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Machine Learning Techniques for Heart Disease Prediction Using a Multi-Algorithm Approach

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Abstract - This analysis explores the efficiency of machine learning systems for heart disease identification through a multi-algorithm approach. The main objective is to identify the best performing algorithm for accurate disease prediction, improving clinical decision making. Using criteria including accuracy, precision, recall, F1 score, and recall, the study assessed four algorithms: Random Forest (RF), Naïve Bayes (NB), Support Vector Machine (SVM), and Decision Tree (DT). The results show that Random Forest outperforms the others, achieving 86.23% precision, 93.76% recall, 89.84% F1 score, and 88.41% accuracy. Random Forest gets an AUC ROC result of 0.94, so Random Forest is considered a superior model in this scenario, especially because it has higher accuracy. The algorithms showed a strong balance between sensitivity and specificity. Decision Tree showed reasonable performance with a precision of 84.18% and a recall of 90.27%, while Naïve Bayes recorded a precision of 87.68% and a recall of 87.03%. SVM showed a precision of 87.40% and a recall of 84.78%, indicating some limitations in capturing positive cases. The novelty of this study lies in the comparative analysis of several algorithms to optimize the heart disease prediction model for clinical use. The random forest algorithm is one of the choices, but there is still a medical standard for classifying people as either indicating or not experiencing heart failure, according to the study.

Keywords: Machine Learning, Random Forest, heart disease, prediction

I. INTRODUCTION

The heart is one of the vital organs in the body [2], [3]. Heart disease remains a topic of profound concern among researchers, and one of the foremost challenges in this field is the accurate detection and precise localization of its occurrence within the human body [1]. Historically, early detection techniques have displayed limited efficiency in identifying heart disease, and even seasoned medical professionals have faced challenges in accurately predicting its onset. Although there are several medical devices that can forecast heart disease, their high cost prevents them from being widely used, and their accuracy in predicting the risk of heart disease in humans is not ideal [3]. For many medical professionals, predicting heart disease is the most important responsibility. Accurate analysis of patient clinical and pathology data is necessary. In these situations, a computerized heart disease prediction system can be useful [4]. By using different patient features to predict the state of heart failure, machine learning provides a novel method of diagnosing heart damage. In order to implement the proper preventative measures and therapies, it is imperative to identify patients who are at risk of developing heart failure [5]. Machine learning can improve the accuracy of heart failure detection, help health practitioners and policy makers to target interventions more effectively, and ultimately, reduce the prevalence of heart failure and avoid negative long-term impacts. Therefore, the use of machine learning in addressing the problem of heart failure is very relevant.

Heart failure is a health condition marked by the heart's inability to pump sufficient blood to fulfill the body's requirements [6]. This disease can be caused by various factors, such as: high blood pressure, congenital heart disease, diabetes, lifestyle factors, obesity, and heredity [7]. Accurately detecting heart failure requires in-depth assessment of a thorough exploration of the patient's medical history, and careful analysis of the results obtained from an extensive series of diagnostic examinations.[8]. In light of technological advancements and the capacity of automated systems to parse and compute data, machine learning techniques have emerged as viable tools for augmenting the diagnostic and prognostic aspects pertaining to this ailment [9]. One of the machine techniques that can be used is classification [10]. Classification techniques in machine learning have many algorithms that can be used in solving problems [11], [12].

Machine learning algorithms are one of the algorithms that can be used to classify heart failure. Machine learning algorithms are algorithms that are used to perform a specific task and find hidden information in the data obtained [13]. The main feature of machine learning is building algorithms that can take input data using different statistical analysis to predict output results. Machine learning algorithms are generally categorized into supervised, unsupervised, and reinforcement. The categories of machine learning techniques, random forest, decision tree, naive bayes, and support vector machine are among the algorithms included in the supervised learning category used for the classification process. The Naïve Bayes (NB), Support Vector Machine (SVM), Random Forest (RF), and Decision Tree (DT) algorithms are algorithms included in the supervised learning category used for the classification process [14]. These methods have different characteristics in their approach to data modeling.

