Journal of Computer Science

Original Research Paper

Cardiovascular Disease Prediction using Various Machine Learning Algorithms

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Article history
Received: 03-07-2022
Revised: 20-08-2022
Accepted: 19-09-2022

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Abstract: Almost one-third of all deaths caused around the world were caused due to cardiovascular diseases. Even if death was not the result, much cost is incurred during the treatment of such diseases. But much of these deaths and treatments could have been prevented with prior action. Advance knowledge of the symptoms and consequently proper care can lead us to avoid such diseases. Thus, current research proposes a highly effective model to predict the presence of heart diseases. Bad eating habits, smoking, stress, and genetics are some of the factors that influence our body mechanisms, which actually cause various irregularities in our hearts and thus adversely affect our bodies. The body mechanisms influenced by external factors have been included to prepare an efficient model to predict the probability of cardiovascular diseases. UCI repository dataset has been utilized for the training and testing purpose in our model. Then accordingly, five different algorithms namely Logistic Regression, Support Vector Machine, Multi-Layer Perceptron (MLP) Classifier with Principal Component Analysis (PCA), Deep Neural Network, Bootstrap Aggregation using Random Forests are executed on our filtered dataset to find which one is the optimum out of all of them. Pre-processing techniques have been extensively used to filter out the dataset. The data processing along with the different models employed make this a sound paper, which could be utilized for real-world cases without any prior modification. Different places around the world would take different factors into account, hence our model can be used as it takes all critical factors from several datasets.

Keywords: Cardiovascular Disease Prediction, Aggregated Dataset, Machine Learning Algorithms, Deep Learning, Bootstrap Aggregation using Random Forests, Logistic Regression, Deep Neural Network, MLP with PCA, SVC

Introduction

With the advancement in technology, though longevity has increased, many lives are still lost to causes that could have been prevented with proper care. Heart attacks are responsible for a fair share of deaths around the world and even the number of deaths that have occurred due to heart attacks are on the rise (Motarwar *et al*., 2020). Moreover, heart attack in the younger ages, an incident seldom seen before, is frequently occurring in the current times. One of the more terrifying attributes of such attacks is that there are not many symptoms or predicaments beforehand. This is a dire situation that needs to be addressed with utmost priority. The better step to take would be to prevent such diseases or at least have a forewarning. Hence, the initial stage toward a healthier body would be the prediction of heart attacks. Current research proposes a system to predict whether heart disease will exist or not (Terrada *et al*., 2020). Numerous relevant factors ergo Age, chest pain, cholesterol, fasting sugar, resting BP, etc., have been incorporated to produce a sound model. Even the data included for this model has been integrated from various places, to give a better simulation comparable to the real-world cases. For data processing, imputing the missing values, then the output column, which indicates the chances of heart-related issues, had to be transformed too along with scaling. Then this filtered data was passed through five different models-namely Logistic regression, Support Vector Machine (SVM), MLP Classifier with Principal Component Analysis, Deep Neural Network, and finally Bootstrap aggregation using Random Forest; to test which one gave us the best performance (Chakarverti *et al*., 2019). Promising accuracy of 97.67% was achieved from Bootstrap aggregation, out of all the models.

Literature Review

Neural Networks require much experimenting with a series of parameters to get the best performance, (Yazid *et al*., 2018) the paper suggests a parameter tuning framework, for the Artificial Neural Network. Statlog heart disease dataset along with the Cleveland dataset was considered to train the model. The inclusion of a variety of datasets would have increased the scope of the model, making it more acceptable (Yazid *et al*., 2018). The accuracy obtained is 90% for the Star log dataset, while 90.9% for the Cleveland one, suggesting that more improvements could be made. In our paper, the current model is built while considering data from various sources to make it more versatile and achieve higher accuracy of 97.67%.

Diwakar *et al*. (2021) in paper explain that diagnosis of the disease before its occurrence can probably save people's lives. A thorough study of the classification methods for machine learning and image fusion has been depicted in this study (Diwakar *et al*., 2021). Age, Sex, FBP-Fasting blood pressure, hypertension, smoking, and many more attributes have been taken into consideration by different methods to diagnose the diseases. Then a basic explanation of various techniques along with outlining of the whole process sums up the constituent of this study, no actual method or model to diagnose or predict the occurrence of the disease has been shown here. While the model proposed by us calculates the probability of occurrence and gives a definite answer whether the disease will occur or not, by considering numerous factors.

As the number of problems related to the heart is increasing with each passing day, problems can even cause death. Hence the authors, (Singh and Kumar, 2020) have suggested a model for different algorithms (Singh and Kumar, 2020). A casual mention of the working of different Machine learning methods, along with their definitions and basic execution of four models namely k-Nearest Neighbor-KNN, decision tree, linear regression, and Support Vector Machine (SVM) has been done. The dataset on which these methods were employed is the UCI repository dataset. Further data processing and tweaking and tuning of the parameters could have resulted in much better performance. Our paper goes in-depth about these workings, which ultimately results in a more sophisticated model, that too with good accuracy of 97.67%.

One of the most critical threats to human beings in the current times is heart-related diseases. The paper (Ambesange *et al*., 2020) uses normalization and outlier detection was done to improve the data, obtained from the UCI repository. Application of several feature selection methods, like the Extra tree's classifier, Random search, and other techniques are made for tuning. Seven models are developed with various features (Ambesange *et al*., 2020). One of the models for which the dimension reduction technique namely Kernel Principal Component Analysis (PCA) was employed on the dataset and then the Grid Search method was used to give 100% accuracy, which suggests the model is over-fitted, thus requiring much more processing. No such anomalies will be found in the paper written by us.

Heart diseases impose a great threat to mankind and one of the first steps to dealing with such diseases is to detect them. Thus, a model is proposed by Yadav *et al*. (2020) to predict the state of heart diseases. UCI dataset has been included to build up the model. A comparison of binary and multi-class classification, along with an explanation regarding various machine learning algorithms has been included here (Yadav *et al*., 2020). Regularization is used to overcome over-fitting. Fuzzy KNN is working better than the other algorithms. Pre-processing of the dataset-imputing missing values, normalization, etc., should have been done to make the dataset better.

