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Classification and Feature Selection Approaches by Machine Learning Techniques: Heart Disease Prediction

N. Satish Chandra Reddy, Song Shue Nee, Lim Zhi Min & Chew Xin Ying
School of Computer Sciences,
11800, Universiti Sains Malaysia, Pulau Pinang, Malaysia
Email: xinying@usm.my

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***Abstract*—The heart disease has been one of the major causes of death worldwide. The heart disease diagnosis has been expensive nowadays, thus it is necessary to predict the risk of getting heart disease with selected features. The feature selection methods could be used as valuable techniques to reduce the cost of diagnosis by selecting the important attributes. The objectives of this study are to predict the classification model, and to know which selected features play a key role in the prediction of heart disease by using Cleveland and statlog project heart datasets. The accuracy of random forest algorithm both in classification and feature selection model has been observed to be 90–95% based on three different percentage splits. The 8 and 6 selected features seem to be the minimum feature requirements to build a better performance model. Whereby, further dropping of the 8 or 6 selected features may not lead to better performance for the prediction model.**

***Keywords*—Machine Learning, Feature Selection, R tool, Classification, Prediction**

I. Introduction

The heart disease is said to be major causes of death globally, according to the World Health Organization (WHO) the mortality rate due to heart disease is around 17.7 million (31%) in 2015 and is estimated to increase by 2020. Every year nearly 20 million people die, indicating the heart disease as a leading cause of death [1]. The group of diseases related to both the heart and blood vessels are referred as cardiovascular disease (CVD). The CVD includes coronary heart disease (CHD) or also known as coronary artery disease (CAD) which refers to the disease of the heart arteries that supply oxygen and blood to the heart, and is associated with life style conditions and age. CHD happens with the narrowing of the coronary arteries due to fatty material (plaque) deposition which is termed as atherosclerosis. The atherosclerosis reduces the blood flow to the heart, and said to be the underlying cause of complications such as angina and heart attacks. An angina is referred to typical pain in the chest, but it can often radiate to the shoulder left arm. The heart attacks, which is also known as myocardial infraction (MI), cardiac or myocardial infarction, and coronary thrombosis or occlusion is a condition when artery ruptures or narrows. A blood clots formed partially or completely during the repair of blood vessels rupture, reduces the blood flow to the heart muscles causing heart attacks. The chest pain, which many also radiate to the left are the signs of heart attacks. The modifiable risk factors are smoking, high blood pressure, high cholesterol, obesity, unhealthy diet, diabetics, depression and stress, on the other hand the non-modifiable risk factors are age, gender, genetic factors, race and ethnicity. Heart failure also known as congestive heart failure where right, left or both sides of the heart are affected once damaged it cannot heal. This is a serious condition when the heart muscle gets damaged, then becomes weak and does not pump blood properly to meets the needs of the rest of the body. Some of the factors, such as heart diseases, high blood pressure and diabetics, cardiomyopathy (a disease of the heart muscle) can over time, leave the heart too weak to fill and pump properly. The other circulatory system malfunctions are peripheral artery disease (PAD) narrowing of the arteries at the regions of arms, legs, stomach and head legs, stomach), venous thromboembolism (VTE: is a blood clot in a vein), aortic aneurysms (the weakened artery allowing it to widen) [2], [3].