Several machine learning models have been identified by prior research [15]. Healthcare practitioners can receive real-time decision support through the integration of machine learning models into clinical workflows [16]. Typical machine learning models include Naïve Bayes, K-Nearest Neighbors (KNN), Decision Trees, Random Forests, Support Vector Machines (SVM), and Logistic Regression [17]. A number of machine learning algorithms that are frequently employed to predict cardiovascular illness will be examined in earlier study [18]. Several studies have been conducted so far to investigate the application of machine learning models in cardiovascular disease prediction. [17]. Further research [19] evaluated the performance of various machine learning models and found that Random Forest outperformed other supervised algorithms in predicting heart disease, achieving an accuracy of 83.52%. Subsequent research by [20] that applies machine learning to develop a predictive model based on 11 clinical features. This research resulted in the SVM model achieving the highest accuracy of 88.41%.

The multi-algorithm approach in machine learning allows researchers to combine the strengths of various algorithms, thereby increasing the accuracy and robustness of prediction models [14], [21]. Machine learning as a developing field of artificial intelligence offers innovative approaches to clinical problems, one of which is heart failure. The approach proposed in this research is classification. Machine learning can increase efficiency in accuracy, precision and speed in detection [22].

II. METHOD

The research carried out is in accordance with the work that has been attached to Fig. 1. The research carried out begins with data preparation, then continues with data preprocessing, splitting the data, testing the machine learning model, getting test results in the form of matrix evaluations, and the final step is comparing the evaluations. model.

Fig. 1 describes many steps in this research, namely the first stage is to search for the heart failure dataset on Kaggle.com for research. The second stage includes data preprocessing activities, namely: checking missing values and data transformation. Missing value checking is carried out to find out whether the dataset contains empty or missing values. If there are empty or missing values it will affect the results of the algorithm's performance. The third stage is split data. The data is divided into two parts, namely 80% training data (734 data) and 20% testing data (184 data). Data is shared with the aim of training the model's performance according to the model being tested, then the model will be tested with new data which is called testing data. The fourth stage is creating a classification model. The classification model tested uses four models, namely: Decision Tree, Random Forest, Support Vector Machine, and Naïve Bayes. Each model tested will produce a different classification model that has the potential to classify heart failure in patients. The fifth stage is to evaluate the model's performance, testing will be carried out using an evaluation matrix known as a confusion matrix. The evaluation matrix produces precision, recall, F1-Score, accuracy, and AUC ROC values. The evaluation is carried out to measure how well an algorithm works in a particular task. These metrics measure the model's ability to make correct predictions. In order to identify the optimal model, the last step involves assessing each of the four tested approaches' model performance using the prior assessment matrix. The purpose of this study is to evaluate the model's ability to determine which method yields the best outcomes when it comes to heart failure detection.

A. *Decision Tree*

A decision tree is a classification method for prediction that resembles a hierarchical or tree structure. Assigning decision rules and data to a decision tree is the basic step of this method. One of the main advantages of using decision trees is its ability to simplify complex decisions. This process helps decision makers in formulating more effective problem solutions. A classification tree is a tree-like model where the target variable can have different values. In this tree structure, the leaves represent class labels, while the branches connect the attributes that contribute to forming the class label [23]. On the other hand, a regression tree is a type of decision tree that is used when the target variable can take on continuous values, usually real numbers.

