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Heart Disease Prediction using SVM

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Abstract

Diagnosing and predicting the outcome of cardiovascular disease are essential tasks in medicine that help ensure patients receive accurate classification and treatment from cardiologists. The use of machine learning in the healthcare sector has grown due to its ability to identify patterns in data. By applying machine learning techniques to classify the presence of cardiovascular diseases, it's possible to decrease the rate of misdiagnosis. This study aims to create a model capable of accurately forecasting cardiovascular diseases to minimize the deaths associated with these conditions. In this paper, two types of SVM model such as linear SVM and polynomial SVM is used. Accuracy, precision, recall and F1 score has been evaluated for comparing linear SVM and polynomial SVM. Polynomial SVM provides better accuracy than linear SVM.

Keywords: Heart disease; Machine Learning; Precision; Recall; SVM; Accuracy.

1. Introduction

Cardiovascular diseases (CVDs) stand as the foremost cause of death and illness globally, contributing to over 70% of all mortalities. The 2017 Global Burden of Disease study indicates that CVDs are behind approximately 43% of all deaths [1, 2]. Key risk factors for heart disease in affluent countries include poor nutrition, smoking, high sugar intake, and being overweight, whereas low- and middle-income countries are witnessing a surge in chronic disease rates [3, 4]. The worldwide economic impact of cardiovascular diseases was projected to hit around USD 3.7 trillion between 2010 and 2015 [5-7].

Moreover, diagnostic tools crucial for identifying coronary heart disease, like electrocardiograms and CT scans, are often prohibitively expensive and unattainable for many, particularly in lower-income regions, contributing to 17 million deaths [5]. Up to 30% of a company's yearly health costs can be traced back to employees suffering from cardiovascular diseases. Thus, early identification of heart disease is imperative to mitigate its health and economic repercussions on individuals and entities alike. The WHO has projected that deaths from CVDs will escalate to 23.6 million by 2030, with heart disease and stroke being the primary affected people, underscoring the urgency of leveraging data mining and machine learning for heart disease prediction to save lives and alleviate societal financial strains [8, 9, 10].

Cardiovascular disease is the leading cause of death worldwide, accounting for more than 70% of all global fatalities. The Global Burden of Disease Study 2017 reported that over 43% of deaths are due to CVDs. The main risk factors include unhealthy diets, smoking, excessive sugar intake, and obesity, predominantly seen in wealthier nations. Nonetheless, the prevalence of chronic illnesses is also climbing in lower- and middle-income countries. Between 2010 and 2015, the global economic cost of CVDs was estimated at approximately USD 3.7 trillion.

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Additionally, essential diagnostic tools for coronary heart disease, such as electrocardiograms and CT scans, are frequently too expensive and inaccessible for many in poorer countries. Early detection of heart disease is crucial to reducing both its health and financial impacts on people and organizations. According to WHO predictions, the total death toll from CVDs will rise to 23.6 million by 2030, primarily due to heart disease and stroke, highlighting the importance of employing data mining and machine learning techniques for early prediction of heart disease to preserve lives and decrease economic burdens.

In the realm of medicine, the vast amount of data produced daily can, through data mining, reveal hidden patterns valuable for clinical diagnosis. Data mining's significance in healthcare is evidenced by the substantial research conducted over recent decades. When predicting heart disease, it's essential to consider various factors such as diabetes, hypertension, high cholesterol levels, and irregular heartbeat rates. Often, the incompleteness of medical data can hinder accurate disease prediction [11-15].

Machine learning is becoming increasingly pivotal in healthcare for diagnosing, detecting, and predicting various diseases [16-26]. There's a burgeoning interest in applying data mining and machine learning to forecast the likelihood of developing specific conditions, with existing studies exploring these techniques for disease prediction. Despite attempts to predict disease progression risk, precise results have often been elusive. This paper focuses on accurately predicting the likelihood of heart disease using machine learning approaches, specifically investigating the efficacy of different algorithms, including Support Vector Machines (SVM).

