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Machine Learning-Based Comparative Study For Heart Disease Prediction

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Abstract

Heart disease is one of the most common causes of death globally. In this study, machine learning algorithms and models widely used in the literature to predict heart disease have been extensively compared, and a hybrid feature selection based on genetic algorithm and Tabu search methods has been developed. The proposed system consists of three components: (1) preprocess of datasets, (2) feature selection with genetic and Tabu search algorithm, and (3) classification module. The models were tested using different datasets, and detailed comparisons and analyses were presented. The experimental results show that the Random Forest algorithm is more successful than Adaboost, Bagging, Logitboost, and Support Vector Machine using Cleveland and Statlog datasets.

Keywords: *Classification, optimization, heart disease, genetic algorithm, tabu search*

1. Introduction

Heart disease is a common disease, accounting for 31% of all global deaths; it ranks first, especially in female deaths [1,2]. One study concludes that a person dies of a heart attack every 34 seconds in the United States [3]. Especially in recent years, the effects of changing world conditions on our lifestyle trigger heart disease. It is argued that viral diseases such as Covid-19 affect the whole world [4], and the drugs used in their treatment also increase the risk of a heart attack. Disease prevention and early diagnosis are essential to overcome such situations and maintain a healthy life. This study offers a model proposal that can be used in the early diagnosis of heart disease.

The heart disease diagnostic system provides information technology to assist healthcare professionals. There is a need for information systems that produce predictions on health issues such as heart disease, where early diagnosis is essential. These systems make predictions based on test results predicted by experts. Making accurate and efficient tools/tests is critical to speed up the decision-making process in disease diagnosis. Accurate and efficient tools/tests are also essential to reduce data storage systems and the costs of testing used for diagnosis.

There are two commonly used data in the literature for diagnosing heart disease. These Cleveland and Statlog are datasets. Both datasets are accessible to researchers in the UCI Repository. The Cleveland dataset contains five classes. However, the number of data for each class is not homogeneous. Studies suggest using this data set by reducing the five class features to two classes. There are two classes in the Statlog data set; patient and not.

In a study [6] using the Statlog data set, the success achieved with the voting classification method using two classifiers was an accuracy of 87.41%. In contrast, the study [1] achieved a value of 92.59% with a new ReliefF and Rough Set-based classification approach.

The study performed with the Cleveland dataset [9] lags behind the 85.48% accuracy rate obtained with the majority voting approach on four different classification methods, the 86.30% value obtained by the multivariate analysis and MLP of the study [5]. When the studies using the Cleveland data set are examined, the accuracy values obtained are 86.87% with SVM [6], 89.30% with clustering-based DT learning [7], and 97.78% with genetic algorithm and recurrent fuzzy neural network [8]. In the study, which draws attention to its high accuracy value [9], the data set was divided into training and testing instead of cross-validation. It has not shown how much success changed when the selected test data was changed.

Especially in recent studies on the Cleveland data set, optimization methods, deep learning, and fuzzy logic-based approaches are encountered. In the study [10], 84.61% accuracy value was reached with the MLP weights trained method with PSO. In a different study [11], test accuracy of 93.33% was achieved using a pre-trained Deep Neural Network for feature extraction, Principal Component Analysis for dimensionality reduction, and Logistic Regression for prediction. In another study [12], which used two methods in feature selection, univariate feature selection, and Relief, the success of the model created with the random forest algorithm was 94.9%. In addition, they presented the model they created in their work as a system that can be performed online with Apache Spark and Apache Kafka in the Twitter application. A study using Cleveland and

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Hungarian datasets [13] proposed an IoT-Cloud-based intelligent health system. Their studies created a model with a fuzzy inference system and recurrent neural network bidirectional LSTM.

One of the essential tasks in creating a recommendation system for disease diagnosis is reliability. The data quality used in the system is necessary while ensuring reliability. For this purpose, two data sets frequently used in the literature were combined and included in this study. Excess data in the data set, inconsistent data, and lack of data can reduce the performance of data mining techniques [16,17]. In this study, the feature selection process was carried out using genetic and tabu search algorithms to increase data quality and prevent data redundancy in the data set. Samples with missing data for missing data were excluded from the data set. In this study, a hybrid optimization method was used to reduce the decision-making process for diagnosing the disease and finding the features that have the disease symptoms. After finding the most valuable features in diagnosis, the classification process was applied.

2. Method and Material

The study examined two data sets for heart disease, frequently used in the literature. It was investigated whether the combination of datasets would positively affect success in predicting heart disease. Optimization algorithms were used to determine the features that can be used to predict the disease to reduce time loss and examination costs in diagnosing heart disease. A hybrid feature selection based on a genetic algorithm and tabu search methods has been developed as an optimization process. Classification results with five different machine learning algorithms with appropriate features are presented. The results are presented and discussed before and after feature selection for comparison.

2.1. Dataset and Preprocessing

The Statlog and Cleveland datasets have similar features on heart disease, which are widely used in the literature, and can be accessed from the UCI Repository. Both datasets contain 14 attributes, 13 attributes, and a class label. There are a total of 303 samples in the Cleveland data set. There are five different classes. In the Statlog dataset, there are 270 samples and two classes.

