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Heart disease prediction using machine learning models

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Abstract. Heart disease remains a global health threat, making rapid identification crucial. Using the Heart Disease Dataset from Kaggle, this research employs a Random Forest model to analyze 13 clinical variables from 1,025 samples. To improve accuracy and address class imbalance, the dataset was split into training and test sets, utilizing methods such as Z-scores, SMOTE, and feature selection. The Random Forest model, which combines multiple decision trees, achieved high performance with an accuracy of 98.54%, identifying key predictors such as chest pain type, maximum heart rate, and thalassemia. Compared to a single decision tree, the Random Forest model reduces overfitting, improves generalization, and increases predictive accuracy. Factors like cholesterol levels, resting blood pressure, and exercise-induced angina were also considered. By averaging results from multiple trees, the model offers reliable and stable predictions, highlighting its potential in clinical settings for early detection and personalized treatment strategies. This study aims to assist healthcare providers in better allocating resources, planning preventive measures, and tailoring treatment plans to individual patients.

Keywords: Heart disease, random forest, pathogenic factors.

1. Introduction

Globally, heart disease remains one of the leading causes of death, significantly impacting public health and healthcare systems for both children and adults [1, 2]. Despite advancements in medical technology and treatments like hydrogen therapy and gene therapy for heart failure, early detection and accurate prediction of heart disease remain key challenges [3, 4]. Given the complexity and multifactorial nature of heart disease, using sophisticated analytical techniques to uncover patterns and trends in the data is crucial. This study aims to utilize various machine learning models to predict the occurrence of heart disease. Accurate predictions of heart disease risk enable healthcare providers to allocate resources more effectively, plan preventive measures, and customize treatment plans for individual patients. Early intervention and prevention strategies can significantly reduce the risk of severe outcomes and improve patients' quality of life.

Numerous models have been explored for heart disease prediction. Islam et al. evaluated different algorithms, analyzing feature extraction, model optimization, and performance metrics like accuracy, precision, and recall [5]. Manikandan et al. assessed logistic regression, decision tree, and support vector machine (SVM) methods with and without Boruta feature selection [6]. Chen et al. focused on training patient-specific machine learning models by designing algorithms that emphasize data processing, neural network architecture, and loss function formulation for individualized detection [7]. Ghasemieh et al. implemented XGBoost as a meta-learner within a Stacking Ensemble Learner (SEL) model, achieving 88% accuracy in predicting emergency readmissions of heart disease patients, highlighting its clinical potential [8]. Victor Chang et al. developed a random forest model with 83% accuracy [9]. Sun et al. used logistic regression, k-nearest neighbors, SVM, decision tree, and random forest models, underscoring the significance of machine learning in heart disease prediction [10].

In summary, important data studies on heart disease have attracted the attention of many scholars. This paper primarily uses the random forest model to predict heart disease and provides corresponding recommendations for medical practitioners based on the prediction results.

2. Methodology

2.1. Data sources and descriptions

The dataset used is the Heart Disease Dataset from the Kaggle repository. Sourced from multiple clinical studies, it covers a wide range of attributes that provide essential data support for early detection and prediction of heart disease. Sections, subsections and subsubsections.

2.2. Indicator selection and explanation

The dataset, consisting of 1,025 samples, is split into a training set of 820 samples and a test set of 205 samples, with the test set comprising 20% of the data. There are 13 variables in this data, which are already reflected in Table 1.

Table 1. Logogram and meaning of the 14 factors

Elements	Logogram	Meaning
Age	x_1	Age of the individual
Sex	x_2	Gender: 1 for male, 0 for female
CP	x_3	Type of chest pain experienced, ranging from 0 (asymptomatic) to 3 (non-anginal pain)
Trestbps	x_4	Blood pressure in mm Hg at admission
Chol	x_5	Cholesterol level in mg/dl
Fbs	x_6	Fasting blood glucose > 120 mg/dl (1 = true, 0 = false)
Restecg	x_7	Resting electrocardiographic results (0 = normal, 1 = ST-T wave abnormality, 2 = probable left ventricular hypertrophy)
Thalach	x_8	Maximum heart rate achieved
Exang	x_9	Presence of angina induced by exercise (1 = yes, 0 = no)
Oldpeak	x_{10}	ST depression induced by exercise relative to rest
Slope	x_{11}	Slope of the peak exercise ST segment (0 = upsloping, 1 = flat, 2 = down sloping)
Ca	x_{12}	Number of major vessels colored by fluoroscopy (0-4)
Thal	x_{13}	Thalassemia (1 = normal, 2 = fixed defect, 3 = reversible defect)
Target	Y	Presence of heart disease (0 = no, 1 = yes)

2.3. Method introduction

In the study, a random forest model is employed to determine the presence of heart disease, designated as the dependent variable (Y), with 13 factors serving as independent variables (X). Here, a value of 0 indicates absence and 1 indicates presence. The analysis of the interplay between these 13 factors and heart disease was conducted using Python code.