Prediction of patterns occurring in the medical sector is a challenge. Prediction of the occurrence of diseases is quite a complicated task in itself. Motarwar *et al*. (2020) employ five algorithm models Random Forest, Naïve Bayes, Support Vector Machine (SVM), Hoeffding Decision Tree, and Logistic Model Tree (LMT) for predicting the occurrence of heart diseases (Motarwar *et al*., 2020). The dataset used for training and testing the model is the Cleveland dataset. Out of 76 attributes present, 13 are selected. Using only one dataset, without any further processing limits the functionality of this model for real-world issues. A brief explanation of the working of each algorithm is done. No methods were used for cleaning the data. The application of such filtering methods would have resulted in a much better efficiency of the model. Thus, much work in detail would have to be performed on this model to make it worthy for the predicting of diseases for any actual scenario working.

Proposed Work

Dataset Description

The proposed system aims to collect and interpret the data from various clinical databases related to heart disease originating from different geographical locations like Switzerland, Hungary, Long Beach, and Cleveland. The different datasets are available at the UCI repository (UCI, 1990).

B. Data Preprocessing

Data Cleaning

The four different datasets cumulatively contribute to a different number of records as shown in Table 1.

The dataset consists of 13 independent features and 1 dependent feature. The dependent feature is a categorical type that indicates the presence (denoted by value 1) or absence (denoted by value 0) of heart disease. The features/attributes mentioned in Table 2 and Fig. 1 depict the whole architecture of the proposed system.

A total of 920 records. The dataset contained a large amount (>50%) of missing values for Thalassemia, Peak exercise, and Vessels colored by fluoroscopy features. The number of records with missing values for each feature is shown in Table 3.

The missing values for Cholesterol are imputed using the mean strategy, while the null values for Vessels colored, fasting sugar, Slope, and Thalassemia are imputed using the mode strategy. The missing values for the Resting ECG, induced angina, Maximum rate, Resting BP, and ST Depression features were negligible and hence the records were removed from the dataset resulting in a total of 854 rows in the dataset.

The target variable of the dataset is categorized into 5 different labels numbered from 0 to 4 (inclusive). The digits 1 to 4 indicate different stages of heart disease. Since the proposed system is based on binary classification, all the labels within the range (Terrada *et al*., 2020; Yazid *et al*., 2018) are replaced with a common digit 1, indicating the presence of the disease.

Heatmaps for features before and after imputing the missing values are shown in Fig. 2 and 3 respectively.

Transforming the Labels

The target variable of the dataset had five unique values in the range [00, 44], where 0 represents no risk of heart attack and the values 11, 22, 33, and 44 indicate the increased risk of a heart attack. To make the dataset suitable for binary classification, the labels in the range (Swain *et al*., 2019ab; 2020) are all replaced by 1. Hence, they now indicate whether the person has a risk of heart attack or not. It no longer gives information about the amount of risk. The count of each label in the dataset is shown in Fig. 4.

Numerical Feature Selection

From all the available numerical features, the top 4 were selected using the ANOVA measure. ANOVA (Analysis of Variance) is a parametric statistical hypothesis procedure used to determine whether the means of two or more samples of data emerge out of the same distribution. This F-statistic score is widely used when the feature is numerical and the target is categorically similar to the problem at hand (Sthle and Wold, 1989). The larger the value of ANOVA more significant the numeric feature. The test concluded that the features 'Age', 'Cholesterol', 'Maximum Heart Rate, and 'ST Depression' are the most significant numerical features.

Table 1: The number of data samples from different datasets

Dataset	Records
Cleveland	303
Hungary	294
Switzerland	123
Long Beach	200

Table 2: Features of the dataset

Type	Feature	Data type
Independent	Age	Numeric
	Chest pain	Categorical
	Cholesterol	Numeric
	Fasting sugar	Categorical
	Induced angina	Categorical
	Maximum rate	Numeric

Table 3: Number of missing values for individual features

Feature	Missing values
Age	0
Chest pain	0
Sex	0
Resting ECG	2
Cholesterol	30
Induced angina	55
Maximum rate	55
Resting BP	59
ST Depression	62
Fasting sugar	90
Slope	308
Thalassemia	477
Vessels colored	606

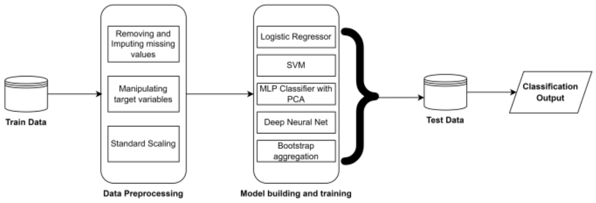


Fig. 1: System architecture

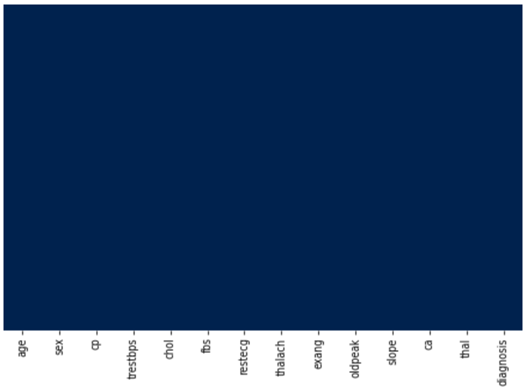


Fig. 2: Missing values before imputation (Yellow lines indicate missing values)