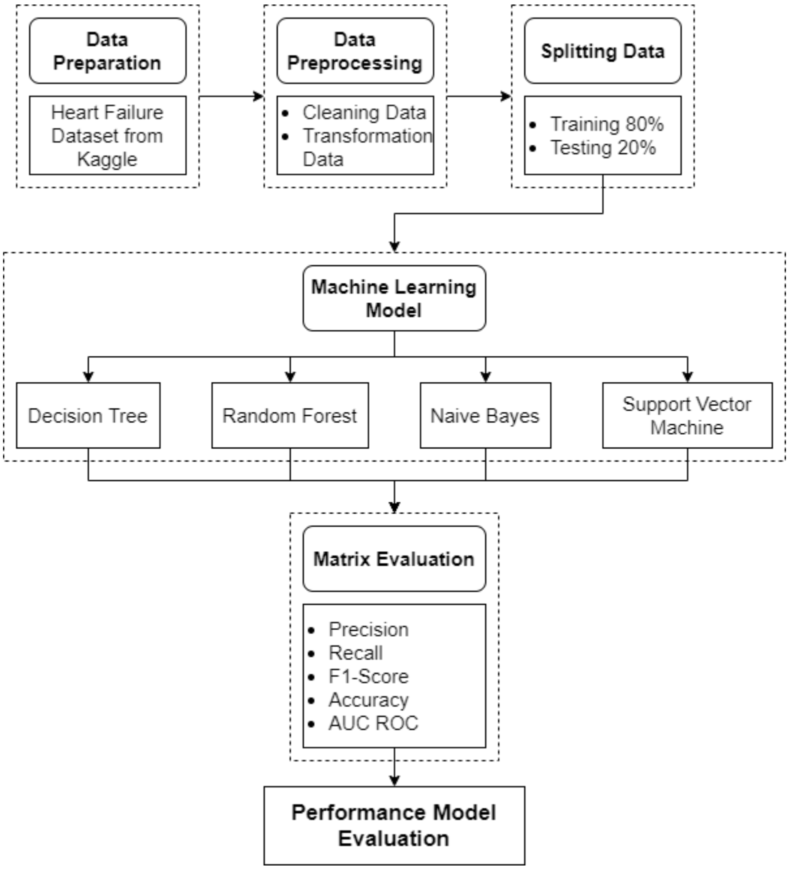


Fig. 1 Research framework

B. Random Forest

Random forest is a method that uses decision trees as a decision-making tool. It consists of a collection of tree classifications that are not tied to a single core model. This method has shown excellent performance in a variety of practical problems, including predictions in the health field [24]. Random forests are not susceptible to noise in the data and do not suffer from overfitting. The model is built by combining predictions from multiple trees, where each tree is drilled independently [25]. In addition, random forests operate quickly and generally show significant performance improvements over many other tree-based algorithms, such as decision trees. Three important decisions that need to be made for random forests are: determining how to split the leaves, choosing which predictors to use in each leaf, and introducing elements of randomness into the tree formation process. The method for calculating entropy as in (1) in determining the level of attribute pollution and information value is obtained through the initial formation of a decision tree using (2).

$$Entropy\ (Y) = \sum_i p(c|Y) log^2 p(c|Y) \tag{1}$$

Explanation:

Y : Case Set
$p(c|Y)$: Proportion of Y value to class c

$$Information\ Gain\ (Y, a) = Entropy\ (Y) - \sum_{v \varepsilon Values(a)} \frac{|Y_v|}{|Y_a|} Entropy(Y_v) \tag{2}$$

Explanation:

$Values(a)$: The values contained in the class set a
Y_v : A subclass of Y with class v related to the class
Y_a : Values that are in accordance with the class

C. Support Vector Machine

A machine learning approach for regression and classification is called Support Vector Machine (SVM). SVM's primary objective is to locate the hyperplane in a feature space that best divides data between two classes. When compared to other models evaluated, the suggested model's accuracy of 99% for Support Vector Machine (SVM) heart disease prediction is a substantial improvement [26]. Because of its versatility in utilizing kernels to construct more intricate decision limits and its capacity to handle high-dimensional data, SVM is frequently used. SVM divides data into two classes by identifying the most effective hyperplane. The distance between the hyperplane and the nearest data points from both classes is called the margin, and this hyperplane maximizes that distance. Nearest to the hyperplane, the data are. By using support vectors, SVM maximizes the margin so that the model generalization is better. A hyperplane in nnn-dimensional space can be defined by the (3).

$$\omega . x + b = 0 \tag{3}$$

Explanation:

ω : weight vector

x : Input vector (features from the data)

b : intercept

SVM aims to find ω and b that determine the best hyperplane that separates two classes, a common linear kernel is used (4).

