Machine Learning Solutions for Heart Disease Diagnosis: Model Choices and Factor Analysis

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Abstract: The prediction of heart disease diagnosis is of paramount importance since it is one of the leading causes of death nowadays. Yet accurately identifying and monitoring the factors relative to heart diseases pose significant challenges. Traditional visual survey methods are time-consuming, often hampered by the lack of data exchange among hospitals and individual doctors, and may not provide real-time data crucial for effective prevention strategies. Machine learning (ML) technologies have become increasingly potent instruments in the diagnosis of diseases in recent years. In this project, several models were investigated. A complete set of data gathered from Long Beach V, Cleveland, Hungary, and Switzerland was utilized. This data set, which encompasses over 13 different factors that are relative to heart diseases, is meticulously preprocessed to ensure data quality. The outcomes not only show how well machine learning techniques can anticipate heart conditions, but they also open the door for the creation of edge computing and mobile applications. These might be installed in far-off places, giving physicians and hospitals access to real-time data and enabling timely treatment decisions. Thus, this study marks a substantial advancement in the use of cutting-edge technologies for the identification of heart disease in real time.

1 INTRODUCTION

An estimated 17.9 million people die from heart disease each year, making it one of the major causes of mortality worldwide. Premature deaths can be avoided by determining who is most at risk for heart disease and making sure they get the right care (World Health Organization, 2021). In less developed countries the increasing population and the rising number of heart disease patients are posing greater challenges. Here, the effectiveness of screening methods for patients exhibiting heart disease signs is still up for debate because of the financial crisis and restricted access to appropriate and equitable healthcare facilities and equipment. Given this, many academics and practitioners have found machine learning-based heart disease detection (MLBHDD) systems to be affordable and adaptable methods since the introduction of machine learning (ML) applications in the medical field (Ahsan & Siddique, 2022).

There are numerous risks to applying ML and ML-based solutions since the behavior of the machine during the process of feature drawing and final prediction is still not clear, thus the credibility of its outputs is still in doubt (Ahsan et al., 2021). Imbalanced performance of ML also occurs when the data is not equally collected, especially in some less developed countries whose majority class has no access to physical examination and medical treatments. It is important to find a reliable data set and use proper methods to ensure the credit of the final diagnosis.

This research applied Random Forest, Naive Bayes, Gradient Boosting, K- Nearest Neighbour Classification (KNN), Logistic Regression and Support Vector Machine (SVM). By comparing different models and analyzing the final outcomes, this research is dedicated to finding a suitable model for heart disease diagnosis and looking for important factors among the 14 attributes.

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2 UNDERSTANDING THE DATA SET

As mentioned earlier, the publicly available and well-liked UCI heart disease data set is used in this study. There are 76 attributes in all in the UCI heart disease data collection.

However, the vast majority of previous research has only used a maximum of 14 attributes. The UCI heart disease data has been used to create a number of datasets. The Cleveland data collection, which has 14 variables, has been primarily utilized by computational intelligence researchers. The majority of the data is in binary form, and computers can easily identify features using this boolean expression. Five class attributes in the data set indicate whether the data set is healthy or one of four sick categories. Five class attributes that correspond to either a healthy state or one of the four sick types make up the data set. Five class attributes, which stand for either a healthy state or one of the four sick categories, make up the data set. Each component is examined separately in this study to ascertain its unique impact. With 0 denoting no disease and 1 denoting disease, the classifier used in the studies is essentially binary. Five datasets were produced as a result. The following symbols are used to refer to the generated datasets: Sick1, Sick2, Sick3, and Sick4, correspondingly, with H-0 standing for healthy. Table 1 shows some important example attributes in this study.

