

Heart disease prediction using machine learning models

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ABSTRACT

Heart disease remains one of the leading causes of death globally, with mortality rates continuing to rise each year. Early detection is critical to reducing the burden of this disease; however, conventional diagnostic methods are often costly, time-consuming, and reliant on specialist expertise. This study aims to evaluate the effectiveness of four machine learning (ML) algorithms—Decision Tree (DT), Random Forest (RF), K-Nearest Neighbors (KNN), and Support Vector Machine (SVM)—in predicting heart disease using clinical datasets. The methodology involves data preprocessing, feature selection using the Random Forest algorithm, and performance evaluation through metrics such as accuracy, precision, recall, F1-score, and support. Experimental results indicate that KNN achieved the highest accuracy after feature selection, while SVM demonstrated the highest recall despite lower precision. RF offered the most balanced performance, making it a reliable model for real-world medical applications. These findings highlight the importance of selecting appropriate algorithms and features to improve the performance of predictive models. The study suggests that future research should incorporate larger datasets, apply systematic hyperparameter tuning, and explore deep learning techniques to further enhance prediction accuracy.

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Introduction

With mortality rates rising annually, heart disease is one of the world's leading causes of death (Gaidai et al., 2023). According to a report from the World Health Organization (WHO), cardiovascular diseases are responsible for more than 17.9 million deaths per year, or about 31% of total global deaths (ReFaey et al., 2021). Risk factors such as hypertension, diabetes, smoking, unhealthy diet and sedentary lifestyle contribute to the increasing prevalence of these diseases (Balwan & Kour, 2021). Early diagnosis plays a crucial role in reducing mortality from heart disease, but conventional methods often require complex and expensive procedures, and rely on the expertise of doctors (Yasmin et al., 2021). Therefore, there is a need for technology-based approaches that can improve the accuracy and efficiency of early detection of heart disease (Tang et al., 2023).

In recent years, Machine Learning (ML) has shown significant potential in the medical field, particularly in clinical data processing and disease prediction (Shehab et al., 2022). ML algorithms are able to analyze large amounts of patient data quickly and produce more accurate predictions than conventional methods (Javaid et al., 2022). Numerous investigations have demonstrated the

effectiveness of ML in diagnosing various diseases, including cancer, diabetes, and cardiovascular diseases (Triantafyllidis et al., 2022). Nevertheless, choosing the best model for heart disease prediction is still a challenge, as each algorithm has its own advantages and limitations (Noroozi et al., 2023). Therefore, a comparative analysis of various ML models is needed to determine the most suitable algorithm to support medical decisions in the early diagnosis of heart disease (Ahsan & Siddique, 2022).

Although many studies have been conducted when using machine learning to forecast heart disease, there are still some unresolved issues (Zhou et al., 2023). Some studies only use one or two algorithms without conducting a thorough comparative analysis. In addition, model evaluation is often limited to accuracy metrics without considering other aspects such as precision, recall, F1-score, and support, which are very important in reducing classification errors. Another problem often encountered is data imbalance, where the number of samples of patients with heart disease is much less than that of healthy patients, which can cause bias in model training. Therefore, this study aims to address these issues by implementing a more comprehensive model evaluation strategy.

Numerous earlier studies have shown how well machine learning works for early heart disease identification (Nagavelli et al., 2022). However, the majority of studies have only focused on developing one particular ML model without conducting an in-depth comparative analysis (Azam et al., 2023). For example, some studies rely on the DT algorithm due to its high interpretability, while others prefer RF due to its ability to handle complex datasets (Gulowaty & Wozniak, 2021). In addition, algorithms such as KNN and SVM are also widely used in various studies, but no research has systematically compared these four models in the context of heart disease prediction (Van Smeden et al., 2022). Therefore, this study aims to fill the gap by comparing the four ML models together, as well as exploring more effective hyperparameter optimization and feature selection methods.

This study aims to evaluate and compare the performance of four ML algorithms, namely DT, RF, KNN, and SVM, in predicting heart disease based on clinical datasets. To identify the best model, a variety of performance criteria were used in the evaluation, including accuracy, precision, recall, F1-score, and support. In addition, this research also aims to identify key factors in the dataset that have a significant influence on heart disease prediction and explore hyperparameter optimization techniques to improve model performance. With this more comprehensive approach, this research is expected to provide evidence-based recommendations on the most effective ML models to be applied in medical decision support systems.