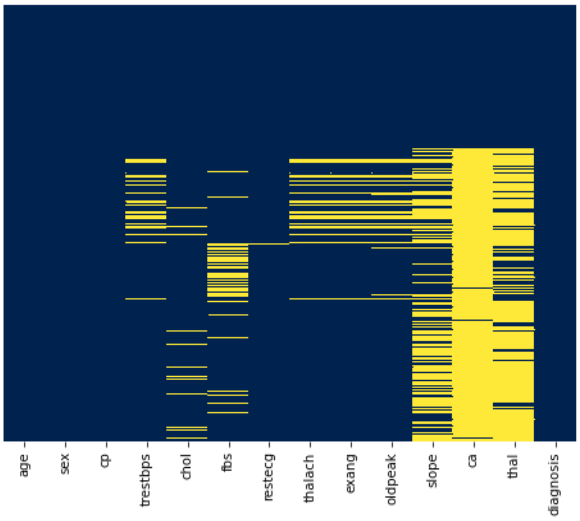


Fig. 3: Missing values after imputation

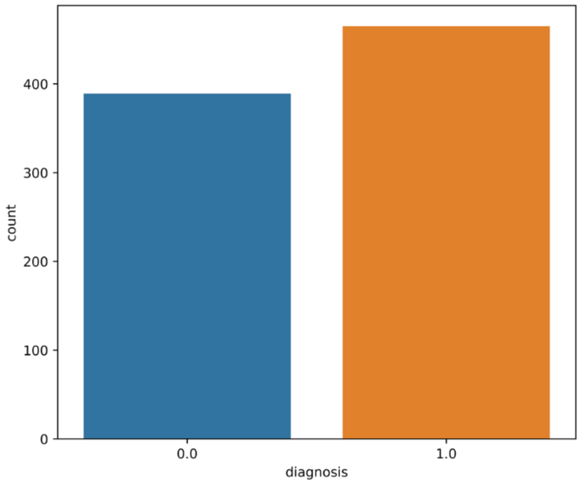


Fig. 4: Count plot for each target variable in the dataset

Categorical Feature Selection

The top 4 categorical features were selected using the Chi-Squared statistic. It is a statistical reliability coefficient that presupposes (the null hypothesis) that the measured and predicted frequencies for a categorical variable match as mentioned and applied in (Spencer *et al.*, 2020). In the context of the chi-squared distribution with the required number of degrees of freedom, we can interpret the test statistic as follows:

- If Statistic (*So*) > = Critical Value (C_o), the result is significant and the null Hypothesis (H0) is rejected
- Otherwise. the null Hypothesis (H0) cannot be rejected

The test concluded that the features 'Chest Pain', 'Induced Angina', 'Vessels Colored', and 'Thalassemia' are the most significant categorical features.

Standard Scaling

The original values of the continuous features have very different scales. While modeling the data, some features tend to dominate others because of their higher range. Hence, to reduce the variance between the features and scale all of them to a certain range, standardization is used. Standardization expects the data to have Gaussian distribution and as observed, the features of the dataset have close to the Gaussian distribution. Standard scaling centers the data points by subtracting them from the mean and scales by dividing them by the standard deviation. Thus standardization is also referred to as 'center scaling'.

Equations 1, 2, and 3 are the equations for Mean, Standard deviation and Standard Scaled values respectively:

$$Mean(\mu) = \frac{1}{n}\sum_{ii=1}^{n} x_{ii} \tag{1}$$

$$Standard\ deviation(\sigma) = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_i - \mu)^2} \tag{2}$$

$$Standard\ scaled\ value(z_i)_f = \frac{(x_i)_f - \mu_f}{\sigma_f}, \tag{3}$$

C. Proposed Models

Various models employing different algorithms were trained on the same training dataset and tested on the same test dataset. The models are as follows:

1) Logistic regression
2) Support vector machine
3) MLP classifier with principal component analysis
4) Deep neural network
5) Bootstrap aggregation using random forest

Logistic Regression

At the core of logistic regression, we have the logistic function, also called the sigmoid function (Wright, 1995). This function can map any real-valued input into the range of (0,1). The function has an S-shaped curve as shown in Fig. 5.

$$Sigmoid = \frac{1}{1+e^x} \tag{4}$$

The output of a logistic regression model indicates the probability of the record belonging to a default class in binary classification. The closer the output is to 1, the higher the probability. The equation used in logistic regression is shown in Eq. 5:

$$y = \frac{e^{(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_n x_n)}}{1 + e^{(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_n x_n)}} \tag{5}$$

where,
$[x_1, x_2, .., x_n]$ = ∈ Input record
β_0 = The bias or intercept term
$[\beta_1, \beta_2, \ldots, \beta_n]$ = Are the coefficients for different feature inputs

Support Vector Machine (SVM)

SVM is a soft margin classifier (derived from the Maximal-Margin Classifier) that learns a hyperplane from the training dataset (Noble, 2006). Tuning parameter C denotes the amount of relaxation that is allowed across all the dimensions of the hyperplane. All the training instances lying with the predefined margin are considered to be the support vectors. The smaller the value of C, the more sensitive the algorithm is to the training dataset and vice versa. SVM algorithm is practically implemented using a kernel. Three different types of kernels are used in SVM:

1) Linear
2) Polynomial
3) Radial

In general, all the SVMs try to find the equation of a hyperplane that maximizes the marginal distance. Doing so allows the algorithm to classify the unknown data samples with higher accuracy. For the given dataset, an SVM model with a linear kernel has been deployed.

Multi-Layer Perceptron (MLP) Classifier with Principal Component Analysis (PCA)

Higher the number of features, the more dimensions and the larger the volume of space. If the number of features is considerably higher concerning the number of data samples, then the sample space does not represent the n-dimensional space with all varieties. This might lead to a lack of information and can lead to unreliable models. To overcome this issue, Principal Component Analysis (PCA) is adopted. It is a technique from linear algebra that uses feature projection methods to reduce the number of features while still maintaining the effectiveness of the data in the dataset. It is often referred to as one of the data compression techniques. PCA adopts the eigen decomposition to calculate the eigenvalues and eigenvectors that are also called the principal components. These components are then sorted in descending order of their eigenvalues. More the eigenvalue, the more impactful the eigenvector (Abdi and Williams, 2010; Krishna and Reddy, 2019).

