



# Prediction of Heart Disease Using Machine Learning Models

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## Abstract

Heart disease remains one of the leading causes of mortality worldwide, highlighting the need for accurate and interpretable prediction systems. This project investigates the use of supervised machine learning methods to classify the presence of heart disease using demographic and clinical features from the Kaggle *Heart Failure Prediction* dataset (918 observations, 12 variables). The analysis follows a structured workflow including exploratory data analysis, data preprocessing, feature standardisation, and systematic hyperparameter optimisation.

Two algorithms—Random Forest (RF) and Support Vector Machine (SVM) with an RBF kernel—were tuned via grid search and cross-validation. Model performance was evaluated using accuracy, sensitivity, specificity, F1-score, and the area under the ROC curve (AUC). The SVM achieved the strongest test performance (Accuracy = 0.891, AUC = 0.944), while the RF model performed competitively across most metrics.

Model interpretability was enhanced using permutation-based feature importance, which identified ECG- and exercise-related predictors such as ST Slope, Chest Pain Type, and Old peak as the most influential factors.

All code, analysis scripts, and generated results are openly available at:  
GitHub Repository.

# Contents

<b>1</b>	<b>Introduction</b>	<b>3</b>
<b>2</b>	<b>Literature Review</b>	<b>4</b>
<b>3</b>	<b>Descriptive Analysis of the Data</b>	<b>4</b>
3.1	Structure of the Training Data . . . . .	5
3.2	Feature Description . . . . .	6
3.3	Distributions of Numeric Variables . . . . .	7
3.4	Class Balance . . . . .	7
3.5	Distributions of Categorical Variables . . . . .	8
3.6	Numeric Variables vs. Heart Disease . . . . .	8
3.7	Categorical Variables vs. Heart Disease . . . . .	9
3.8	Correlation Between Numeric Predictors . . . . .	9
3.9	Scatter Plots of Numeric Predictors vs. Age . . . . .	10
3.10	Smoothed Trend Between Age and MaxHR . . . . .	10
3.11	Scatter Plot of MaxHR vs. Oldpeak by Sex . . . . .	11
3.12	Statistical Hypothesis Testing of Feature Differences . . . . .	11

<b>4 Mathematical Overview of Machine Learning Methods</b>	<b>12</b>
4.1 Random Forests . . . . .	12
4.2 Support Vector Machines . . . . .	14
<b>5 Model Training, Tuning, and Diagnostics</b>	<b>16</b>
5.1 Hyperparameter search space . . . . .	17
5.2 Hyperparameter Tuning Results . . . . .	17
5.3 Hyperparameter Tuning Visualisation . . . . .	18
5.4 Training–Validation Diagnostics . . . . .	19
<b>6 Model Evaluation</b>	<b>20</b>
6.1 Decision Threshold Selection . . . . .	20
6.2 Evaluation Metrics . . . . .	21
6.3 Confusion Matrices . . . . .	22
6.4 ROC Curves . . . . .	23
6.5 Final Train–Test Evaluation . . . . .	24
<b>7 Interpretation of the Trained Models Using XAI Techniques</b>	<b>25</b>
7.1 Global Importance Structure . . . . .	25
7.2 Agreement Between RF and SVM . . . . .	25
7.3 Summary of Feature Contributions . . . . .	25
7.4 Limitations of Global Feature Importance . . . . .	26
7.5 Overall Interpretation . . . . .	26
<b>8 Conclusion</b>	<b>26</b>

## List of Figures

1 Histograms of numeric features in the training data. . . . .	7
2 Proportion of HeartDisease classes in the training data. . . . .	7
3 Bar plots of categorical predictors. . . . .	8
4 Numeric predictors separated by heart disease outcome. . . . .	8
5 Proportions of heart disease within each category. . . . .	9
6 Correlation matrix of numeric predictors. . . . .	9
7 Scatter plots of Age versus key numeric predictors. . . . .	10
8 LOESS smoothing of Age vs. MaxHR. . . . .	10
9 Scatter plot of MaxHR vs. Oldpeak, faceted by Sex. . . . .	11
10 Illustration of a Random Forest: many decision trees trained on bootstrap samples, with predictions aggregated by averaging. . . . .	13
11 Geometric interpretation of the SVM classifier showing the maximal margin hyperplane and support vectors. . . . .	15

12	Complete hyperparameter tuning visualisation for Random Forest and SVM models. Colours represent cross-validated ROC performance across all evaluated hyperparameter combinations. . . . .	19
13	Training vs. validation accuracy for RF and SVM. . . . .	19
14	Confusion matrices for Random Forest and SVM on the training and test sets. . . . .	22
15	ROC curves for Random Forest and SVM on the test set. . . . .	23
16	Comparison of key performance metrics (Accuracy, Sensitivity, Specificity, Precision, F1, and AUC) for Random Forest and SVM on the test set. . .	24
17	Permutation feature importance for RF and SVM models. . . . .	26

## List of Tables

1	Feature Description Based on the Raw CSV Data . . . . .	6
2	Hyperparameter search spaces used for grid search in Random Forest and SVM models. . . . .	17
3	Sample rows from the Random Forest hyperparameter tuning grid. . . .	18
4	Sample rows from the SVM (RBF kernel) hyperparameter tuning grid. .	18
5	Training and validation metrics for RF and SVM (rounded to 4 decimals). .	20
6	Optimal decision thresholds selected using Youden's index. . . . .	20
7	Training performance metrics for Random Forest and SVM. Bold values indicate the higher value between the two models. . . . .	24
8	Test performance metrics for Random Forest and SVM. Bold values indicate the higher value between the two models. . . . .	24

## 1 Introduction

Cardiovascular disease is the leading cause of mortality worldwide, making early and accurate risk prediction an important component of modern clinical decision support. Machine learning (ML) techniques provide effective tools for analysing complex patient profiles and identifying patterns that traditional statistical methods may not capture. This study develops and compares ML models for predicting whether a patient has heart disease using demographic and clinical variables.

The target variable, Heart Disease, indicates the presence or absence of heart disease. The predictors include demographic attributes such as Age and Sex, as well as clinical measurements including Chest Pain Type, Resting BP, Cholesterol, Max HR, Exercise Angina, Old peak, and ST Slope. These variables are commonly used in cardiovascular assessment and stress-test analysis.

The data originate from the Heart Failure Prediction dataset on Kaggle (fedesoriano), which is publicly available at [Dataset Link](#).

It contains 918 observations and 12 features with no missing values. The dataset integrates clinical, ECG, and exercise-related measurements, making it a widely used benchmark for machine-learning classification tasks.

The dataset was divided into training (60%), validation (20%), and test (20%) subsets. Two supervised learning algorithms, Random Forest (RF) and Support Vector Machine (SVM) with a radial basis function (RBF) kernel, were trained and tuned using cross-validation and grid search. A comprehensive exploratory data analysis was conducted beforehand to examine feature distributions and relationships.

This project aims to build accurate ML models for heart-disease prediction, evaluate their performance using standard classification metrics, compare their generalisation ability on unseen data, and identify the most influential clinical variables contributing to the predictions. The overall goal is to develop interpretable and reliable models that can support clinical decision-making and provide insight into important risk factors for cardiovascular disease.

## 2 Literature Review

Machine learning has become an essential tool for predicting heart disease because of its ability to uncover complex, nonlinear relationships in clinical data. A number of studies have demonstrated that supervised learning algorithms—such as Support Vector Machines (SVM), Random Forests (RF), Logistic Regression, and boosting-based ensemble methods—achieve strong performance on standard cardiovascular datasets. Kumar et al. [1] provide a comprehensive review showing that ML approaches consistently outperform traditional statistical methods for heart-disease risk assessment. Similarly, Ekle et al. [2] compared multiple supervised models and reported that tree-based ensembles and SVM are the most reliable classifiers across datasets such as Cleveland, Statlog, and Framingham. Hossain et al. [3] found that Random Forest achieved the highest accuracy and robustness compared to decision trees, Naive Bayes, and logistic regression on a clinical heart-disease dataset. Other comparative studies—including Rimal et al. [4] and Baxani and Edinburgh [5]—also show that SVM and RF consistently rank among the top-performing models for heart-disease prediction, particularly when combined with systematic feature preprocessing and cross-validation. Overall, the literature strongly supports the use of RF and SVM models, aligning with the modelling choices adopted in this study.