Although various studies have examined the application of ML in heart disease prediction, there are still some gaps in the literature that need to be addressed (Rahim et al., 2021). Most of the previous studies were limited to one or two ML models without conducting a broader comparison. In addition, the feature selection techniques used in some studies are still suboptimal, so there is a possibility that important information has not been fully explored. The hyperparameter tuning approach used in many studies is also often unsystematic, which can lead to suboptimal model performance in real-world applications (Slade et al., 2024). Therefore, this study aims to bridge the gap by applying a more systematic approach in model selection, performance metrics evaluation, and feature and hyperparameter optimization.

This study's primary contribution is its all-encompassing methodology of comparing four major ML models with multi-metric based analysis. Furthermore, this study helps to increase the accuracy of heart disease prediction by optimizing feature selection methods and hyperparameter tuning. Unlike previous studies that tend to use conventional approaches in feature selection, this study will apply data-driven strategies to identify the most significant variables in heart disease detection. The main justification for this research is the urgency in improving medical decision support systems for early diagnosis of heart disease, given that it is still the leading cause of death globally. With a more robust and systematic methodology, the results of this research are expected to provide more accurate recommendations for medical practitioners in choosing the most suitable ML algorithm to support early detection of heart disease. In addition, this research also has practical implications in improving the efficiency and accuracy of medical diagnosis, which in turn can help reduce the mortality rate due to this disease.

Method

Decision Tree (DT)

For classification and regression problems, the decision tree algorithm is utilized (Charbuty & Abdulazeez, 2021). The decision tree algorithm is used for problems involving regression and classification that are most significant in determining the outcome (Althnian et al., 2021). Decisions are made through a set of feature value-based rules, which are visualized in the form of a tree with nodes as features and branches as possible decisions (Kairgeldin & Carreira-Perpiñán, 2024).

1. Entropy is used to measure the irregularity in the dataset:

$$\text{Entropy}(S) = -\sum p_i \log_2 p_i \quad (1)$$

2. Information Gain (IG) measures how much a feature can reduce disorder:

$$IG(S, A) = \text{Entropy}(S) - \sum \frac{|S_v|}{|S|} \text{Entropy}(S_v) \quad (2)$$

The primary benefit of decision trees is its ability to capture complex relationships in data without requiring much preprocessing. However, the model is prone to overfitting if pruning or limiting the depth of the tree is not done.

Random Forest (RF)

Random Forest is an ensemble consisting of many decision trees trained independently on different subsets of data (Salman et al., 2024). It uses bootstrap aggregation (bagging) techniques to improve accuracy and reduce the risk of overfitting by combining predictions from multiple trees (Tahraoui et al., 2022).

1. The final prediction is calculated based on the average prediction of all trees (for regression) or majority voting (for classification):

$$RF(x) = a_0 + \sum_{n=1}^n h_i(x) \quad (3)$$

2. Where $h_i(x)$ is the prediction of the i -th decision tree.

One of Random Forest's benefits is its capacity to manage big datasets, reduced bias compared to a single Decision Tree, and robustness against irrelevant features. However, this model can be slow in training and inference if the number of trees is too large.

K-Nearest Neighbors (KNN)

A new data point's K nearest neighbors are found using the non-parametric K-Nearest Neighbors algorithm, which then assigns a label based on the labels of the majority of the neighbors (Halder et al., 2024). To determine how close together data are, it mainly uses the distance metric (Mallick et al., 2022).

1. Euclidean Distance formula, one of the most commonly used distance metrics:

$$d(x, y) = \sqrt{\sum_{i=1}^n (x_i - y_i)^2} \quad (4)$$

2. After calculating the distance to the K nearest neighbors, the final decision is determined based on the majority of the labels of those neighbors (for classification) or the average value of the neighbors (for regression).

KNN has the advantage of simplicity and does not require explicit training, but its performance can suffer on large datasets due to high search time, especially without the use of optimization

techniques such as KD-Tree or Ball-Tree(Pham & Wagner, 2025).