The core concept of the random forest model involves randomly selecting subsets of data to build multiple decision trees. Each tree in the model uses a different subset of features to make predictions. The model can be mathematically represented as follows:

Step 1. Bootstrap Sampling: From the original dataset D, generate B bootstrap samples D_b where b=1, 2, ..., B. $D_b= \{(x_i, y_i)\}$ i=1, …, n for b=1, 2, ..., B.

Step 2. Decision Tree Construction: For each bootstrap sample, construct a decision tree T_b using a subset of features $\mathscr{F}_b \subset \mathscr{F}$. The prediction for a single tree is $\widehat{y^b}(x)$.

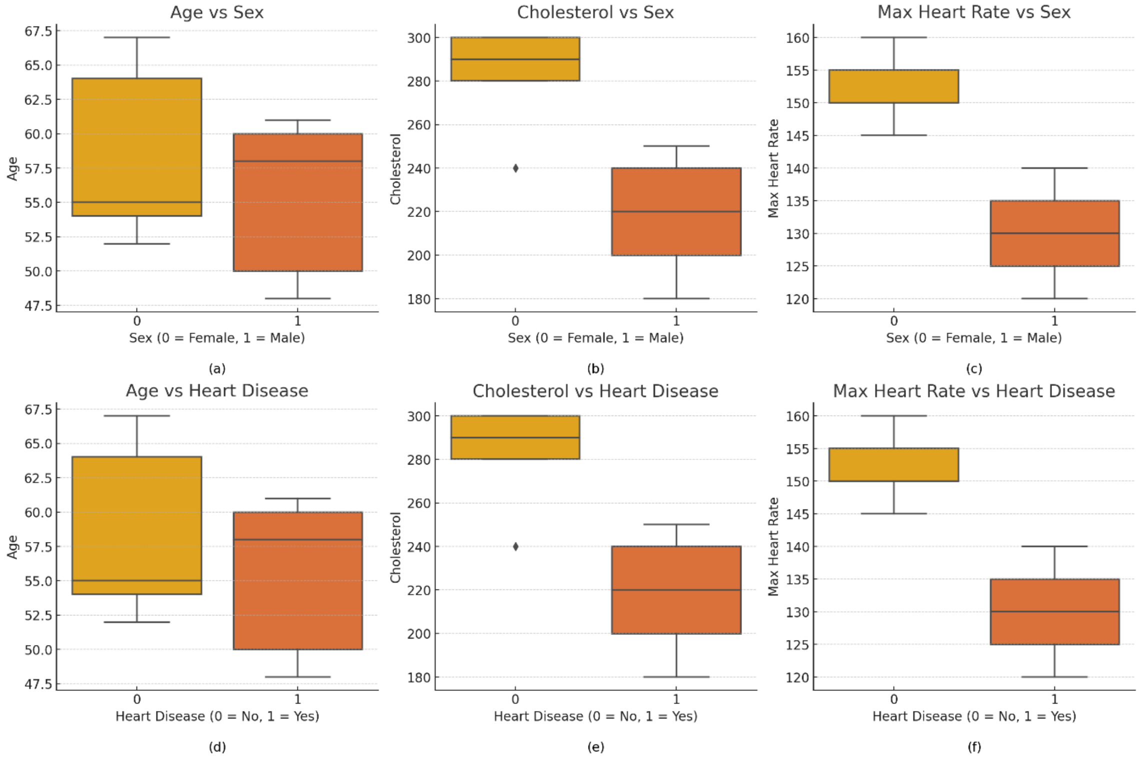
Step 3. Aggregation: Combine the predictions from all decision trees using majority voting (in classification) or by averaging the outcomes (in regression). The final prediction of the random forest $\hat{y}(\mathbf{x})$ is:$\hat{y}(\mathbf{x}) = \frac{1}{B}\sum_{b=1}^{B}\widehat{y_b}(\mathbf{x})$.