$$x_i, x_j = x_i . x_j \tag{4}$$

D. Naïve Bayes

The Naive Bayes algorithm for classification is predicated on the idea that all features, or input variables, are unrelated to one another. It is based on the Bayes theorem [27]. Naive Bayes frequently performs exceptionally well in a variety of classification problems to determine the probability of an event based on past knowledge of related circumstances, even though this assumption is rarely accurate in real-world data. The basic formula is (5).

$$P(y|X) = \frac{P(y).P(X|y)}{P(X)} \tag{5}$$

Explanation:

$P(y|X)$: The likelihood that a hypothesis or class y is accurate in light of information or characteristics X

$P(y)$: Prior probability, or the starting probability of class Y without examining the data

$P(X|y)$: The likelihood, or probability, that data X will emerge if class Y is true

$P(X)$: The likelihood of data X taken as a whole (proof or stabilizing factor)

We presume in naïve Bayes that every feature $x_1, x_2, \ldots, x_n$ are independent of one another, regardless of class. This means that the joint probability of these features can be calculated as the product of their individual probabilities. The Naive Bayes formula (6) based on this assumption becomes:

$$P(y|X) = \frac{P(y)\prod_{i=1}^{n} P(x_i|y)}{P(X)} \tag{6}$$

E. Matrix Evaluation

To evaluate classification models, confusion matrices can be used in machine learning, which allows a deeper analysis of the performance of the algorithms being compared [28].

Accuracy stands as a pivotal evaluation metric within the domain of classification modeling in machine learning. It quantifies the model's ability to accurately predict class labels across the entirety of the test data. Accuracy represents the percentage of correct predictions in relation to the overall test dataset [29]. The equation of accuracy can be seen in the (7).

$$Accuracy = \frac{TP+TN}{TP+FN+FP+TN} \tag{7}$$

Precision is a highly relevant evaluation metric in assessing the performance of classification models in machine learning. Precision gives an idea of how accurate the model is in classifying the data as positive. This metric is particularly important in situations where the consequences of false positives are high, such as in disease or security threat detection [30]. The formula for precision is expressed as (8).

$$Precision = \frac{TP}{TP+FP} \tag{8}$$

Recall, sometimes known as sensitivity or True Positive Rate, is an important statistic used in the examination of confusion matrices in the context of machine learning classification. It focuses on the model's ability to correctly identify and capture positive instances from the dataset. Recall is highly relevant in critical situations to avoid potentially fatal misclassification, such as in medical diagnosis [30]. The formula equation of recall can be seen in (9).

$$Recall = \frac{TP}{TP+FN} \tag{9}$$

The F1-Score is an evaluation metric that serves as the harmonic mean of precision and recall within the framework of confusion matrix analysis in machine learning. The F1-Score proves particularly useful in situations where achieving a balance between precision and recall is of paramount importance, and where the avoidance of potentially costly errors is a key concern. It provides a single, comprehensive measure that encapsulates the model's performance, taking into account the trade-off between precision and recall, which is crucial in scenarios where the consequences of false positives and false negatives have significant implications [30]. F1-Score is calculated using (10).

$$f1 - score = \frac{2(precision+recall)}{precision+recall} \tag{10}$$

Area Under Curve (AUC) is a useful metric with a value ranging from 0 to 1. The higher the AUC value, the better the model performance. If the model is able to perfectly distinguish between two classes, the AUC will reach 1. Conversely, if the model is unable to distinguish between examples from both classes, the AUC will be 0.

III. RESULT AND DISCUSSION

A. Dataset Preparation

This analysis uses a dataset sourced from Kaggle. This dataset consists of 918 data that have been used by previous studies. This dataset is divided into two, namely 734 training data and 184 testing data. Testing data is used to test the model built, while training data is used to train and build a model. This dataset contains 12 attributes as in Fig. 2.