Support Vector Machine (SVM)

A classification algorithm called Support Vector Machine finds the best hyperplane in the data that divides two classes by the greatest amount (Zhang, 2001a). This model uses the concept of Support Vectors to determine the best decision boundary(Zhang, 2001b).

1. The general equation of a hyperplane in feature space is:

$$w \cdot x + b = 0 \quad (5)$$

2. To maximize the margin, the following optimization is used:

$$\max \frac{2}{\|w\|} \quad (6)$$

3. With the restriction that all data in the dataset fulfill:

$$y_i(w \cdot x_i + b) \geq 1 \quad (7)$$

If the data cannot be linearly separated, kernel functions are used to project the data to a higher dimension, allowing for better separation. Some commonly used kernel functions include:

1. Kernel Linier:

$$K(x_i, x_j) = x_i^T x_j \quad (8)$$

2. Kernel Polinomial:

$$K(x_i, x_j) = (x_i^T x_j + c)^2 \quad (9)$$

3. Kernel Radial Basis Function (RBF):

$$K(x_i, x_j) = e^{-\gamma \|x_i - x_j\|^2} \quad (10)$$

SVM is known to have high accuracy in many classification tasks, especially in high-dimensional datasets(Kafrawy et al., 2021). However, they can be slow to train on large datasets and are sensitive to kernel parameter selection.

Tools and Libraries

In this study, four Machine Learning algorithms, namely DT, RF, KNN, and SVM, were used to build a heart disease prediction model. Decision Tree works by dividing the dataset based on the most significant features using entropy and information gain calculations, but is prone to overfitting. Random Forest, as an ensemble method, combines many Decision Tree to improve accuracy and reduce variance with bootstrap aggregation technique. KNN determines the label of a data set based on the majority of the K nearest neighbors using the Euclidean distance metric, while SVM searches for the optimal hyperplane that separates two classes by the largest margin, using different types of kernels to handle non-linearly separable data.

This research was conducted using Google Colab with various Python libraries for data processing, model training, and visualization of results. NumPy and Pandas libraries were used for data manipulation and analysis, while Matplotlib and Seaborn helped in exploratory visualization. Scikit-learn provides important functions such as train_test_split to split the dataset, StandardScaler for data normalization, and several machine learning techniques, including RandomForestClassifier, SVC, KNeighborsClassifier, and DecisionTreeClassifier. In addition, GridSearchCV and StratifiedKFold are

used for parameter optimization and model validation, while `accuracy_score` and other evaluation metrics, `classification_report`, and `confusion_matrix` are used to measure model performance. With this combination of tools, the research can be conducted in an efficient and structured manner.

To optimize the model, two experiments were conducted. The first experiment used all the features in the dataset to see the basic performance of each model. To increase the model's effectiveness and interpretability, the second experiment employed Random Forest to identify the most significant attributes. The best model for predicting heart disease was identified by comparing the outcomes of the two studies using assessment measures like precision, recall, F1-score, and support.

Research Stage

This research focuses on building a heart disease prediction model by analyzing various risk factors that contribute to the patient's health condition. The research object includes a classification process based on medical parameters such as blood pressure, cholesterol levels, medical history, and other variables related to heart health. The methods used in this research involve various Machine Learning algorithms, namely DT, RF, KNN, and SVM. The used datasets were from reliable sources and underwent a number of crucial steps, including feature selection, data preprocessing, model training, and performance evaluation of the model using metrics like support, accuracy, precision, recall, and F1-score. With this approach, the research aims to identify the best model in detecting potential heart diseases and provide ideas for the creation of prediction systems based on artificial intelligence systems in the medical field. The following are the stages of research carried out based on the flowchart used:

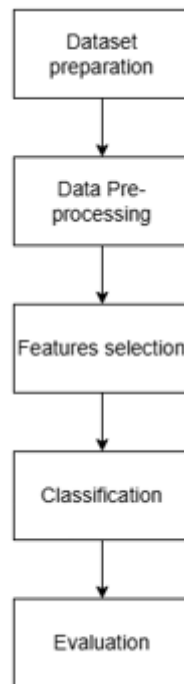


Figure 1 Flowchart of Research Phase

Dataset Preparation

In the Dataset Preparation stage, this study uses the Cleveland Dataset from the University of California (UCI), which is one of the standard datasets in heart disease research. This dataset consists of 303 rows of data with 14 columns, where 13 columns are features that include various risk factors such as blood pressure, cholesterol levels, maximum heart rate, and other medical history, while the other 1 column is a label that indicates the patient's condition (whether they have heart disease or not). This dataset was chosen because it has comprehensive information and has been widely used in various Machine Learning studies related to heart disease prediction.