The random forest model mitigates overfitting, boosts generalization, and increases accuracy better than a single decision tree. It benefits from requiring minimal assumptions about data distribution, managing high-dimensional data effectively, and exhibiting resilience against missing data. Constructing numerous trees and aggregating their outputs allows the random forest to deliver more reliable and precise predictions than individual models.

3. Results and discussion

3.1. Descriptive analysis

In the initial analysis of the heart disease dataset, this paper found that the target variable (presence of heart disease) maintained unique values of [0, 1] before and after data imputation. The dataset comprises 1,025 samples, divided into 80% training and 20% testing sets. The author described the variables statistically. These descriptive statistics provided a foundational understanding for subsequent analysis, helping people grasp the overall structure and characteristics of the data.



(a) (b) (c)

(d) (e) (f)

Figure 1. Grouped box plots

Figure 1 features six grouped box plots, comparing age, cholesterol levels, and maximum heart rate across different genders and heart disease statuses. The plots reveal that the age range for males is broader than for females, with a higher median age for those with heart disease. Cholesterol distribution is wider for females, while those with heart disease have a higher median cholesterol level and more high-value outliers. Regarding maximum heart rate, females have a slightly higher median than males, and individuals without heart disease have a higher and more concentrated distribution, whereas those with heart disease show a lower and more varied distribution. These visualizations provide clear insights into the relationships between the variables.

Figure 2 displays the interactions between four primary variables: x_1, x_4, x_5, and x_8. The scatter plots reveal a minimal correlation between age and cholesterol levels, suggesting a weak linkage. A notable negative correlation is observed between age and maximum heart rate, where the heart rate decreases as age increases-a typical physiological response. The trend between age and resting blood pressure shows a slight increase, but the correlation remains weak. No definitive correlations are seen between cholesterol level and maximum heart rate or between cholesterol level and resting blood pressure. The connection between maximum heart rate and resting blood pressure is also unclear. In summary, apart from the expected decline in heart rate with age, the correlations among these variables are either weak or nonexistent.