Based on the disease statistics, it is noted that the rate of heart disease is increasing and cannot be identified from the visual prospective since it is caused by many risk factors, and does not show noticeable symptoms. However, the continuous monitoring of different vital signs such as heartbeat, blood pressure, glucose levels, ECG, EEG, EMG, respiratory rate and temperature would be useful to track the early detection of different disease abnormalities. This monitoring has been made possible with an advancement in wireless communication technology "Wireless Body Area Network (WBAN) which consists of tiny Bio-Medical Sensors (BMSs)" which are at reasonable cost. The three methods of BMS deployment includes on body wearable (to monitor blood pressure, ECG and EMG), in-body implantation (to monitor lungs, liver and kidney), and off body (to monitor physical health conditions, body position, arm positions, walking and running). The monitoring of these BMS is done through Body Area Network Coordinator (BANC) following star network topology [4]. The monitoring of the patients is categorized as non-emergency (a normal reading of vital signs such as temperature and glucose levels) and emergency data (signs such as low respiratory rate and high blood pressure). The Medium access control (MAC) Superframe structures uses IEEE 802.15.4 as a protocol [5]. The heterogeneous nature of the patient's data is classified into Ordinary Packet (OP), Reliability Data Packet (RP), Critical Data Packet (CP) and Delay Data Packet (DP). Though these classifications help to deliver without loss in patient data to medical doctors, and with less energy consumption of BMSs, they lack the consideration of low and high threshold values of vital signs in emergency data categorization. This has been overcome with the help of a traffic priority based MAC protocol and slot allocation based on the alert signals to BMSs respectively, in which the vitals such as heart rate, blood pressure, respiratory rate and temperature has been categorized into threshold ranges of low, normal and high values. These values are useful to provide appropriate and dedicated timeslots to non-emergency and emergency based BMSs. Based on the severities of the threshold values of vital signs BANC allocate slots, apart from resolving the conflict of slots allocation. This protocol improves throughput, reduces packets delay for non-emergency and emergency data, consume minimum energy of BMSs and BANC [6], [7].

The enormous amount of the data is being produced from different hospitals and medical centers or an organization. This data is not being used in a proper way, although it contains potential information for further proceedings such as clinical decision support, disease surveillance and population health management [8], [9]. On the other hand, the clinical decisions made by doctors indicate that there is a chance of leaving the hidden quality from the data leading to errors and unwanted biases. This might affect the medical costs and quality of health services provided to the patients [10]. The decrease in medical errors and unwanted practice variation, improve patient outcome and safety, can be achieved by the integration of clinical decision support with computer-based patient records. The researchers and clinicians are studying different heart disease datasets with different machine learning classification algorithms and features selection methods to bring up possible predictions for heart disease [11], [12]. In this paper, the main objectives are to build a model with prevails performance, and to identify which selected features play a key role in the prediction of heart disease by using Cleveland and statlog project heart datasets from UCI [13] with R tool.

II. Literature Review

This section reviews some work related to classification and feature selection methods applied for the prediction of heart diseases. Heart being one of the main organs of the body allows the pumping of the blood through blood vessels (i.e., circulatory system). The oxygen and other materials such as nutrients, hormones and waste substances are carried out to the other parts of the body through blood. Thus, heart is referred to play an important role in circulatory system. The condition where the impairment of the heart occurs is referred to as heart disease. The heart disease or cardio vascular disease refers to the disorders of heart and blood vessels. The different types of heart diseases are coronary heart disease, heart attacks (blocked vessels or myocardial infarction) and angina (coronary artery disease). The coronary heart disease leads to heart attack and is said to be one of the major causes for the individual death globally (WHO). The non-modifiable risks factors such as age, gender, genetic or family history, ethnicity or race, and modifiable risk factors such as cholesterol, high blood pressure, hypertension, lack of physical exercise, smoking, obesity and stress are responsible for heart diseases [14] [15].

A. Data Mining and Machine Learning Algorithms

Data mining is a process of exploring the new and valuable information from data, this could significantly improve the quality of clinical decisions and play an important role in intelligent medical system. The data mining consists of various disciplines, among them machine learning is one discipline, and consists of different techniques such as classification, clustering, regression, association analysis, and outlier detection [16]. The various classification machine learning algorithms used for the prediction of heart disease are reviewed below:

1) K-Nearest Neighbor's Algorithm

It is a simple classifier that cannot handle noises, easy to implement and understand, requires short training time and whole training set is used for prediction. The K-Nearest Neighbors (K-NN) with weighting parameter has been used for the prediction of heart disease. Among 13 attributes mentioned in UCI heart disease dataset, the selection of 8 attributes due to simple measurements has been taken into consideration for this study. The study shows the accuracy of 81.9 % and also mentioned that 8 attributes such as age, sex, chest pain, trestbps, trestbpd, restecg, thalrest, exang are more than enough to predict heart disease [17]. The similar techniques (KNN) have been used along with the feature selection technique such as particle swarm optimization (PSO) for the heart disease prediction where it shows 100% accuracy [18].