Table 1 dataset information

Variabel Name	Description
age	The patient's age in years
sex	The patient's gender (0 = male, 1 = female)
cp	Types of chest pain include atypical angina, non-anginal discomfort, atypical angina, and asymptomatic.
trestbps	Blood pressure at rest in millimeters Hg
chol	mg/dl of serum cholesterol
fbs	Fasting blood sugar level, categorized as above 120 mg/dl (1 = true, 0 = false)
restecg	Results of a resting electrocardiogram: 0: Normal, 1: Abnormal ST-T wave, and 2: Presumably or definitely exhibiting left ventricular hypertrophy
thalach	The highest heart rate attained during a stressful exam
exang	Angina brought on by exercise (1 = yes, 0 = no)
oldpeak	Exercise-induced ST depression in comparison to rest
slope	The peak exercise's slope ST segment: flat, downsloping, and upsloping (0, 1, 2).
ca	Number of main vessels (0-4) that fluoroscopes can color
thal	0: Normal, 1: Fixed Defect, 2: Reversible Defect, and 3: Not described are the results of the Thallium stress test
target	Status of heart disease (0 = absence of disease, 1 = existence of disease)

Data Pre-processing

Once the dataset is ready, the next step is data preprocessing, which aims to ensure data quality before entering the modeling stage. This process includes handling missing values, normalizing or standardizing features, and encoding category variables into a numerical format that can be used by Machine Learning algorithms. Techniques such as StandardScaler are used to equalize the scale of the data, so that the model can work more optimally.

Table 2 Pieces of Data Pre-processing Result

age	sex	cp	trest	chol	fbs	rest	thal	exa	oldpeak	slope	ca	tal	target
63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

Features Selection

To find the most pertinent characteristics for heart disease prediction, feature selection is carried out at this point. The Random Forest method is used to pick features, which ranks features based on their importance. By selecting significant features, the complexity of the model can be reduced without sacrificing performance, making the model more efficient and interpretative.

Classification

Once the best features are selected, the next step is to train classification models using various Machine Learning algorithms, namely DT, RF, KNN, and SVM. Each model was tested using two scenarios: first, with all features, and second, with features that had been selected using Random Forest. This process aims to compare the effectiveness of each model in predicting heart disease.

Evaluation

Model assessment is the final step, which evaluates the model's performance using a variety of evaluation measures, including accuracy, precision, recall, F1-score, and support. The best model with the most accurate predictions is chosen based on the evaluation findings. In addition, the advantages and disadvantages of each model are analyzed to provide recommendations for using the most suitable model in real cases.

Results and Discussions

First Try

In the second experiment, I applied feature selection using the Random Forest algorithm to determine the most influential features in predicting patient conditions as shown in Figure 2. From the results of the importance feature analysis displayed in the graph, it can be seen that the features 'cp', 'thalach', 'oldpeak', 'thal', 'chol', 'ca', 'age', 'trestbps', 'slope', 'exang'.