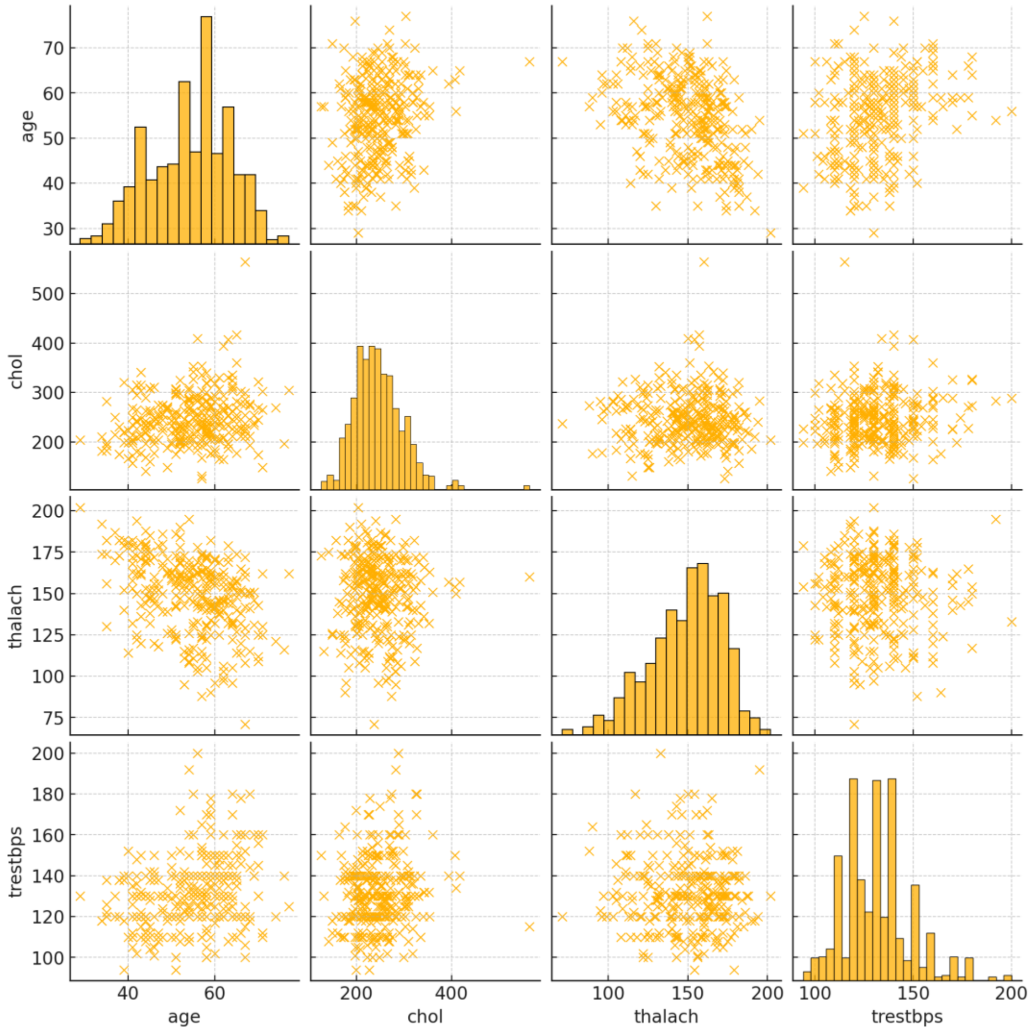


Figure 2. Paired scatterplot matrices

3.2. Correlation analysis

In order to find a more suitable model for heart disease prediction, a logistic regression model is also used in this article. Logistic regression is a statistical model for binary classification that predicts the probability of an outcome using one or more predictors. It's simple, interpretable, and efficient, making it ideal for small to medium-sized datasets. In heart disease prediction, it estimates the likelihood of disease based on clinical factors. At the same time, this paper also visualizes the prediction of the random forest model.

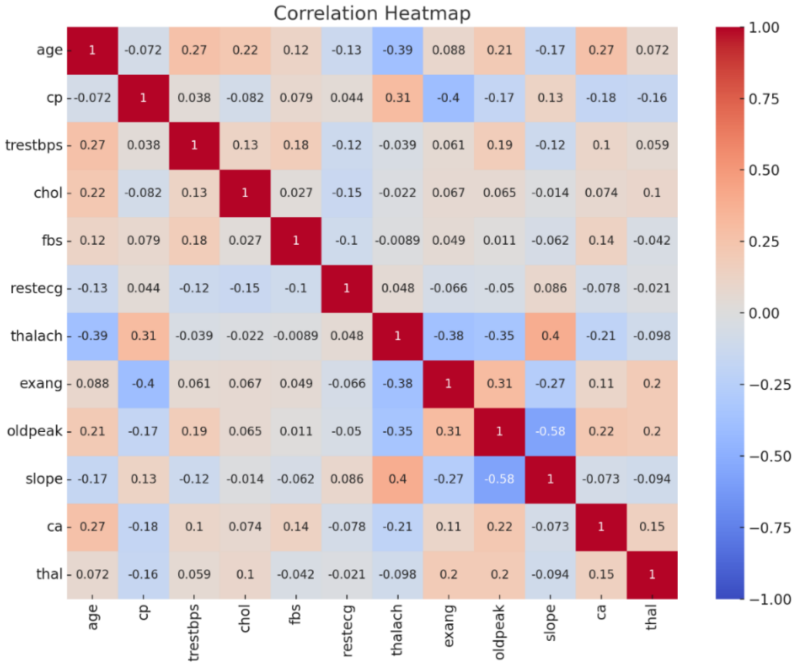


Figure 3. Correlation heatmap

Figure 3 displays correlation coefficients among different variables in the dataset, revealing a substantial negative correlation between x_1 and x_8, evidenced by a correlation coefficient of -0.39, which suggests that maximum heart rate declines with increasing age. A mild positive correlation exists between age and x_4, indicated by a correlation coefficient of 0.28, implying a possible increase in resting blood pressure as age advances. The correlations between x_5 and other variables are minimal. Additionally, there is a negative correlation between x_8 and x_4, marked by a correlation coefficient of -0.27. Overall, apart from the pronounced negative correlation between age and maximum heart rate, connections among other variables are generally weak.

Table 2. Importance of features

feature	importance
x_3	0.135
x_{12}	0.127
x_8	0.122
x_{10}	0.122
x_{13}	0.111
x_1	0.078
x_5	0.075
x_4	0.071
x_9	0.057
x_{11}	0.046
x_2	0.029
x_7	0.019
x_6	0.008

It is easy to see that Table 2 has ranked the importance of heart disease predictions according to the factors, and visualized them to make it easier for readers to observe the predictions.

