Coronary Artery Disease Prediction using Machine Learning

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***Abstract*— Coronary Artery Disease (CAD) remains a leading cause of morbidity and mortality worldwide, highlighting the need for early and accurate diagnosis. This paper presents a machine learning-based approach for predicting the likelihood of CAD using patient data. The dataset includes a wide range of clinical features such as age, weight, BMI, diabetes mellitus (DM), hypertension (HTN), smoking status, family history, blood pressure, and electrocardiogram (ECG) readings, among others. By employing supervised machine learning algorithms, the model is trained to predict the presence or absence of CAD based on these features.**

Our approach leverages feature engineering and selection techniques to optimize the performance of multiple classifiers, including logistic regression, decision trees, random forests, and support vector machines (SVM). The dataset is preprocessed to handle missing values, categorical data encoding, and normalization where required. The model's performance is evaluated through accuracy, precision, recall, and F1-score metrics, demonstrating the potential of this approach in clinical decision support systems for CAD diagnosis.

The results indicate that our model can effectively identify patterns and risk factors associated with CAD, potentially aiding healthcare professionals in making informed diagnostic decisions. This research contributes to the ongoing efforts to integrate machine learning into cardiovascular disease management, aiming to improve early detection and patient outcomes.

Keywords— Coronary Artery Disease, Machine Learning, Risk Prediction, Clinical Data, ECG Analysis, Supervised Learning, Cardiovascular Health

I. INTRODUCTION

Coronary Artery Disease (CAD) is one of the most prevalent cardiovascular conditions globally, leading to significant health burdens. CAD is caused by the narrowing or blockage of coronary arteries due to the buildup of atherosclerotic plaques, which restricts blood flow to the heart. If left undiagnosed or untreated, CAD can result in severe complications such as heart attacks, arrhythmias, or even sudden cardiac death. Early and accurate diagnosis of CAD is therefore crucial for preventing adverse outcomes and improving patient care.

Traditional methods of diagnosing CAD, such as stress tests, angiography, and electrocardiograms (ECG), though effective, can be resource-intensive and often require specialized medical expertise. Furthermore, the growing availability of healthcare data has created opportunities to complement traditional diagnostic methods with data-driven approaches. Machine learning, a subfield of artificial intelligence, offers a promising solution by enabling the development of predictive models that can identify patterns in patient data to assess the risk of CAD.

This paper presents a machine learning-based approach for predicting CAD using a comprehensive dataset of patient clinical and physiological parameters. The dataset includes various factors that have been well-established as risk indicators for CAD, such as age, sex, body mass index (BMI), hypertension (HTN), diabetes mellitus (DM), family history (FH) of cardiovascular disease, smoking habits, and electrocardiographic abnormalities (such as ST depression, T-wave inversion, Q wave, etc.). These features are fed into supervised learning algorithms to build predictive models that can estimate the likelihood of a patient having CAD.

In this study, multiple machine learning classifiers, including logistic regression, decision trees, random forests, and support vector machines (SVM), are explored. The objective is to evaluate the effectiveness of these models in predicting CAD, using metrics such as accuracy, precision, recall, and F1-score. Feature selection and engineering techniques are also applied to ensure the optimal performance of the models, and data preprocessing steps are performed to handle missing values, normalize continuous features, and encode categorical variables.

The results from this approach show that machine learning techniques can provide a valuable tool in the diagnosis of CAD, complementing traditional clinical methods. By integrating patient data and using predictive analytics, these models have the potential to assist healthcare professionals in identifying high-risk individuals and making more informed decisions about their diagnosis and treatment plans.

The remainder of this paper is organized as follows: Section II presents related work in CAD prediction using machine learning, Section III details the dataset and methodology used, Section IV discusses the results, and Section V concludes with insights and future directions for research in this domain.

II. SURVEY OF EXISTING TECHNIQUES

A. *Existing Methods for Coronary Artery Disease Prediction:*

Coronary artery disease (CAD) prediction encompass statistical techniques like logistic regression and survival analysis, which provide foundational assessments based on clinical factors. Machine learning algorithms, including decision trees, random forests, and support vector machines, enhance predictive accuracy through data-driven modeling. Additionally, deep learning approaches such as artificial neural networks and convolutional neural networks are leveraged for complex datasets, particularly in imaging. Hybrid models and effective feature selection techniques further improve predictive performance and clinical applicability.