Fig. 2 is a visualization of the dataset used for this study. Visualization of the attribute distribution helps in depicting the characteristics of patients based on various attributes relevant to heart health. Age covers the age range from 29 to 77 years, providing an overview of the age distribution of patients, which is important because the risk of heart disease tends to increase with age. The Sex attribute groups patients based on gender, either male or female to evaluate whether there is a difference in risk between these two groups. Furthermore, ChestPainType categorizes the level of chest pain with codes such as TA (Typical Angina), ATA (Atypical Angina), NAP (Non-Anginal Pain) and ASY (Asymptomatic) which reflect the variation in the type of pain experienced by patients. RestingBP describes the blood pressure at rest which is an important factor in determining the risk of hypertension and heart disease. The patient's fasting blood sugar level is displayed by FastingBS, where a value of 1 indicates that the blood sugar level is more than 120 mg/dl, which can indicate diabetes, and 0 indicates normal levels. Cholesterol describes the patient's cholesterol level, which is also a major indicator of heart disease risk. The electrocardiogram readings at rest are displayed on a resting electrocardiogram (ECG), which has a score ranging from 0 to 2, signifying possible irregularities in the heart's electrical activity. With a range of 71 to 202, MaxHR indicates the maximal heart rate during physical activity and is a crucial indicator of how the heart reacts to exercise. ExerciseAngina indicates whether the patient experiences angina during physical activity where 1 indicates the presence of angina and 0 otherwise. Oldpeak indicates the level of ST segment depression which helps in detecting problems such as ischemia, while ST_Slope describes the slope of the ST segment during exercise where an upward, flat, or downward slope can indicate different heart conditions. And finally, HeartDisease is a target variable indicating whether the patient has heart disease (1) or not (0). Overall, the distribution of these attributes provides important insights into the patient's health condition and the risk factors that influence the likelihood of heart disease.

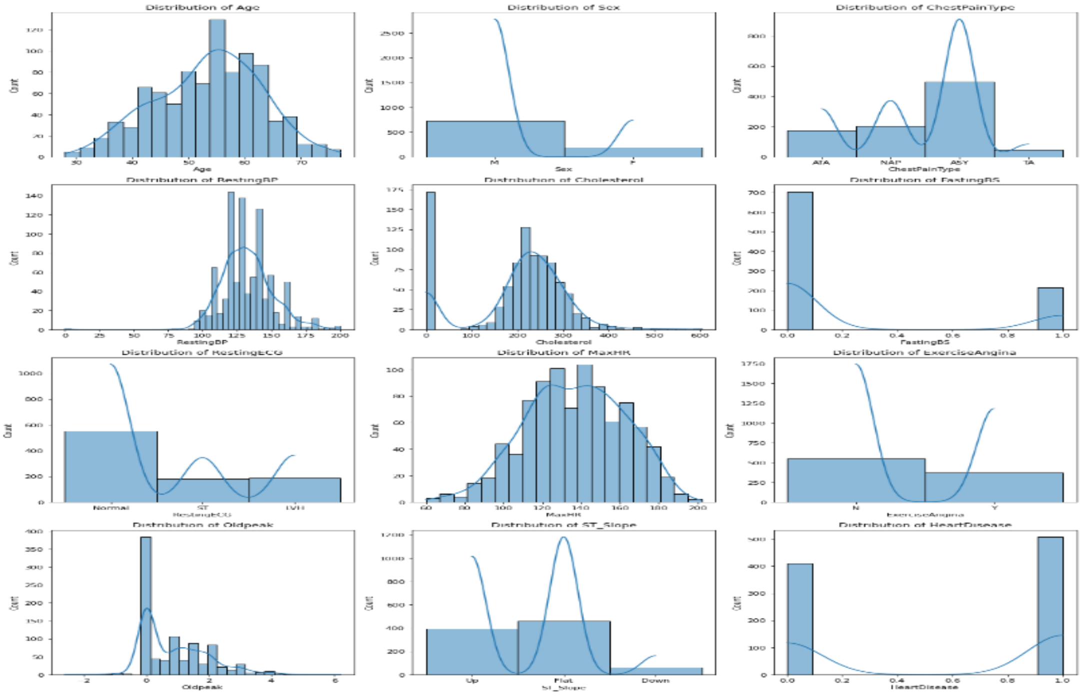


Fig. 2 Attribute distribution

B. Dataset Preprocessing

A step in the process of removing noise from data or looking for missing data is called missing value. A missing value is a value that is either incomplete or nonexistent, and it can have an impact on the outcomes of data analysis. Data entry and deletion are the methods used to handle missing values. There were no missing values found in the dataset used for this study (Fig. 3).