## 3 Descriptive Analysis of the Data

This section provides a descriptive and statistical overview of the variables in the Heart Failure Prediction dataset. We summarise the structure of the data and provide a detailed description of each feature included in the modelling process. These insights guide the

modelling choices and help identify predictors likely to hold discriminatory value.

### 3.1 Structure of the Training Data

The dataset contains 918 observations and 12 variables, consisting of six numeric and five categorical predictors, along with the binary target variable Heart Disease. Among the 918 samples, 410 patients are labelled 0 (no heart disease) and 508 are labelled 1 (heart disease), which indicates a mild class imbalance but still allows for reliable model training. No missing values were found in the dataset.

Several categorical variables in the raw data are encoded as text labels rather than numeric values. For example, Sex is represented as M/F and Chest Pain Type includes categories such as ATA, NAP, ASY, and TA. While this improves human readability, these variables require conversion to numerical form (e.g., one-hot or ordinal encoding) prior to modelling. A detailed overview of each feature, including its data type and meaning in the raw CSV file, is provided in Table 1.

All numeric variables were standardised using the  $z$ -score transformation:

$$z = \frac{x - \mu}{\sigma},$$

where  $\mu$  and  $\sigma$  denote the mean and standard deviation of each feature. This standardisation ensures that all numeric predictors contribute comparably during model fitting, particularly benefiting algorithms such as SVM that rely on distance or kernel computations.

### 3.2 Feature Description

Table 1: Feature Description Based on the Raw CSV Data

No.	Feature	Data Type	Description (as in CSV)
1	Age	Numeric	Patient's age in years.
2	Sex	Nominal	Sex of the patient: M = Male, F = Female.
3	ChestPainType	Nominal	Chest pain type: ATA = Atypical angina, NAP = Non-anginal pain, ASY = Asymptomatic, TA = Typical angina.
4	RestingBP	Numeric	Resting blood pressure (mm/Hg).
5	Cholesterol	Numeric	Serum cholesterol level (mg/dl).
6	FastingBS	Nominal	Fasting blood sugar: 0 = $\leq 120$ mg/dl, 1 = $> 120$ mg/dl.
7	RestingECG	Nominal	Resting ECG results: Normal, ST = ST-T wave abnormality, LVH = Left ventricular hypertrophy.
8	MaxHR	Numeric	Maximum heart rate achieved.
9	ExerciseAngina	Nominal	Exercise-induced angina: Y = Yes, N = No.
10	Oldpeak	Numeric	ST depression induced by exercise relative to rest.
11	ST_Slope	Nominal	Slope of peak exercise ST segment: Up = Upsloping, Flat = Flat, Down = Downsloping.
Target Variable			
12	HeartDisease	Nominal	1 = Heart disease present, 0 = No heart disease.

### 3.3 Distributions of Numeric Variables

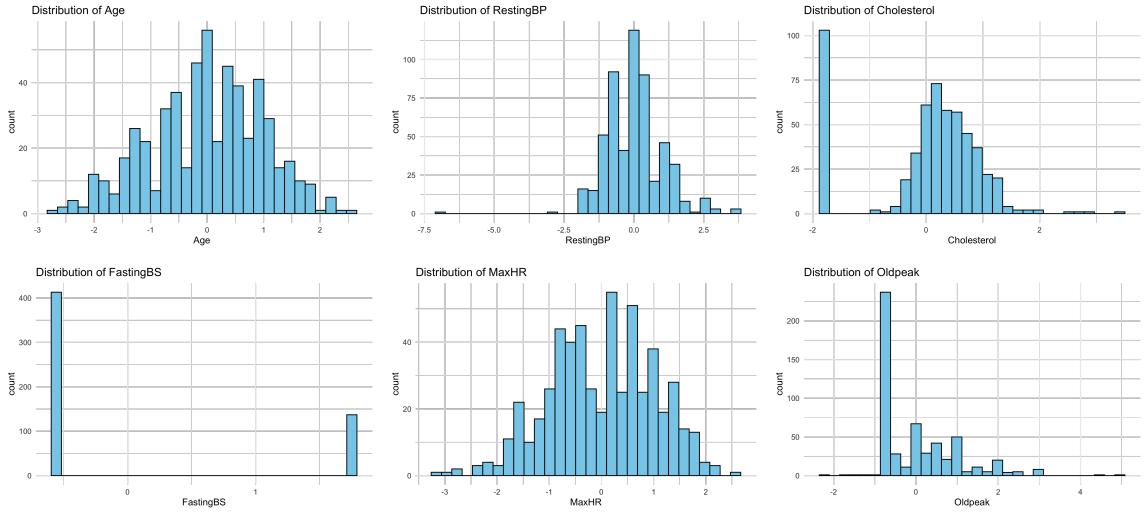


Figure 1: Histograms of numeric features in the training data.

The numeric variables show different distribution shapes. Age and Max HR follow smooth, unimodal distributions. Resting BP, Cholesterol, and Old peak display clear right-skewness, including some high-value outliers. Fasting BS behaves as a binary variable with two peaks. These differences in skewness and scale support the use of standardisation before model training.

### 3.4 Class Balance

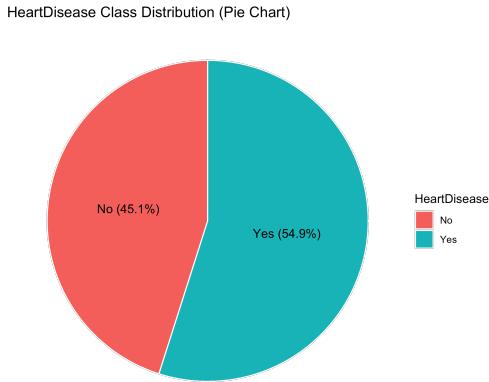


Figure 2: Proportion of HeartDisease classes in the training data.

The two outcome classes are well balanced, reducing the risk of biased model learning and eliminating the need for class imbalance correction techniques. This balance also means that both classes are equally represented in the plots, making visual patterns and group comparisons easier to interpret. It further ensures that the models do not favour one class simply due to its frequency.

### 3.5 Distributions of Categorical Variables

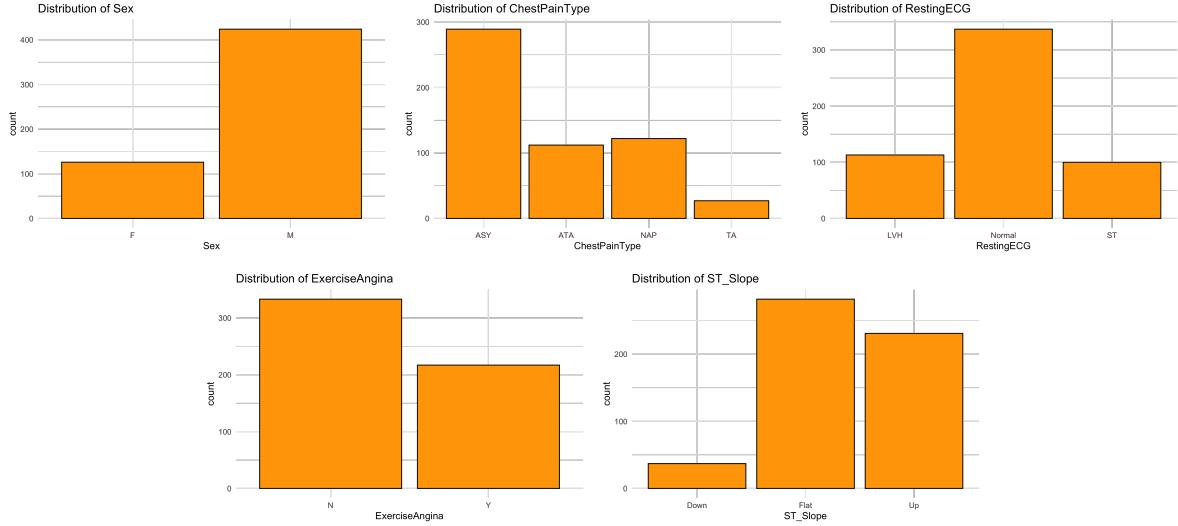


Figure 3: Bar plots of categorical predictors.

Most patients are male, have asymptomatic chest pain ASY, and show a normal resting ECG. A large majority present a flat ST Slope, a pattern consistent with typical clinical heart disease datasets.