After reducing the dimensions of the dataset down to only 3, using PCA, a Multi-Layer Perceptron (MLP) is trained using the reduced features. An MLP classifier is a fully connected, feed-forward neural network that utilizes backpropagation for updating the weight matrices (Sonawane and Patil, 2014; Terrada *et al*., 2020).

Deep Neural Network

The architecture of the neural network is shown in Fig. 6. The model consists of 3 hidden layers each with 64 neurons and ReLU as their activation function. A dropout layer is used between every hidden layer to prevent overfitting. The output layer has one neuron and it uses a sigmoid as its activation function (Karayılan and Kılıç, 2017). Other parameters tuned for the model are listed in Table 4.

Bootstrap Aggregation using Random Forest

Bootstrap aggregation also called bagging, is a powerful ensemble method. The method combines the predictions from multiple machine learning algorithms to provide an even more accurate prediction. In bootstrap aggregation, multiple models are fed and trained on the resamples of the same training dataset with replacement. The individually trained models are expected to learn different patterns from the same dataset which are then combined to give an accurate prediction.

Random forests are also a powerful bootstrap aggregation algorithm. The algorithm utilizes multiple decision trees that are trained on the resamples of the training dataset. Decision trees work greedily, i.e., at each split point, they select the feature that most optimally minimizes the error. This nature can in turn produce a high correlation between the predictions of the individual decision trees. Bagging algorithms rely upon independent models that have high variance and low bias so that there is a very weak correlation between their predictions. To overcome this issue, random forests limit the search space of the features that a decision tree can go through at a split point. This little tweak allows random forests to generate weakly correlated decision trees (Hastie *et al*., 2009).

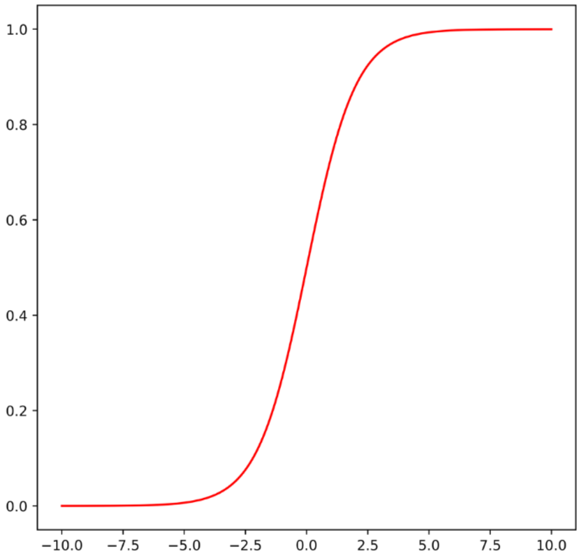


Fig. 5: Curve of the sigmoid function

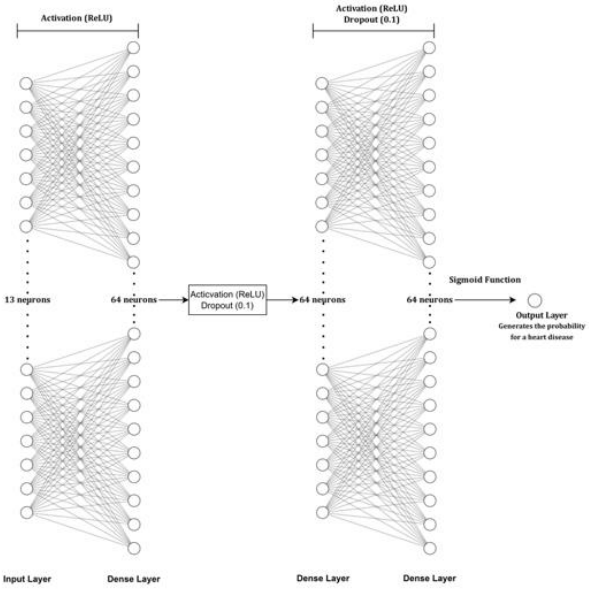
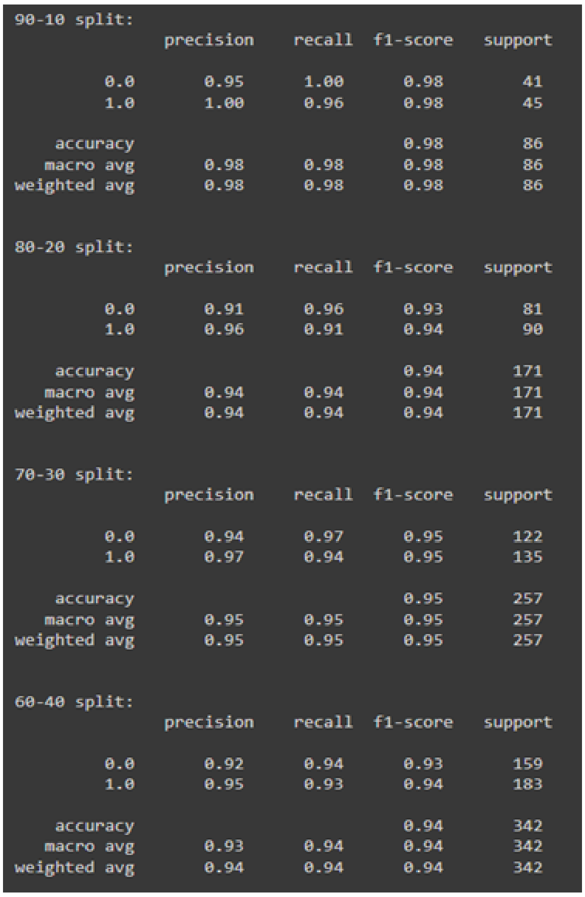


