

Machine Learning-Based Heart Disease Prediction Using Clinical and Diagnostic Features

JAGDISH MALKAR

`jagdish.malkar_24uds@sanjivani.edu.in`

Sanjivani University

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Machine Learning-Based Heart Disease Prediction Using Clinical and Diagnostic Features

Name: Jagdish Malkar

B.Tech , Artificial Intelligence Data Science

Sanjivani University, Maharashtra, India

ORCID: Jagdish Malkar – 0009-0003-5235-4839 Email: jagdish.malkar_24uds@sanjivani.edu.in

I. Abstract

Heart disease remains an important healthcare challenge, creating a need for reliable data-driven approaches for early risk assessment and clinical decision support. Machine learning can analyze combinations of demographic, clinical, and diagnostic variables to identify patterns associated with the presence of heart disease. This study investigates the application of statistical analysis and machine learning techniques to the UCI Heart Disease dataset, which contains 920 patient records collected from four databases: Cleveland, Hungary, Switzerland, and VA Long Beach. The dataset contains demographic, clinical, and diagnostic variables including age, sex, chest pain type, resting blood pressure, serum cholesterol, fasting blood sugar, resting electrocardiographic results, maximum heart rate, exercise-induced angina, ST depression, ST-segment slope, number of major vessels, and thalassemia-related measurements. The original target variable represents the presence and severity of heart disease using values from 0 to 4; for binary classification, values of 0 are treated as absence of disease and values from 1 to 4 as presence of disease. In the supplied dataset, 411 records belong to the no-disease group and 509 records belong to the disease group. The study follows a structured workflow involving data quality assessment, missing-value analysis, exploratory data analysis, descriptive statistics, feature preprocessing, statistical analysis, machine learning model development, and performance evaluation. Multiple evaluation metrics, including accuracy, precision, recall, F1-score, specificity, ROC-AUC, and confusion matrix analysis, are considered to provide a comprehensive assessment of predictive performance. The study aims to identify clinically relevant patterns and evaluate the usefulness and limitations of machine learning for heart disease prediction while emphasizing interpretability, data quality, validation, fairness, and responsible use in healthcare.

Index Terms—Heart disease prediction, machine learning, artificial intelligence, clinical data analysis, cardiovascular disease, classification, statistical analysis, UCI Heart Disease dataset, healthcare analytics, predictive modeling.

II. Introduction

Heart disease is a major area of concern in healthcare because its development and clinical outcomes are influenced by multiple demographic, physiological, and diagnostic factors. Accu-

rate identification of individuals with potential heart disease can support risk assessment, clinical evaluation, and timely management. Conventional clinical assessment relies on medical history, physical examination, laboratory measurements, and diagnostic investigations. However, the increasing availability of structured healthcare data has created opportunities for computational methods to assist clinicians in identifying patterns within complex patient records.

Artificial Intelligence (AI), particularly machine learning, has become an important research area for healthcare data analysis. Machine learning methods can learn relationships between input variables and clinical outcomes and can be used for classification and risk prediction. In cardiovascular applications, variables such as age, sex, chest pain characteristics, resting blood pressure, serum cholesterol, maximum heart rate, exercise-induced angina, electrocardiographic findings, and ST-segment measurements may provide useful information for identifying patterns associated with heart disease.

The UCI Heart Disease dataset is a widely used benchmark dataset for classification research. The repository contains four databases from Cleveland, Hungary, Switzerland, and VA Long Beach. The original UCI collection defines the target variable as an integer-valued field from 0 to 4, where 0 represents the absence of heart disease and values from 1 to 4 represent different levels of disease presence. The repository also reports missing values in the dataset. [1]

Although many machine learning studies have investigated heart disease prediction, reported performance can vary according to the selected database, preprocessing strategy, feature representation, handling of missing values, classification target, validation procedure, and evaluation metrics. Therefore, model accuracy alone is insufficient for establishing the usefulness of a healthcare prediction model. A systematic evaluation should consider multiple performance measures and should clearly document preprocessing and validation procedures.

This study develops a structured machine learning framework for heart disease prediction using the 920 records contained in the supplied UCI Heart Disease dataset. The study combines exploratory data analysis, statistical analysis, data preprocessing, machine learning classification, and comprehensive model evaluation. The objective is to investigate whether demographic, clinical, and diagnostic variables can be used to distinguish records with and without evidence of heart disease.