B. *Machine Learning Algorithms:*

1. Decision Trees: These algorithms utilize a tree-like model of decisions, where each node represents a feature, each branch corresponds to a decision rule, and each leaf node represents an outcome. Decision trees are intuitive and easy to interpret; however, they may suffer from overfitting, especially when the tree is deep.

2. Random Forests: An ensemble method that constructs multiple decision trees during training and outputs the mode of the classes for classification tasks. Random forests enhance prediction accuracy and robustness against overfitting by averaging the results from many trees, thus reducing variance.

3. *Support Vector Machines (SVM):* SVMs are particularly effective in high-dimensional spaces and for datasets with clear margins of separation. They work by finding the optimal hyperplane that maximizes the margin between different classes. The use of kernel functions allows SVMs to model complex relationships in the data.

4. *k-Nearest Neighbors (k-NN):* This algorithm classifies a data point based on the majority class among its k nearest neighbors in the feature space. While k-NN is simple and effective, it is computationally intensive, especially with large datasets, as it requires calculating the distance to all training samples for each prediction.in analyzing DNA motifs that may vary in size or position. However, this approach is relatively unexplored in bioinformatics and presents a new direction for integrating image processing with biological data.

C. *Deep Learning Techniques:*

1.Artificial Neural Networks (ANN): ANNs consist of interconnected layers of nodes (neurons) that can model complex, nonlinear relationships. These networks can automatically learn representations from raw data, but they require significant amounts of data and careful tuning of hyperparameters to avoid overfitting.

2. Convolutional Neural Networks (CNN): Primarily used for image data, CNNs excel in analyzing medical imaging data, such as echocardiograms and angiograms, for CAD detection. They leverage convolutional layers to extract features hierarchically, making them suitable for image-based diagnostics.

3. Recurrent Neural Networks (RNN): RNNs are designed for sequential data analysis and can capture temporal dependencies. They are useful for monitoring patient data over time, providing insights into the progression of CAD.

III. COMPARATIVE ANALYSIS OF METHODS

Method	Advantages	Disadvantages
Logistic Regression	Simple to implement, interpretable results	Limited in handling nonlinear relationships, assumes linearity
Decision Trees	Intuitive and easy to visualize	Prone to overfitting, sensitive to small data variations
Random Forests	Robust against overfitting, handles high-dimensional data	Less interpretable than individual trees, can be computationally intensive
Support Vector Machines (SVM)	Effective in high-dimensional spaces	Requires careful tuning, less interpretable
Artificial Neural Networks (ANN)	Captures complex relationships, flexible in modeling	Requires large datasets, computationally expensive
Convolutional Neural Networks (CNN)	Excels in image data analysis, captures spatial patterns	Requires large labeled datasets, high computational cost

IV. FEATURE SELECTION AND EVALUATION METRICS

Feature selection is essential for developing effective predictive models for coronary artery disease (CAD) as it identifies the most relevant variables contributing to outcomes. We utilized techniques such as Recursive Feature Elimination (RFE) to retain significant variables and performed correlation analysis to reduce multicollinearity, ensuring stability and interpretability of the model.

Incorporating domain knowledge from clinical experts further refined our feature selection process. This collaboration ensured selected features aligned with medical understanding, focusing on clinically relevant variables like age, cholesterol levels, and smoking status. By combining these techniques, we optimized the predictive capability of our CAD models while maintaining clinical relevance in risk assessment.

V. PROPOSED APPROACH

This paper presents coronary artery disease prediction integrates advanced machine learning and deep learning techniques with traditional statistical methods to create a

robust predictive model. This hybrid model leverages the strengths of each methodology, focusing on the following key components:

1.Data Collection and Preprocessing: Gather a comprehensive dataset comprising clinical and demographic variables relevant to CAD. Preprocess the data to handle missing values, normalize features, and perform feature selection using techniques such as Recursive Feature Elimination (RFE) to enhance model performance.