### 3.6 Numeric Variables vs. Heart Disease

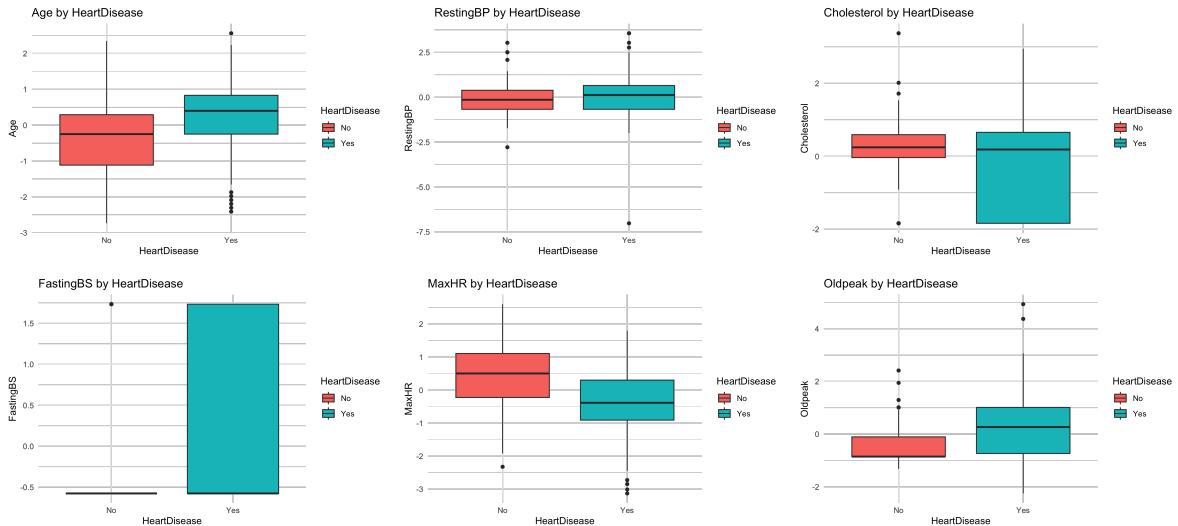


Figure 4: Numeric predictors separated by heart disease outcome.

Patients with heart disease are generally older, show lower Max HR, and exhibit substantially higher Old peak. Fasting BS equals 1 more often among the disease group. Differences in Resting BP and Cholesterol are weaker but still visible.

### 3.7 Categorical Variables vs. Heart Disease

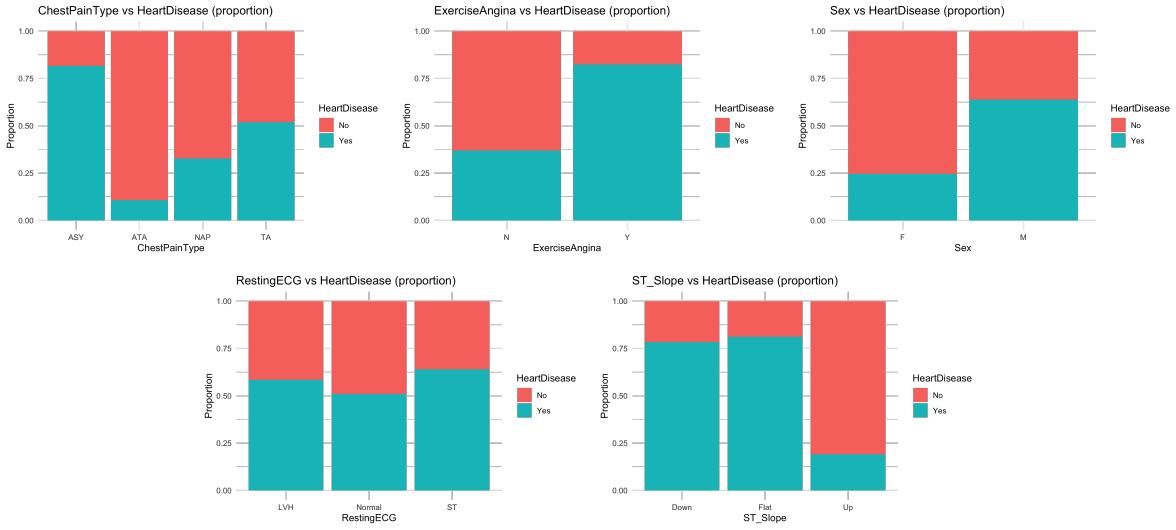


Figure 5: Proportions of heart disease within each category.

Chest Pain Type shows the strongest categorical separation. Exercise-induced angina and downward or flat ST slopes are also strongly associated with heart disease, whereas Resting ECG shows little differentiation.

### 3.8 Correlation Between Numeric Predictors

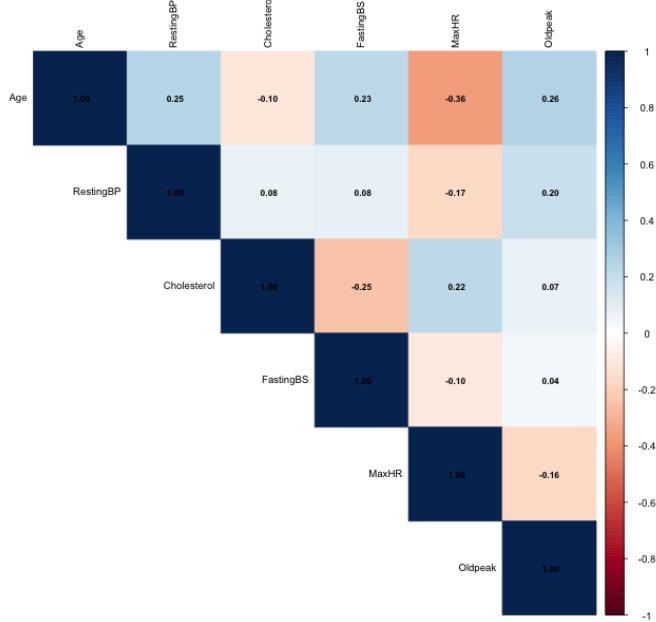


Figure 6: Correlation matrix of numeric predictors.

Overall, the correlation matrix shows that the numeric predictors are mostly weakly related to one another. The only noticeable pattern is the expected negative relationship between Age and Max HR, reflecting that older patients usually reach lower maximum heart rates.

There is also a mild positive relationship between Age and Old peak, indicating slightly higher exercise-induced ST depression in older individuals.

All other variable pairs show minimal or no linear association, meaning that each numeric feature contributes largely independent information to the modelling process.

### 3.9 Scatter Plots of Numeric Predictors vs. Age

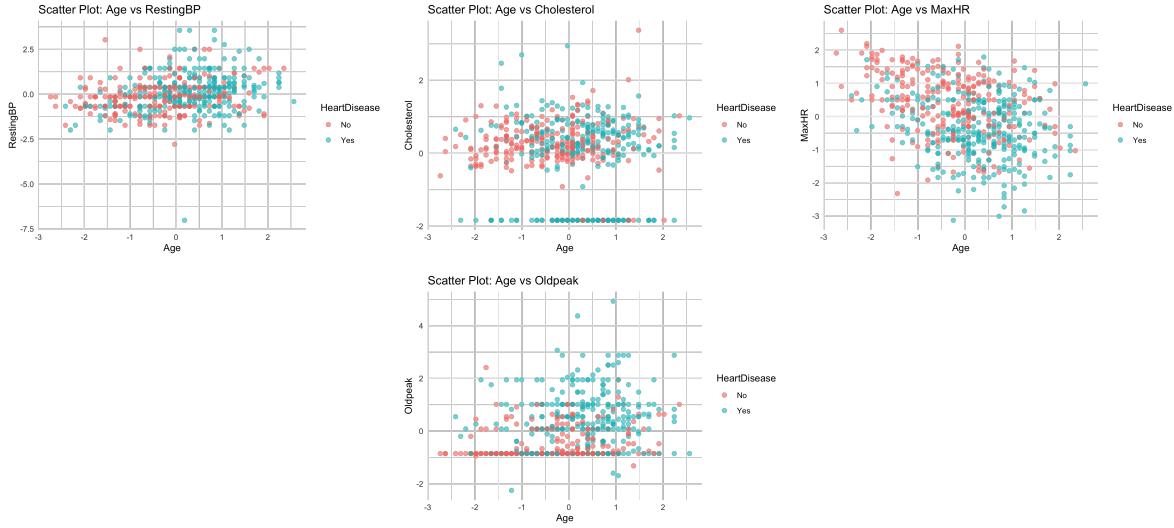


Figure 7: Scatter plots of Age versus key numeric predictors.