A description of the research data without any missing values may be found in Fig. 3. The dataset does not require any changes to handle missing values, as the "False" output shows that all of the attributes are present and there are no missing values. In this study, the "isnull()" method in the pandas library is used to determine whether or not there is a missing value in the data. The dataset that was used has a missing value if the outcome that is produced is "True". The results of data transformation are shown in Fig. 4. ExerciseAngina (Yes and No), ChestPainType (TA, ATA, NAP, and ASY), StSlope (Up, Flat, and Down), and gender (M and F) are the modified attribute values.

C. Splitting Data

The train_test_split function from the scikit-learn module is typically used in Python to split data. The dataset is split into training and testing sets via this function. In this study, training data were split into 80% and testing data into 20%. Splitting the data with a ratio of 80% training and 20% testing can use **X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)**.

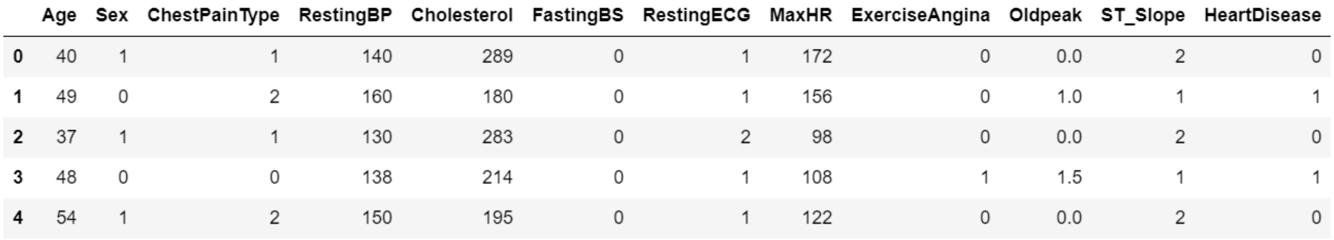
D. Performance Model Evaluation

Confusion matrix analysis in machine learning can be used to assess the classification model and provide a more thorough examination of the performance of the competing algorithms. An explanation of how well a classification model performs when applied to a set of test data whose real values are known is sometimes provided via a table called a confusion matrix. Each implemented algorithm's confusion matrix may be successfully acquired, at which point metric values like accuracy, precision, recall, f1-score, and AUC-ROC curve can be determined (Fig. 5).

```
data.isnull()
```

	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	False	False	False	False	False	False	False	False	False	False	False	False
1	False	False	False	False	False	False	False	False	False	False	False	False
2	False	False	False	False	False	False	False	False	False	False	False	False
3	False	False	False	False	False	False	False	False	False	False	False	False
4	False	False	False	False	False	False	False	False	False	False	False	False
...	...	...	...	...	...	...	...	...	...	...	...	...
913	False	False	False	False	False	False	False	False	False	False	False	False
914	False	False	False	False	False	False	False	False	False	False	False	False
915	False	False	False	False	False	False	False	False	False	False	False	False
916	False	False	False	False	False	False	False	False	False	False	False	False
917	False	False	False	False	False	False	False	False	False	False	False	False

Fig. 3 As a result of a missing value



	Age	Sex	ChestPainType	RestingBP	Cholesterol	FastingBS	RestingECG	MaxHR	ExerciseAngina	Oldpeak	ST_Slope	HeartDisease
0	40	1	1	140	289	0	1	172	0	0.0	2	0
1	49	0	2	160	180	0	1	156	0	1.0	1	1
2	37	1	1	130	283	0	2	98	0	0.0	2	0
3	48	0	0	138	214	0	1	108	1	1.5	1	1
4	54	1	2	150	195	0	1	122	0	0.0	2	0