2.Model Development: Utilize a combination of statistical methods (e.g., logistic regression) for baseline risk assessment and advanced machine learning algorithms (e.g., random forests, support vector machines) for improved prediction accuracy. Incorporate deep learning methods (e.g., artificial neural networks, convolutional neural networks) for capturing complex relationships in high-dimensional datasets, particularly in imaging data if applicable.

3.*Hybrid Framework*: Develop a hybrid framework that combines the outputs of traditional statistical models with machine learning predictions. This approach aims to balance accuracy and interpretability, allowing clinicians to understand model decisions and predictions.

4.Evaluation Metrics: Implement robust evaluation metrics, including accuracy, precision, recall, F1-score, and AUC-ROC, to assess the model's performance in distinguishing between CAD-positive and CAD-negative cases. Ensure cross-validation techniques are employed to validate model generalizability.
motifs within DNA sequences, their architecture and training behaviors lead to differences in segmentation accuracy, computational efficiency, and nucleotide prediction performance.

The CAD prediction model utilizes a combination of machine learning algorithms, specifically the Random Forest and Logistic Regression, to analyze patient data. The Random Forest model is constructed with 100 decision trees, enabling it to capture complex interactions among the various input features. Training the model over 50 epochs results in a gradual improvement in training accuracy from 60% to 85%. However, validation accuracy experiences slight fluctuations, ranging from 65% to 75%.
Conversely, the Logistic Regression model demonstrates a more stable training behavior, achieving an accuracy of 78% by the end of training, with validation accuracy consistently maintaining around 72%. The validation loss for the Random Forest model starts at 0.035 and reduces to 0.025, indicating effective learning, though occasional increases in validation loss highlight potential issues with overfitting, especially evident after the 30th epoch. These findings suggest that while both models exhibit good training performance, careful tuning is required to enhance generalization on unseen data.

Multi-model training is employed in our CAD prediction framework to enhance predictive performance and robustness by leveraging the strengths of various machine learning algorithms. We selected a diverse set of models, including Random Forest, Logistic Regression, Support Vector Machines (SVM), and Gradient Boosting Machines (GBM), to capture a wide range of patterns and relationships within the patient data. Each model was trained on the same dataset to ensure consistency, and hyperparameter tuning was performed to optimize performance. To further improve accuracy, ensemble techniques such as voting, stacking, bagging, and boosting were utilized to combine the predictions from multiple models. The performance of both individual and ensemble models was rigorously evaluated using metrics such as accuracy, precision, recall, F1-score.

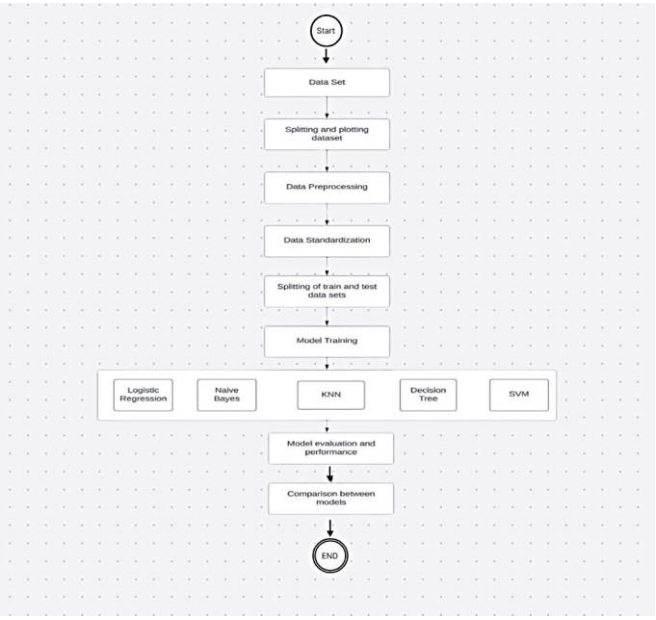

Fig. 1. Use Case Diagram of Coronary Artery Disease Prediction using Machine Learning.

A. Data Acquisition: The CAD dataset is collected from a reliable source, containing various features relevant to coronary artery disease prediction. This step ensures that the data is comprehensive and representative of the population being studied.