A strong negative trend is observed between Age and Max HR, while older patients tend to show higher Old peak. Other variables show no meaningful age-related structure. These patterns agree with clinical expectations: maximum heart rate naturally declines with age, and exercise-induced ST depression Old peak often becomes more pronounced in older individuals. Overall, the plots suggest that age plays an important role mainly through its relationship with exercise-related measures, rather than through resting clinical variables.

### 3.10 Smoothed Trend Between Age and MaxHR

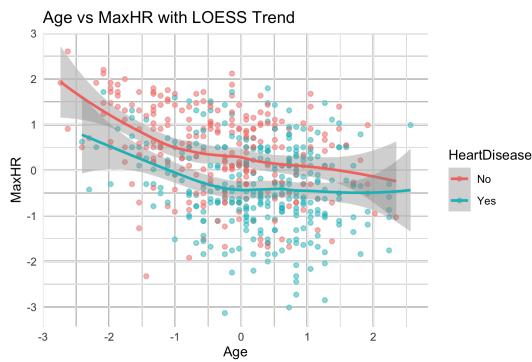


Figure 8: LOESS smoothing of Age vs. MaxHR.

The LOESS curve confirms a smooth decline in Max HR with age. Across all ages, patients with heart disease tend to have consistently lower Max HR. This pattern suggests that reduced heart performance during exercise is strongly linked to disease presence. The smooth trend also indicates that the relationship is stable and not driven by a few extreme values. Overall, the plot highlights Max HR as an important indicator of cardiovascular health.

### 3.11 Scatter Plot of MaxHR vs. Oldpeak by Sex

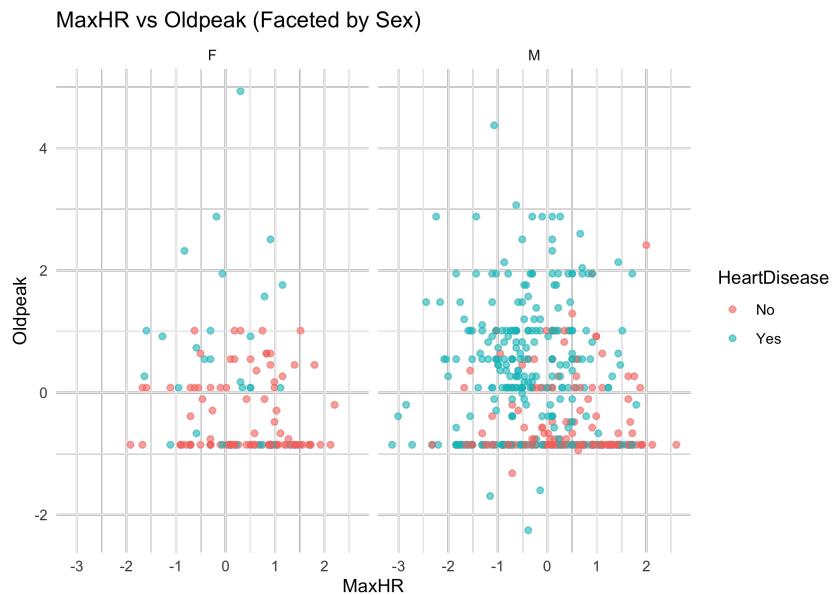


Figure 9: Scatter plot of MaxHR vs. Oldpeak, faceted by Sex.

Male patients exhibit a wider spread in Max HR and tend to show higher Old peak values. A dense cluster of low Max HR and high Old peak is strongly associated with heart disease, particularly among men.

### 3.12 Statistical Hypothesis Testing of Feature Differences

To validate the visual patterns, statistical tests were used to assess whether each feature differs between patients with and without heart disease. Numeric variables were tested using Welch's two-sample  $t$ -test, and categorical variables using the chi-square test of independence. All tests used a 5% significance level ( $\alpha = 0.05$ ) with 95% confidence intervals.

#### Numeric Variables

All numeric features differ significantly between groups:

- Age: Higher for disease patients ( $p < 10^{-11}$ ).
- Resting BP: Slightly higher in the disease group ( $p = 0.002$ ).
- Cholesterol: Higher for non-disease patients ( $p < 10^{-6}$ ).

- Fasting BS: Higher in the disease group ( $p < 10^{-8}$ ).
- Max HR: Markedly lower for disease patients ( $p \approx 0$ ).
- Old peak: Markedly higher for disease patients ( $p \approx 0$ ).

## Categorical Variables

Most categorical features show strong associations with heart disease:

- Sex: Significant association ( $p < 10^{-14}$ ).
- Chest Pain Type: Very strong relationship ( $p \approx 0$ ).
- Exercise Angina: Highly significant ( $p \approx 0$ ).
- ST Slope: Strongest association among categorical variables ( $p \approx 0$ ).
- Resting ECG: Not significant ( $p = 0.051$ ).

Both the descriptive visualisations and the statistical tests highlight clear and clinically meaningful differences between patients with and without heart disease. Exercise-related variables—Max HR, Old peak, ST Slope, and Exercise Angina—show the strongest separation and are therefore expected to be important predictors in the subsequent modelling steps. In contrast, Resting ECG shows no significant difference between groups. These findings provide a strong empirical foundation for the machine learning models developed in the following sections.

## 4 Mathematical Overview of Machine Learning Methods

This section provides a formal mathematical description of the two supervised learning methods used in this study: Random Forests and Support Vector Machines (SVMs). The presentation emphasizes the optimisation principles, underlying assumptions, and decision functions that govern both models.

### 4.1 Random Forests

Random Forests (RF), introduced by Breiman [10], are an ensemble method consisting of a large number of decision trees trained on bootstrap samples of the data. Their strength lies in variance reduction through aggregation and the ability to capture nonlinear feature interactions.

## Node impurity and optimal splitting

Let the dataset be

$$\mathcal{D} = \{(x_i, y_i)\}_{i=1}^n, \quad x_i \in \mathbb{R}^p, y_i \in \{0, 1\}.$$

At each node of a decision tree, the algorithm searches over a subset of features (`mtry`) and possible thresholds to find the split that minimises impurity. For classification, a common impurity measure is the Gini impurity:

$$G(t) = \sum_{k=0}^1 \hat{p}_{k,t}(1 - \hat{p}_{k,t}), \quad \hat{p}_{k,t} = \frac{1}{N_t} \sum_{i \in t} \mathbf{1}(y_i = k).$$

An alternative and scientifically equivalent impurity measure is the entropy (used in information gain-based tree algorithms):

$$H(t) = - \sum_{k=0}^1 \hat{p}_{k,t} \log \hat{p}_{k,t}.$$

Both Gini and entropy quantify node impurity and typically lead to very similar splits, with Gini being slightly faster to compute.

The optimal split  $(j^*, s^*)$  solves

$$(j^*, s^*) = \arg \min_{j,s} \left[ \frac{N_{\text{left}}}{N_t} I(R_{\text{left}}(j, s)) + \frac{N_{\text{right}}}{N_t} I(R_{\text{right}}(j, s)) \right],$$

where  $I(\cdot)$  denotes the chosen impurity measure (Gini or entropy).

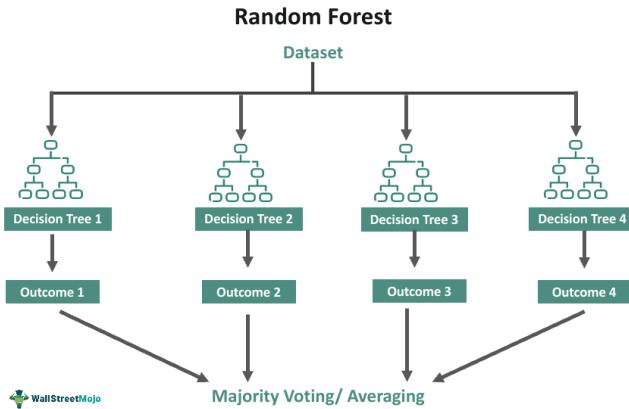


Figure 10: Illustration of a Random Forest: many decision trees trained on bootstrap samples, with predictions aggregated by averaging.