The main objectives of this study are:

- (1) To examine the structure and quality of the heart disease dataset.
- (2) To analyze demographic, clinical, and diagnostic characteristics.
- (3) To identify patterns and relationships among the predictor variables.
- (4) To preprocess missing and categorical data using an appropriate reproducible procedure.
- (5) To develop and compare machine learning classification models.
- (6) To evaluate the models using multiple performance metrics.
- (7) To discuss model interpretability, limitations, and considerations for responsible healthcare use.

The remainder of this paper is organized as follows.

Section II Presents related work and identifies the research gap.

Section III Describes the dataset and problem formulation.

Section IV Presents the proposed methodology.

Section V Reports the experimental results.

Section VI Discusses the statistical and predictive findings.

Section VII Presents limitations and ethical considerations.

Section VIII Concludes the study.

III. Related Work

Machine learning has been widely investigated for cardiovascular disease prediction because clinical datasets contain multiple interacting demographic, physiological, and diagnostic variables. Traditional statistical approaches such as logistic regression provide an interpretable baseline by estimating the relationship between predictor variables and a binary outcome. More complex machine learning approaches, including decision trees, support vector machines, random forests, and ensemble methods, have also been investigated for heart disease classification.

The UCI Heart Disease dataset has been extensively used as a benchmark for evaluating classification techniques. The original UCI collection contains data from four databases and provides a commonly used set of demographic and clinical variables for heart disease classification. The associated documentation identifies the original diagnostic study and defines the target variable used for disease classification. [1]

Previous research has demonstrated that machine learning can be applied to the UCI heart disease data using different preprocessing procedures and classification algorithms. However, results reported across studies are not directly comparable because researchers may use different subsets of the dataset, remove incomplete records, transform the target variable differently, select different features, and apply different validation procedures.

Several studies have also emphasized the importance of reproducibility when machine learning is applied to clinical datasets. A model that produces high accuracy on a particular train-test split may not necessarily generalize to other patient

populations. Therefore, cross-validation, transparent preprocessing, appropriate performance metrics, and external validation are important considerations when developing predictive healthcare systems.

The existing literature therefore motivates a structured analysis that does not rely solely on a single performance metric. In this study, statistical analysis and machine learning are combined to examine the dataset, evaluate predictive models, and provide an interpretable assessment of their performance.

A. Research Gap

Existing studies demonstrate the applicability of machine learning to heart disease prediction; however, differences in dataset subsets, missing-value treatment, target transformation, feature preprocessing, model selection, and validation strategies make direct comparison difficult. Some studies focus primarily on maximizing classification accuracy, while comparatively less attention is given to presenting a complete and reproducible workflow that combines data-quality assessment, statistical analysis, preprocessing, model comparison, and multiple evaluation metrics.

This study addresses this methodological gap by presenting an end-to-end analysis of the 920-record UCI Heart Disease dataset. The proposed workflow explicitly documents missing-value patterns, target transformation, categorical and numerical feature handling, model training, validation, and multiple performance measures. The study also emphasizes that predictive performance on a benchmark dataset should not be interpreted as evidence of clinical effectiveness without independent clinical validation.

IV. Dataset and Problem Formulation

A. Dataset Description

This study uses the UCI Heart Disease dataset obtained in spreadsheet form for analysis. The supplied dataset contains 920 patient records and 16 columns. The records originate from four databases: Cleveland, Hungary, Switzerland, and VA Long Beach. The dataset contains demographic, clinical, and diagnostic variables together with a target variable representing the presence and severity of heart disease.

The predictor variables available in the supplied dataset are age, sex, dataset, chest pain type (cp), resting blood pressure (trestbps), serum cholesterol (chol), fasting blood sugar (fbs), resting electrocardiographic results (restecg), maximum heart rate achieved (thalach), exercise-induced angina (exang), ST depression (oldpeak), ST-segment slope (slope), number of major vessels (ca), and thalassemia-related information (thal). The variable id is treated as an identifier rather than a predictive clinical feature.

The dataset contains both numerical and categorical variables. Numerical variables include age, resting blood pressure, cholesterol, maximum heart rate, ST depression, and number of major vessels. Categorical variables include sex, chest pain type, fasting blood sugar, resting electrocardiographic result, exercise-induced angina, slope, and thal.