2. Literature Reviews

In [27], Ayatollahi et al. conducted a comparative study between the artificial neural network (ANN) and support vector machine (SVM) approaches for classification based on the positive predictive value of cardiovascular disease. They utilized medical data records from various hospitals, specifically for coronary artery disease patients. The dataset consisted of 1324 instances, 25 attributes, and was split into training and testing sets with a ratio of 70% and 30% respectively. The experimental results revealed that SVM outperformed ANN in terms of accuracy and performance.

In another study by M. F. Rabbi [28], the most common classification models used in data mining were proposed. They applied the k-nearest neighbor (K-NN), artificial neural network (ANN), and support vector machine (SVM) using MATLAB's multilayered feed-forward back-propagation. The heart disease Cleveland dataset from the UCI machine learning repository, containing 303 instances and 76 attributes, was analyzed. After preprocessing the dataset and conducting experiments, the results showed that SVM achieved a classification accuracy of 85%, surpassing K-NN and ANN which achieved approximately 82% and 73% respectively.

A. S. Ebenezer et al. [29] selected ten different algorithms for coronary artery disease risk assessment. They chose artificial neural network (ANN), decision tree (DT), support vector machine (SVM), random forest (RF), CHAID, rule induction, naïve bayes (NB), k-nearest neighbor (KNN), [30] and decision stump (DS) for the classification task. The PIMA dataset from an online repository was used for their analysis, which comprised 303 patient records with 14 attributes. Their results revealed that NB and SVM performed well in predicting heart disease.

In [31], the authors compared the performances of classification algorithms for machine learning. They specifically selected Random Forest (RF) and Logistic Regression (LR) techniques to predict the risk level of heart disease in patients. The United States National Inpatient Sample (NIS) data for 2011-2013 was utilized. Based on their experimental analysis, LR demonstrated a better accuracy performance of 89% compared to RF with 88%.

Desai et al. [32] conducted experiments with logistic regression (LR) and back-propagation neural network (BFNN) to assess the accuracy of classification techniques for heart disease prediction. They performed a comparative study of parametric and non-parametric methods in classifying heart disease. The Cleveland dataset, consisting of 270 records and 13 features, was obtained and used to validate their analysis. A 10-fold cross-validation method was employed to measure the unbiased estimate of their classification models. Their results showed that LR achieved an accuracy of 0.91% compared to BFNN with an accuracy of 0.88%.

3. Methodology

In this section, the proposed methodology will be discussed in details.

3.1. Description of Dataset

The dataset used is obtained from the UCI repository online [33] to analyze and compare the algorithms chosen for this study. The dataset has 303 samples and 14 variables. age (Age), sex (Sex), cp (ChestPain), trtbps (RestingBloodPressure), chol (Cholesterol), fbs (FastingBloodPressure), restecg (RestingECG), thalachh (MaxHeartRate), exng (EscerciseAngina), slope (STSlope), caa(nMajorVessels), thall (Thalium), and output (Status) are int64 (13 variables). oldpeak (OldPeak) is float64 (1 variable). Table 1 describes the Statistical summary of numerical attributes existed in the dataset. Heart disease status can be defined as 0: no disease and 1: presence of disease.

Table 1 Statistical summary of numerical data

Attributes	count	mean	standard deviation	min	25%	50%	75%	max
Age	303.0	54.366337	9.082101	29.0	47.5	55.0	61.0	77.0
Resting Blood Pressure	303.0	131.623762	17.538143	94.0	120.0	130.0	140.0	200.0
Cholesterol	303.0	246.264026	51.830751	126.0	211.0	240.0	274.5	564.0
Max Heart Rate	303.0	149.646865	22.905161	71.0	133.5	153.0	166.0	202.0
Old Peak	303.0	1.039604	1.161075	0.0	0.0	0.8	1.6	6.2
nMajorVessels	303.0	0.729373	1.022606	0.0	0.0	0.0	1.0	4.0

3.2. Histogram and Box Plot Analysis:

Figure 1 shows the histogram and box plot analysis of Max Heart Rate. The skewness of the MaxHeartRate variable is -0.537, indicating a left-skewed distribution. A left-skewed distribution means that there are more individuals with higher maximum heart rates and fewer individuals with lower maximum heart rates compared to a symmetric distribution.

