Prediction of Heart Disease using Ensemble Learning and Particle Swarm Optimization and Genetic Algorithm

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Student Name	Enrollment	Contributions
	no.	
Patmanjari Nautiyal	00401042019	Wrote introduction and Performed Ensemble Meth-
		ods: Random Forest and AdaBoost and applied fea-
		ture selection on Random Forest, Decision Tree and
		AdaBoost.
Nupur Goel	04001042019	Read the abstract, introduction and data section of
		papers [6],[5],[2],[12] and wrote their summaries.
		Performed SVM. Applied Genetic Algorithm on
		SVM, KNN and LR.
Manya	04801042019	Read the abstract, introduction and data section
		of papers. [8], [7], [9], [3] and wrote their sum-
		maries. Performed ANN and applied feature selec-
		tion on ANN and KNN.
Chhavi Bhadana	05001042019	Wrote the abstract and has given a brief description
		of base paper in related work section. Performed
D IZ	0.0001040010	Decision Tree, Naive Bayes and Logistic Regression.
Prerna Khera	06301042019	Read the abstract, introduction and data section of
		papers [1], [4], [10], [11] and wrote their summaries.
		Performed KNN. Wrote about Genetic Algorithm
		and Applied Genetic Algorithm on Random Forest,
		AdaBoost and Decision Tree. Represented Tables 12
Priya Chaturvedi	06801042019	and 13 in graphical form and wrote the conclusion. Visualize the data by analyzing the dataset at-
i iiya Chaturvedi	00001042019	tributes, label encoding and plotting graphs or
		charts. Applied PSO on various Machine Learning
		Algorithms like Bagged Tree, AdaBoost, KNN and
		Decision Tree.
		Dodolon 1100.

Abstract

With the world becoming a smaller and paced space. The pace has led us to a number of health problems. With the advancement of technology the lazy man's lifestyle has become a host to heart problems. Every year the number of people affected by heart diseases increases by a concerning number. Early and accurate prediction has become a requirement. Heart diseases do not have clear early signs and health professionals being humans can do as much as their human potential dictates. In addition taking tests for heart diseases is not a common and economical process. Hence prediction using Artificial Intelligence and machine learning can be a serviceable tool. Models with high accuracy have been built but heart diseases being a crucial health problem need a 100 percent accuracy. AI and ML technologies have great abilities and that can help health professionals as well as patients to identify numerous diseases in early stages. Assisting reduction of mortality rate, number of surgeries performed and other complications. To find a tool with the highest possible accuracy in predicting cardiovascular disease at early stages, we used multiple feature selection methods like PSO and Genetic Algorithm and found that PSO (Particle swarm Optimization) paired with Bagged Tree ensemble returned 90% accuracy and PSO with LR gave the highest accuracy of 100%.

1 Introduction

Cardiovascular disease or commonly known as heart disease is a class of diseases that includes conditions that affect the heart. Types of heart diseases are coronary artery disease, cardiomyopathy, congenital heart disease, pulmonary embolism, stroke, and peripheral artery disease. The most common symptoms of heart disease may include chest pain, chest discomfort, and shortness of breath. Other symptoms may include pain in the neck, jaw, upper abdomen, or back, fatigue, nausea, weakness in the legs and hand (narrowed blood vessels). Sometimes heart disease can go undiagnosed until a person experiences a heart attack, arrhythmia, or heart failure. High blood pressure, high cholesterol, and diabetes are leading medical conditions that increase the risk of heart diseases. Lifestyle choices like obesity, smoking, and excessive use of alcohol can also affect the heart. Family history of heart problems and age can also lead to serious heart problems. In 2019 nearly 18 million people died due to heart disease which contributes to 32 percent of all global deaths. China has the highest number of deaths due to heart conditions followed by India, Russia, and the United States. Death rates due to heart disease were lowest in Japan, France, and Peru. More than 50 million cases of heart diseases are registered every year. According to surveys conducted, the annual death rate due to heart disease has increased by more than 50 percent from 1990 to 2017. Studies have shown that people aged between 45-60 years are highly prone to a heart attacks. Also, deaths caused by cardiovascular diseases are higher in men than in the female. We can protect ourselves from heart problems by improving our lifestyle and being active. It is necessary to detect heart disease at an early stage to get proper medical guidance and treatment. Therefore various methods are used by the healthcare system to prevent such medical conditions. These methods make data easily accessible and save both time and effort. One such is the data mining concept which plays a vital role in the health care industry. Data mining helps in the proper usage of data and analytics by the health system. It also identifies patterns and predicts various diseases such as liver disease, heart disease, etc. Due to the early detection of high-risk diseases by using data mining, patients receive better and more affordable health care treatment that eventually increases their life span. It also manages customer relationships and detects waste, insurance fraud, and abuse. Data mining has introduced various methods and techniques to predict heart diseases in the medical industry. One such system is a radial base function with a support vector machine. But this system could not provide satisfactory classification results. There was another system that used a genetic support vector machine to predict heart valve conditions. Another system uses multiple data mining technologies which predict heart disease. All these methods are highly complex and difficult to understand. Also, different factors can lead to heart problems in both males and females. In data mining, the classification is trained and tested to predict a patient's medical condition. It also helps in predicting if a person is suffering from heart disease. Due to a significant increase in cases of heart disease, there is an urgent requirement for a higher level of classification accuracy that a traditional classifier cannot provide. In such a case ensemble classifier is used. Ensemble classifier combines the prediction of different components and then gives the output. An ensemble classifier gives maximum accuracy and is better than an individual classifier. Feature subset selection removes irrelevant data, which helps in improving the accuracy. Particle swarm optimization and Genetic Algorithm are feature selection techniques. They remove the extra features from an enormous amount of data, which helps to increase the accuracy of the classifier. In some cases, PSO gives better accuracy as compared to GA while in some other Machine Learning models GA performs better. The rest of the paper is organised as follow: Section 2 discusses the prior work as well as our work in the field. Section 3 deals with data set description and visualise the data. The main contributions of this paper are:

- 1. Using different ensemble classifier methods to get the accuracy that is useful for the prediction of heart disease.
- 2. Removing irrelevant data using the feature selection method to increase the accuracy
- 3. Applying different types of feature selection methods like Particle Swarm Optimization, and Genetic Algorithm on the dataset to extract relevant features that affect heart disease.
- 4. Selecting the best performance-based algorithm which gives the highest accuracy for the prediction of heart disease.

2 Related Work

Base paper(s): We selected the work of Indu Yekkala, Sunanda Dixit and M.A.jabbar [?] as our base paper and worked on dataset used by them. They used ensemble learning and particle swarm optimization(PSO) to predict Coronary heart disease. Their paper analysed various ensemble methods accompanied by PSO as a subset feature selection. The results displayed an accuracy of 100 percent in one of the methods.

Important paper(s): M.A.Jabbar, B.L.Deekshatulu, and Priti Chandra [9] proposed a classification model which uses the random forest as their classifier with chi square and genetic algorithm as their feature selection measures. Chi square and genetic algorithm are used to select attributes that will contribute more to diagnosis. The model showed an accuracy of 83.70 Per for the heart stat-log dataset...

Jabbar [6] proposed a decision support system in which KNN is used as classifier and PSO as feature subset selection measure to predict heart disease.

Author's main aim is to increase the performance of KNN classifier. Their method reached to an accuracy of 100 Per with hybrid feature selection. Sensitivity and TP rate of this model was 100 Per.

Emakhu et al. [5] implemented ensemble classifiers for the prediction of heart disease. Data mining classification techniques include AdaBoost, Random Forest, Bagging and Voting Ensemble that is applied to ensemble classifier. Random Forest Ensemble classifier is used to enhance accuracy of the model. This method achieved an accuracy of 87.04 Per.

H. Benjamin [4] introduced various ensemble learning methods and illustrated that higher performance and better accuracy in the prediction of heart disease could be achieved using these methods. He used Support Vector Machine, Naive Bayes and K-Nearest Neighbours classifiers for constructing the ensemble. He performed Bagging, Stacking and AdaBoost algorithms and evaluated their performances across various folds of cross-validation. He also indicated that the folds of improved the the values of precision, recall and f-measure. It became evident from his results that the AdaBoost algorithm outperformed the others.

Other papers: Rajwant Kaur [8] used a dataset the contains 50 people data collected by American Heart Associations. She tested data using the Support Vector Machine (SVM) classifier and Genetic Algorithm for predicting heart diseases based on the risk factor. As of result SVM and Genetic algorithm gives higher accuracy as compared to Neural network and Genetic algorithm. Accuracy of system for SVM+Genetic Algorithm = 0.95152 whereas for Neural Network = 0.904444.

Kathleen H. Miao .[7] used methods like Ensemble learning classification and prediction models have been used to detect coronary heart disease. The developed Ensemble classification and prediction models are based on an adaptive Boosting algorithm. For the result, an average sensitivity of 86.61~% (the presence of disease) and an average specificity of 83.76~% (the absence of disease) were obtained. The accuracy of testing result for different datasets were 80.14~% for CCF, 89.12~% for HIC, 77.78~% for LBMC, and 96.72~% for SUH.

Jabbar [3] used alternating decision tree method with Principal component analysis (PCA) for diagnosing heart disease. The data was collected from the corporate hospital in Hyderabad for about 96 patients with 10 features. The accuracy for the approached model was increased by 3.13 % for the full Hyd training set. Also, the accuracy for the model was increased by 2.11% as compared to J48 for the heart disease full Hyd training set.

Jabbar et al. [2] used this research paper in Andhra Pradesh to predict risk score of heart disease. Author investigated to predict heart disease by using feature subset selection and classification. Associative classification is used to

amend the classification accuracy.

Latha.B et al. [12] proposed ensemble classifier for classification and also used particle swarm optimization as feature subset selection to predict heart disease. An ensemble classifier like AdaBoost and PSO is used to improve learning accuracy of this model. Accuracy of this model is 84.88 % by using AdaBoost and PSO and the error rate is 4%.