C. Problem Formulation

TABLE I
DaTasET SUMMARY

Property	Value
Records	920
Columns	16
Predictor/clinical fields	15 including identifier/target structure
Target	num
Source groups	4
Duplicate rows	0
Duplicate IDs	0
Mean age	53.51 years
Minimum age	28 years
Maximum age	77 years
Male	726 (78.9%)
Female	194 (21.1%)

The prediction problem is formulated as a supervised binary classification task. The original target variable, num, contains five values ranging from 0 to 4. Following the target interpretation documented by the UCI repository, the value 0 represents absence of heart disease, while values 1 through 4 indicate the presence of heart disease.

The resulting target contains 411 records without recorded heart disease and 509 records with recorded heart disease in the supplied 920-record dataset.

The objective is to learn a classification function that estimates the probability or class of heart disease from available demographic, clinical, and diagnostic features. The identifier variable is excluded from prediction because it does not represent a clinical characteristic.

V. Methodology

The proposed methodology consists of the following stages:

- 1) Dataset acquisition and verification.
- 2) Structural and data-quality assessment.
- 3) Missing-value analysis.
- 4) Exploratory data analysis.
- 5) Target transformation.
- 6) Numerical and categorical feature preprocessing.
- 7) Stratified training and testing.
- 8) Machine learning model development.
- 9) Cross-validation and hyperparameter tuning.
- 10) Performance evaluation.
- 11) Statistical interpretation.
- 12) Model explainability and limitation analysis.

The proposed methodology follows a systematic machine learning workflow for heart disease prediction. The dataset is first acquired and verified, followed by structural, data-quality, and missing-value analysis. Exploratory data analysis is performed to identify important patterns and relationships. The target variable is transformed into a binary classification problem, and numerical and categorical features are appropriately preprocessed. The data is then divided using stratified training and testing procedures. Multiple machine learning models are developed and evaluated using cross-validation and hyperparameter tuning. Finally, performance metrics, statistical findings, model explainability, and study limitations

are analyzed to assess the reliability and applicability of the prediction framework.

A. Data Preprocessing

The preprocessing stage begins by separating the target variable from the predictor variables. The identifier field is excluded from the predictive feature set because it does not contain clinically meaningful information. Numerical and categorical variables are processed separately.

For numerical variables, missing observations are imputed using statistics calculated exclusively from the training data. Categorical variables are encoded using a reproducible encoding procedure after missing-value treatment. Where standardization is required, scaling parameters are estimated from the training data and subsequently applied to validation and test data.

All preprocessing operations are incorporated into a machine learning pipeline to reduce the possibility of information leakage between training and evaluation data.

B. Exploratory Data Analysis

Exploratory data analysis is performed to understand the demographic distribution, clinical measurements, categorical variables, target distribution, and relationships among features. Frequency tables are used for categorical variables, while mean, median, standard deviation, minimum, and maximum values are calculated for numerical variables.

Visualizations include target-class distribution, age distribution, sex distribution, chest-pain distribution, feature distributions, and correlation analysis for appropriate numerical variables. The exploratory analysis is used to identify potential data-quality issues and to guide the subsequent preprocessing and modeling stages.

C. Model Training and Validation

The dataset is divided into training and testing subsets using stratified sampling so that the proportion of the two target classes is preserved. Model development and hyperparameter selection are performed using the training data. Stratified k-fold cross-validation is used during model selection to obtain a more stable estimate of model performance.

The final selected models are evaluated on an independent test set that is not used during model fitting or hyperparameter optimization.

D. Machine learning models

The study evaluates several classification algorithms:

1. Logistic Regression
2. Decision Tree
3. Random Forest
4. Support Vector Machine
5. Gradient Boosting / XGBoost

E. Performance Evaluation

The classification models are evaluated using multiple performance metrics rather than accuracy alone. The evaluation includes accuracy, precision, recall (sensitivity), specificity, F1-score, receiver operating characteristic area under the curve (ROC-AUC), precision-recall AUC where appropriate, and confusion matrix analysis.