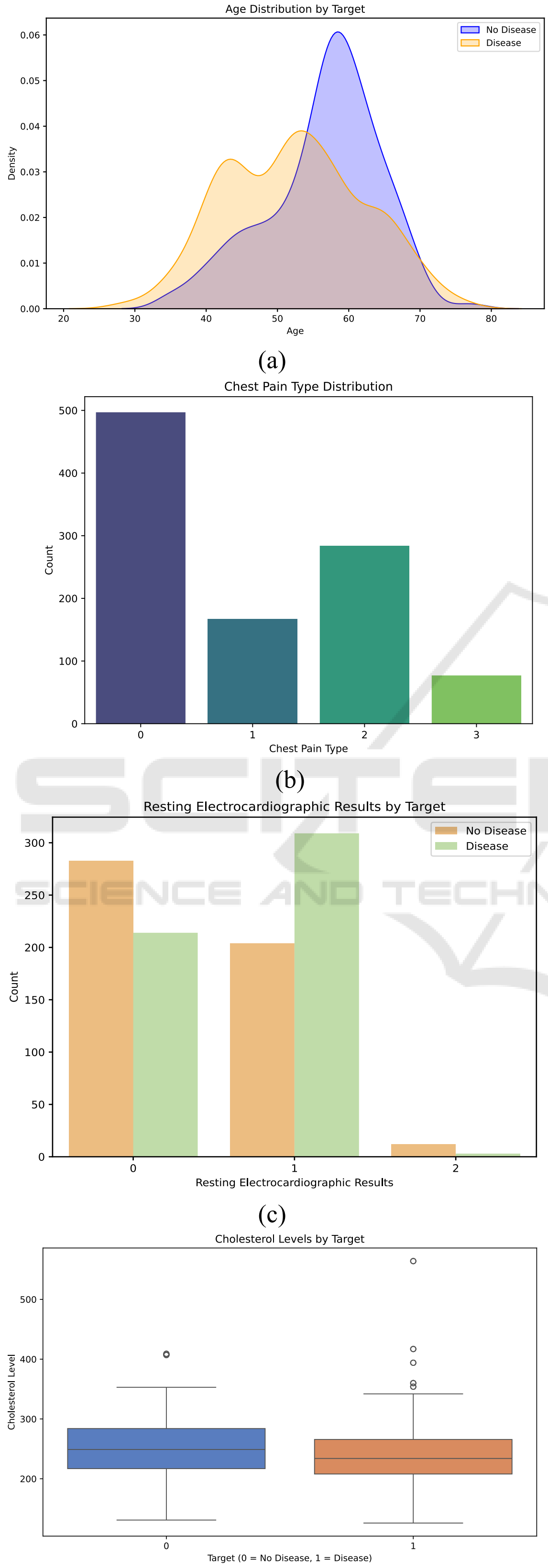
Table 1: Explanation of Partial Attributes

Name	Description
Age	age (numeric)
Sex	male, female (nominal)
Chest pain type (CP)	4 chest pain types
Trestbps	resting blood pressure, mm/Hg
Chol	Serum cholesterol, mg/dekadaliter
Fbs	Whether the blood sugar levels after fasting exceed 120 mg/dl: (0 = False; 1 = True)
Restecg	Three different kinds of values. Normal (norm), aberrant (abn): exhibiting ventricular hypertrophy (hyp) or abnormal ST-T waves.
Thalach	highest heart rate reached
Exang	whether angina brought on by exercise has occurred: 0 indicates no, whereas 1 indicates yes.
Oldpeak	Exercise-induced ST depression compared to rest
Slope	the ST segment's slope at maximal exertion. Three different value types: downsloping, flat, and upsloping
Ca	number of main fluoroscopy-colored vessels (0‑3)
Thal	heart issue (reversible, fixed, or normal)
The class attributes	either cardiac illness or healthy.

Figure 1(a) displays a distribution for age and heart disease frequencies. The frequencies of the age groups 50 - 60 years old and 60 - 70 years old are relatively high, showing a pattern similar to a normal distribution.