The study examined and removed repetitive and null values on the data set. Since only one sample repeats the value in our dataset, duplicates and samples with six blank data were excluded. There are 567 pieces of data in total in the combined data set. Five different class information in the Cleveland data set was reduced to two and expressed as Cleveland (2 classes) in the study.

2.2. Feature Selection Process

Feature selection is an essential step in solving problems with many features. It can be defined as the subset finding process representing the original dataset with fewer data. Thanks to this process, the data size to be processed is reduced. This often speeds up model production and testing. Data quality is improved as the feature selection process removes noisy/less effective/unnecessary data. This helps to increase model quality. The reduction in the number of data provides advantages in data collection, data processing, and data storage.

Sample number distributions of data sets according to classes are shown in **Table 1**. In the combined dataset, there are 567 data after clearing the invalid data.

Table 1. *Distribution of the number of samples found in the class labels of the data sets*

Data sets	Diagnosis of healthy	Diagnosis of Heart Disease			
Statlog	Class 1	Class 2			
	150	120			
Cleveland	Class 0	Class 1	Class 2	Class 3	Class 4
	164	55	36	35	13
Cleveland + Statlog	Class 1	Class 2			
	314	259			
Cleveland + Statlog (cleaned)	310	257			

Deterministic methods can extract the most suitable feature set from the original data set. However, this approach is costly as all possible clusters will be examined. For example, in the data set used in this study, the most suitable feature set among 13 features can be found by examining all possible sets.

In this case, the number of clusters to be examined is:
Let C(n,r) be the number of subsets containing r data of a set with n elements (the r combination of n)
The formula for all possible situations:

$$C(13,1) + C(13,2) + C(13,3) + \ldots\ldots\ldots + C(13,11) + C(13,12) + C(13,13) = 8191 \text{ set of pieces}$$

A solution close to the successful solution can be reached by examining a much less number of examples with non-deterministic optimization methods. Instead of examining 8191 cases, an optimization method that will be prepared with a combination of Genetics and Taboo Techniques can be used. The cost of the deterministic approach can be observed more clearly in data sets containing more than 13 features.

2.3. Genetic Algorithm

The Genetic Algorithm is an optimization technique proposed by Holland [25] based on simulating the natural evolutionary process. In the algorithm, a population consists of chromosomes, each can solve the problem. The effect of the presence of each chromosome in the population is related to its fitness value. The fitness value may differ for each problem. The population is refreshed until the specified number of generations or termination operator is satisfied. The regeneration process involves forming a new generation by crossing over and then diversifying by mutation. When the regeneration process stops, the chromosome with the most suitable fitness value for the problem in the population is chosen as the solution. Thanks to crossover and mutation, the search space is not unidirectional.

Thanks to its wide search area and its solution to intermittent and linear problems, the genetic algorithm has a wide range of uses. In the literature, genetic algorithm is preferred for solving many problems. Some of those; In solving the multi-mode multi-objective problem [18], it is used as a solution sequencing problem [18], in the solution of the effect maximization problem in social networks [19], in the solution of the dual-objective routing problem in dynamic networks [21], in the solution of the multi-objective reactive power distribution strategy problem for wind energy integrated systems [20], shape optimization [23], biomedicine [24]. Genetic algorithm is frequently preferred in the feature selection process, especially in recent years [26-30]

2.4. Tabu Search Algorithm

Tabu Search Algorithm is a local search algorithm proposed by Fred Glover [31] and developed by Hansen [32]. A single solution is generated when the algorithm stopping criterion is met. The algorithm starts with the initial solution. All possible neighbor solutions are examined, and the best neighbor solution is determined as the solution. The algorithm keeps all its operations in memory. One of his strengths is his memory, which prevents him from re-examining situations he has studied before.

Tabu search algorithm is used in many fields such as scheduling problems [33,35] and route planning [34].

2.5. Classification Algorithm

Five different classifiers were used in this study. These are Support Vector Machines (SVM) and ensemble learning algorithms. The purpose of SVM is to maximize the separation of the two hyperplanes to obtain an optimal hyperplane separated in space. Ensemble learning produces multiple models rather than a single model. It is divided into Bagging and Boosting. Each model created in the bagging method is independent of the other [39]. In the classification process, the result produced by each model is examined, and the value determined by the majority is assigned as a result. The Random Forest algorithm extends the Bagging algorithm by combining random selection in a subset of data. The Boosting method is an ensemble learning technique developed to increase the performance of a learning algorithm [39]. It weights the data set to increase the model's success with weak learning. The weak model is strengthened by training with weighted data sets and works as a single model. Logitboost is one of the boosting methods introduced by Schapire and Singer [37]. Adaboost, proposed by Freund and Schapire [38], is an algorithm that can work with small datasets and uses the Bayesian classifier to create a model that includes the optimization process.

2.6. Performance Evaluation Metrics

In the experiments conducted within the scope of this study, Accuracy, Precision, Recall, and F1 Score, which are traditional classification performance measures, were used. When comparing the study with other studies in the literature, this value was discussed because the common evaluation metric in all studies was Accuracy. These metrics are based on the four values (TP, FN, TN, FP) of the confusion matrix.