Madhumita Pal et al. [10] proposed a heart disease prediction system using Random Forest algorithm. The authors used a dataset consisting of 303 instances and 14 attributes. They expressed the outcomes of the dataset with a classification accuracy of 86.9 %, sensitivity value of 90.6%, and specificity value of 82.7%. They expressed results in a confusion matrix and plotted an ROC curve using Random Forest Algorithm and predicted a diagnosis rate of 93.3 Per.

Mohammed et al. [1] Proposed that various heart diseases can be predicted with the help of data mining and machine learning algorithms. For this, they used a classification algorithm under the supervision of Random Forest and Naive Bayes for classification and prediction purposes. They used 384 instances with 14 attributes of Cleveland, Hungarian and Switzerland datasets. By performing filter method and feature selection wrap method, they obtained that Naive Bayes has more accuracy over Random Forest.

Dhyan Chandra Yadav et al. [11] Proposed a system of prediction of heart disease by using feature selection methods and applying them on tree-based classification algorithms. By using Pearson Correlation, Recursive Features Elimination and Lasso Regularization and applying them on M5P, Random Tree and Reduced Error Pruning with Random Forest Ensemble method they calculated the values of classification accuracy, precision, sensitivity and ROC. They concluded that Pearson Correlation and Lasso Regularization along with Random Forest gave 99 Per accuracy.

Table 1: Comparative analysis between prior research works who have used

same dataset as the basepaper.

Author(s)	Brief Description	Results
Jabbar [6] ^a	Author proposed a decision support	Accuracy with hybrid fea-
	system in which KNN is used as classi-	ture selection was 100 Per.
	fier and PSO as feature subset selection	Sensitivity and TP rate of
	measure to predict heart disease. Au-	this model was 100% .
	thor's main aim is to increase the per-	
	formance of KNN classifier.	
Emakhu et al. $[5]$ ^b	Author implemented ensemble classi-	Accuracy of this model
	fiers for the prediction of heart dis-	for feature selection using
	ease. Data mining classification tech-	PSO + Bagged Tree gave
	niques include AdaBoost, Random For-	100 %value, PSO + Ran-
	est, Bagging and Voting Ensemble that	dom Forest gave 90.37% ,
	is applied to ensemble classifier. Ran-	PS O + AdaBoost gave
	dom Forest Ensemble classifier is used	88.89 %.
	to enhance accuracy of the model.	
M.A.Jabbar et	Proposed a classification model which	The model showed an ac-
al.[9] c	uses the random forest as their classifier	curacy of 83.70% for the
	with chi square and genetic algorithm	heart stat-log dataset
	as their feature selection measures.Chi	
	square and genetic algorithm are used	
	to select attributes that will contribute	
	more to diagnosis.	
H. Benjamin [4]	Author introduced various ensemble	The model indicated
	learning methods and illustrated that	that the folds of cross-
	higher performance and better accu-	validation improved the
	racy in the prediction of heart disease	values of precision, recall
	could be achieved using these meth-	and f-measure. It was evi-
	ods. He used Support Vector Machine,	dent from his results that
	Naive Bayes and K-Nearest Neighbours	the AdaBoost algorithm
	classifiers for constructing the ensem-	outperformed the others.
	ble. He performed Bagging, Stacking	
	and AdaBoost algorithms and evalu-	
	ated their performances across various	
	folds of cross-validation.	

 $[^]a \rm https://www.researchgate.net/publication/317357702$ $^b \rm https://www.researchgate.net/publication/350620141$ $^c \rm https://ieeexplore.ieee.org/abstract/document/7057816$

Table 2: Prior research works related to our problem but using different datasets.