2) Support Vector Machine (SVM)

Based on the kernel functions the support vector classifiers are divided into different types such as linear, nonlinear, radial basis function (RBF), sigmoid and polynomial. The hyperplane or support vector machine separates the support vector or data points. The different classification techniques such as K-Nearest Neighbors, J48 Decision tree, SMO and Naive Bayes based on 8 attributes with 10 fold cross validation in WEKA was used. The four features have been extracted using gain ratio evaluation technique. The highest accuracy is found to be in J48 with 83.73% [19]. In another study, the different datasets of heart, diabetes and cancer were classified using SVM, RBF and Naïve Bayes in Weka. Among 3 classifiers SVM showed the highest accuracy of 93.75% and also seem to be most effective and robust classifier in predicting diseases [20].

3) Random Forest

Random forest constructs a multitude of decision trees at training time and output the mode prediction of the classes for classification and the mean prediction for regression. The different patterns in the data are evaluated by the decision tress. The class prediction is based on the majority vote for classification. The random forest with 10 fold cross validation along with feature selection methods such as chi square and genetic algorithm was used to for the prediction of heart disease. The single UCI heart dataset was used in this study and the accuracy as found to be 83.70 % and found to be better when compared with other algorithms such as Naïve Bayes, decision tree and neural nets [21]. In another study, the Cleveland heart disease was used with random forest and 10 fold cross validation to get an accuracy of 85.81%, the feature selection approach has given better accuracy [22].

4) Naïve Bayes

Naïve Bayes is a classifier that is based on Bayes theorem, and it assumes the probability of the features which are independent of other features. The different classification algorithms REPTREE, J48, CART, Naïve Bayes and Neural networks have been used on the data collected from medical practitioners in South Africa. Weka tool is used for this purpose and the accuracy of Naïve Bayes is found to be 85.92% [23]. In another study, The single UCI heart disease dataset has been used for the prediction of heart disease using K-NN, decision tree, SVM and Naïve Bayes. The Weka software was used, and the Naïve Bayes shows highest accuracy [24].

5) Neural Network

Neural network is inspired by the biological neural network that constitute in the brain or central nervous system, this is also called as an artificial neural network. It is used in machine learning algorithm, and can be used of classification/supervised learning. The neurons and synapse are interconnected each other that allow passage of messages with in them. The three major parts of the neural network are the input layer, hidden layer and output layer.

The three algorithms such as Neural Networks, J-48 Decision Tree and Naïve Bayes along with feature selection method CfsSubsetEval attribute filter with Best First search method on single UCI heart disease dataset was used. Weka tool was used for this study, and the highest accuracy is shown by Naïve Bayes both with and without feature selection [25]. In another study, the Neural Network with feature correlation analysis (NN-FCA) was studied on Sixth Korea National Health and Nutrition Examination Survey (KNHANES-VI) dataset. In this study, it is found that chronic renal failure and triglyceride were closely related to coronary heart disease. The NN-FCA showed the highest accuracy of 82.51% [26].

B. Feature Selection Approaches

The huge amounts of data produced by different sources have become a fundamental importance for capturing, storing, searching, sharing, and are hard to interpret and analyze [27]. The huge volume of data and the increase in diagnosis cost made to look for feature selection which in turn increases the accuracy of the model, and give a better result for the prediction of disease. The initial dataset consists of number of attributes, some of them may not be useful thus it is necessary to remove them during data preprocessing [28]. Thus one of the important steps in data preprocessing is feature selection, by this unnecessary features can be removed and improve the performance to build a better classification model. The various feature selection methods such as wrapper methods, filter, embedded and ensemble and hybrid methods have been applied to study the heart disease prediction [29].

1. Trstbps, Restecg, slope, CA, Thal, Age are the best selected features with the approach of novel feature selection, with the selected features the accuracy was found to be 93% and 89 % in neural network and SMO algorithms respectively [28].

2. The recursive Feature Elimination (RFE) has been applied along with stochastic gradient boosting algorithm and the selected features was found to be chest pain, ca, and Thal with the accuracy of 95.45% [30].

3. The 4 feature selection methods have been applied and 12 classification algorithms has been used for heart disease prediction. The application of different feature selection methods showed different best selected features. The highest accuracy was found to be in SVM-linear and Naïve Bayes with an accuracy of 84.81% [31].