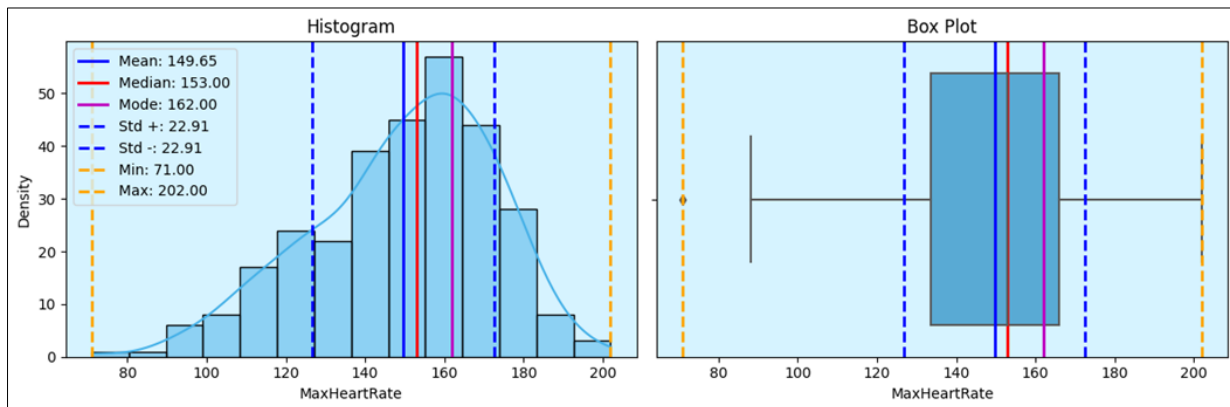


Figure 1 Histogram and Box plot analysis of Max Heart Rate

Mean: The average maximum heart rate is 149.65, representing the central value of the distribution.

Median: The median maximum heart rate is 153, indicating the middle value when the data is ordered from lowest to highest.

Mode: The most frequent maximum heart rate is 162, representing the most common value observed in the dataset.

Standard Deviation: With a value of 22.91, it measures the spread of maximum heart rates around the mean.

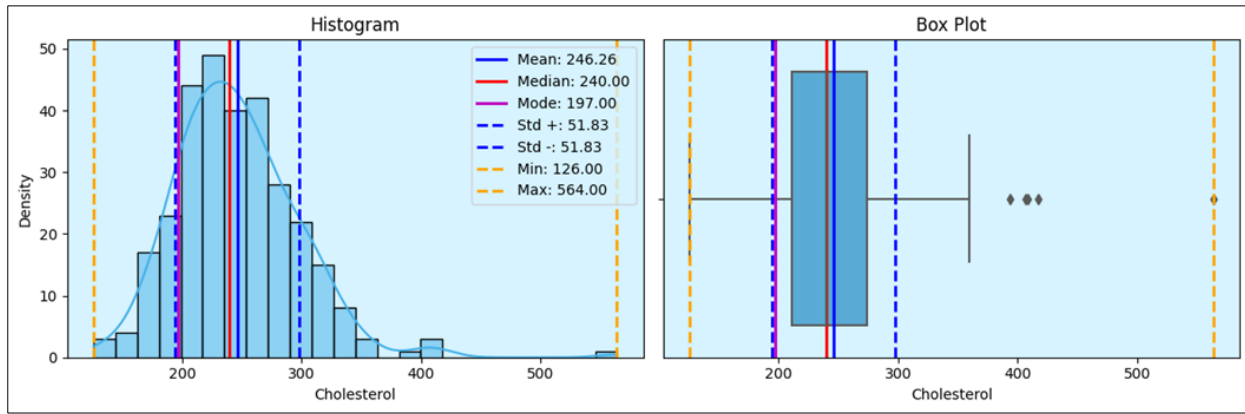


Figure 2 Histogram and Box plot analysis of Cholesterol

Figure 1 shows the histogram and box plot analysis of Cholesterol. The skewness of the cholesterol distribution is quantitatively expressed as 1.143, indicating a right-skewed or positively skewed distribution. This skewness signifies a predominance of individuals with lower cholesterol levels and a relative paucity of individuals with elevated cholesterol levels, compared to what would be observed in a symmetric distribution.