Author(s)	DataSet	Brief Description
Jabbar et	14 datasets from UCI data	Author used this research paper in Andhra Pradesh
al.[2]	were taken and experi-	to predict risk score of heart disease. Author investi-
	ments were conducted on	gated to predict heart disease by using feature subset
	them by using 10 cross	selection and classification. Associative classification
	fold validation	is used to amend the classification accuracy.
Latha.B et	Dataset was taken from	Author proposed ensemble classifier for classification
al.[12]	kaggle.	and also used particle swarm optimization as feature
		subset selection to predict heart disease. An ensem-
		ble classifier like AdaBoost and PSO is used to im-
		prove learning accuracy of this model. Accuracy of
		this model is 84.88 % by using AdaBoost and PSO.
Rajwant	The author used a dataset	She tested data using the Support Vector Machine
Kaur et	the contains 50 people	(SVM) classifier and Genetic Algorithm for predict-
al.[8]	data collected by Ameri-	ing heart diseases based on the risk factor. As of
	can Heart Associations.	result SVM and Genetic algorithm gives higher ac-
		curacy as compared to Neural network and Genetic
		algorithm. Sensitivity of system for SVM+Genetic
		algorithm = 0.957895 whereas for Neural Network
		= 0.954545. Accuracy of system for SVM+Genetic
		Algorithm = 0.95152 whereas for Neural Network =
TZ /11 II	H + D: D + G +	0.904444.
Kathleen H.	Heart Disease Data Set	Author used methods like Ensemble learning classi-
Miao al.[7]	$link^a$ of this dataset	fication and prediction models have been used to detect coronary heart disease. The developed Ensemble
		classification and prediction models are based on an
		adaptive Boosting algorithm. For the result, an aver-
		age sensitivity of 86.61 perr(the presence of disease)
		and an average specificity of 83.76per(the absence
		of disease) were obtained. The accuracy of testing
		result for different datasets were 80.14 per for CCF,
		89.12per for HIC, 77.78 per for LBMC, and 96.72 per
		for SUH.
Jabbar et	The data was collected	Author used alternating decision tree method with
al.[3]	from the corporate hospi-	Principal component analysis (PCA) for diagnos-
	tal in Hyderabad(Hyd) for	ing heart disease. The accuracy for the approached
	about 96 patients with 10	model was increased by 3.13% for the full Hyd train-
	features.	ing set. Also, the accuracy for the model was in-
		creased by 2.11% as compared to J48 for the heart
		disease full Hyd training set.
Madhumita	The datasets b are col-	Author proposed a heart disease prediction system
Pal et al.[10]	lected and gathered from	using Random Forest algorithm. She used a dataset
	the Machine Learning	consisting of 303 instances and 14 attributes. She
	Repository (UCI). It	expressed the outcomes of the dataset with a classifi-
	contains 303 instances	cation accuracy of 86.9 %, sensitivity value of 90.6%,
	with 14 attributes.	and specificity value of 82.7 %. She expressed results in a confusion matrix and plotted an POC curve us
		in a confusion matrix and plotted an ROC curve us- ing Random Forest Algorithm and predicted a diag-
		nosis rate of 93.3 %.
		HOSIS LATE OF 30.0 /0.

 $[^]a \\ https://archive.ics.uci.edu/ml/datasets/Heart+Disease \\ ^b \\ http://archive.ics.uci.edu/ml/datasets/Heart+Disease$

Table 3: In continuation with Table 2 Mohammed Mohammed et Al. Proposed that various heart dis-The datasets are colet Al. [1] lected and gathered from eases can be predicted with the help of data min-Machine Learning ing and machine learning algorithms. For this, they Repository (UCI). It conused a classification algorithm under the supervitains 394 datasets copies sion of Random Forest and Naive Bayes for claswith 14 attributes. sification and prediction purposes. They used 384 instances with 14 attributes of Cleveland, Hungarian and Switzerland datasets. By performing filter method and feature selection wrap method, they obtained that Naive Bayes has more accuracy over Random Forest. The dataset ² was taken Dhyan Proposed a system of prediction of heart disease by Chandra from the Machine Learnusing feature selection methods and applying them Yadav et al. ing Repository (UCI). It on tree-based classification algorithms. By using contains 1025 instances Pearson Correlation, Recursive Features Elimina-[11]with 14 attributes. tion and Lasso Regularization and applying them on M5P, Random Tree and Reduced Error Pruning with Random Forest Ensemble method they calculated the values of classification accuracy, precision, sensitivity and ROC. They concluded that Pearson Correlation and Lasso Regularization along with Random Forest gave 99% accuracy.

3 Dataset Description

Dataset has been obtained from UCI Machine Learning which is a treasure of dataset where a person can search or download the data set according to size/dimensions or Machine learning function . This data set is known as Statlog(heart) Dataset which is used to predict absence or presence of heart disease.

Table 4 is describing the dataset information through counts of some key entities involved in the dataset.

Table 4: Dataset description

Table I. Battaset description	Table I. Bacaset description				
Details	count/type				
Number of instances/rows	270				
Number of attributes/columns	13				
Data set feature	multivariate				
Attribute feature	categorical,real				
Missing values	no				

Table 5 describes the attributes of the dataset. Also in text here, explain those attributes briefly. As evident, there are so and so many attributes.

Table 5: Attribute Description

Attribute Name	Attribute brief de-	Attribute	Domain values
	scription	Data type	
Age	Age of patient	real	29-77
Sex	Gender	binary	0 - female 1 - male
			1- typical angina
Chest	Type of chest pain	nominal	2- atypical angina
Chest	Type of chest pain	пошша	3- nonanginal pain
			4 - asymtomatic
Resting blood pres-	Normal blood pressure	real	94 - 200
sure(mmHg)			
Serum	It is the sum of high	real	126-564
cholestoral(mg/dl)	density and low density		
	(HDL+LDL) cholestoral		
	in blood.		
Fasting blood	A test used to retrieve the	binary	1 - yes
sugar<100mg/l	patient's blood sugar after	billary	0 - no
54841 (1001118/1	a overnight fasting.		
	a overlight lasting.		0 - normal
Resting electro-	A process used to emulate	nominal	1- having St-t unusual
cardiographic	the root of different heart		2 - left ventricular hypertropy
results(ECG)	conditions.		2 felt ventileatar hypertropy
			<141 - low
Maximum Heart	Measurement of a person's	real	111-194 - moderate
Rate achieved	heart rate during a physi-		152>- high
	cal activity.		
E1	Tt to:	1. :	1- yes
Exercise induced	It triggers when you ex-	binary	0 - no
angina	erted yourself with physi-		
	cal activity like exercise.		<2 - low
Old peak	ST depression causes by	real	1.5-4.2 - risk
Old peak	exercise	1 Cai	2.5>- high
	CACICISC		1 - upward
Slope	Displacement of ST seg-	nominal	2- flat
prohe	ment with respect to in-	nommai	3- downward
	duced exercise in heart		5- downward
	rate		
Number of major	Major vessels colored by	nominal	0-3
vessels	flouroscopy(blood flow by		
V CODCID	coronary artery)		
			3 - normal
Thal	Anemia can be induced by	nominal	6 - fixed defect
- 11W1	Thalassemia		7 - reversible defect
Class	Heart Disease	binary	0 - absent 1 - present
		1	- Coccini