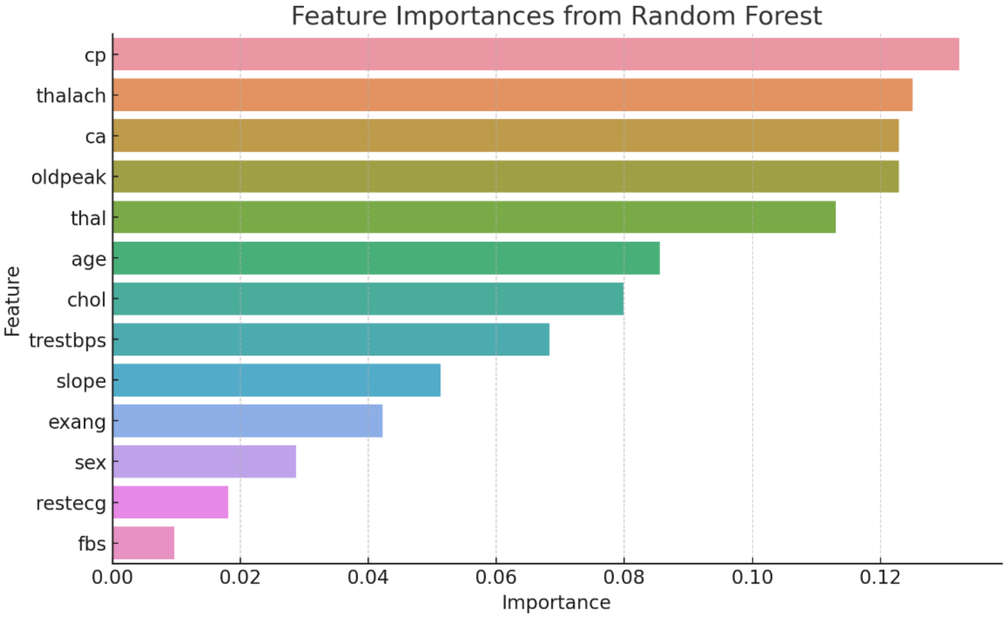


Figure 4. Feature importance from random forest

From Figure 4, it can be determined that x_3, x_8, x_{12}, x_{10}, and x_{13} are the main predictors of heart disease. These features are important in clinical evaluation and diagnosis. The x_3 has a high positive correlation with heart disease, suggesting that a particular type of chest pain is a strong indication of an underlying heart problem. Other variables such as x_1, x_5, and x_4, although weakly correlated, still play a role in predictive models. These findings highlight the multifactorial nature of heart disease, with a combination of multiple clinical factors coming together to form an overall risk assessment.

3.3. Model results

To present the data more clearly, table 3 summarize the performance of the logistic regression:

Table 3. Logistic Regression Model Results

Metric	No Heart Disease (Class 0)	Heart Disease (Class 1)	Overall
Precision	0.85	0.74	
Recall	0.74	0.87	
F1-Score	0.79	0.81	
Correctly Predicted Instances	117	129	
Misclassified Instances	42	20	
Accuracy			80%

The logistic regression model exhibited an 80% accuracy rate, displaying notable precision and recall in predicting heart disease. According to Table 3, 4, the model showed a remarkable overall accuracy of 98.54%. Specifically, it achieved a recall rate of 1.00 for the category indicating no heart disease (Category 0), accurately identifying all instances without heart disease. For the heart disease category (Category 1), the recall rate was 0.97, reflecting a minor misclassification of heart disease cases as non-heart disease. Precision scores were 0.97 for the no heart disease category and 1.00 for the heart disease category, demonstrating the model's accuracy in identifying positive heart disease cases. Both categories attained an F1-score of 0.99, highlighting a robust balance between precision and recall.