III. DATASET

A. Data Sources

In this study, the five heart disease datasets (Cleveland, Switzerland, Hungarian, V.A. Medical and Statlog project heart disease) are collected from publicly available source UCI machine learning repository webpage [13]. The five datasets were combined into single dataset (i.e., combined dataset) for better model performance. The combined dataset consists of 1190 instances with 14 attributes. The characteristics of five heart disease datasets and combined dataset are shown in Table 1.

TABLE 1. Characteristics of five and combined dataset of heart Disease

Datasets	**No of Instances**	**No of Attributes**	**Missing Values**
Statlog project	270	14	No
Cleveland	303	14	No
Hungarian	294	14	Yes
V.A. Long Beach	200	14	Yes
Switzerland	123	14	Yes
Combined Dataset	1190	14	Missing values replaced with Mode Value

B. Attributes Description

The dataset consists of 14 attributes. The predictable attribute is referred to "Diagnosis" and rest of 13 as input attributes. The attribute descriptions are shown in Table 2.

TABLE 2. Description of attributes in the dataset

Features	**Type**	**Description, Value**
Sex	Discrete	1 = male; 0 = female

Chest Pain	Discrete	Value 1: typical angina;
		Value 2: atypical angina;
		Value 3: non-anginal pain;
		Value 4: asymptomatic

FBS	Discrete	Fasting Blood Sugar, 0 = false (FBS <120 mg/dl) 1 = true (FBS > 120 mg/dl)
Restecg Rest Electrocardiographic	Discrete	Value 0: normal; Value 1: having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV); Value2 : showing probable or definite left ventricular hypertrophy by Estes' criteria
Exang	Discrete	Exercise induced angina. 1 = yes; 0 = no
Slope	Discrete	Peak exercise slope measure, Value 1: upsloping, Value 2: flat, Value 3: down sloping
ca	Discrete	number of major vessels colored by flourosopy (0-3)
thal	Discrete	Patient heart rate, 3 = normal; 6=fixed defect; 7 = reversable defect
Age	Continuous	Patients age , 28 to 77
Trestbps	Continuous	Resting blood pressures of patients measured in mm Hg on admission to the hospital 80-200.
Chol	Continuous	Patient serum cholesterol measured in mg/dl. 85, 100 - 200 - 394, 400-603
thalach	Continuous	Patient maximum heart rate achieved.60-202, Low: below 50, Normal:51-119, High: 120-202 [6] [7]
oldpeak	Continuous	ST depression made by exercise relative to rest -2.6 to -0.1, 0, 0.1 to 6.2, 120
Diagnose	Discrete	0: No heart disease; 1: Heart disease

IV. Methodology

A. Data Preprocessing

In the data preprocessing stage, missing values are replaced with mode value based on the particular datasets source. Second, taking into consideration that heart disease patients might have high values of respective attributes (i.e., referred as outliers in the dataset) are not removed. The normalization (normalize <- function(x) {return ((x - min (x)) / (max(x) - min(x)))} has been carried out since dataset consists of different measuring units.

B. Data Analysis

After data normalization to build a classification model, the combined dataset with 14 attributes is divided into training and testing data with a percentage split of 60–40%, 70–30% and 80–20% respectively with set.seed (123). The R -based CARET package (https://cran.r-project.org/web/packages/) is used for data splitting, pre-processing steps such as normalization, classification algorithms such as K-Nearest Neighbor (KNN, library “caret”, method = 'knn', tuneLength = 10), Support Vector Machine (SVM, library “caret”, method = 'svmLinear', tuneLength =10), Random Forest (RF, library “randomForest”,method='rf',ntree=500,importance=TRUE), Naïve Bayes (NB, library “e1071”, method = ‘naïve_bayes’) and Neural Network (NN, library “nnet”, method = 'nnet', trace= FALSE) with 10 fold cross validation (method = "cv", number = 10) are evaluated based on the fore mentioned training and testing data. The different feature selections methods such as correlation matrix (library “mblench”), recursive feature elimination (RFE) method with random forest algorithm (library “mblench”, functions=rfFuncs, method="cv", number=10). The variable importance estimations such as regression method to calculate variable importance (library “mblench”), rank feature by Importance (library “class” and “mblench”) with learning vector quantization model (LVQ) is addressed using CARET package in R tool (http://topepo.github.io/caret/index.html).The performance of a model on test data is calculated by accuracy, sensitivity/recall, and specificity in R tool. Sensitivities and specificity measures the true positives (risk class) and the true negatives (normal class) respectively. Thus the predictive capabilities of the classifiers are measured by sensitivity and specificity values.