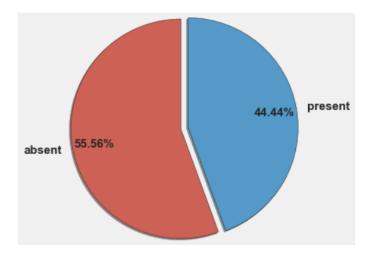


Figure 1: This is a pie chart depicting percentage contribution of present (1) and absent (0) data member of class attribute where 44.44% of present and 55.56% of absent data member.

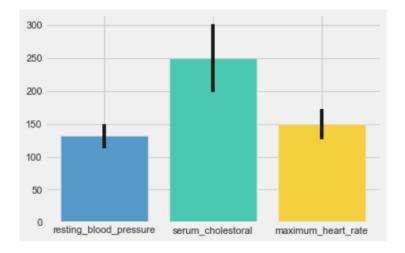


Figure 2: Bar charts helps us to visualize the magnitudes of a quantitative variable so, here we have taken 3 attributes and the black vertical line shows the variability in the data set larger the black line more will be the variability i.e values are varying too much from the mean like here serum cholestoral have the highest variability.

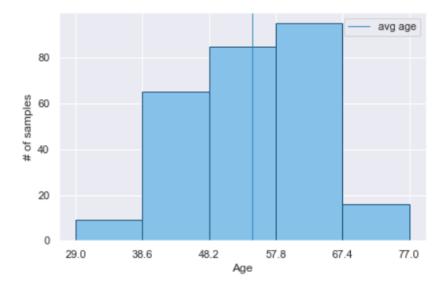


Figure 3: Histograms are univariate i.e one requires only one continuous variable to plot a histogram here we have used age attribute from the dataset and the long vertical blue line shows the average age .

4 Proposed Methodology

4.1 Data Pre-processing

The main focus of this research paper is to intensify the ensemble classifier for classification with Particle swarm optimization as a feature subset selection for detection of heart disease. At first Load the data set and then data-cleaning and pre processing which includes renaming features to appropriate name , converting features to categorical variables, feature encoding , filling missing values has to be done . After this step we will also detect and remove the outlier using z score.

 $\mathbf{z} = (\mathbf{x} - \mu)/\sigma$ where, z=standard score x=observed score μ =mean σ =standard deviation

There are 16 data points which are outliers and all will be removed. Now before splitting data set into train and test we first encode categorical features as dummy features and segregate feature and class variable. Then we will normalize all the numeric feature in the range of 0 to 1 and cross validation will also be done and final step will be model building or evaluation.

4.2 Proposed Workflow/Architecture

Different models will be evaluated on most important evaluation metrics are sensitivity, specificity, Precision, F1-measure, PPV, NPV. The confusion matrix

is used to measure the accuracy, sensitivity, and specificity.

Table 6: Confusion Matrix

	TRUE(1)	FALSE(0)
TRUE(1)	TP	FN%
FALSE(0)	FP	TN%

Where

TP – Positive tuples that are correctly labelled by the classifier.

TN – Negative tuples that are correctly labelled by the classifier.

FN – Positive tuples that are incorrectly labelled by the classifier.

FP -Negative tuples that are incorrectly labelled by the classifier

To evaluate the performance of ensemble methods we have used following classification measures

- Sensitivity = TP/(TP+FN)
- Specificity = TN/(FP+TN)
- Positive predictive value (PPV) = TP/(TP+FP)
- Nega+tive predictive value (NPV) = TN/(FN+TN)
- Accuracy = (TP+TN)/(TP+TN+FP+FN)

We apply feature selection methods like PSO and Genetic Algorithm on data set and Remove least ranked attributes and keep predominant features.

Apply ensemble classifiers on primary features (Bagging, Random Forest, and AdaBoost) At last measure the performance of proposed method.

5 Experiment Design

Random forest: it is a type of ensemble classifier which is used for predicting better accuracy. It is used to help in medical application. Random Forest algorithm constructs N number of decision trees by using random attributes as their input. In Random Forest, the bias remains the same but the number of tree can vary. With increase in number of trees the variance of model decreases. The prediction can be made by average voting or majority voting.