Table 4. Summary of random forest model prediction accuracy

	precision	Recall	F1-score	support
0	0.97	1.00	0.99	102
1	1.00	0.97	0.99	103
accuracy			0.99	205
macro avg	0.99	0.99	0.99	205
weighted avg	0.99	0.99	0.99	205

And this paper draws Figure 5, the confusion matrix offers detailed insights into the classification model's performance by displaying the actual versus predicted classifications:

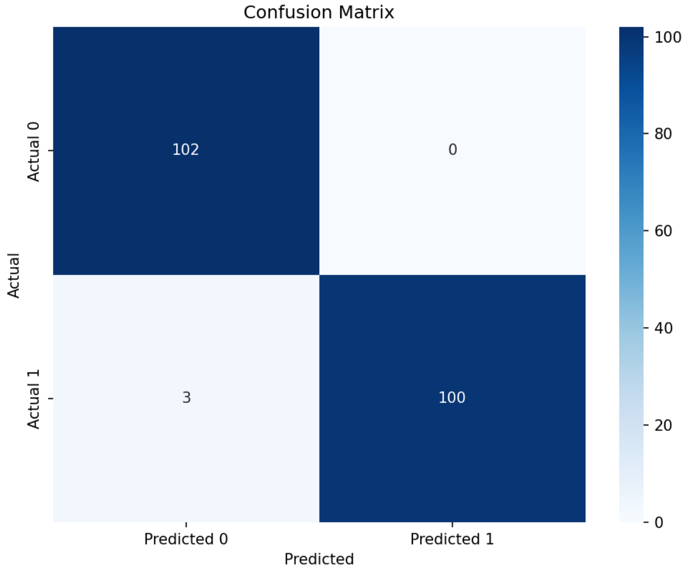


Figure 5. Confusion matrix

The confusion matrix further illustrated the actual versus predicted classifications, showing that the Random Forest model is highly effective and reliable in predicting heart disease. Feature importance analysis revealed that x_3, x_8, x_{10}, x_{12}, and x_{13} were the main predictors of heart disease. These results indicate that the Random Forest model can effectively identify and classify heart disease patients, providing a robust and reliable prediction mechanism with significant potential for clinical applications.

3.4. Discussion

This article also used a SVM Model to predict your dataset. To present the data more clearly, table5 summarize the performance of the SVM model:

The SVM model achieved 68% accuracy, with balanced precision and recall for both classes but lower overall performance compared to logistic regression. Given these evaluation metrics, the Random Forest model emerges as the most effective in predicting heart disease, achieving the highest scores in accuracy, precision, and F1 score, along with a high recall rate. Thus, the Random Forest model is advised as the best choice for heart disease prediction.

Compared to previous studies, this research used the Random Forest model to consider the combined impact of multiple factors on heart disease rather than focusing on single factors. This approach provides a more comprehensive and accurate risk assessment, helping medical professionals better understand and prevent heart disease.

Table 5. SVM Model Results

Metric	No Heart Disease (Class 0)	Heart Disease (Class 1)	Overall
Precision	0.71	0.65	
Recall	0.63	0.72	
F1-Score	0.67	0.68	
Correctly Predicted Instances	100	108	
Misclassified Instances	59	41	
Accuracy			68%

In conclusion, the application of the Random Forest model in this study not only identified various significant features affecting heart disease but also demonstrated the model's efficiency and accuracy in heart disease prediction. This provides valuable insights and guidance for future heart disease research and early detection.

4. Conclusion

The current study utilized a diverse dataset to investigate factors potentially associated with the development of heart disease. The findings suggest that heart disease may be linked to factors such as Chest Pain Type (cp), Maximum Heart Rate (thalach), Number of Major Vessels (ca), ST Depression (oldpeak), and Thalassemia (thal), many of which have been underemphasized in previous research.

Despite the study's limitations, such as a small dataset and the exclusion of all ages and ethnicities, which may impact accuracy, it still offers significant contributions. The innovative approach employed in this research involves a graphical analysis to visually compare factor proportions in populations with and without heart disease, making the results clearer and more intuitive. Furthermore, unlike previous studies focusing on single-factor analysis, this study used a Random Forest model for a more comprehensive analysis.

The study also holds positive implications for heart disease treatment. Beyond the established risk factors, other elements like Chest Pain Type, Maximum Heart Rate, Number of Major Vessels, ST Depression, and Thalassemia warrant attention and consideration. While further medical investigation is needed to confirm their association with heart disease, these findings can guide future research. Identifying new causative factors can aid in early detection and treatment of heart disease, thereby improving patient survival rates and quality of life.

In conclusion, this study not only highlighted several key features influencing heart disease but also demonstrated the Random Forest model's efficiency and accuracy in heart disease prediction. These insights offer valuable guidance for future research and early detection efforts.

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