## Bootstrap aggregation (bagging)

Each tree is trained on a bootstrap sample of size  $n$ :

$$\mathcal{D}_b \sim \text{SampleWithReplacement}(\mathcal{D}, n).$$

Random feature selection additionally decorrelates trees, improving ensemble stability.

## Ensemble decision rule

Let  $T_b(x)$  denote the predicted probability from tree  $b$ . For  $B$  trees, the RF estimator is

$$\hat{p}_{RF}(y = 1 \mid x) = \frac{1}{B} \sum_{b=1}^B T_b(x).$$

The class prediction is

$$\hat{y}(x) = \begin{cases} 1 & \text{if } \hat{p}_{RF}(x) > \tau, \\ 0 & \text{otherwise,} \end{cases}$$

where  $\tau$  is a probability threshold (tuned in this project using Youden's index).

Random Forests excel in capturing nonlinear structure and interactions while maintaining robustness against noise and overfitting.

## 4.2 Support Vector Machines

Support Vector Machines (SVMs) [12] construct a decision boundary that maximizes the margin between two classes. Only a subset of the training points, the *support vectors*, determine the optimal boundary.

### Hard-margin optimisation

For linearly separable data, the SVM solves

$$\min_{w,b} \frac{1}{2} \|w\|^2$$

subject to

$$y_i(w^\top x_i + b) \geq 1.$$

The margin equals  $2/\|w\|$ , so minimizing the norm of  $w$  maximizes the distance between the supporting hyperplanes, yielding the maximal margin classifier.

### Soft-margin formulation

Real-world data are rarely perfectly separable. Introducing slack variables  $\xi_i \geq 0$  allows controlled margin violations:

$$\min_{w,b,\xi} \frac{1}{2} \|w\|^2 + C \sum_{i=1}^n \xi_i$$

subject to

$$y_i(w^\top x_i + b) \geq 1 - \xi_i, \quad \xi_i \geq 0.$$

The parameter  $C > 0$  regulates the trade-off between maximizing the margin and

penalizing violations.

**Effect of the margin parameter  $C$  and slack variables  $\xi_i$ .** The slack variables quantify the degree of constraint violation:

$$\xi_i = \begin{cases} 0 & \text{correctly classified and outside the margin,} \\ 0 < \xi_i < 1 & \text{inside the margin but correctly classified,} \\ \xi_i > 1 & \text{misclassified.} \end{cases}$$

A large value of  $C$  imposes a high penalty on non-zero  $\xi_i$ , encouraging a narrow margin and a solution close to the hard-margin classifier. This prioritizes minimizing training errors but may overfit in noisy scenarios. In contrast, a small  $C$  tolerates larger slack values, producing a wider margin that can improve generalization by reducing sensitivity to outliers and label noise. This interpretation aligns with the regularization view of SVMs.

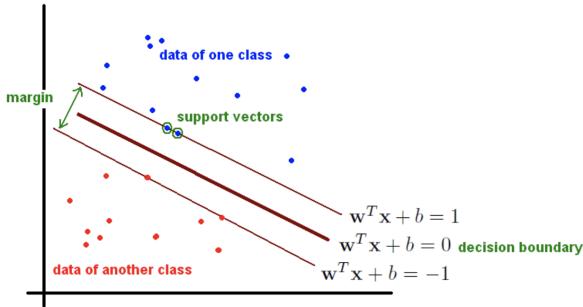


Figure 11: Geometric interpretation of the SVM classifier showing the maximal margin hyperplane and support vectors.

### Kernel-based nonlinear decision functions

Although the SVM is inherently a linear classifier, nonlinear decision boundaries can be constructed using kernel functions  $K(x, z)$ , which implicitly map the data to a high-dimensional feature space.

A widely used choice is the radial basis function (RBF) kernel:

$$K(x, z) = \exp(-\gamma \|x - z\|^2),$$

where  $\gamma$  controls the width of the Gaussian basis and thus the smoothness of the decision boundary.

In the dual representation, the SVM decision function is

$$f(x) = \sum_{i=1}^n \alpha_i y_i K(x_i, x) + b,$$

where  $\alpha_i$  are Lagrange multipliers. Only support vectors satisfy  $\alpha_i > 0$ , so inference depends on a subset of training points. The kernel mapping enables SVMs to model complex, curved boundaries in the original feature space while retaining convex optimisation in the dual problem.

## 5 Model Training, Tuning, and Diagnostics

Before model fitting, all numeric predictors were standardised to have mean 0 and unit variance, while categorical variables were encoded as factors. The dataset was split into training (60%), validation (20%), and test (20%) sets. All tuning procedures were performed on the training set only, and the validation set was used for intermediate model comparison prior to final testing.

Both Random Forest and SVM models were trained using the `caret` package, which provides a unified interface for model training, resampling, and hyperparameter tuning. To obtain robust performance estimates, cross-validation was used during tuning: 5-fold cross-validation for Random Forest and 5-fold cross-validation for SVM. This reduces variance in performance estimates and helps prevent overfitting to any particular partition of the data.

Hyperparameter tuning was carried out using an exhaustive grid search. For each model, a predefined grid of hyperparameter combinations was evaluated, and each configuration was trained and assessed using cross-validation. Performance was measured using the area under the ROC curve (AUC), which provides a threshold-independent measure of classification quality and is particularly suitable for balanced binary outcomes such as this dataset.

The best model configuration was selected based on the highest cross-validated AUC. Secondary metrics such as accuracy, sensitivity, and specificity were also monitored to ensure models performed well across different evaluation criteria. Once tuning was complete, the optimal hyperparameters were used to fit a final model on the combined training and validation data. This final model was then evaluated on the held-out test set, ensuring an unbiased estimate of generalisation performance.

Diagnostic plots—such as confusion matrices, ROC curves, and training vs. validation accuracy comparisons—were used to assess whether the final models exhibited signs of overfitting or underfitting. Both models demonstrated consistent performance between training and validation sets, indicating well-controlled variance and good generalisation.

## 5.1 Hyperparameter search space

Table 2 summarises the complete hyperparameter grids used during the tuning of the Random Forest and SVM (RBF kernel) models. The Random Forest models were tuned using 5-fold cross-validation, while the SVM models were tuned using 5-fold cross-validation.

Model	Hyperparameter	Values Explored
Random Forest	mtry	{1, 2, 3, 4, 5, 6, 7, 8, 9, 10}
	min.node.size	{1, 2, 3, 4, 5, 10, 15, 20}
	splitrule	{gini, extratrees, hellinger}
SVM (RBF)	Cost (C)	{1, 5, 10, 20, 50, 100, 200, 500, 1000}
	sigma ( $\sigma$ )	{0.0001, 0.001, 0.005, 0.01}

Table 2: Hyperparameter search spaces used for grid search in Random Forest and SVM models.

The Random Forest grid consisted of

$$10 \times 8 \times 3 = 240$$

hyperparameter combinations, resulting from all possible choices of `mtry`, `min.node.size`, and `splitrule`. The SVM grid included

$$9 \times 4 = 36$$

combinations of cost values and kernel width parameters. Each combination was evaluated using the respective cross-validation scheme, and the configuration with the highest ROC value was selected for final model training.

## 5.2 Hyperparameter Tuning Results

The full hyperparameter grids for both Random Forest (RF) and Support Vector Machine (SVM) models contain a large number of evaluated configurations. To illustrate their structure, representative sample rows from the grid search are presented below. These samples show how performance metrics such as ROC and Accuracy vary across different combinations of tuning parameters. The ellipsis (...) indicates that additional configurations were evaluated during cross-validation.

mtry	min.node.size	ROC	Accuracy
1	5	0.9208	0.7890
2	5	0.9204	0.7985
3	10	0.9198	0.7937
5	5	0.9185	0.7850
8	15	0.9174	0.7810
:	:	:	:

Table 3: Sample rows from the Random Forest hyperparameter tuning grid.

Cost (C)	Sigma	ROC	Accuracy
1	0.0001	0.9162	0.8020
5	0.0001	0.9167	0.8267
50	0.0001	0.9223	0.8147
10	0.001	0.9208	0.8093
20	0.001	0.9214	0.8120
:	:	:	:

Table 4: Sample rows from the SVM (RBF kernel) hyperparameter tuning grid.