Adaptive Boosting: It is another type of ensemble classifier method. It converts weak learner into strong learner. It works by choosing a base classifier such as decision tree. We can improve it by taking misclassified attributes from the dataset in an iterative method. Equal weights are assigned to the attributes and a base classifier is choosen.

ANN: It is one of the models used for experimenting in this project. The dataset on which we trained our model was Stat-log heart diseases dataset. We trained the dataset using multilayer perceptron classifier (MLP). MLP consist of an input, hidden and an output layer. For this dataset we had only one hidden layer and max iteration = 300. After training the dataset we got 83.33% as the mean accuracy of the given test data and labels.

KNN: K-Nearest Neighbors belongs to the supervised learning domain and finds intense application in pattern recognition, data mining and intrusion detection. KNN works on a principle assuming every data point falling in near to each other is falling in the same class. KNN algorithms decide a number k which is the nearest Neighbor to that data point that is to be classified. The optimal value of K using cross-validation. It gives high accuracy.

SVM: Support Vector Machines are popular Supervised Learning Algorithm which is used for both classification and regression problems. But primarily, it is used in classification problems. This is popular because it can handle multiple continuous and categorical variables. It's main goal is to create best line or decision boundary which separate n-dimensional space into classes and this decision boundary is known as hyperplane. It selects extreme points that hepls in creating the hyperplane.

LR: Logistic Regression is a popular algorithm based on the sigmoid function. It is linear algorithm with a non-linear transform on output. It does assume a linear relationship between the input variables with the output. NB: Gaussian Naive Bayes is a variant of Naive Bayes that follows Gaussian normal distribution and supports continuous data. DT: It is a tree-structured classifier, where internal nodes represent the features of a dataset, branches represent the decision rules and each leaf node represents the outcome. In a Decision tree, there are two nodes, which are the Decision Node and Leaf Node. Decision nodes are used to make any decision and have multiple branches, whereas Leaf nodes are the output of those decisions and do not contain any further branches

Table 7: Ensemble methods Approaches

	Ensemble	Accuracy	Precision	Sensitivity	Specificity	F1 Score	Positive	Negative
	method						Pre-	Pre-
							dictive	dictive
							Value	Value
							(PPV)	(NPV)
1.	Bagged	82%	91%	91%	93%	94%	92%	92%
	Tree							
2.	Random	77.78%	73.07%	79.17%	76.67%	76%	87%	86%
	Forest							
3.	AdaBoost	74%	70.83%	70.83%	76.67%	70.83%	75%	88%

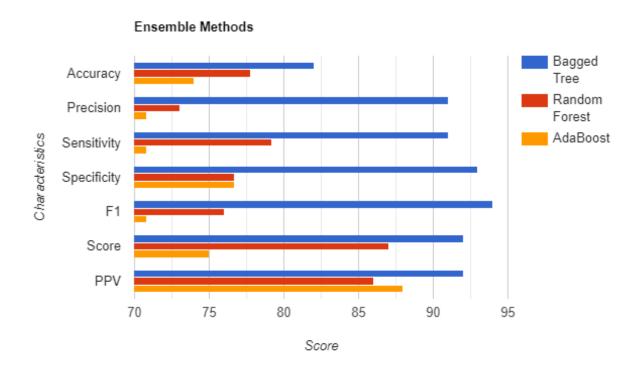


Figure 4: Comparison for different measures

Table 8: Comparison with various models

S.no	Techniques	Accuracy
1.	Decision Tree	75.30%
2.	Naïve-Bayes	77.78%
3.	KNN	83.33%
4.	SVM	85.19%
5.	ANN	77.7%
6.	LR	80.25%

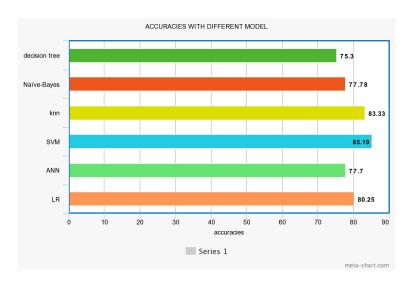


Figure 5: Accuracies with different Classifiers

Table 9: Feature selection with Different models

$\overline{}$	Tuble 9: Teature beleetion with Binerent models							
S.	Ensemble	Accuracy	Precision	Recall	F1	Sensitivity	Specificity	
No	Method				Score			
1.	Random For-	75%	79%	75%	77%	76%	75%	
	est							
2.	AdaBoost	79%	75%	77%	83%	75%	77%	
3.	ANN	88.88%	89.28%	88.87%	89.28%	89.28%	88.46%	
4.	KNN	72.22%	84%	73.71%	73.68%	65.62%	81.81%	
5.	Decision Tree	79%	78%	78%	82%	86%	70%	

6 Result/Observations

6.1 Feature engineering

In order to enhance the performance of these models various approaches are used which also require re-engineering or re-processing the dataset. Data gathered from the real world can be tremendously disorganized. Therefore, feature engineering is needed to modify the data into something that is more significant. And new features can be produced from raw data. Features can be weakly significant or strongly significant. Weakly significant features are those which are carrying the information of other features might fully or partially might carry. Strong features are those which carry information which other features do not whereas weak features can carry either partially or fully features of others. It's considered a good practice to have extra features than to miss out on a few important ones. The process of feature selection includes not only attaching

features but also deleting few not so known or unnecessary features. Therefore, feature selection techniques can be used in order to reduce or avoid overfitting.