Fig. 6: Neural network architecture



```
90-10 split:
              precision    recall  f1-score   support

         0.0       0.95      1.00      0.98        41
         1.0       1.00      0.96      0.98        45

    accuracy                           0.98        86
   macro avg       0.98      0.98      0.98        86
weighted avg       0.98      0.98      0.98        86

80-20 split:
              precision    recall  f1-score   support

         0.0       0.91      0.96      0.93        81
         1.0       0.96      0.91      0.94        90

    accuracy                           0.94       171
   macro avg       0.94      0.94      0.94       171
weighted avg       0.94      0.94      0.94       171

70-30 split:
              precision    recall  f1-score   support

         0.0       0.94      0.97      0.95       122
         1.0       0.97      0.94      0.95       135

    accuracy                           0.95       257
   macro avg       0.95      0.95      0.95       257
weighted avg       0.95      0.95      0.95       257

60-40 split:
              precision    recall  f1-score   support

         0.0       0.92      0.94      0.93       159
         1.0       0.95      0.93      0.94       183

    accuracy                           0.94       342
   macro avg       0.93      0.94      0.94       342
weighted avg       0.94      0.94      0.94       342
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Fig. 7: Classification report for bootstrap aggregation using random forests

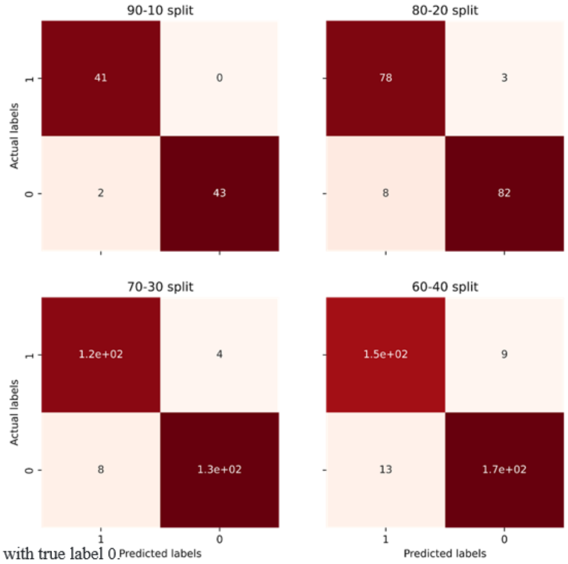

Fig. 8: Confusion matrix for bootstrap aggregation using random forests

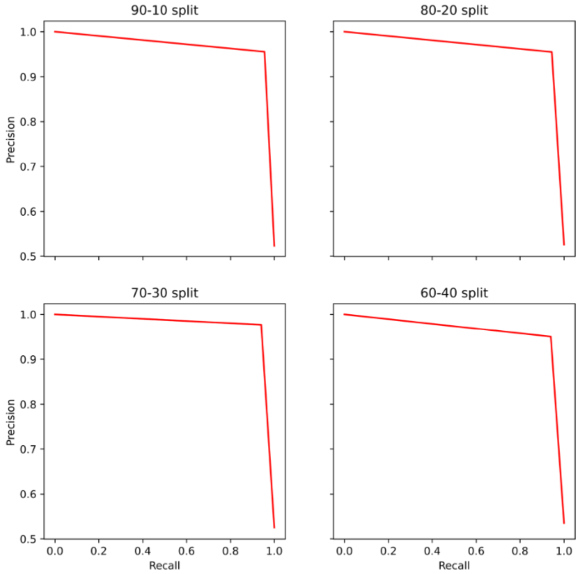

Fig. 9: Precision-Recall (PR) curve of logistic regression model

Result and Performance Analysis

The proposed approach is evaluated using several splitting models and analysis is then undertaken. The confusion matrix in Table 3 is used to illustrate the model's performance. Classification Accuracy is defined as the percentage of correctly categorized points to the total test data points (Swain *et al*., 2019a; 2020). The accuracy of the proposed classifier was 97.67%. The model's Cohen Kappa Score (E1. 6), R2 Score (Eq. 7), and AUC Score (Eq. 8) is determined to be 95.34, 90.67, and 97.77%, respectively. Furtherly, as illustrated in Fig. 7 the classification report shows the F1 score which is used to evaluate the model's testing accuracy in terms of recall and precision for binary classification (Swain *et al*., 2020; 2018). For sensitive applications where an error-free diagnosis is a must, recall and precision are primarily seen as critical performance aspects.

Cohen Kappa (***κκ***):

$$\kappa = \frac{\left(\rho_0 - \rho_e\right)}{1 - \rho_e} \qquad (6)$$

where,

ρ_0 = Empirical probability of agreement on the label assigned to the sample (the observed agreement ratio)

ρ_0 = Expected agreement when both annotators assign labels randomly

R2 score:

$$R^2 = \frac{1 - s_{res}}{s_{tot}} \qquad (7)$$

where,

ꞩ = Sum of squares of the residual errors

ꞩ = Total sum of the errors

$$AUC = \frac{1}{mn}\sum\nolimits_{i=1}^{m}\sum\nolimits_{i=1}^{n} 1 p_{i>pj} \qquad (8)$$

where,

$p_{ii} > p_{jj}$ = Probability score by the classifier to data points *i* and *j*