There are four forms of chest pain. From a medical perspective, (i) is defined as substernal discomfort brought on by emotional or physical stress (Jones et al., 2020). A patient with typical angina has a high risk of coronary artery blockages since their past medical history exhibits the typical symptoms. (ii) Chest pain that doesn't match the definition of typical or classic chest pain is referred to as atypical (Cleveland Clinic, 2023). (iii) The stabbing or knife-like, protracted, dull, or uncomfortable condition that can persist for brief or extended periods of time is known as non-angina pain (Constant, 1990). (ⅳ) Asymptomatic pain does not manifest any signs of illness or disease and may not be the source of or a sign of a disease. The distribution of chest pain types is as follows in Figure 1(b).

The rest distribution is as Figure 1(c) with three resting electrocardiographic results 0, 1 and 2, representing 3 different ranges. Cholesterol level can be classified into two categories according to a target value and can be inferred in Figure 1(d), while Exang can be inferred in Figure 1(e).

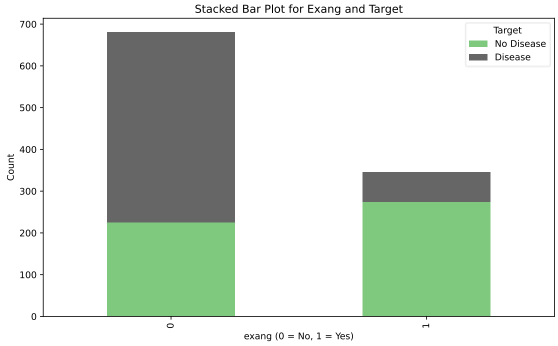


(a)

(b)

(c)

(d)



(e)

Figure 1: Analysis of the important attributes. (a) is the Age distribution by target, (b) is the Chest Pain type distribution, (c) is the Resting Electrocardiographic results by target, (d) is the Cholesterol Levels by target, (e) is the stacked bar plot for Exang and Target. (Photo/Picture credit: Original).

3 MACHINE LEARNING IN HEALTHCARE

Machine learning is a growing topic in recent healthcare, which analyzes vast volumes of medical data using algorithms. In the medical field, machine learning algorithms are essential. Their pattern-recognition capabilities in large datasets are well-suited for genomics and proteomics applications. They aid significantly in illness diagnosis and detection, enabling better treatment decisions. As medical data grows, the role of machine learning will expand, promising more personalized and efficient healthcare (Shailaja et al., 2018).

3.1 Explanation of Algorithms Used for Diagnosis

Random forest, K-Nearest Neighbors (KNN), Logistic Regression, Naive Bayes, Gradient Boosting and Support Vector Machine (SVM) are evaluated for heart disease diagnosis. Random forest is one ensemble learning approach that exemplifies an information mining methodology. It employs multiple classifiers that work in tandem to identify the class label for a new, unlabeled instance within a data set (Parmar et al., 2019). A majority vote among the individual decision trees determines the final forecast for classification. Every tree makes a class prediction, and the random forest predicts the class with the most votes. Compared to a single decision tree, random forests have the advantage of being able to handle high-dimensional data well, being reasonably resistant to overfitting, and being able to identify intricate non-linear correlations in the data.

KNN is a learning algorithm that is instance-based. When a new sample is provided, the KNN algorithm locates the K samples in the training dataset that are the most comparable (closest in distance) and then uses the classes of these K neighbors to forecast the new sample's class. Manhattan distance, Euclidean distance, and other methods are typically used to measure the distances between samples. It is extensively utilized in domains including recommendation systems, text categorization, and image recognition. It is quite flexible with regard to data distribution and does not require a training procedure. One of its drawbacks is its high computational complexity, which rises sharply with data volume. Additionally, it is susceptible to local noise in the data, and the model's performance may be impacted by the K value selection.