6.2 Feature Selection

Feature Selection is the process of decreasing the number of disordered or disarranged features under inspection generating only a smaller set of predominant features. Higher the number of features, the more tough to visualize and train the machine learning models with the dataset. Many of the features might be tally and hence, their impact would be needless. This is where the feature selection algorithms come into the picture. Therefore, Particle Swarm Optimization (PSO) and Genetic Algorithm (GA) were the techniques used for feature selection .

6.3 Particle Swarm Optimization (PSO)

This method was originally proposed by Kennedy and Eberhart it is a algorithm based on the concept of swarm intelligence. The particles that constitute the PSO system fly around in a multidimensional search space; each particle regulate its position as stated by its own experience during its flight, and the experience of the neighboring particles, utilizing the best position face by itself and its neighbors.

Heart stalog data set contains 14 instances.PSO removed 6 least ranked features and selected 7 as predominant features which will enhance the accuracy of the ensemble classifier.

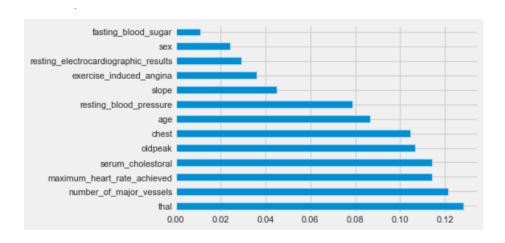


Figure 6: Comparison for different measures

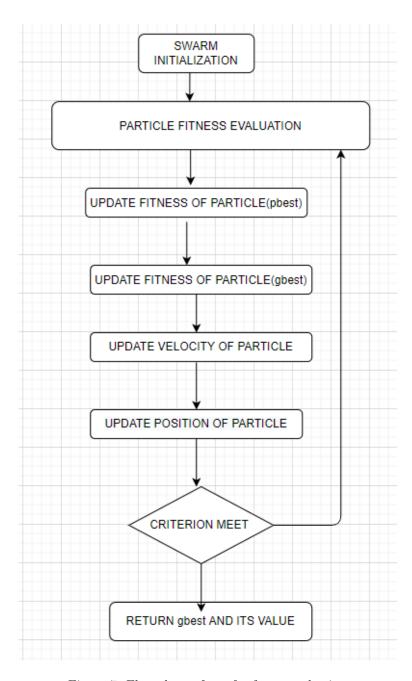


Figure 7: Flow chart of pso for feature selection

Table 10: Features selected by PSO

S.no	Selected Features
1.	Thal
2.	$number_of_major_vessels$
3.	maximum_heart_rate_achieved
4.	serum_cholestoral
5.	old peak
6.	chest
7.	age

Table 11: Accuracy of our proposed method for feature selection using PSO

S.no	Proposed Methodolgy	Accuracy
1.	PSO+ BAGGED TREE	90.6%
2.	PSO+RANDOM FOREST	83.3%
3.	PSO+ADABOOST	74.05%
4.	PSO+KNN	55.5%
5.	PSO + LR	100%
6.	PSO + DT	91.24%
7.	PSO + NB	90.06%

Table 11 records the accuracy of the proposed method using feature subselection method PSO. By using PSO feature selection measure on Bagged Tree, accuracy obtained is 90.6%. With feature selection method PSO on Random Forrest algorithm, accuracy is 83.3%. With feature selection method PSO on AdaBoost accuracy is 74%.

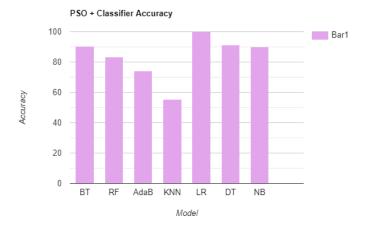


Figure 8: Comparison of Accuracy with Particle Swarm Optimization

6.4 Genetic Algorithm

The Genetic Algorithm is a model of biological evolution based on Charles Darwin's theory of natural selection. It was introduced by John Holland in the year 1975. It is a randomized algorithm that is developed to mimic the mechanics of natural selection and natural genetics. Holland used crossover and recombination, mutation, and selection to enhance the algorithm's problem-solving strategy. It supports the "survival of the fittest" concept for solving a problem and generates high-quality solutions for optimization problems.

The genetic algorithm works by initializing a population of chromosomes and determining its fitness. Then we perform the selection operation through which the parents of the next generation are selected. Crossover between the selected parents creates a new population. The new population is mutated to maintain its diversity. Ultimately, the fitness for this new generation is estimated.