Fig. 4 As a result of a transformation

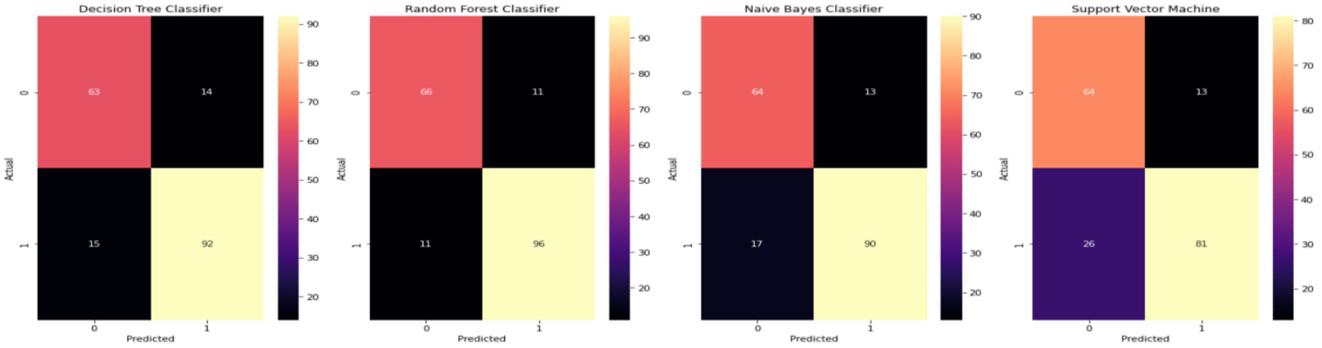


Fig. 5 Confussion matrix

Fig. 5 shows the model categorizing 184 test data with DT, NB, RF, and SVM algorithms. These matrices offer valuable insights into the classification of true positives, true negatives, false positives, and false negatives, facilitating a nuanced evaluation of the model's efficacy in distinguishing between classes. This has different results from testing. The confusion matrix using the Decision Tree model gets the result TP [Prediction 1, Actual 1] or the number of data correctly entered into the positive class and predicted to be the positive class is 92 data. while the confusion matrix using gets the result TN [Prediction 0, Actual 0] is 63. The Confusion Matrix FP [Prediction 1, Actual 0] is 14 and the Confusion Matrix of FN [Prediction 0, Actual 1] is 15. An example of the calculation performed using the Decision Tree model is:

$$Accuracy = \frac{92+63}{92+63+15+14} = 88.04\%$$

$$Precision = \frac{92}{92+14} = 86.79$$

$$Recall = \frac{92}{92+15} = 85.98$$

$$F1 - Score = \frac{2(86.79+85.98)}{86.79+85.98} = 86.38$$

Table I presents the results of the confusion matrix, which shows significant differences in accuracy between the various classification algorithms tested. In this analysis, accuracy serves as the main parameter to evaluate the performance of the model in classifying heart failure disease. The evaluation results indicate that the Random Forest algorithm achieved the highest accuracy, which is 88.41%. This figure shows that the Random Forest model has a very good ability to identify and classify patients at risk of heart failure. Furthermore, the Naïve Bayes algorithm also showed good performance with an accuracy of 86.23%, which reflects its ability to handle classified data even with a simpler approach. Decision Tree recorded a lower accuracy, which is 85.42%, indicating that although it is still effective, this algorithm is less capable in some aspects of classification compared to the previous two models. Finally, Support Vector Machine (SVM) had the lowest accuracy among all the algorithms tested, which was 85.01%. This accuracy comparison provides important insights into the effectiveness of each algorithm in the context of disease classification, and all the accuracy values obtained can be seen in detail in Table 1.

Fig. 6 presents the performance evaluation of five classification algorithms in an effort to detect heart failure. AUC is a very relevant metric in this context, because it provides a clear picture of the model's accuracy in classifying data. This metric is especially important in sensitive classification cases, such as heart failure detection, where decisions taken can have a significant impact on heart health interventions. By utilizing AUC, researchers can comprehensively evaluate the effectiveness of each algorithm, so that the most appropriate method can be selected to support data-based decision making in efforts to overcome the problem of heart failure.