1 $p_{jj} > p_{jj}$ = Indicator Function (Output 1 if the condition is satisfied) *i* run over all *m* data points with true label 1 and *j* runs over all n data points with true label 0

The classification report and confusion matrix for each of the deployed models are generated, as shown in Fig. 7 and 8 for Bootstrap Aggregation using Random Forests. Accuracy, Precision, Recall, and F1 Score measurements are used to evaluate the system's performance. The robust performance of the proposed classifier is demonstrated by the significant number of these metrics.

The Precision-Recall (PR) curves for different models are illustrated in Fig. 9-13.

It can be observed that for the majority of the models, which include Logistic Regression, SVM, MLP with PCA, and Bootstrap aggregation, the 90-10 split of the dataset gave the best PR curve among the four splits. The results of the PR curves for these four models are as expected since the model always learns better when exposed to more training data. The exception of the DNN model having a slightly better PR curve for the 80-20 split than the 90-10 split, is likely to be the result of overfitting in the 90-10 split DNN model. Among the five models, the PR curve corresponding to the 90-10 test dataset split for the Bootstrap aggregation model is the best.

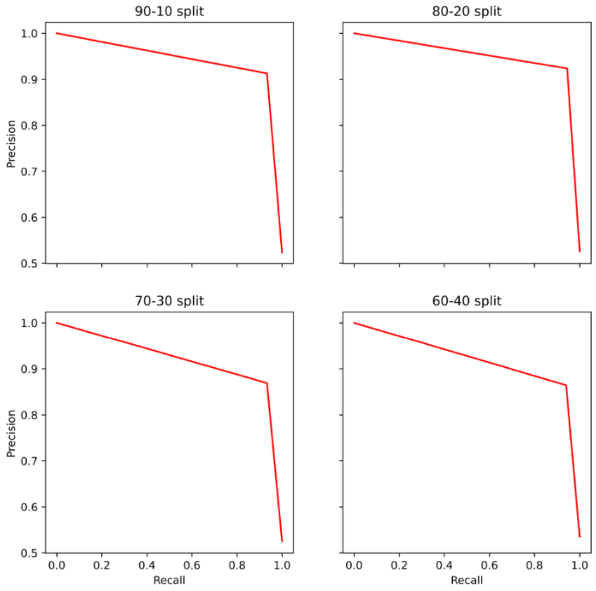

Fig. 10: Precision-Recall (PR) curve of simple vector machine

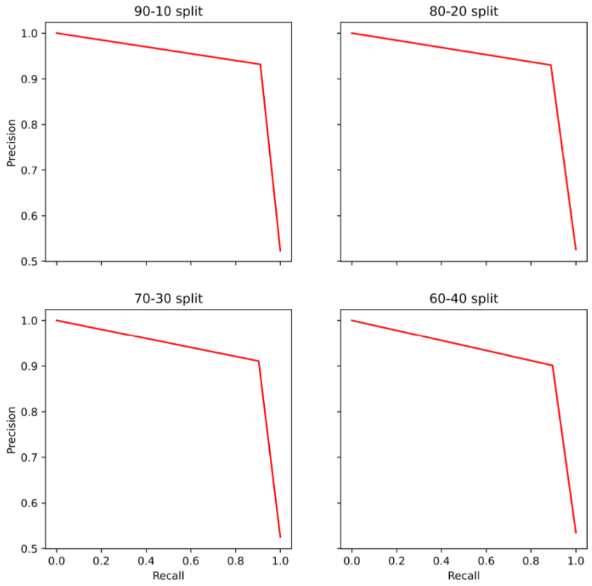

Fig. 11: PR curve of Multi-Layer Perceptron (MLP) Classifier with Principal Component Analysis (PCA) model

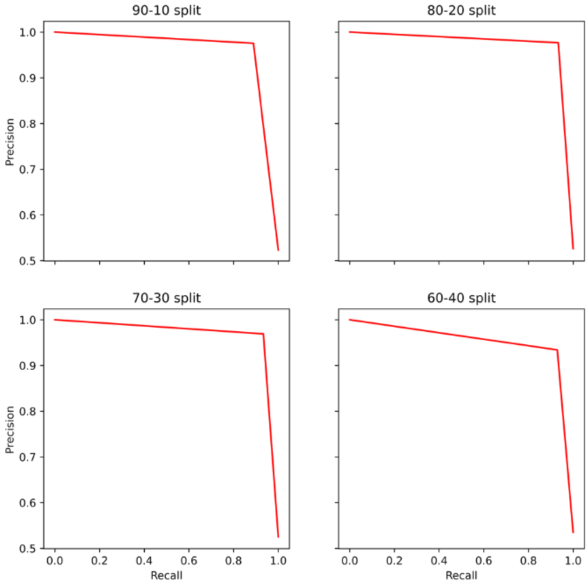

Fig. 12: Precision-Recall (PR) curve of the deep neural network model

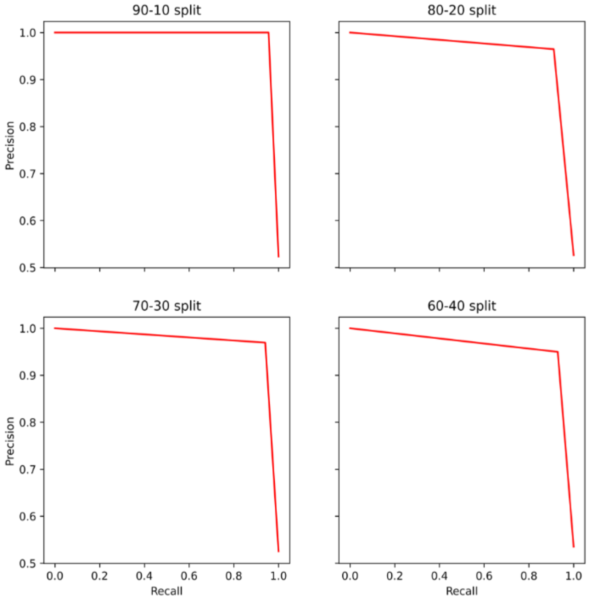

Fig. 13: PR curve of bootstrap aggregation using random forests model

Receiver Operating Characteristic (ROC) curve values for all the models are illustrated in Fig. 14-18. A trend similar to that for the PR curves can be observed for the ROC curves. All the models, except for the DNN, trained on a 90-10 split training dataset outperformed the ones trained with other split proportions. The Bootstrap aggregation model produces the best AUC score (0.9778) among the other models with all their splits (Jerome, 2006; Hamel, 2009).

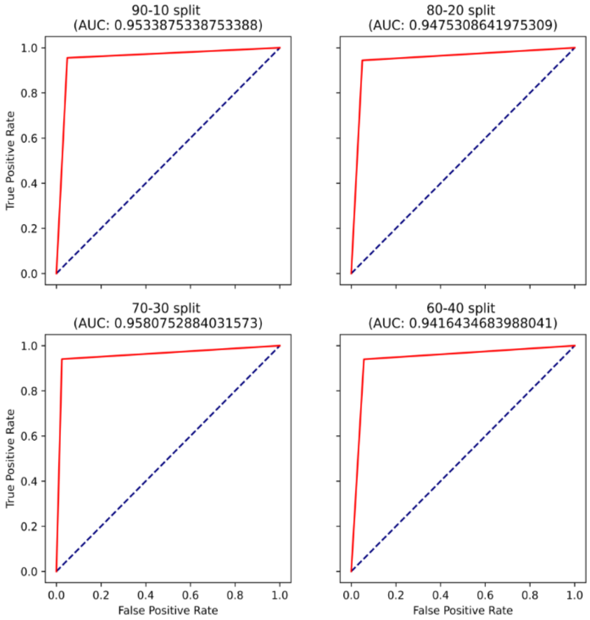

Fig. 14: ROC curve for logistic regression model history

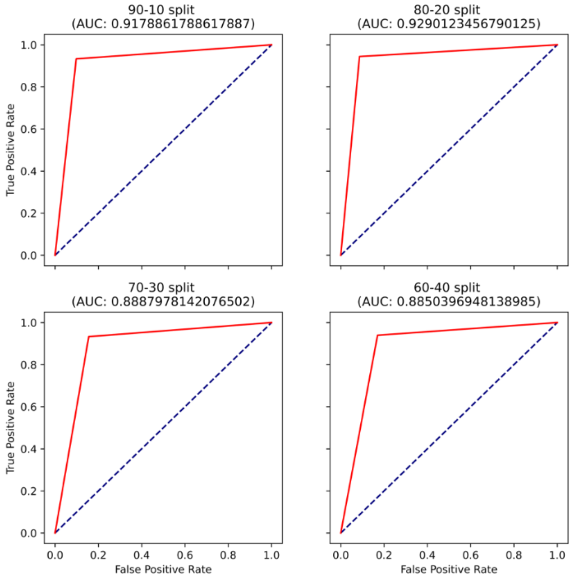

Fig. 15: ROC curve of Simple Vector Machine (SVM) model history

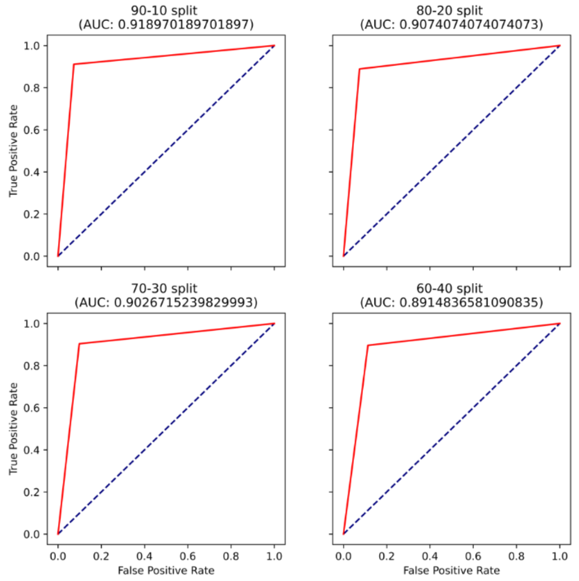

Fig. 16: ROC curve of Multi-layer Perceptron (MLP) Classifier with Principal Component Analysis (PCA) model history

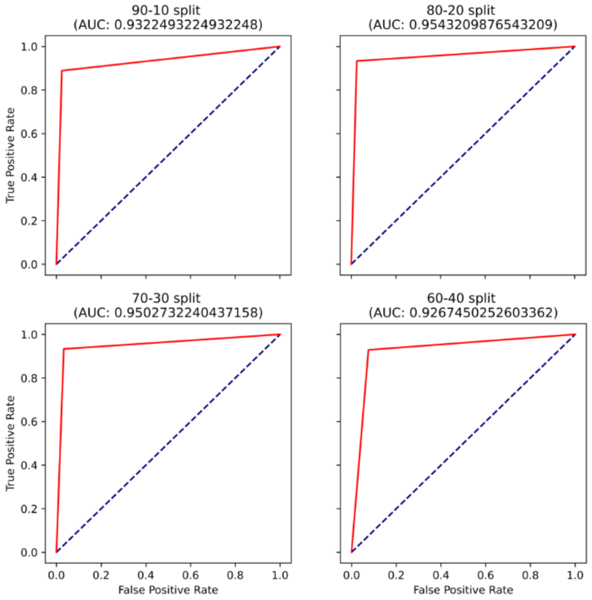

Fig. 17: ROC curve of deep neural network model history

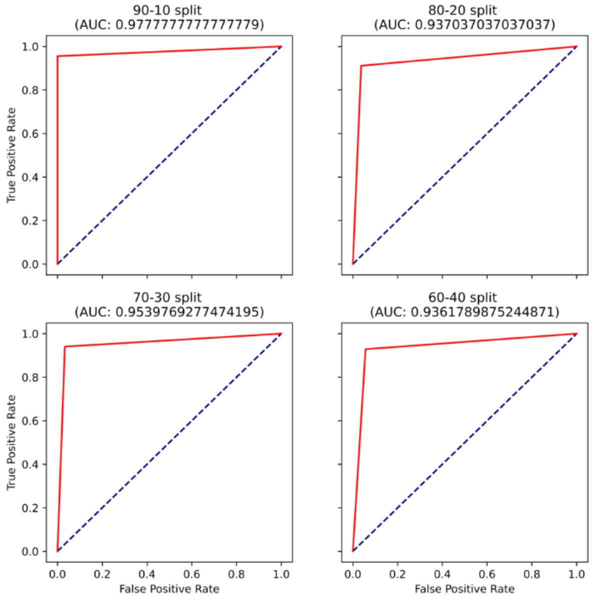

Fig. 18: ROC curve of bootstrap aggregation using random forests model history

Table 4: Hyperparameters used for the model

Hyperparameters	Value/type
Activation function for the hidden layers	ReLU
Activation function for the output layer	Sigmoid
The technique used to prevent overfitting	Early stopping
Optimizer	Stochastic gradient Descent
Loss function	Binary cross entropy
	pochs 1000
Batch size	8

Results of five evaluation metrics for all the models trained on different splits are mentioned in Table 5.