V. Results

A. Performance on Combined Dataset

To the best of author knowledge, there is no studies addressed with the combined dataset (i.e., of five heart disease datasets: Cleveland, Switzerland, Hungarian, V.A. Medical and Statlog project heart disease with the five mentioned algorithms in this study) [24] [32]. R tool is selected to understand which classification model has a better performance on combined dataset with 13 features. The performance measures are in accordance with the accuracy of each classification algorithm. Among the five classification algorithms used, the highest accuracy in three percentage splits (60–40, 70–30, and 80–40) has been observed in random forest with a range of 91.39%–94.96%, and average accuracies (85.92–89.41%) respectively (refer to Table 3).

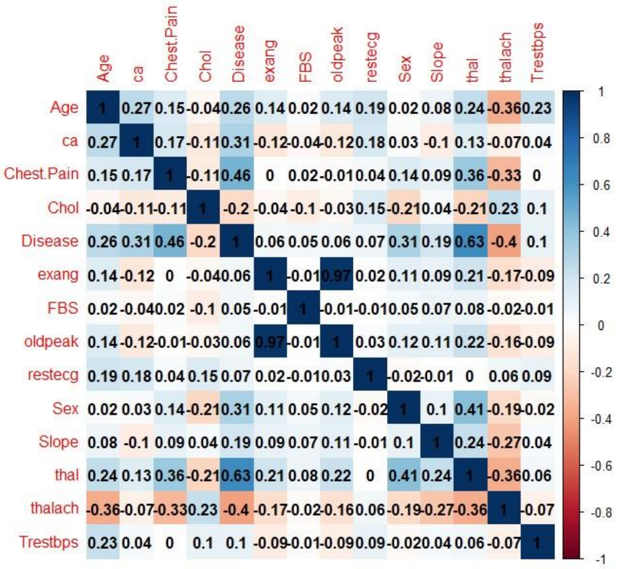
TABLE 3. The performance comparisons of different percentage splits of combined dataset with 13 features

Algorithms	60 - 40			70 - 30			80-20		
	Accu	Sensi	Speci	Accu	Sensi	Speci	Accu	Sensi	Speci
KNN	84.03	0.7917	0.8808	83.75	0.8176	0.853	86.55	0.847	0.879
SVM	84.45	0.791	0.888	85.15	0.786	0.904	87.82	0.8381	0.909
Random Forest (RF)	91.39	0.856	0.961	92.16	0.880	0.954	94.96	0.904	0.985
Naïve Bayes	84.45	0.842	0.846	85.71	0.729	0.959	88.66	0.800	0.954
Neural Network	85.29	0.773	0.919	85.43	0.786	0.909	89.08	0.876	0.902
Avg Accuracy	85.92	0.810	0.898	86.44	0.799	0.915	89.41	0.853	0.925

Accu: Accuracy; Sensi: Sensitivity; Speci: Specificity; k-nearest neighbors algorithm (k-NN), Support vector machine (SVM)

B. Performance on Feature Selection Attributes

The feature selection is performed on the combined dataset to select a subset of relevant features for model building that aims to improve model accuracy. In this study, a correlation analysis was performed to know the highly correlated attributes, in this case the correlation has been found to be between exang and oldpeak attributes with a given correlation cutoff at 0.75 (refer to Figure 1).