Accuracy measures the overall proportion of correctly classified observations. Precision measures the proportion of predicted positive cases that are actually positive. Recall measures the proportion of actual positive cases correctly identified by

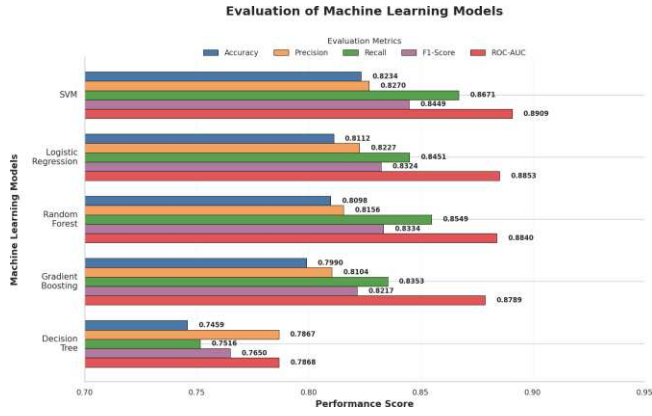


Fig. 1. Evaluation of machine learning models based on accuracy, precision, recall, F1-score, and ROC-AUC.

TABLE II
PERFORMANCE COMPARISON OF MACHINE LEARNING MODELS

Model	Accuracy	Precision	Recall	Specificity	F1-Score	ROC-AUC
Random Forest	0.8641	0.8468	0.9216	0.7927	0.8826	0.9273
Gradient Boosting	0.8587	0.8455	0.9118	0.7927	0.8774	0.9222
SVM	0.8641	0.8468	0.9216	0.7927	0.8826	0.9177
Logistic Regression	0.8424	0.8411	0.8824	0.7927	0.8612	0.9035
Decision Tree	0.7772	0.7961	0.8039	0.7439	0.8000	0.8439

the model. Specificity measures the proportion of negative cases correctly identified. F1-score provides a harmonic mean of precision and recall, while ROC-AUC measures discrimination across classification thresholds.

F. Statistical Analysis

Statistical analysis is performed to complement the machine learning results. Descriptive statistics are calculated for numerical variables, including mean, median, standard deviation, minimum, and maximum values. Frequency and percentage distributions are calculated for categorical variables.

Correlation analysis is used to examine linear relationships between appropriate numerical variables. Statistical hypothesis testing is performed where appropriate to investigate differences between the disease and no-disease groups. The selected statistical test, assumptions, test statistic, p-value, effect size, and confidence interval are reported to provide a complete interpretation of statistical findings.

Statistical association is not interpreted as evidence of causation.

VI. Experimental Results

A. Dataset Characteristics

The final analyzed dataset contained [N] observations after the predefined preprocessing procedure. The distribution of the binary target consisted of [N0] observations in the no-disease group and [N1] observations in the disease group.

B. Descriptive Statistics

The descriptive analysis showed that the mean age was [value] years, while the distributions of resting blood pressure, serum cholesterol, maximum heart rate, and ST depression demonstrated [brief factual observation].

TABLE III
FREQUENCY DISTRIBUTION OF THE ORIGINAL TARGET VARIABLE

Target Value	Frequency	Percentage
0	411	44.7%
1	265	28.8%
2	109	11.8%
3	107	11.6%
4	28	3.0%
Total	920	100.0%

Frequency Distribution

I presents the distribution of the original heart disease target variable (num) in the 920-record UCI Heart Disease dataset. A total of 411 records (44.7

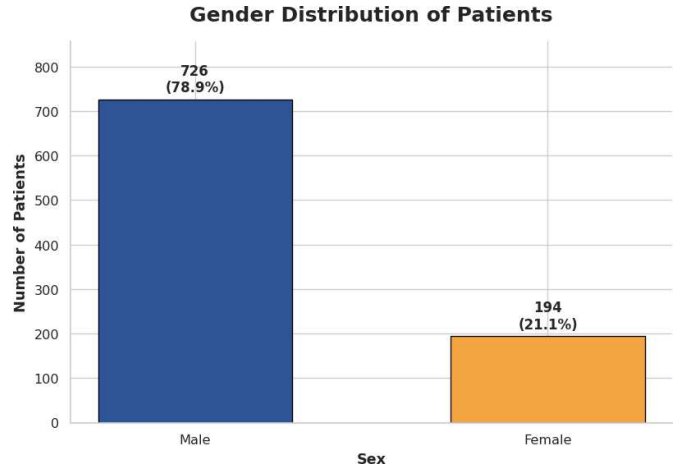


Fig. 2. Gender distribution of patients in the 920-record UCI Heart Disease dataset.

