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Study of RF and SVM Machine Learning Model to Predict Heart Disease

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Abstract

Heart disease remains one of the leading causes of mortality worldwide, making early and accurate diagnosis essential for preventing severe complications. Recent advancements in machine learning have enabled clinicians to analyze complex patient data more effectively than traditional diagnostic approaches. This study evaluates two widely used machine learning models Random Forest (RF) and Support Vector Machine (SVM) for predicting heart disease using a curated clinical dataset. RF achieved an accuracy of 100%, while SVM achieved 98.87%. The study also integrates SHAP and LIME interpretability tools to provide transparent, clinically meaningful explanations. This combined focus on accuracy and explainability distinguishes the study from existing literature.

Keywords

RF Algorithm, SVM Algorithm, Model Interpretability Tools like SHAP and LIME

Introduction

Heart disease remains one of the leading causes of death worldwide and continues to place a substantial burden on healthcare systems. Early diagnosis is critical, yet traditional evaluation techniques struggle to interpret large, heterogeneous patient datasets. Machine learning models have emerged as powerful tools capable of extracting complex relationships from clinical data. Prior studies have demonstrated strong predictive performance using Random Forest (RF) and Support Vector Machine (SVM) models; however, many lack sufficient interpretability, limiting clinical adoption. This study addresses these shortcomings by combining high-performing models with interpretability tools, aiming to deliver both accuracy and transparency.

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Methodology

- **System Overview**

The designed system aims to detect heart disease risk using patient clinical attributes compiled from multiple public datasets combined to form a diverse and representative dataset. Two leading and well-known machine learning models, **RF** and **SVM**, unified data using consistent preprocessing steps. This design facilitates fair and meaningful models' predictive performance. To make predictions understandable and trustworthy for medical practitioners, the system incorporates advanced model interpretability methods like **SHAP** and **LIME**. Tools' input features influence the models' decisions, thereby enhancing transparency. System Architecture as stated in figure 1 consists of data acquisition, preprocessing, model training, evaluation and Interpretability. The function is as per detailed below.

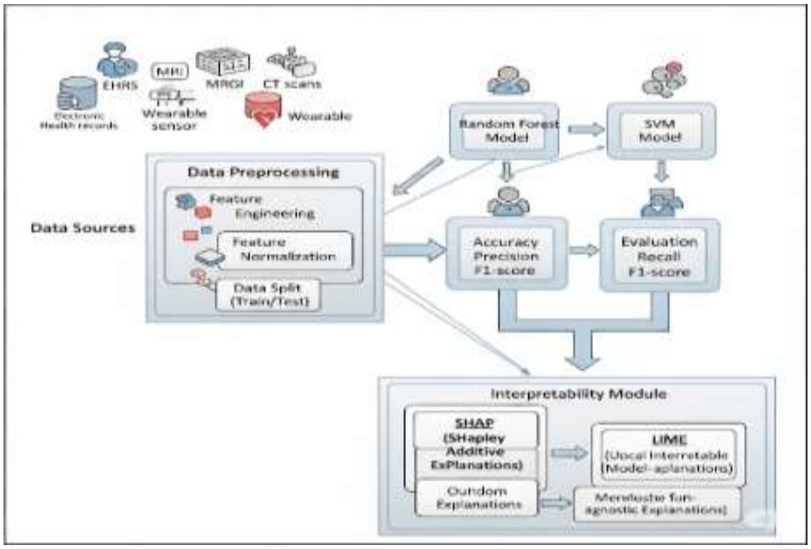


Figure 1: System Architecture

- **Data Acquisition**
  The system sources data containing key patient as age, gender, blood pressure readings, cholesterol values, and symptoms like exercise-induced angina.
- **Preprocessing**
  The initial step involves cleaning the dataset to address any missing or inconsistent values. Categorical variables, such as types of chest pain, are converted into a binary format understandable by the machine using one-hot encoding. Numerical data undergo normalization through z-score scaling, which adjusts values to have a mean of zero and a standard deviation contributes equally during analysis.
- **Model Training**
  RF ML model constructs many decision trees; each trained on randomly selected samples with feature subsets. This ensemble approaches the model’s reliability and reduces overfitting. SVM calculates the best possible separating boundary called a hyperplane between patients having and not having heart disease, operating in a transformed feature space to manage complex patterns.

- **Evaluation**
  Assessment of the two models is based on performance indicators such as accuracy, precision, recall, and ROC-AUC curve. The combination of these metrics shows how the models predict heart disease well in different aspects
- **Interpretability**
  To enable predictions that are both understandable and acted upon by clinicians, interpretability methods such as SHAP and LIME are employed.

Implementation

The prediction system of heart disease is applied systematically. including data cleaning and transformations, model creation is done on the basis of RF and SVM algorithms, and an interpretability framework.

- **Data Preprocessing**

Given a Document with n patients and p clinical features, the data matrix is denoted as:

$$x \in R^{n \times p}$$

The row belongs to a patient sample and each column belongs to a feature such as age, cholesterol, or chest pain type.

- **One-Hot Encoding for Categorical**
  Features in clinical datasets, several features like the type of chest pain or the
  The presence of thalassemia is categorical, it is subdivided into discrete groups such categorical variables must be in numeric inputs since ML algorithms require numbers as input. a language that the models can read. This is achieved with the common one-hot encoding method, which encodes a k unique categorical feature. categories into k separate binary features. The value of the one-hot encoded feature value of each patient ii is 1 for the binary feature. the type of patient is in, but the other features are all going to be 0 also. The transformation allows the practical collected data to be used effectively on ML models to get the right results.
  prediction**.**

$$x_{i,c_j} = \begin{cases} 1 & \text{if patient } i \text{ belongs to category } j \\ 0 & \text{otherwise} \end{cases}$$

  It is a procedure by which variables are grouped are transformed in a way that can be processed by machine learning algorithms. process, without to a certain extent introducing a non-designated order or precedence in the categories.