The development of artificial intelligence in the field of medical sciences has sparked a plethora of studies aimed at lowering the death rate by using various approaches to machine learning. The proposed model compared the outcomes of all the aforementioned procedures and arrived at the 97.674% accurate decision to employ the Bootstrap Aggregation with Random Forest technique which is illustrated in Table 6.

Table 5: Performance of all the models

Model	Split	Accuracy	Cohen Kappa	R2 Score	AUC
Logistic Regression	90-10	0.95348	0.90677	0.81355	0.9533
	80-20	0.94736	0.89450	0.78888	0.9475
	70-30	0.95719	0.91434	0.82835	0.9580
	60-40	0.94152	0.88255	0.76492	0.9416
Support Vector Machine (SVC)	90-10	0.91860	0.83667	0.67371	0.9178
	80-20	0.92982	0.85908	0.71851	0.9290
	70-30	0.89105	0.78067	0.56308	0.8887
	60-40	0.88888	0.77519	0.55335	0.8850
MLP with PCA	90-10	0.91860	0.83703	0.67371	0.9189

Table 5: Continue

	80-20	0.90643	0.81280	0.62469	0.9074
	70-30	0.90272	0.80502	0.60989	0.9026
	60-40	0.89181	0.78264	0.56510	0.8914
Deep neural network	90-10	0.93023	0.86076	0.72032	0.9322
	80-20	0.95321	0.90640	0.81234	0.9543
	70-30	0.94941	0.89877	0.79714	0.9502
	60-40	0.92690	0.85313	0.70615	0.9267
Bootstrap aggregation with random forests	90-10	0.97674	0.95348	0.90677	0.9777
	80-20	0.93567	0.87138	0.74197	0.9370
	70-30	0.95330	0.90652	0.81275	0.9539
	60-40	0.93567	0.87092	0.74141	0.9361

Table 6: Comparison analysis with previous research

Past Proposed work	Limitations Observed in previous work	Currently proposed methodology
Yazid *et al*. (2018)	For data analysis, Statlog, and Cleveland datasets are used. For the Statlog dataset, accuracy was 90%, while for the Cleveland dataset, it was 90.9%.	To increase versatility and reach a greater accuracy of 97.67%, the current model was constructed while taking data from a variety of sources into account
Diwakar *et al*. (2021)	A general overview of several methodologies and an outline of the entire process presented; no actual method or model used for identifying the disease or predicting its the occurrence has been demonstrated.	The proposed Model calculates the probability of occurrence and gives a definite answer whether the disease will occur or not, by considering numerous factors
Singh and Kumar's (2020)	Performance may have been much improved by data processing, parameter tuning, and tweaking.	An in-depth discussion of mentioned mechanisms in our paper leads to a more detailed model, achieving an accuracy of 97.67%
Ambesange *et al*. (2020)	Grid Search was used to give 100% accuracy after Kernel Principal Component Analysis (PCA) was applied to the dataset, implying that the model is over-fitted.	The current proposed paper does not contain any such abnormalities
Yadav *et al*. (2020)	The dataset has to be improved; normalization and entry of missing values were not seen during pre-processing.	Dataset utilized in the currently proposed methodology was properly pre-processed using all preprocessing methods
Motarwar *et al*. (2020)	Since adequate pre-processing methods weren't users, the accuracy was limited to 95.08%.	Bootstrap aggregation outperformed all other models with a promising accuracy of 97.67%

Conclusion and Future Work