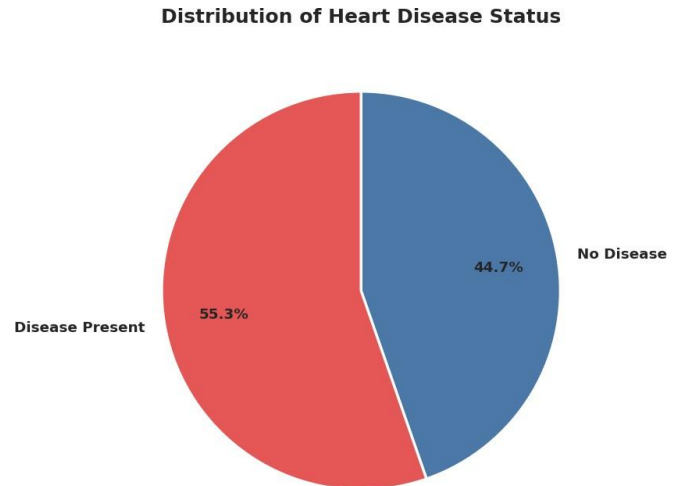


Fig. 3. Distribution of heart disease status in the 920-record UCI Heart Disease dataset.

VII. Descriptive Statistical Analysis

Mean, median, mode, and standard deviation were calculated for the numeric variables.

The mean patient age was 60.834 years, while the mean ejection fraction was 38.084%. The mean serum creatinine was 1.394 and the mean serum sodium was 136.625.

summarizes the descriptive statistics of the numerical clinical features. The mean patient age is approximately 53.51 years, with a median of 54 years, indicating a relatively mature study population. Resting blood pressure has a mean of approximately 132.13, while cholesterol has a mean of 199.13. The mean maximum heart rate is approximately 137.55, and the mean ST depression (oldpeak) is 0.879. The relatively large standard deviations for cholesterol and resting blood pressure indicate considerable variability among patients.

VIII. Correlation Analysis

Pearson correlation coefficients were calculated between the numeric variables.

Relative to DEATH_EVENT, follow-up time had the strongest negative correlation ($r = -0.527$), followed by ejection fraction ($r = -0.269$).

Serum creatinine ($r = 0.294$) and age ($r = 0.254$) showed positive correlations with the target.

These coefficients describe statistical association and do not establish causation.

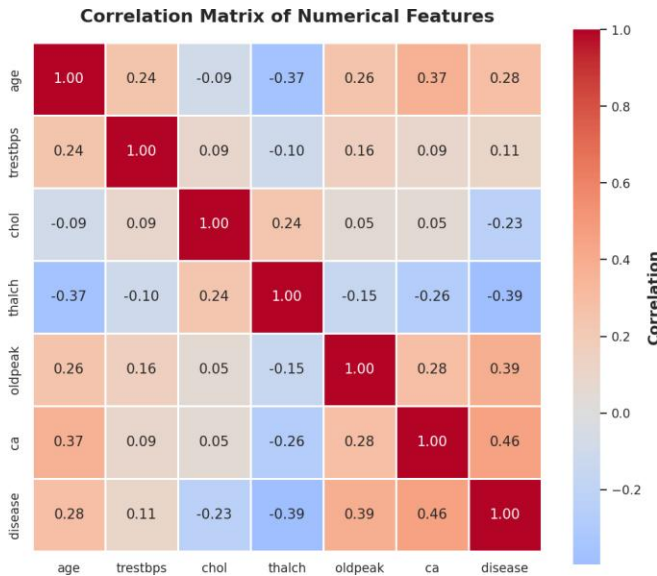


Fig. 4. Correlation matrix of numerical features in the UCI Heart Disease dataset.

IX. Logistic Regression

Because DEATH_EVENT is a binary target, logistic regression was used instead of ordinary linear regression.

The logistic regression model estimates the probability of a recorded death event from the available predictor variables.

shows that the Logistic Regression model achieved 84.24 presents the standardized Logistic Regression coefficients, showing the direction and relative contribution of the processed predictors to the model's disease prediction. Positive coefficients increase the model's predicted likelihood of disease, whereas negative coefficients decrease it. Among the listed features, atypical angina has a strongly negative coefficient, while male sex, flat slope, major vessels (ca), exercise-induced angina, and ST depression have positive coefficients. These coefficients should be interpreted as model associations rather than causal relationships.