Logistic regression is a linear model for classification issues. It represents the likelihood that a sample belongs to a particular class by mapping the outcomes of linear regression to probability values between 0 and 1. The likelihood function is maximized in the model to estimate parameters, and gradient descent is a popular solution technique. The model can effectively handle linearly separable data and is straightforward, interpretable, and computationally efficient. Its restrictions on data distribution, which typically call for feature independence, are its drawbacks. Its capacity to fit complex non-linear data is restricted, and it can only handle linear relationships.

The Bayes theorem and the feature conditional independence assumption form the foundation of the Naive Bayes classification technique. It computes the posterior probability of each class given the features and makes the assumption that each feature is independent given the class. The prediction outcome is chosen from the class with the highest posterior probability. This model is insensitive to missing values, works well on small-scale data, and trains quickly. The drawback is that the feature conditional independence assumption is highly sensitive to the input data's representation form and is frequently challenging to meet in practice, which could compromise the model's accuracy.

Based on the concept of ensemble learning, gradient boosting trains a number of weak learners iteratively before combining them to create a strong learner. The approach gradually improves the performance of the model by modifying the training of the subsequent weak learner based on the gradient of the current model's loss function in each iteration. Numerous data kinds, including categorical and numerical data, can be handled by it. It performs well in generalization and has a strong fit for intricate non-linear relationships. However, it is time-consuming to train, prone to overfitting, and very sensitive to hyperparameter selection, necessitating adjustment.

SVM maximizes the margin between the two classes of samples by identifying the best hyperplane to divide them. A kernel function is used to translate the data to a high-dimensional space in order to make it linearly separable in the high-dimensional space while dealing with non-linear situations. SVM performs well in handling both linear and non-linear issues, has strong generalization ability, and successfully prevents overfitting when working with small sample data. The drawbacks include a lengthy training period and considerable computational complexity, particularly when working with huge amounts of data. It also necessitates specific tuning abilities and is highly sensitive to the kernel functions and parameter choices.