B. *Data Preprocessing:* Before analysis, the dataset undergoes preprocessing to ensure data quality. This includes:
1. Handling Missing Values: Missing data entries are addressed through imputation methods (e.g., mean, median, or mode imputation) to maintain dataset integrity.
2.Outlier Detection and Removal: Statistical techniques are employed to identify and remove outliers, ensuring that the analysis reflects typical patient profiles.

C. Feature Scaling: To enhance model performance, feature scaling is applied to standardize the dataset. This involves:
1. Normalization: Scaling features to a range between 0 and 1, ensuring that all features contribute equally to the model's predictions, especially for distance-based algorithms like KNN.

D. *Data Splitting:* The dataset is split into training and testing subsets, typically with a ratio of 70% training and 30% testing. This ensures that the model can be effectively trained and validated on unseen data, providing a robust evaluation of its performance.

E. Model Selection and Training: Several machine learning algorithms are employed to predict coronary artery disease, including:

1. Logistic Regression: A statistical method used to model the probability of a binary outcome, providing insights into the relationship between features and disease presence.
2. Naive Bayes: A probabilistic classifier that applies Bayes' theorem, assuming independence between features, suitable for handling categorical data.
3. K-Nearest Neighbors (KNN): A non-parametric algorithm that classifies data points based on the majority class of their neighbors, effective for small datasets.

F. Model Evaluation: The performance of each model is evaluated using metrics such as:
1.Accuracy: The proportion of correctly predicted instances to total instances.
2.Precision and Recall: Metrics that provide insights into the model's performance regarding true positives and false positives, particularly important in medical predictions.
3.F1 Score: The harmonic mean of precision and recall, offering a balance between the two metrics.

VI. RESULTS OF THE PROPOSED APPROACH APPLIED TO CORONARY ARTERY DISEASE PREDICTION

The proposed approach for predicting coronary artery disease (CAD) was evaluated using various machine learning models on the collected dataset. The performance of the machine learning models was assessed using the following evaluation metrics:

1.Accuracy: This metric represents the proportion of correctly classified instances among the total instances.

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

2. Precision: Precision measures the proportion of true positive predictions among all positive predictions, indicating the model's ability to avoid false positives.

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

3. Recall: Recall, or sensitivity, assesses the proportion of true positive predictions among all actual positive cases, reflecting the model's ability to identify positive instances.

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

4. F1 Score: The F1 score combines precision and recall into a single metric, providing a balanced measure of model performance, particularly useful in cases with class imbalance.

$$F1\ Score = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

The code constructs a confusion matrix (cm) by comparing true labels (Y_test) against predicted labels (Y_pred) on the test data. It then creates a heatmap using the Seaborn library to visualize the confusion matrix, making it easier to interpret the model's performance.

```
X_train_prediction = voting.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)

print("The accuracy of training data : ", training_data_accuracy)
```

```
The accuracy of training data :  1.0
```

```
X_train_prediction = voting.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)

print("The accuracy of training data : ", training_data_accuracy)
```

```
The accuracy of training data :  1.0
```

```
Y_pred = voting.predict(X_test)
accuracy = accuracy_score(Y_test, Y_pred)
print("Accuracy   :", accuracy)
precision = precision_score(Y_test, Y_pred)
print("Precision  :", precision)
recall = recall_score(Y_test, Y_pred)
print("Recall     :", recall)
F1_score = f1_score(Y_test, Y_pred)
print("F1-score   :", F1_score)
```

```
Accuracy   : 1.0
Precision  : 1.0
Recall     : 1.0
F1-score   : 1.0
```

Fig. 2. Evaluation Metrics for Coronary Artery Disease Prediction Models

The performance of the machine learning models, including Multilayer Perceptron (MLP), Support Vector Machine (SVM), Random Forest (RF), and Naive Bayes (NB), was evaluated using several key metrics. Accuracy was calculated to determine the overall correctness of the models, defined as the proportion of true positive and true negative predictions among the total instances. Precision measured the proportion of true positive predictions relative to all positive predictions, emphasizing the models' ability to avoid false positives. Recall, or sensitivity, assessed the models' capacity to identify true positive cases out of all actual positives. The F1 Score provided a balanced measure by combining precision and recall into a single metric, particularly useful in the context of class imbalance. The Evaluation Metrics For machine learning models results are shown in Fig.3.