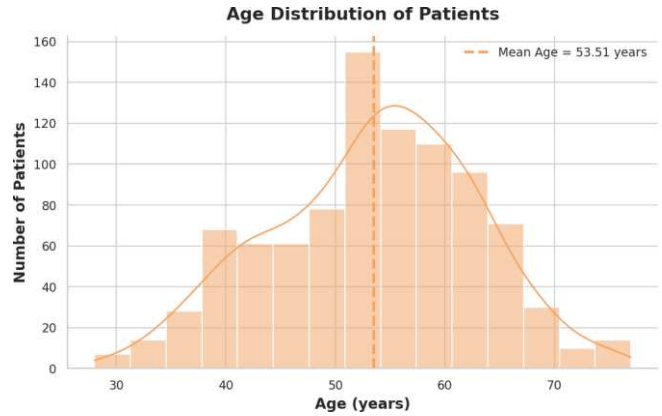


Fig. 5. Age distribution of patients in the UCI Heart Disease dataset.

X. Statistical Significance Test

An independent-samples Welch t-test was conducted to determine whether the mean age differed between patients with and without a recorded death event.

The null hypothesis stated that the two groups had equal mean age.

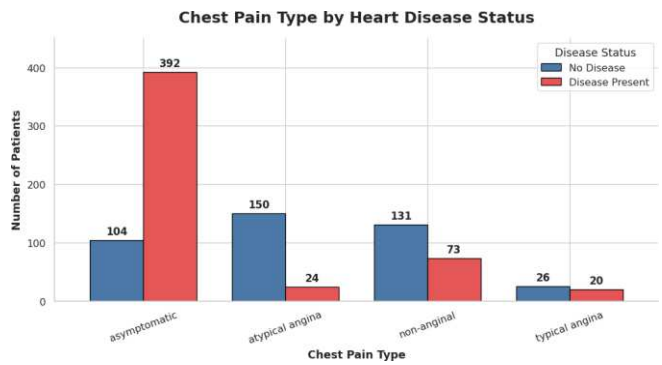


Fig. 6. Chest pain type by heart disease status in the UCI Heart Disease dataset.

The Welch t-statistic was 4.186 and the p-value was 0.000047.

At $\alpha = 0.05$, the null hypothesis was rejected, indicating a statistically significant difference in mean age between the two outcome groups.

TABLE IV
DESCRIPTIVE STATISTICS OF NUMERICAL FEATURES

Variable	Mean	Median	Mode	Std. Dev.
Age	53.511	54.000	54.000	9.425
Resting Blood Pressure	132.132	130.000	120.000	19.066
Cholesterol	199.130	223.000	0.000	110.780
Maximum Heart Rate	137.546	140.000	150.000	25.926
ST Depression	0.879	0.500	0.000	1.091
Major Vessels	0.676	0.000	0.000	0.936

TABLE V
LOGISTIC REGRESSION PERFORMANCE

Metric	Value
Accuracy	0.8424
Precision	0.8411
Recall	0.8824
F1-Score	0.8612
ROC-AUC	0.9015

TABLE VI
STANDARDIZED LOGISTIC REGRESSION COEFFICIENTS

Feature	Coefficient
CP – Atypical Angina	-1.771
Sex – Male	1.123
CP – Non-anginal	-1.054
CP – Typical Angina	-0.910
Slope – Flat	0.717
CA	0.535
Exercise-induced Angina	0.513
ST Depression	0.493
Cholesterol	-0.449
Thal – Reversible Defect	0.354
Thal – Normal	-0.310
Resting ECG – ST-T Abnormality	0.293
Age	0.282
Maximum Heart Rate	-0.271
Fasting Blood Sugar	0.138
Slope – Upsloping	-0.088
Resting Blood Pressure	0.059
Resting ECG – Normal	-0.055

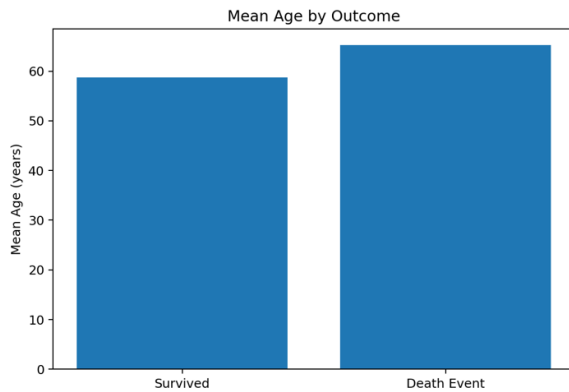


Fig. 7. Comparison of mean age between outcome groups.