Table 12: Comparison Of Ensemble Methods

	Table 12. Comparison of Ensemble Methods							
S.	Ensemble	Accuracy	Precision	Recall	F1	Sensitivity	Specificity	
No	Method				Score			
1.	Random For-	77.78%	73.07%	79.17%	76%	79.17%	76.67%	
	est							
2.	AdaBoost	74.07%	70.83%	70.83%	70.83%	70.83%	76.67%	
3.	Genetic Algo-	79.63%	78%	75%	77%	75%	83.33%	
	rithm + Ran-							
	dom Forest							
4.	Genetic Algo-	79.63%	78%	75%	77%	75%	83.33%	
	rithm + Ad-							
	aBoost							

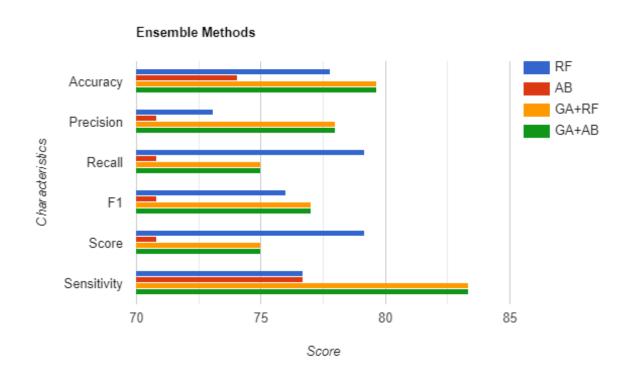


Figure 9: Comparison of Ensemble Methods before and after GA

Table 13: Comparison Of Various Machine Learning Models

S.no	ML Tech-	Accuracy	Precision	Recall	F1 Score	Sensitivity	Specificity
	niques	-					
1.	DT	64.81%	60%	62.5%	61.22%	62.55%	66.67%
2.	SVM	85.19%	80.77%	87.5%	84%	87.5%	83.33%
3.	KNN	83.33%	80%	83.33%	81.63%	83.33%	83.33%
4.	LR	85.19%	80.77%	87.5%	84%	87.5%	83.33%
5.	GA + DT	75.93%	87%	54%	67%	54%	80%
6.	GA +	88.89%	87.5%	87.5%	87.5%	87.5%	90%
	SVM						
7.	GA +	87.04%	84%	87.5%	85.71%	87.5%	86.67%
	KNN						
8.	GA + LR	92.59%	91.67%	91.67%	91.67%	91.67%	93.33%

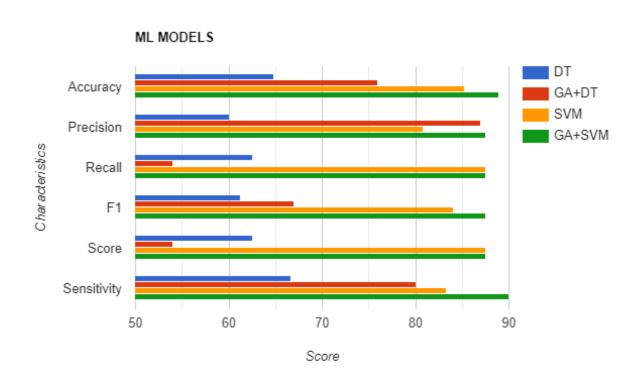


Figure 10: Comparison of ML Models before and after GA

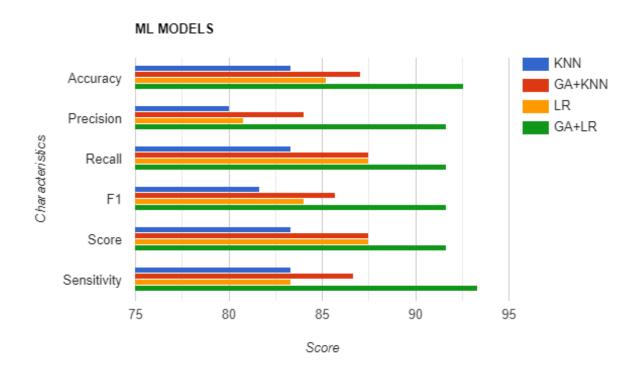


Figure 11: Comparison of ML Models before and after GA

6.5 CONCLUSION

In this paper, we have applied various machine learning algorithms on heart stat-log data set from UCI Repository and we have used those results for the prediction of heart diseases. The proposed approach uses PSO and Genetic Algorithm (GA) as a feature selection method to reduce the less important features. Then applied ensemble methods as a classifier to decrease misclassified rate and to enhance the classification production. The experimental results by applying 2 different feature selection algorithms, i.e. PSO and GA, on the same data set we got different results. Some machine learning models like DT, KNN, LR and AdaBoost classifier performed better with GA while some other models like RF gave better results with PSO. It has been shown that PSO + BT gives a high accuracy of 90.6% while PSO + LR gives the highest accuracy of 100%. Therefore, these models will help medical specialists to accurately predict and early diagnosis of heart diseases using a subset of features. In future we would want to develop an intelligent system that can determine the probability of a person developing a heart disease. And once such a system is developed focus can be shifted towards developing models that specify the line of treatment for a diagnosed patient based on past records.

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