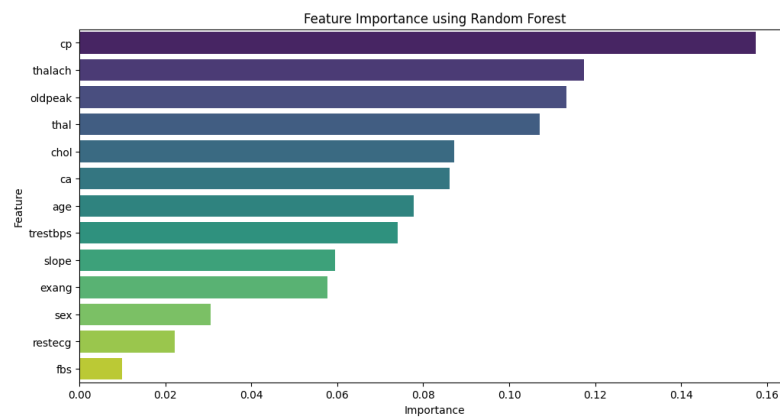


Figure 2 Feature Selection Results With Random Forest Algorithm

After feature selection using the Random Forest algorithm, the model is evaluated using only the top 10 features that have a significant influence on predicting patient conditions. Based on the visualization of the evaluation results in Figure 3, the KNN model still shows the highest accuracy, followed by RF and SVM, while Decision Tree has the lowest accuracy.

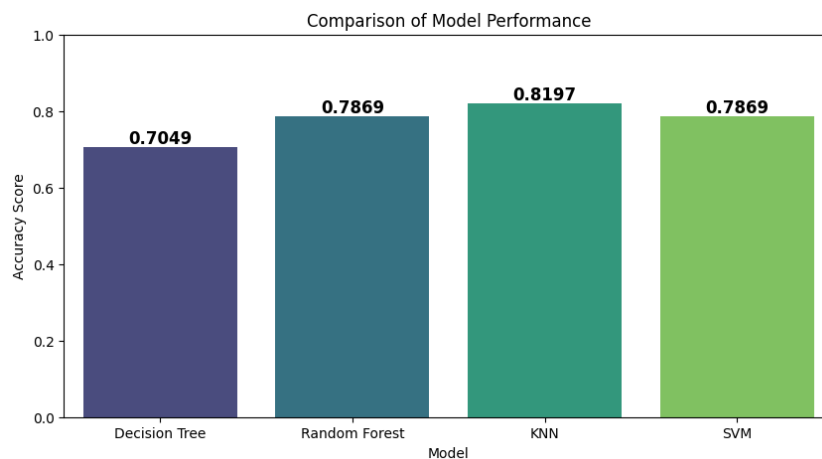


Figure 3 Evaluation Results Using Feature Selection

Only the top ten features that significantly influenced the patient's condition prediction were used to test the model after feature selection using the Random Forest technique. Based on the visualization of the evaluation results, the KNN model still shows the highest accuracy, followed by RF and SVM, while Decision Tree has the lowest accuracy.

Although feature selection succeeded in improving the efficiency of the model by reducing the number of variables used, the resulting score accuracy is still suboptimal. This indicates that the model

can still be improved, either through the selection of a more suitable algorithm, hyperparameter tuning, or exploration of other feature selection methods.

Second try

In the second experiment, the model was built using all available features without performing a feature selection process. The performance evaluation of the model is done with the recall metric for the positive class, which measures the extent to which the model is able to detect positive cases correctly.

Based on the results obtained in Figure 4, SVM showed the best performance with a recall of 1.00 (100%), which means all positive cases were successfully detected without error. RF achieved a recall of 0.88 (88%), which is still quite high but slightly lower than SVM. KNN and DT have the same recall of 0.85 (85%), which shows a fairly good performance but still below RF and SVM.

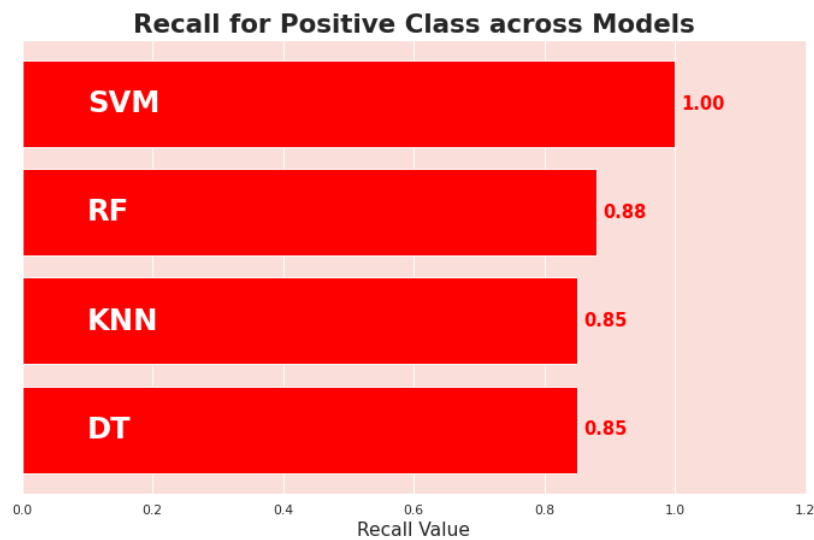


Figure 4 Recall For Positive Class Across Models

Besides accuracy, there are other performance metrics to see the performance of each model such as precision, recall, F1-Score, support.