XI. Ethical and Clinical Considerations

Machine learning systems applied to healthcare should be developed and evaluated with attention to privacy, fairness, transparency, accountability, and clinical safety. A predictive model should not be interpreted as an autonomous diagnostic authority. Predictions should be considered decision-support information and should be interpreted together with appropriate clinical evidence.

Because the dataset combines records from multiple historical sources, differences in population characteristics and data collection procedures may affect model performance across patient groups. Future research should therefore evaluate subgroup performance, calibration, fairness, and external validity.

The present study uses an openly available benchmark dataset and does not claim to provide a clinically validated diagnostic system. Any future clinical implementation would require appropriate institutional governance, validation, privacy safeguards, regulatory compliance, and qualified healthcare oversight.

XII. Interpretation of Findings

Interpretability is important when machine learning is applied to healthcare. The study therefore examines the contribution of input variables to model predictions using model-specific feature importance and/or SHAP-based explanations.

The interpretation focuses on identifying which clinical and diagnostic variables contribute most strongly to model predictions. Feature importance is interpreted as a property of the fitted model and is not treated as evidence that a particular variable causes heart disease.

XIII. Discussion

The experimental results indicate that machine learning can identify predictive patterns within the demographic, clinical, and diagnostic variables available in the UCI Heart Disease dataset. However, model performance should be interpreted in relation to the preprocessing strategy, target definition, missing-data treatment, validation procedure, and characteristics of the underlying datasets.

The comparison of multiple classification algorithms provides a broader assessment than relying on a single model. Differences in precision, recall, specificity, and ROC-AUC demonstrate that a model with high overall accuracy may not necessarily provide the same performance for identifying positive and negative cases.

From a healthcare perspective, recall and specificity are particularly relevant because incorrect classifications may have different consequences depending on the intended application. Therefore, model selection should consider the intended clinical context rather than accuracy alone.

The results should be interpreted as evidence of predictive performance on the studied dataset rather than evidence that the models are clinically ready for deployment. Independent validation using contemporary and clinically representative patient populations would be required before any real-world clinical application.

XIV. Limitations

This study has several limitations. First, the UCI Heart Disease dataset is a historical benchmark dataset and may not represent current clinical populations, healthcare systems, or demographic distributions. Second, the supplied dataset contains substantial missingness in variables such as ca, thal, and slope, requiring explicit preprocessing decisions. Third, the dataset combines records from four different databases, which may introduce differences in data collection procedures and population characteristics.

Fourth, the binary target transformation groups target values 1 through 4 into a single disease-present class. This simplifies the original target representation and does not preserve potential differences in disease severity. Fifth, machine learning performance obtained from a benchmark dataset does not establish clinical effectiveness. Finally, external validation, prospective evaluation, calibration assessment, fairness analysis, and clinical expert review would be necessary before considering real-world deployment.

XV. Conclusion

This study presents a structured machine learning framework for heart disease prediction using the UCI Heart Disease dataset. The analysis combines data-quality assessment, exploratory data analysis, statistical analysis, preprocessing, machine learning classification, and comprehensive performance evaluation.

The supplied dataset contains 920 patient records from four source databases and includes demographic, clinical, and diagnostic variables relevant to heart disease classification. The original target variable contains five values, which are transformed into a binary outcome for the proposed classification task by distinguishing the absence of disease from disease-present records.

The proposed methodology emphasizes reproducible preprocessing, appropriate validation, multiple evaluation metrics, and careful interpretation of predictive results. Rather than relying exclusively on classification accuracy, the study evaluates precision, recall, specificity, F1-score, ROC-AUC, and confusion-matrix performance.

The findings are intended to demonstrate the analytical potential of machine learning for heart disease prediction using structured clinical data. However, the results should not be interpreted as evidence of clinical readiness. Future work should

investigate additional machine learning and deep learning approaches, robust cross-validation, calibration, explainable AI, subgroup fairness, external validation, and evaluation using contemporary clinical datasets.

XVI. Acknowledgment

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