Mean: The mean cholesterol level, calculated as 246.26 mg/dl, serves as an indicator of the central tendency within the distribution. This metric elucidates the average cholesterol concentration across the sampled population.

Median: The median cholesterol value, identified as 240 mg/dl, delineates the central data point within the distribution, offering a measure that is less susceptible to outliers compared to the mean.

Mode: The mode, observed at a cholesterol level of 197 mg/dl, signifies the most recurrently encountered value within the dataset, providing insight into the most common cholesterol concentration among the subjects.

Standard Deviation: The standard deviation, quantified as 51.83, assesses the variability or dispersion of cholesterol levels around the mean, indicating the extent to which individual cholesterol measurements deviate from the average.

4. Experimental Results

In a binary classification context, there are two possible classes: positive (P) and negative (N). The confusion matrix organizes predictions into four categories based on the combination of the predicted class and the actual class [34-44]:

- True Positives (TP): The count of cases correctly identified by the model as positive.
- True Negatives (TN): The count of cases correctly identified by the model as negative.
- False Positives (FP): The count of cases incorrectly identified as positive.
- False Negatives (FN): The count of cases incorrectly identified as negative.

The evaluation criteria used to measure the algorithm's performance are based on specific metrics such as $f1_score$, precision, recall, and accuracy. In this paper, Support vector machine (SVM) model has been used for the classification of heart disease. Figure 3 shows the confusion matrix for original data with linear kernel and $C=0.3$. For training data, TP is 82- Instances correctly predicted as class 1. TN is 103. FP and FN is 11 and 15, respectively. For test data, the value of TP, TN, FP and FN is 33, 38, 7, and 12 respectively. Table 2 and 3 shows the classification report for training and testing data using Linear SVM. Accuracy is 0.88 and 0.79, respectively for training and testing data.