These tables demonstrate the variability in model performance across the grid search and highlight the types of parameter combinations that yield higher ROC scores. However, they provide only a partial view of the complete tuning landscape. To better understand how performance behaves across all evaluated hyperparameter combinations, a visualisation of the full grid search is presented next.

### 5.3 Hyperparameter Tuning Visualisation

While the sample rows illustrate individual tuning outcomes, they do not fully reflect the structure of the entire search space. Figure 12 therefore provides heatmap visualisations of the full tuning surfaces for both models.

The Random Forest heatmap (left) shows that ROC performance is stable across a wide range of `mtry` and `min.node.size` values, indicating that the model is generally robust to moderate changes in its hyperparameters. By contrast, the SVM heatmap (right) reveals a more concentrated high-performance region, with the best results observed for moderate  $C$  values and smaller  $\sigma$ , reflecting the greater sensitivity of SVMs to these parameters.

Overall, the heatmaps confirm that the selected hyperparameters lie within strong, well-performing regions of the search space for both models.

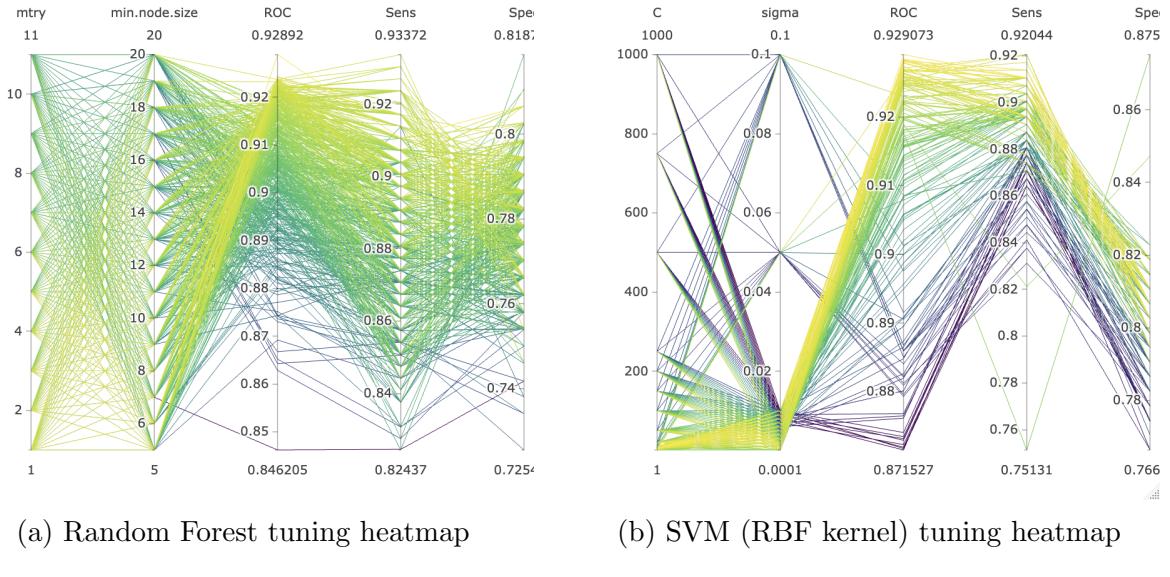


Figure 12: Complete hyperparameter tuning visualisation for Random Forest and SVM models. Colours represent cross-validated ROC performance across all evaluated hyperparameter combinations.

## 5.4 Training–Validation Diagnostics

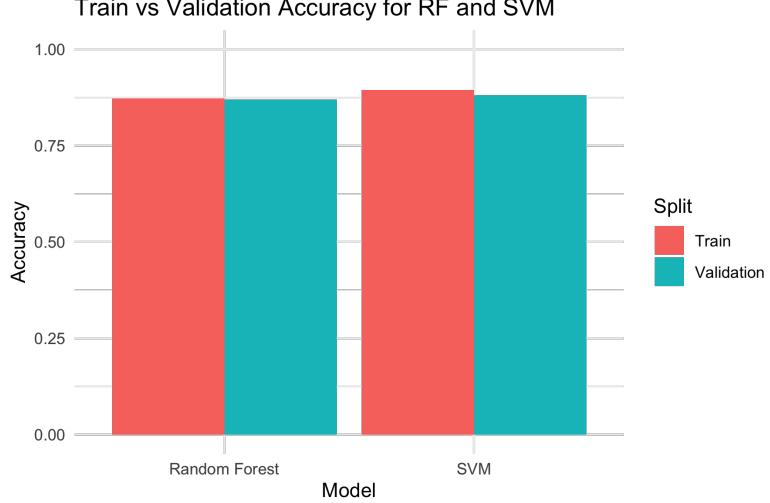


Figure 13: Training vs. validation accuracy for RF and SVM.

Figure 13 provides a visual comparison of training and validation accuracy for both the Random Forest and SVM models. In both cases, the training and validation bars lie very close to each other, indicating that neither model exhibits a large generalisation gap. This suggests that overfitting is limited and that both models maintain stable predictive behaviour on unseen data. The slightly higher accuracy of the SVM is already visible in the plot, although the difference is modest.

To provide a more detailed quantitative view, Table 5 summarises the main performance

metrics—Accuracy, Sensitivity, Specificity, Precision, F1, and AUC—on both the training and validation sets, derived from the CSV summary.

Dataset	Accuracy	Sensitivity	Specificity	Precision	F1	AUC
Train_RF	0.8727	0.9272	0.8065	0.8537	0.8889	0.9332
Val_RF	0.8696	0.8981	0.8289	0.8818	0.8899	0.9204
Train_SVM	0.8945	0.9338	0.8468	0.8813	0.9068	0.9479
Val_SVM	0.8804	0.8889	0.8684	0.9057	0.8972	0.9247

Table 5: Training and validation metrics for RF and SVM (rounded to 4 decimals).

The numerical metrics corroborate the conclusions drawn from the accuracy plot. Training and validation performance remain closely aligned across all metrics for both models, reinforcing the observation that neither RF nor SVM suffers from substantial overfitting. The SVM achieves slightly higher accuracy and AUC, while the Random Forest shows marginally higher sensitivity on the training set. Overall, both models demonstrate strong and balanced discrimination performance.

## 6 Model Evaluation

This section presents the full evaluation of the Random Forest (RF) and Support Vector Machine (SVM) models. We describe the threshold selection method, define the evaluation metrics, and compare model performance using confusion matrices, ROC curves, and final train–test results.

### 6.1 Decision Threshold Selection

Although a default cutoff of 0.5 is common in binary classification, it does not always maximise predictive performance. Therefore, thresholds were selected using Youden’s index:

$$J = \text{Sensitivity} + \text{Specificity} - 1.$$

Model	Optimal Threshold
Random Forest	0.4886
SVM (RBF)	0.4957

Table 6: Optimal decision thresholds selected using Youden’s index.

These thresholds were used for all final predictions and confusion matrices. Applying model-specific thresholds ensures a better balance between false positives and false negatives, which is particularly important in medical diagnosis. We use Youden’s index because it selects the cutoff that jointly maximises sensitivity and specificity, while a fixed

threshold of 0.5 does not account for class imbalance or differences in model calibration. This optimisation slightly improved both sensitivity and overall classification stability compared to using the standard 0.5 cutoff.

## 6.2 Evaluation Metrics

Model performance was evaluated using standard binary classification metrics. These metrics quantify different aspects of predictive behaviour and are defined in terms of true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN).

Accuracy measures the overall proportion of correct predictions:

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

Sensitivity (also called Recall or True Positive Rate) indicates how well the model identifies patients with heart disease:

$$\text{Sensitivity} = \frac{TP}{TP + FN}.$$

Specificity (True Negative Rate) measures the ability to correctly identify patients without heart disease:

$$\text{Specificity} = \frac{TN}{TN + FP}.$$

Precision quantifies how many predicted positive cases are actually positive:

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

F1-score is the harmonic mean of Precision and Sensitivity, providing a balanced measure when false positives and false negatives are both important:

$$\text{F1-score} = 2 \cdot \frac{\text{Precision} \cdot \text{Sensitivity}}{\text{Precision} + \text{Sensitivity}}.$$

Area Under the ROC Curve (AUC) evaluates the model's ability to distinguish between positive and negative cases across all possible thresholds:

$$\text{AUC} = \int_0^1 \text{TPR(FPR)} d(\text{FPR}).$$

AUC can also be interpreted as the probability that a randomly selected positive case receives a higher predicted score than a randomly selected negative case. A higher AUC indicates stronger overall discriminative ability.