TABLE I
CONFUSION MATRIX RESULT

Algorithm	**Precision**	**Recall**	**F1-Score**	**Accuracy (%)**
Decision Tree	84.18	90.27	87.12	85.42
Random Forest	86.23	93.76	89.84	88.41
Naïve Bayes	87.68	87.03	87.35	86.23
Support Vector Machine	87.40	84.78	86.07	85.01

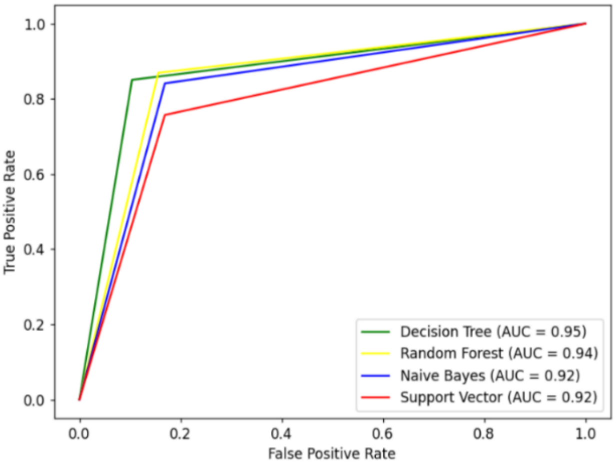


Fig. 6 ROC AUC curve

Based on Fig. 6, Random Forest can be considered as the best model. This is due to several factors. High accuracy indicates that Random Forest has a strong ability to distinguish heart failure cases with good accuracy. In this case, the AUC produced by each algorithm is as follows: Decision Tree (0.95), Random Forest (0.94), Naïve Bayes (0.92) and Support Vector Machine (0.92). Random Forest has also shown a balanced performance in previous evaluation metrics that Random Forest has high precision (89.71%) and good recall (89.71%). Random Forest provides a good balance between the ability to identify failure cases. The high F1-score and high AUC further emphasize that Random Forest is the best model compared to the other three algorithms.

IV. CONCLUSION

This study Using four machine learning algorithms Decision Tree, Random Forest, Naive Bayes, and Support Vector Machine this study aims to categorize heart failure and determine which model performs best. With an accuracy of 88.41% and an AUC value of 0.94, the Random Forest algorithm beats the other models in the comparative analysis, establishing itself as the best model for categorizing instances of heart failure. Metrics such as precision, recall, F1-score, and overall accuracy from the confusion matrix can be used to assess how well each machine learning system predicts heart failure. The algorithm known as Decision Tree exhibits 84.18% precision, 90.27% recall, 87.12% F1-score, and 85.42% accuracy. Its poor precision belies its effective identification of affirmative cases (high recall). In contrast, Random Forest achieves 88.41% accuracy, 89.84% F1-score, 93.76% recall, and 86.23% precision. This algorithm provides a good mix between sensitivity and specificity, which makes it a great choice for heart disease prediction due to its high precision and recall. With a precision of 87.68%, recall of 87.03%, F1-score of 87.35%, and accuracy of 86.23%, Naïve Bayes also outperformed the competition. The algorithm demonstrated its ability to generate reasonably accurate predictions; nevertheless, its recall was marginally lower than that of the other algorithms, suggesting that certain positive cases were overlooked. The Support Vector Machine's (SVM) accuracy, F1-score, recall, and precision were 85.01%, 86.07%, and 84.78%, respectively. SVM had a lower recall than the other algorithms, which meant that there was a greater possibility of false negatives despite its high precision. All things considered, Random Forest turned out to be the best-performing algorithm in this situation, combining high recall and precision a crucial combination in medical applications where accurate disease detection lowers the possibility of misdiagnosis. Despite its strong performance, Decision Tree and SVM demonstrated certain limitations with regard to the trade-off between precision and recall. While Naïve Bayes produced good results as well, it might not be as balanced as Random Forest. In summary, the selection of an appropriate algorithm is crucial for enhancing the precision and efficacy of heart disease prognosis, with Random Forest emerging as a prominent approach. Future studies could use larger and more diverse datasets from different sources (hospitals, clinics, countries) to improve the generalizability of the model. Variations in patient characteristics, such as age, gender, and medical history, could also be added to see if the model can maintain its performance across different subgroups.

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