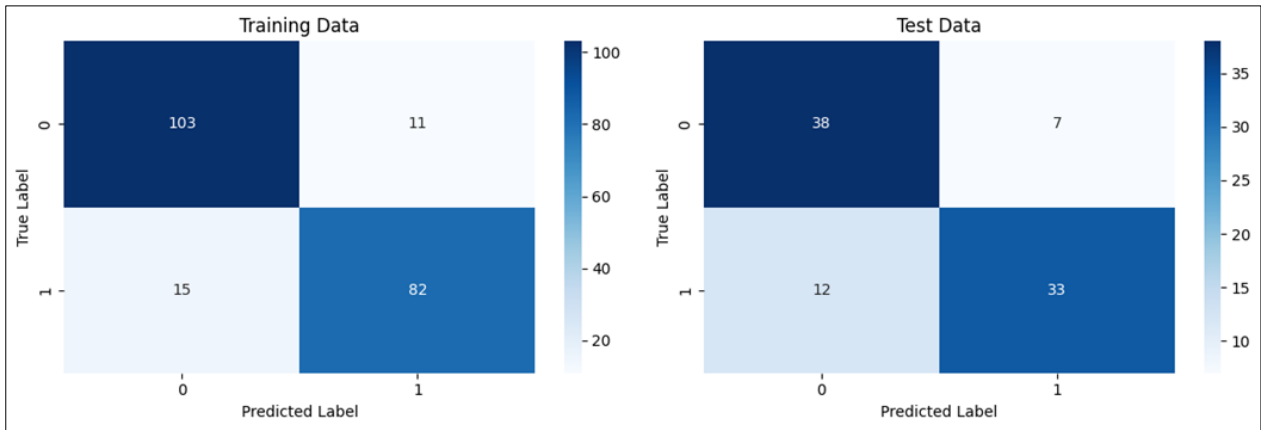


Figure 3 Confusion Matrix for original data with linear kernel and C=0.3

Table 2 Classification Report for training data using Linear SVM

Class	Precision	Recall	F1 Score
0	0.87	0.90	0.89
1	0.88	0.85	0.86

Table 3 Classification Report for testing data using Linear SVM

Class	Precision	Recall	F1 Score
0	0.76	0.84	0.80
1	0.82	0.73	0.78

Figure 4 shows the confusion matrix for transformed data with linear kernel and C=0.3. For training data, TP is 82- Instances correctly predicted as class 1. TN is 103. FP and FN is 11 and 15, respectively. For test data, the value of TP, TN, FP and FN is 34, 41, 4, and 11 respectively. Table 4 and 5 shows the classification report for training and testing data using Linear SVM. Accuracy is 0.88 and 0.83, respectively for training and testing data.

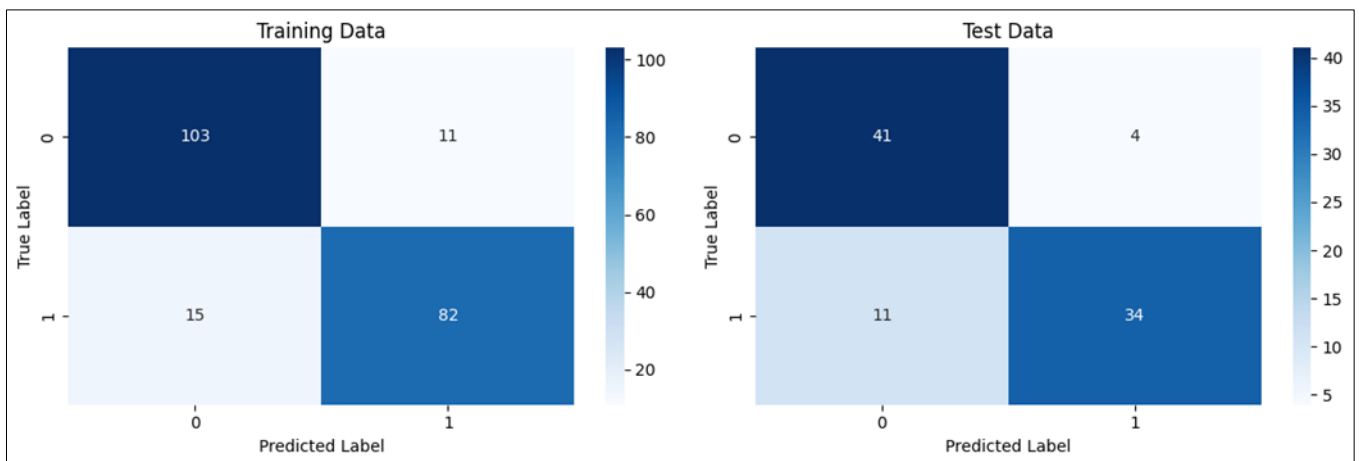


Figure 4 Confusion Matrix for transformed data with linear kernel and C=0.3

Table 4 Classification Report for training data using Linear SVM

Class	Precision	Recall	F1 Score
0	0.87	0.90	0.89
1	0.88	0.85	0.86

Table 5 Classification Report for testing data using Linear SVM

Class	Precision	Recall	F1 Score
0	0.79	0.91	0.85
1	0.89	0.76	0.82

4.1. Train SVM on original data with poly kernel and C=0.7

Figure 5 and 6 shows the confusion matrix for original data and transformed data, respectively. Here, poly kernel and C=0.7 is used. Table 6 and 7 shows the classification report for training and testing data (transformed data) using polynomial SVM. Accuracy is 0.91 and 0.80, respectively for training and testing data.