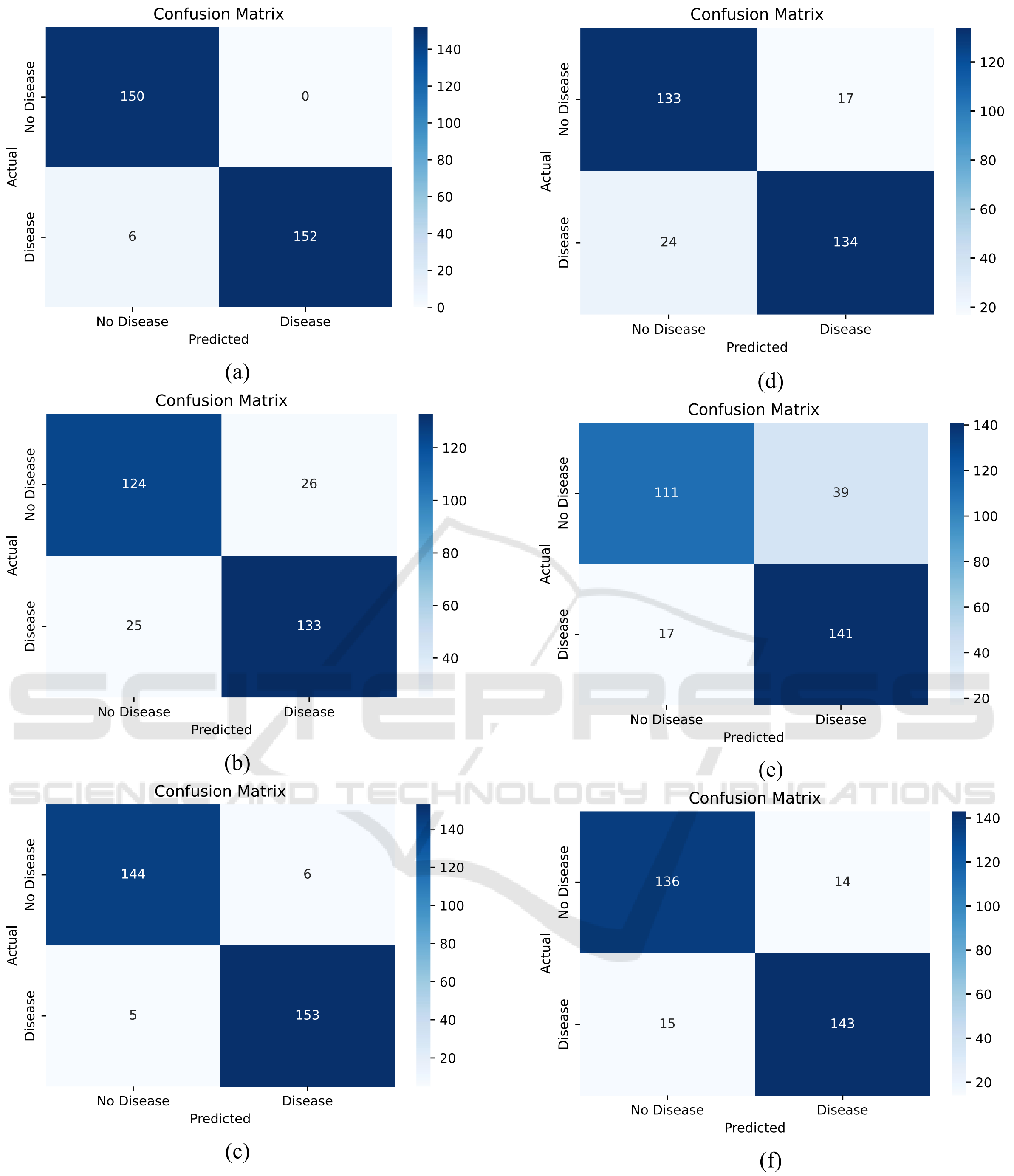
4 MODEL TRAINING AND COMPARISON

The six algorithms are properly applied in the process of training and show different performances. To evaluate the functionality of each algorithm, accuracy and F1-score are calculated in Equation (1), and Equation (2), using True Positive (TP), True Negative (TN), False Positive (FP), False Negative (FN), with P refers to precision and R refers to recall.

$$Accuracy = \frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{TN} + \mathrm{FP} + \mathrm{FN}} \tag{1}$$

$$F1 = \frac{2\mathrm{PR}}{\mathrm{P} + \mathrm{R}} \tag{2}$$

A key tool for assessing the effectiveness of diagnostic tests, particularly in binary classification settings, is the ROC curve (Srinivasan & Mishra, 2024), which is also used to compare various models. A greater area under the curve typically indicates higher performance. Figure 2 shows the inferred confusion matrix reports, each of which represents an algorithm. Table 2 lists the F1 Scores and Accuracy. Figure 3 shows the ROC curve.



(a)

(d)

(b)

(e)

(c)

(f)

Figure 2: Confusion matrix for each model. (a) is the Random Forest confusion matrix, (b) is the Naive Bayes confusion matrix, (c) is the Gradient Boosting confusion matrix, (d) is the KNN confusion matrix, (e) is the Logistic Regression confusion matrix, (f) is the SVM confusion matrix. (Photo/Picture credit: Original).

Table 2: F1 score and accuracy.

	Random Forest	Naive Bayes	Gradient Boosting	KNN	Logistic Regression	SVM
F1 for 0	0.98	0.83	0.96	0.87	0.80	0.90
F1 for 1	0.98	0.84	0.97	0.87	0.83	0.91
Accuracy	0.98	0.83	0.96	0.87	0.82	0.91

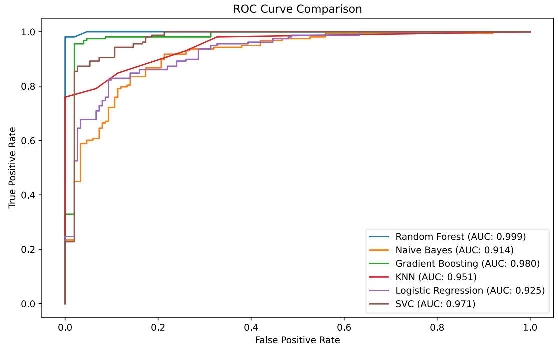


Figure 3: ROC curve for each model. (Photo/Picture credit: Original).