	Age	ca	Chest.Pain	Chol	Disease	exang	FBS	oldpeak	restecg	Sex	Slope	thal	thalach	Trestbps
Age	1	0.27	0.15	-0.04	0.26	0.14	0.02	0.14	0.19	0.02	0.08	0.24	-0.36	0.23
ca	0.27	1	0.17	-0.11	0.31	-0.12	-0.04	-0.12	0.18	0.03	-0.1	0.13	-0.07	0.04
Chest.Pain	0.15	0.17	1	-0.11	0.46	0	0.02	-0.01	0.04	0.14	0.09	0.36	-0.33	0
Chol	-0.04	-0.11	-0.11	1	-0.2	-0.04	-0.1	-0.03	0.15	-0.21	0.04	-0.21	0.23	0.1
Disease	0.26	0.31	0.46	-0.2	1	0.06	0.05	0.06	0.07	0.31	0.19	0.63	-0.4	0.1
exang	0.14	-0.12	0	-0.04	0.06	1	-0.01	0.97	0.02	0.11	0.09	0.21	-0.17	-0.09
FBS	0.02	-0.04	0.02	-0.1	0.05	-0.01	1	-0.01	-0.01	0.05	0.07	0.08	-0.02	-0.01
oldpeak	0.14	-0.12	-0.01	-0.03	0.06	0.97	-0.01	1	0.03	0.12	0.11	0.22	-0.16	-0.09
restecg	0.19	0.18	0.04	0.15	0.07	0.02	-0.01	0.03	1	-0.02	-0.01	0	0.06	0.09
Sex	0.02	0.03	0.14	-0.21	0.31	0.11	0.05	0.12	-0.02	1	0.1	0.41	-0.19	-0.02
Slope	0.08	-0.1	0.09	0.04	0.19	0.09	0.07	0.11	-0.01	0.1	1	0.24	-0.27	0.04
thal	0.24	0.13	0.36	-0.21	0.63	0.21	0.08	0.22	0	0.41	0.24	1	-0.36	0.06
thalach	-0.36	-0.07	-0.33	0.23	-0.4	-0.17	-0.02	-0.16	0.06	-0.19	-0.27	-0.36	1	-0.07
Trestbps	0.23	0.04	0	0.1	0.1	-0.09	-0.01	-0.09	0.09	-0.02	0.04	0.06	-0.07	1

Fig. 1. Correlation plot of the combined dataset

After the removal of exang and oldpeak from the combined dataset the different feature selection methods (see data analysis) implemented in R tool has been applied. The 10 selected features/attributes such thal, ca, chestpain, age, thalach, chol, trestbps, slope, restecg and sex are common across 3 feature methods. The attribute FBS is observed in regression method and rank feature by Importance. The selected features by 3 methods showed the similar order of arrangement/topology with minor differences in the ranking order (refer to Table 4).

Based on the order of the features (refer to Table 4), the common 8 and 6 selected features (refer to Table 5) are taken into consideration to build a model. In 8 selected features, the highest accuracy in three percentage splits (60–40, 70–30, and 80–40) has been observed in random forest with a range of 91.18–94.96%, and average accuracy (85.99–89.07%) respectively (refer to Table 6). Similarly with respect to 6 selected features the highest accuracy in three percentage splits (60–40, 70–30, and 80–40) has been observed in random forest with a range of 89.64–92.44%, and average accuracy (85.20–88.40%) respectively (refer to Table 7).

TABLE 4. The order of best selected features after the removal of exang and old peak attributes

Recursive Feature Elimination	**Regression to Calculate Variable Importance**	**Rank Feature by Importance**
thal	thal*** 12.650	thal 0.816
ca	ChestPain*** 7.368	ChestPain 0.766
ChestPain	ca *** 7.159	thalach 0.734
oldpeak	thalach*** 4.330	exang 0.711
thalach	Trestbps** 2.731	oldpeak 0.704
Trestbps	Sex * 2.520	ca 0.664
Age	Slope * 2.226	Age 0.657
Chol	Restecg 1.721	Sex 0.632
exang	Chol 0.628	Slope 0.605
Slope	Exang 0.622	Trestbps 0.547
Sex	FBS 0.427	Chol 0.546
restecg	oldpeak 0.057	Restecg 0.542
FBS	Age 0.050	FBS 0.532

Significance code: ***: 0, **:0.001, *: 0.01

TABLE 5. The common selected features

8 selected features	thal, chest pain, ca, thalach, trestbps, age, sex and chol
6 selected features	thal, chest pain, ca, thalach, trestbps, age

The highest accuracy in 8 and 6 selected features is found to be in random forest (refer to Table 6 & 7) which is in agreement with the combined dataset with 13 features (refer to Table 3). The 8 selected features show average accuracies with an insignificant of ±0.5% in 70–30 and 80–40 percentage split (refer to Table 6), whereas the 6 selected features (refer to Table 7) showed the decrease in average accuracies (1.24% in 70–30% split and 1.18% in 80–40%) which could be due to the dip in the performance of SVM, RF (in both 70–30% and 80–40%), and NN (80–40%) to that of combined dataset with 13 features (refer to Table 3).