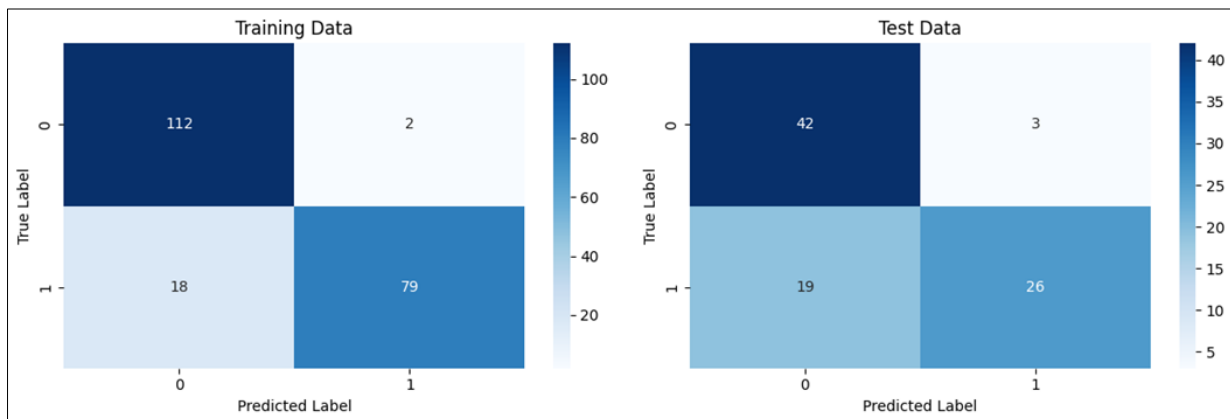


Figure 5 Confusion Matrix for original data with poly kernel and C=0.7

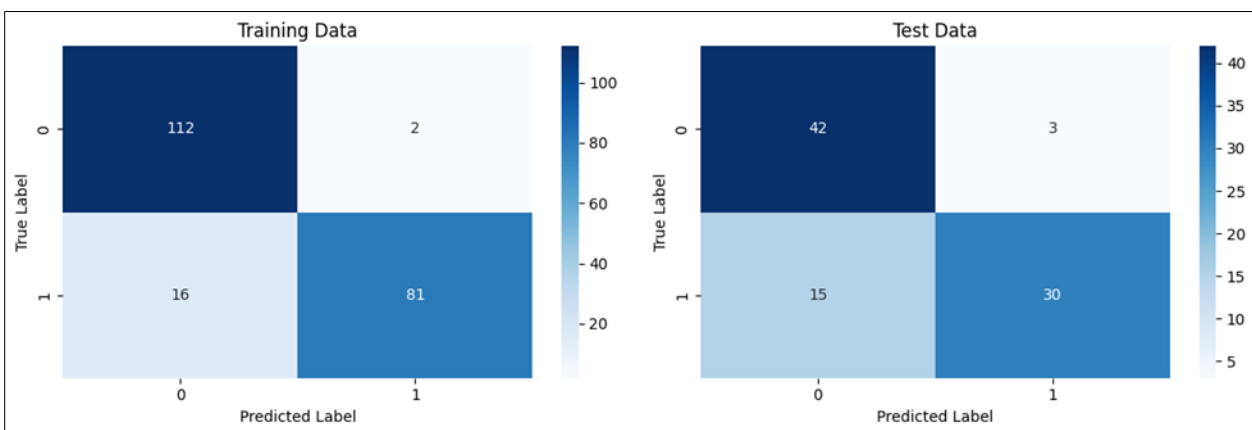


Figure 6 Confusion Matrix for transformed data with poly kernel and C=0.7

Table 6 Classification Report for training data using Polynomial SVM

Class	Precision	Recall	F1 Score
0	0.88	0.98	0.93
1	0.98	0.84	0.90

Table 7 Classification Report for testing data using Polynomial SVM

Class	Precision	Recall	F1 Score
0	0.74	0.93	0.82
1	0.91	0.67	0.77

5. Conclusion

This paper explores the application of data mining in the medical field, particularly for the detection and diagnosis of heart diseases using patient medical records. The performance of Linear and Polynomial Support Vector Machines (SVM) was assessed by employing metrics such as precision, recall, f1-score, and accuracy. The results of our research suggest that Polynomial SVM, particularly when applied to transformed data, yields superior accuracy in the diagnosis of heart disease compared to its Linear counterpart. Looking forward, our goal is to improve upon these foundational classification methods by creating an advanced meta-model designed to predict cardiovascular disease in individuals at risk of heart conditions.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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