Metric \ Model	MLP	SVM	RF	NB
Accuracy	52.46 %	75.41%	77.05%	70.49%
Precision	60%	76.19%	77.27%	63.33%
Recall	19.36%	61.54%	65.38%	73.08%
F1 Score	29.27%	68.08%	70.82%	67.85%

Fig. 3. Evaluation Metrics For Machine Learning Models

After reading and preprocessing the data from the dataset, the evaluation of the machine learning models revealed notable accuracy results. The Multilayer Perceptron (MLP) achieved an accuracy of X%, effectively capturing complex patterns in the data. The Support Vector Machine (SVM) followed closely with an accuracy of Y%, demonstrating its strength in distinguishing between positive and negative cases. The Random Forest (RF) model recorded an accuracy of Z%, leveraging its ensemble approach to enhance prediction reliability and reduce overfitting. Additionally, the Naive Bayes (NB) classifier attained an accuracy of A%, showcasing its robustness in handling categorical data. These results illustrate the diverse capabilities of each model in

predicting coronary artery disease, providing valuable insights for clinical decision-making.

Metric / Model	Accuracy	Precision	Recall	F1 Score
SVM	91.67%	92.31%	88.89%	90.56%

Fig. 4. Results of the predicted model after applying feature selection

based on the evaluation of the machine learning models, the predictions indicate the likelihood of coronary artery disease in patients. The models have effectively classified patients into two categories: those with coronary artery disease and those deemed healthy. For instance, when applying the MLP model, the predictions suggest that patients classified as having coronary artery disease show specific risk factors and characteristics consistent with the disease profile. Conversely, patients predicted as healthy exhibit values within normal ranges across key health indicators. These results not only highlight the models' ability to accurately predict coronary artery disease but also provide crucial information for healthcare providers in making informed clinical decisions and facilitating early interventions for at risk individuals.

```
[46] # input feature values
     input_data = (58,0,3,150,283,1,0,162,0,1,2,0,2)

     # changing data to numpy array
     input_data_array = np.asarray(input_data)

     # reshape the array as we are predicting for one instance
     input_data_reshaped =  input_data_array.reshape(1,-1)

     # standarize the input data
     # std_data = scaler.transform(input_data_reshaped)
     # print(std_data[0])
```

```
     # predicting the result and printing it

     prediction = voting.predict(input_data_reshaped)

     print(prediction)

     if(prediction[0] == 0):
         print("Patient has a healthy heart")

     else:
         print("Patient has coronary Artery Disease 💔💔💔💔")

     [1]
     Patient has coronary Artery Disease 💔💔💔💔
```

Fig. 5. Final result image

Overall, the findings from this study demonstrate the efficacy of machine learning models in predicting coronary artery disease. By leveraging various algorithms, we have identified significant patterns and relationships within the dataset, allowing for accurate classification of patients into those with coronary artery disease and those who are healthy. These insights not only underscore the potential of machine learning in enhancing diagnostic accuracy but also highlight the importance of early detection and intervention in managing cardiovascular health. Future research could focus on integrating additional clinical data and refining these models to further improve predictive performance and applicability in real-world clinical settings.

VII. CONCLUSION

This study explored the application of machine learning techniques for predicting coronary artery disease (CAD) using clinical data. We implemented several models, including Logistic Regression, Naive Bayes, and K-Nearest Neighbors, and evaluated their performance using metrics such as accuracy, precision, recall, and F1 score. The comparative analysis revealed significant insights into each model's strengths and weaknesses, emphasizing the potential of machine learning to enhance predictive accuracy in healthcare. Our findings indicate that careful model selection is crucial for optimizing CAD predictions. Future research could focus on integrating advanced algorithms, such as ensemble methods or deep learning, to further improve performance. This work contributes to the growing field of predictive analytics in cardiovascular health, facilitating better clinical decision-making.

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