### 6.3 Confusion Matrices

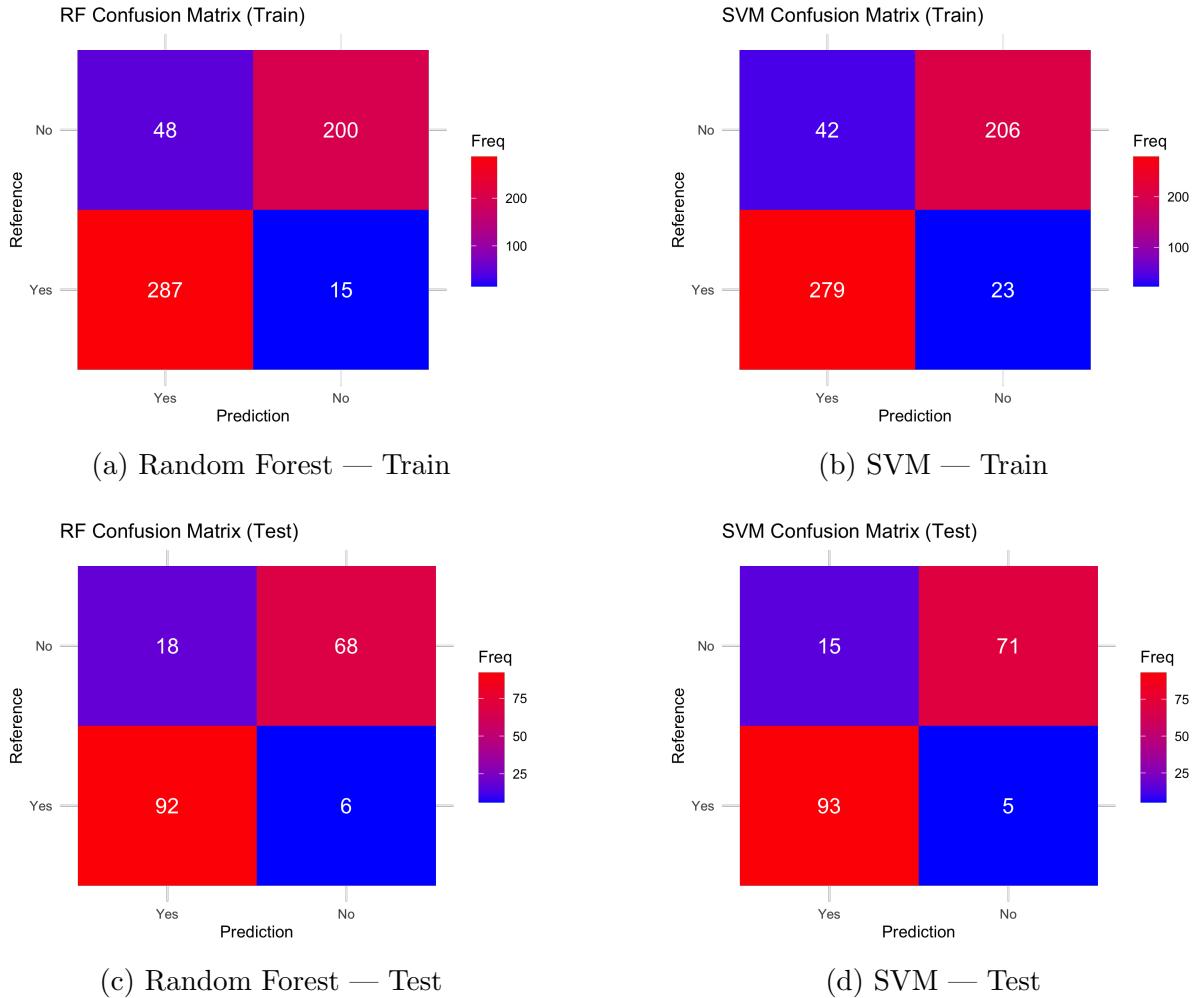


Figure 14: Confusion matrices for Random Forest and SVM on the training and test sets.

The confusion matrices show how many samples each model classified correctly or incorrectly. The diagonal cells show the correct predictions, while the off-diagonal cells show mistakes.

On the training set, the SVM identifies more true heart-disease cases than the Random Forest and makes fewer false negatives. This means the SVM is better at avoiding missed disease cases. Both models produce a noticeable number of false positives, meaning they sometimes classify healthy patients as having heart disease.

On the test set, both models still perform well, but the SVM again makes fewer false negatives. This is important in medical settings, because false negatives represent patients who actually have heart disease but are predicted as healthy. The SVM also shows slightly fewer false positives overall.

In summary, both models work well, but the SVM provides better detection of true heart-disease cases and makes fewer high-risk mistakes. This matches the metric comparison results reported earlier.

## 6.4 ROC Curves

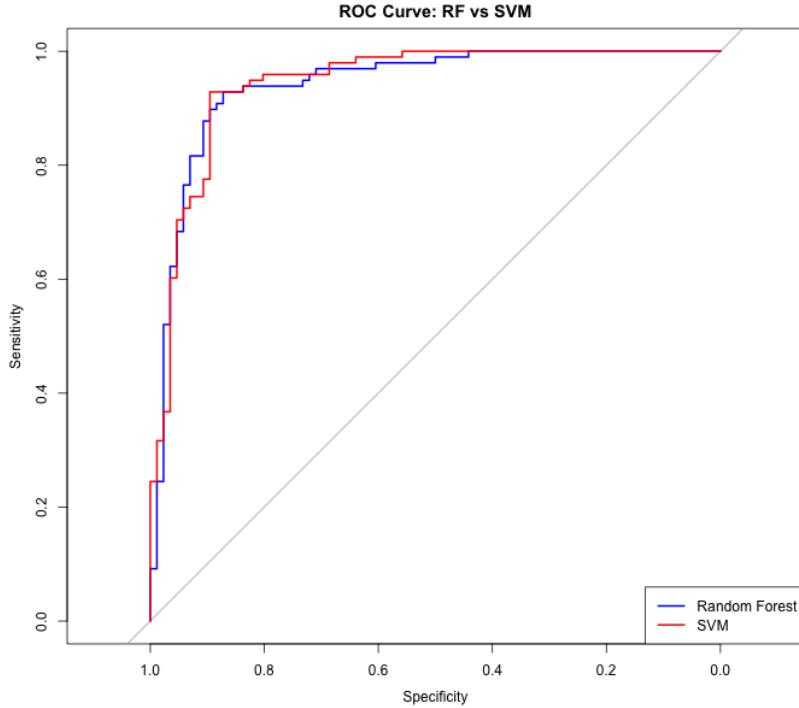


Figure 15: ROC curves for Random Forest and SVM on the test set.

The ROC curves provide a threshold-independent view of model performance by showing how sensitivity and specificity change across all possible decision cutoffs. Both models achieve an AUC above 0.94, which indicates excellent ability to distinguish between patients with and without heart disease.

The SVM curve lies slightly above the Random Forest curve across most of the threshold range. This means the SVM consistently achieves a better trade-off between true positive rate and false positive rate. In practical terms, the SVM is more reliable at ranking patients so that true heart-disease cases receive higher risk scores than non-disease cases.

Overall, the ROC analysis supports the earlier results showing that the SVM provides slightly stronger predictive performance than the Random Forest.