Compared to other models, the Random Forest classifier and Gradient Boosting performed better. With the highest accuracy of 0.98, the Random Forest classifier is closely followed by the Gradient Boosting classifier, which has an accuracy of 0.96. This suggests that in comparison to the other classifiers, Random Forest and Gradient Boosting do better overall at accurately classifying instances in this data set. Random Forest has the highest precision (0.96 & 1.00), whereas Gradient Boosting comes in second (0.97 & 0.96). Gradient Boosting has a recall of 0.96 and 0.97, both much higher than other models, whereas Random Forest has a perfect recall of 1.00 for class 0 and 0.96 for class 1. With the greatest f1-scores of 0.98 & 0.98 and 0.96 & 0.97, respectively, Random Forest and Gradient Boosting demonstrate a good trade-off between recall and precision. Figure 3 shows the ROC curves. Based on the Area Under ROC Curve (AUC) values, the Random Forest model performs the best, followed by Gradient Boosting and SVM. In contrast, Naive Bayes, KNN, and Logistic Regression are all above 0.900, indicating fairly high functionalities, but they are all relatively weaker.

Random Forest or Gradient Boosting would be the best options if overall high accuracy and strong performance in both classes are the primary objectives. These classifiers appear to be capable of producing precise predictions and effectively capturing the patterns in the data. Regarding feature selection, Random Forest and Gradient Boosting produced encouraging results when paired with the computerized feature selection process (CFS) and the medical knowledge-based motivated feature selection process (MFS) (Nahar et al., 2013). This suggests that it can improve its discriminatory power by efficiently leveraging the improved feature sets.

Additionally, SVM does fairly well, with an accuracy of 0.91. If Random Forest or Gradient Boosting has too high of a computational cost, this can be an acceptable substitute.

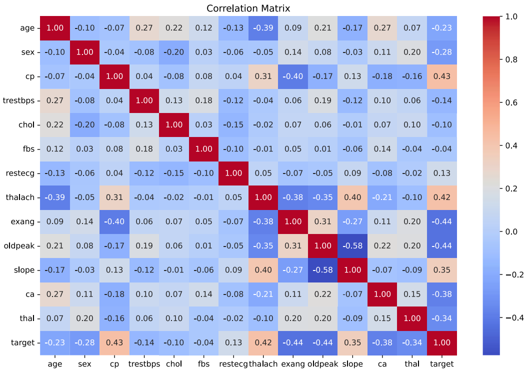
KNN performs mediocrely, with an accuracy of 0.87. It might work well with data sets when the local similarity assumption is valid, but in this instance, the best-performing classifiers exceed it.

The accuracy of Naive Bayes and Logistic Regression is comparatively lower. The feature independence assumed by Naive Bayes might not hold true for this set of data. The intricacy of the decision boundary in the data may be a limitation of logistic regression. Despite its poorer performance, logistic regression may still be taken into consideration if interpretability and simplicity are important since it can shed light on the link between the target variable and the features.

5 RESULTS AND INTERPRETATION

Using the six different methods of training, a correlation matrix can be established in Figure 4. The diagonal elements are all 1, indicating that each variable is perfectly correlated with itself.

The correlation values are represented in the matrix by a color gradient. A positive correlation is shown in red and a negative correlation in blue. Positive correlations imply that when one variable rises, the other one tends to rise as well. When one variable rises, the other one tends to fall, according to negative correlations. For instance, there is a somewhat negative association (-0.07) between age and cp. Conversely, there is a moderately positive connection (r = 0.22) between chol and trestbps.