V. Discussion

In this study, the heart disease prediction has been evaluated with the classification and feature selection algorithms implemented in CARET package of R tool using combined dataset. The highest accuracy is shown by random forest in three percentage split (without and with feature selection). This shows the performed random forest algorithm shows the best performance with the existing model accuracies [22] [33]. The average accuracies of 8 selected feature shows similar results with the combined dataset, indicating these features could be used for the prediction of heart disease as mentioned in the previous studies where KNN algorithm was used [17].

TABLE 6. The performance comparisons of different percentage splits of combined dataset with 8 features

Algorithms	**60 - 40**			**70 - 30**			**80-20**		
	Accu	**Sensi**	**Speci**	**Accu**	**Sensi**	**Speci**	**Accu**	**Sensi**	**Speci**
KNN	83.82	0.796	0.873	83.47	0.811	0.853	86.97	0.866	0.872
SVM	84.24	0.777	0.896	81.79	0.748	0.873	85.71	0.828	0.879
Random Forest	91.18	0.875	0.942	91.60	0.880	0.944	94.96	0.914	0.977
Naïve Bayes	86.76	0.810	0.915	87.39	0.811	0.924	89.5	0.857	0.924
Neural Network	85.29	0.777	0.915	85.71	0.773	0.924	88.24	0.838	0.917
Avg Accuracy	86.25	0.807	0.908	85.99	0.804	0.903	89.07	0.860	0.913

Accu: Accuracy; Sensi: Sensitivity; Speci: Specificity; k-nearest neighbors algorithm (k-NN), Support vector machine (SVM)

TABLE 7. The performance comparisons of different percentage splits of combined dataset with 6 features

Algorithms	**60 - 40**			**70 - 30**			**80-20**		
	Accu	**Sensi**	**Speci**	**Accu**	**Sensi**	**Speci**	**Accu**	**Sensi**	**Speci**
KNN	85.5	0.812	0.892	85.15	0.792	0.899	87.82	0.847	0.902
SVM	82.77	0.773	0.873	82.07	0.735	0.888	83.61	0.809	0.857
Random Forest	90.76	0.870	0.938	89.64	0.886	0.904	92.44	0.923	0.924
Naïve Bayes	86.97	0.824	0.907	84.03	0.792	0.878	90.76	0.885	0.924
Neural Network	85.5	0.791	0.907	85.15	0.786	0.904	87.39	0.828	0.909
Avg Accuracy	86.3	0.814	0.903	85.20	0.798	0.894	88.40	0.858	0.903

Accu: Accuracy; Sensi: Sensitivity; Speci: Specificity; k-nearest neighbors algorithm (k-NN), Support vector machine (SVM)

However, the further analysis with 6 selected features showed the decrease in average accuracies with that of combined dataset, this could be due to under fitting of the attributes and the performance of the classifier under default conditions. These results are in general agreement with the previous studies where 5 out of 6 selected features in this study were used with different feature selection method [11], thus indicating this features as a minimum number to build a reliable model. It is expected that the further drop in 6 selected features to build a model may not give a better prediction. However, this is in contrast where 3 selected features such as chest pain, ca, Thal showed 95.45% with different feature selection method. On the other hand, it is shown the 3 selected features might be important for accuracy improvement [30].

VI. CONCLUSION

It is known that the accuracy of the model depends on the database, preprocessing, analytical tools and techniques. The present study shows it is important to select minimum and prominent attributes to improve the performance when compared to the use of whole features from the dataset. This study shows that the random forest can be used as a good classification algorithm for the accurate prediction of heart disease with an accuracy of 90–95 %. However, the addition of dataset with the inclusion of other non-modifiable risk factors (genetic factors), and modifiable risk factors such as smoking, lack of physical exercise, alcohol consumption could result in better risk prediction of the heart disease. The less variation of accuracy differences between dataset and selected features (8 and 6) indicates these features can be useful for the prediction of heart disease. However, drop of the 6 selected features may not lead to better model prediction.

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