Due to increasingly stressful lives, unhealthy lifestyles which include snacking too much on fatty foods have all led to unhealthy lives for people. These all problems have a big effect on reducing the overall average longevity of the general population. One such case is increasing pollutants like lead, arsenic, mercury, and other contaminants that can change the viscosity of our blood, while adversely affecting the walls of our heart. These agents can impact some of the vital factors responsible for maintaining our hearts, thus indirectly influencing our survival chances. We look at these vital factors like chest pain, gender, thalassemia, cholesterol, and many more, to understand how cardiovascular diseases are caused. This was the first step toward understanding the major factors involved in heart diseases.

Five different models were trained and tested using the CDA's composite dataset. Table 5 depicts that the Bootstrap Aggregation model performed best for the 90-10 (train-test) split of the dataset, with the highest accuracy among all of 97.674%.

The logistic model employed along with the sigmoid function gives a surprising accuracy of 95.38%. Multi-Layer Perceptron (MLP) classifier with Principal Component Analysis (PCA) is used to overcome when some information may not be included. The average accuracy of 91.86% is obtained, which has increased to these levels due to backpropagation techniques. The Deep neural network has three layers and is using ReLu as its activation function while giving an optimal accuracy of 95.32% among all splits. Here, the 90-10 split gets overfitted a little, hence the 80-20 split performs better overall. On the other hand, the SV Classifier performed worst when employed with the 60-40 (train-test) dataset split at 88.88% accuracy.

The hyper-parameters of all the models were finely tuned using random search to optimize the model. The Bootstrap Aggregation model performed exceedingly well as compared to the other systems, the reason being it had the advantage of multiple model predictions. This allowed the model to use the "crowd-vote" system to understand the dynamics of the dataset better and cancel out any bias that an individual model may possess. The purpose behind the building up of these models is to start predicting accurately the occurrence of the diseases, so we can start on the next step of treating or even preventing them from happening.

Acknowledgment

The authors of this manuscript would like to express their appreciation and gratitude to their universities for supporting this research.

The authors would like to thank the editors for their efforts in handling the manuscript and all reviewers for the constructive comments which improved the original submission.

Author's Contributions

Debabrata Swain: Problem identification, Implementation.

Badal Parmar, Hansal Shah and Aditya Gandhi: Implementation.

Manas Ranjan Pradhan, Harprith Kaur and Biswaranjan Acharya: Data Set Identification and Preprocessing.

Ethics

This study is original and innovative and contains unpublished material. The corresponding author confirms that all the other authors have read and approved the manuscript and no ethical issues involved or conflicts of interest to release.

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