	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
age	1.00	-0.10	-0.07	0.27	0.22	0.12	-0.13	-0.39	0.09	0.21	-0.17	0.27	0.07	-0.23
sex	-0.10	1.00	-0.04	-0.08	-0.20	0.03	-0.06	-0.05	0.14	0.08	-0.03	0.11	0.20	-0.28
cp	-0.07	-0.04	1.00	0.04	-0.08	0.08	0.04	0.31	-0.40	-0.17	0.13	-0.18	-0.16	0.43
trestbps	0.27	-0.08	0.04	1.00	0.13	0.18	-0.12	-0.04	0.06	0.19	-0.12	0.10	0.06	-0.14
chol	0.22	-0.20	-0.08	0.13	1.00	0.03	-0.15	-0.02	0.07	0.06	-0.01	0.07	0.10	-0.10
fbs	0.12	0.03	0.08	0.18	0.03	1.00	-0.10	-0.01	0.05	0.01	-0.06	0.14	-0.04	-0.04
restecg	-0.13	-0.06	0.04	-0.12	-0.15	-0.10	1.00	0.05	-0.07	-0.05	0.09	-0.08	-0.02	0.13
thalach	-0.39	-0.05	0.31	-0.04	-0.02	-0.01	0.05	1.00	-0.38	-0.35	0.40	-0.21	-0.10	0.42
exang	0.09	0.14	-0.40	0.06	0.07	0.05	-0.07	-0.38	1.00	0.31	-0.27	0.11	0.20	-0.44
oldpeak	0.21	0.08	-0.17	0.19	0.06	0.01	-0.05	-0.35	0.31	1.00	-0.58	0.22	0.20	-0.44
slope	-0.17	-0.03	0.13	-0.12	-0.01	-0.06	0.09	0.40	-0.27	-0.58	1.00	-0.07	-0.09	0.35
ca	0.27	0.11	-0.18	0.10	0.07	0.14	-0.08	-0.21	0.11	0.22	-0.07	1.00	0.15	-0.38
thal	0.07	0.20	-0.16	0.06	0.10	-0.04	-0.02	-0.10	0.20	0.20	-0.09	0.15	1.00	-0.34
target	-0.23	-0.28	0.43	-0.14	-0.10	-0.04	0.13	0.42	-0.44	-0.44	0.35	-0.38	-0.34	1.00

Figure 4: Correlation Matrix. (Photo/Picture credit: Original).

Table 3: significant correlations.

trestbps and chol	exang and oldpeak	age and exang	thalach and exang
0.22	0.40	-0.39	-0.38

Some significant correlations were included in this correlation matrix and are shown in Table 3. Trestbps is associated with higher chol and the same as exang and oldpeak. Thalach and age are associated with a lower likelihood of exang.

The feature cp has the highest importance value, close to 0.25, while features like ca and thal also have relatively high importance values, around 0.15. On the other hand, features such as fbs, restecg, sex, and exang have rather low importance values, with fbs, nearly 0. Features with very low importance values like fbs might be considered for removal if the goal is to streamline the model.

6 CONCLUSIONS

Early diagnosis of heart disease plays a crucial role in saving lives. Recognizing the significance of data mining in facilitating heart disease diagnosis is of utmost importance. This paper has elaborated on the comparison of various classifiers for detecting heart disease. It was noted that the Random Forest and Gradient Boosting have emerged as a potentially effective classification algorithm in this domain, especially when total accuracy is regarded as the performance metric. The results can also help in feature selection, where less important features can be removed to simplify the model without significantly sacrificing accuracy. It also allows medical practitioners to focus on the crucial aspects during patient evaluations, potentially leading to earlier and more accurate diagnoses.

There is an urgent need for further researches and applications in this field to harness its full benefits and continuously enhance the quality of healthcare, ensuring more lives are saved and better health outcomes are achieved.

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