Table 3 Evaluate The Optimized Model On The Test Data

	Precision_1	Recal_1	F1-score_1	Support_1
DT	0.78	0.85	0.81	33
RF	0.83	0.88	0.85	33
KNN	0.85	0.85	0.85	33
SVM	0.54	1.00	0.70	33

Based on the model performance evaluation results displayed in the line diagram in Figure 5, it can be seen that there are significant variations in the Precision, Recall, and F1-Score metrics among the tested models. DT shows a balance between precision (0.78), recall (0.85), and F1-score (0.81). Although the recall was high, the lower precision indicates that the model produced some false positive predictions. RF gave better results with precision (0.83), recall (0.88), and F1-score (0.85). This model showed more stable performance compared to DT, especially in capturing positive classes with better recall. KNN has a balanced performance with precision (0.85), recall (0.85), and F1-score (0.85). This model can be said to be quite stable and does not experience a trade-off between precision and recall.

SVM shows a stark difference with a very low precision (0.54) but a perfect recall (1.00). While the support values are all the same at 33.

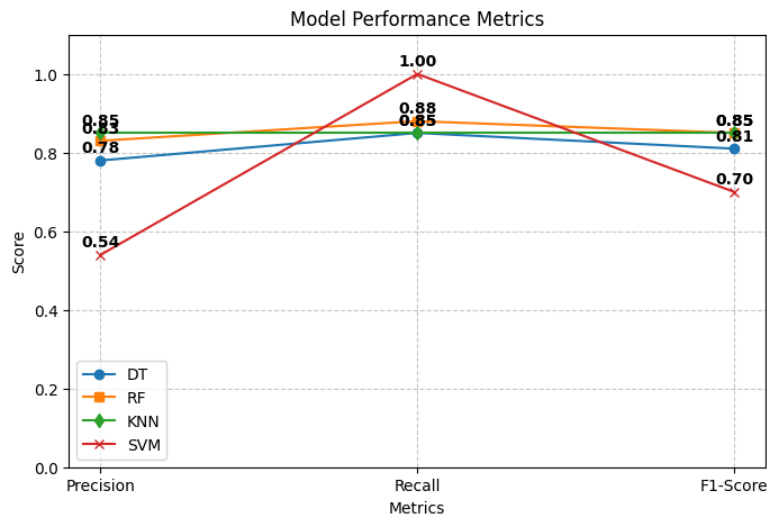


Figure 5 Model Performance Metrics

Overall, the Random Forest and KNN models show better and balanced performance compared to the others. However, the accuracy and F1-score results are still generally less than optimal, so further exploration is needed such as refining feature selection, tuning hyperparameters, or trying other model approaches to improve classification performance.

Conclusions

This study shows that the Support Vector Machine (SVM) algorithm without feature selection is the best model in detecting heart disease, as it has the highest recall value (1.00), which means it is able to identify all patients with heart disease without error. This confirms that in the context of medical applications, especially for early detection of diseases with serious consequences, high recall is preferred over other metrics to minimize the risk of misdiagnosis. The findings imply that SVM-based models can be applied in medical decision support systems to improve the accuracy of early diagnosis and assist medical personnel in identifying high-risk patients. However, this study still has limitations, especially in terms of the imbalance between recall and precision, which may lead to an increase in the number of false positives. In addition, external validation on a larger and more diverse dataset is necessary to make the model more reliable in various patient populations. Therefore, future research is recommended to explore hyperparameter optimization techniques in SVM, apply more adaptive feature selection methods, and combine ensemble learning and deep learning approaches to improve overall model performance.

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