## 6.5 Final Train–Test Evaluation

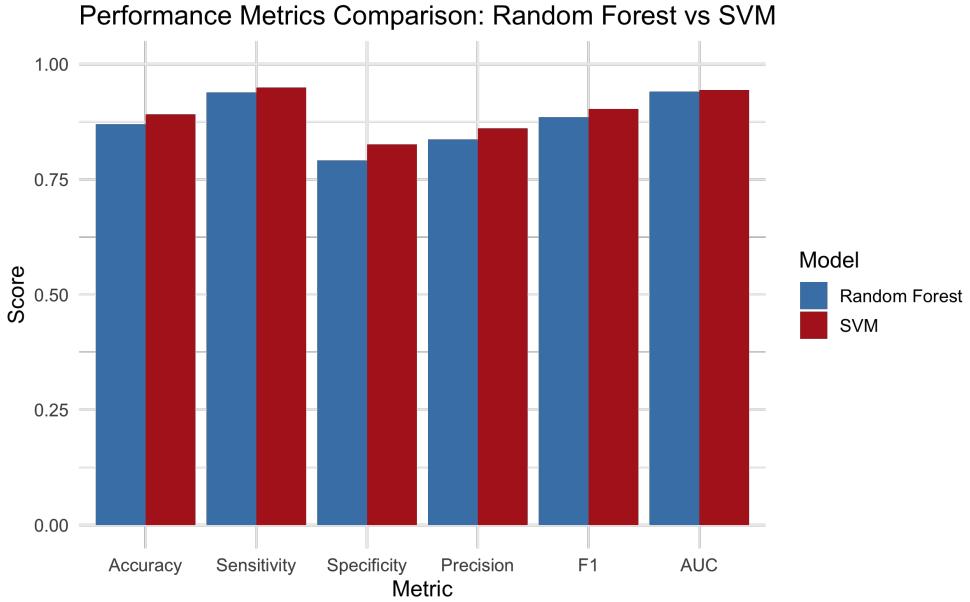


Figure 16: Comparison of key performance metrics (Accuracy, Sensitivity, Specificity, Precision, F1, and AUC) for Random Forest and SVM on the test set.

Figure 16 provides a visual summary of how the two models perform across the main evaluation metrics. The SVM generally shows slightly higher values across most metrics—particularly Sensitivity, Precision, F1-score, and AUC—whereas Random Forest shows a small advantage in Specificity. The close height of the bars indicates that both models perform consistently, but the SVM holds a modest overall edge on the test set. This visual pattern agrees with the quantitative results reported in the tables below.

Model	Accuracy	Sensitivity	Specificity	Precision	F1	AUC
RF	0.885	0.950	0.806	0.857	0.901	0.959
SVM	0.882	0.924	0.831	0.869	0.896	0.944

Table 7: Training performance metrics for Random Forest and SVM. Bold values indicate the higher value between the two models.

Model	Accuracy	Sensitivity	Specificity	Precision	F1	AUC
RF	0.870	0.939	0.791	0.836	0.885	0.940
SVM	0.891	0.949	0.826	0.861	0.903	0.944

Table 8: Test performance metrics for Random Forest and SVM. Bold values indicate the higher value between the two models.

Both models show strong generalisation on unseen data. The SVM model achieves the highest accuracy = 0.891, sensitivity = 0.949, F1-score = 0.903, and AUC = 0.944,

indicating better overall performance. Random Forest also performs well but has lower specificity 0.791 and slightly weaker discrimination AUC = 0.940. Together with the confusion matrices and ROC analysis presented earlier, these results confirm that the SVM with RBF kernel is the stronger and more reliable model for this classification task.

## 7 Interpretation of the Trained Models Using XAI Techniques

To better understand how the Random Forest (RF) and Support Vector Machine (SVM) models arrive at their predictions, we computed global permutation feature importance (PFI). PFI quantifies how much the model performance decreases when a feature is randomly permuted; a larger drop indicates a more influential feature. Thus, PFI provides a global view of how strongly each predictor contributes to classification performance.

### 7.1 Global Importance Structure

Figures 17a and 17b display the PFI rankings for RF and SVM. In both models, ST\_Slope emerges as the most influential feature, highlighting the dominant role of ECG-derived stress-test information in the prediction of heart disease. Several other features consistently appear with high importance across both models, including Chest Pain Type, Sex, Exercise Angina, Cholesterol, and Old peak. Although the numerical values differ slightly between the two algorithms, the overall ranking of key predictors is highly similar.

### 7.2 Agreement Between RF and SVM

Both models show strong agreement in which features carry predictive value. Symptom-related variables for instances, Chest Pain Type, Exercise Angina and stress-test metrics for instances, ST Slope, Old peak consistently appear at the top of the rankings. This convergence suggests that the underlying signal in the dataset is robust and that different learning algorithms capture similar clinical patterns. Lower-ranked features such as Age, Resting BP, and Resting ECG contribute comparatively little in this modelling context, although this does not necessarily diminish their clinical relevance.

### 7.3 Summary of Feature Contributions

Across both RF and SVM, the feature importance structure can be summarised as:

- Most important: ST Slope
- Moderately important: Chest Pain Type, Sex, Exercise Angina, Cholesterol, Old peak, Max HR, Fasting BS
- Least important: Age, Resting BP, Resting ECG

These results indicate that the models rely primarily on exercise-related ECG characteristics and symptom profiles when predicting heart disease.

## 7.4 Limitations of Global Feature Importance

Although PFI is useful for identifying influential predictors, it provides only a limited type of explanation. Specifically, PFI does not indicate:

- whether higher feature values increase or decrease predicted risk,
- whether effects are linear or non-linear,
- interactions or joint effects between features,
- case-specific explanations for individual patients.

Gaining such insights would require methods such as SHAP values, partial dependence plots (PDP), or individual conditional expectation (ICE) curves.

## 7.5 Overall Interpretation

Overall, the feature importance analysis shows that RF and SVM rely on a coherent and clinically meaningful set of predictors, with ST Slope consistently emerging as the dominant feature. The strong agreement between both models increases confidence in the stability and interpretability of the findings. These results provide a global understanding of the underlying decision logic driving the models' predictions.

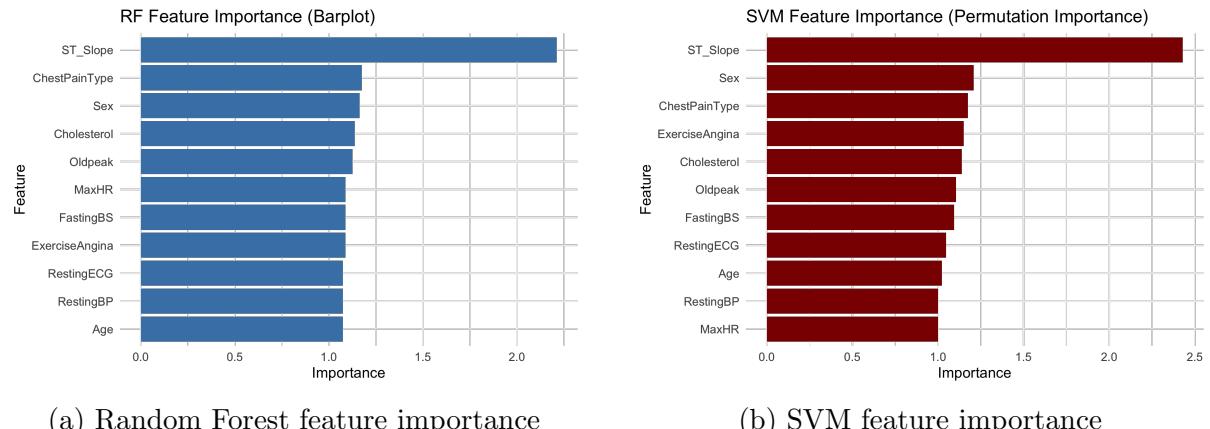


Figure 17: Permutation feature importance for RF and SVM models.

## 8 Conclusion

This project investigated the use of supervised machine learning methods for predicting heart disease using a structured clinical dataset containing demographic, ECG, and exercise-related variables. Through a systematic workflow that included exploratory data analysis, feature standardisation, hyperparameter optimisation, and independent

test evaluation, two models—Random Forest and Support Vector Machine with an RBF kernel—were developed and compared.

Both models demonstrated strong and stable predictive performance. The SVM achieved the highest overall accuracy, sensitivity, F1-score, and AUC on the test set, indicating superior discrimination between patients with and without heart disease. Random Forest also performed well but showed slightly lower specificity and weaker generalisation. Across all evaluations, the SVM model proved to be the more reliable classifier for this task.

Model interpretability was examined using permutation feature importance, which revealed that exercise-related and ECG-derived variables—particularly ST Slope, Chest Pain Type, Exercise Angina, Old peak, and Max HR—were the most influential predictors. These findings align with established clinical knowledge and confirm that the models capture clinically meaningful patterns.

Overall, the results show that machine learning techniques are effective tools for heart-disease prediction and can support clinical decision-making by highlighting key risk factors. Future work may incorporate larger and more diverse datasets, apply advanced interpretability methods such as SHAP values, or extend the analysis to probabilistic and deep-learning models to further improve predictive performance and explanatory depth.

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