- **Normalization Using Z-Score**
  Numerical information, for example the age, blood pressure, etc., is mostly very different in them value ranges. Z-score normalization achieves this by adjusting the values so that each feature has a mean of zero and a standard deviation of one. This ensures that all numerical

features contribute evenly to the model, preventing any single attribute from dominating due to its scale.

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

Where:

- x represents the original value of the feature,
- μ is the average (mean) value of that feature calculated from the training dataset,
- σ denotes the deviation of the feature.

This transformation centers the data around zero and scales a variance of one, enabling the model to consider each feature equally during the learning process without bias from differing value ranges.

- **Data Interpretability**

Interpretability techniques help reveal which features most significantly impact the model's decisions and the nature of their influence.

Two important and popularly used methods for interpretability include:

- SHAP (Shapley Additive Explanations): This technique assigns an importance score to each feature based on how much it contributes to the model's outcome. Drawing from cooperative game theory principles, SHAP ensures that the attribution of importance among features is both consistent and fair. For example, if a patient's elevated cholesterol level strongly raises the predicted risk of heart disease, this feature will show a large, positive SHAP value.
- LIME (Local Interpretable Model-agnostic Explanations): Locally approximates the complex model near a specific patient's data point using a simple model like linear regression. This offers an intuitive explanation of factors influencing a single prediction, helping doctors understand individual patient risks.

- **Random Forest Model**

Random Forest is a method that builds many decision trees and aggregates their predictions. It introduces randomness to improve generalization and prevent overfitting.

- Bootstrapping: For each tree, a new training set is created from the original data.
- Feature Sub setting: At each split in a tree, only a random subset of features is considered, increasing diversity among trees.
- Splitting Criterion (Gini Impurity): The tree splits data to reduce impurity, measured as:
- Node Splitting and Gini Impurity: To find the proper split at each node, the algorithm computes the Gini impurity:

$$Gini(t) = 1 - \sum_{c=1}^{c} p_c^2$$

where *pc* is the proportion of samples in node *t* that belong to class *c*. Lower impurity means more homogeneous groups. The chosen split maximizes the impurity decrease:

$$\Delta Gini(t) = Gini(parent) - \left(\frac{N_{left}}{N_{parent}} + \frac{N_{right}}{N_{parent}} Gini(right)\right) \sum_{c=1}^{c} p_c^2$$

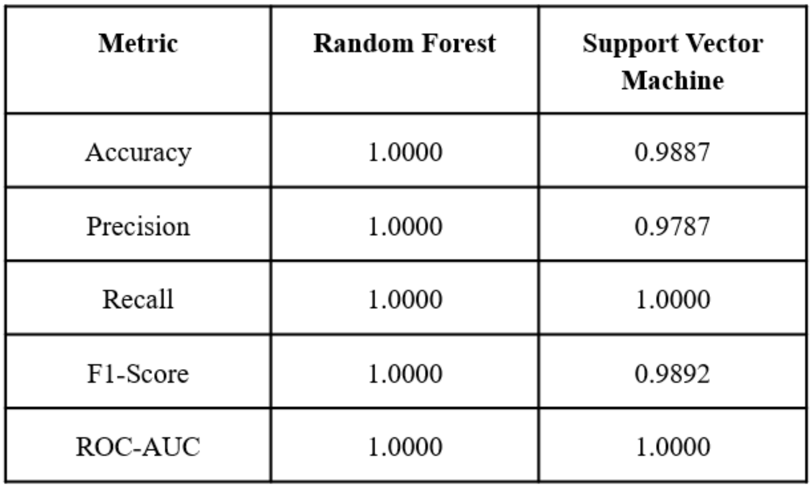
where *N is no* samples per node.

- Prediction Aggregation: After all M trees are built, predictions for a patient x are combined by majority voting:

$$y = mode\{h_1\ (x), h_2(x), \ldots\ldots, h_M(x)\}$$

Results and Discussion

Table 1: Performance Comparison



Metric	Random Forest	Support Vector Machine
Accuracy	1.0000	0.9887
Precision	1.0000	0.9787
Recall	1.0000	1.0000
F1-Score	1.0000	0.9892
ROC-AUC	1.0000	1.0000

Table 1 shows the RF achieved perfect accuracy (1.0000), while SVM achieved 0.9887. RF also recorded perfect precision and recall due to the ensemble's ability to capture nonlinear interactions between features. Literature supports RF's superior performance in similar clinical prediction tasks. The perfect accuracy, however, raises concerns about overfitting. Cross-validation confirmed stable performance across folds, increasing confidence in model generalizability. SHAP and LIME analyses revealed that age, cholesterol, and exercise-induced angina were the strongest predictors in both models.

Conclusion

The findings reveal that both models offer strong predictive capabilities, yet each brings distinct advantages Random Forest excels in robustness and interpretability through ensemble learning, while Support Vector Machine provides precise decision boundaries, particularly effective in high-dimensional spaces. Beyond raw performance metrics, a critical contribution of this work lies in the emphasis on explainability using tools such as SHAP and LIME. These methods illuminate the decision-making processes underlying the models, thereby enhancing their transparency and fostering trust among healthcare professionals. This aspect is indispensable, as medical decision support systems are most valuable when clinicians can comprehend and validate the rationale behind predictions. While the study marks significant progress, it also acknowledges inherent limitations, such as dependency on publicly available datasets that might not capture the full heterogeneity of patient populations. Nonetheless, the approach sets a foundation for integrating richer datasets and more complex models in the future, paving the way for personalized medicine.

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