The confusion matrix has positive and negative labels for the actual and predictive classes. Data with a positive label in the real class; Having a positive label in the prediction class is expressed as “True Positive (TP)”, and having a negative label in the prediction class is expressed as “False Negative (FN)”. Data with negative labels in the actual class; Having a positive label in the prediction class is expressed as “False Positive (FP)”, and having a negative label in the prediction class is expressed as “True Negative (TN)”.

Accuracy is the ratio of the total number of samples predicted correctly by the model to the total number of samples tested, and its formula is given in Equation 1. Precision: the ratio of the number of positive samples correctly predicted by the model to the total number of positive samples predicted, and its formula is given in

Equation 2. Recall is the ratio of the number of positive samples predicted by the model to the total number of true positive samples and its formula is given in Equation 3. F1-Score is calculated by taking the harmonic average of the precision and sensitivity values and its formula is given in Equation 4.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \tag{1}$$

$$\text{Precision} = \frac{TP}{TP + FP} \tag{2}$$

$$\text{Recall} = \frac{TP}{TP + FN} \tag{3}$$

$$\text{F1} - \text{Score} = 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{4}$$

2.6. Methodology

In this study, analyses were carried out with different data sets to create a more stable structure in heart disease. Datasets were preprocessed on features and samples. To not affect the stable structure, samples with invalid data in the data sets were removed. The feature selection process was applied for the disease prediction process with the fewest features, which is one of the study's aims. Optimization was achieved by combining the Genetic algorithm and Tabu search technique in the selection process.

A Genetic algorithm can produce good, fast, and efficient results for exploring the complex solution space (spherical search), but it can give ineffective results in the optimal local area. Tabu search algorithm is superior in local search but insufficient in global search.

In the study, the memory capability of the Tabu search algorithm was added after the basic structures of the genetic algorithm, crossover, and mutation processes. Thanks to this addition, the population continues through more suitable solutions in local search.

Table 2. *Parameters used in the feature selection process*

Parameters	Value
Population size	32
Iteration size	50
Crossover process	Two-point crossover
Mutation probability	%15
Selection	Elitism
Initial population	Opposite-based population distribution
Population size	32

One of the essential parameters in the genetic algorithm is the selection of the initial population. In this study, a counter-based approach was used for the initial population. Opposite-based approach: the opposite is generated by randomizing the generated half-solution and the other half to prevent all solutions from failing on one side of the search space. The created population is kept in the tabu list in memory. In this way, multiple examinations of the same solution are avoided. The model algorithm, which provides the highest accuracy in the classification process performed before the feature selection process, was used to calculate the chromosome fitness value. The fitness value is the accuracy value of the model produced by the algorithm. The chromosome with the highest accuracy value in the population obtained at the end of the determined parameters was chosen as the solution chromosome. The parameter values used in the experiments are shown in **Table 2**.

In the standard genetic algorithm, the population size is kept constant. To avoid the classification cost in this study, we excluded the previously reviewed solution from the population to reevaluate. Thus, the population size changed.

3. Experimental Results

In this study, the results of the models created before and after the feature selection process are listed to examine the effect of the feature selection process in detail. All data set in **Tables 3** and **4** were classified using the 10-fold cross-validation method.

Table 3. *The success values of the models are created with five different algorithms of the data sets before the feature selection process is applied.*

Data sets	Algorithm	Accuracy	F1-Score	Precision	Recall
Cleveland (4 class)	Random Forest	60.3	56.4	54.1	60.4
	SVM	58.7	55.1	52.3	58.7
	Adaboost	51.4	-	-	51.5
	LogitBoost	57.0	54.8	52.8	57.1
	Bagging	57.4	52.2	49.2	57.4
Cleveland (2 class)	Random Forest	80.5	80.5	80.5	80.5
	SVM	85.1	85.1	85.2	85.1
	Adaboost	83.4	83.5	83.5	83.5
	LogitBoost	81.8	81.9	81.9	81.8
	Bagging	80.5	80.5	80.5	80.5
Cleveland+ Statlog (2 Class)	Random Forest	97.5	97.6	97.6	97.6
	SVM	85.6	85.6	85.9	85.7
	Adaboost	83.8	83.8	83.8	83.8
	LogitBoost	84.6	84.6	84.6	84.6
	Bagging	88.3	88.2	88.4	88.3

When **Table 3** is examined, the number of samples increased by the combination of the data set improved the model's performance by an average of 5.64%. In particular, it provided the highest difference, with 17.03%, between the models created with the Random Forest Algorithm.

The feature selection process was applied to the three prepared data sets separately. The data sets created due to the application were trained and tested with five different classifiers. The best feature set shared in the study includes nine features, class information, and ten features. These; The success of sex, cp, fbd, resterg, exang, oldpeak, slope, ca and thal Models are shown in **Table 4**.

Table 4. *The success values of the models created with five different algorithms of the new data sets with the feature selection process applied.*

Data sets	Algorithm	Accuracy	F1-Score	Precision	Recall
Cleveland (4 class)	Random Forest	56.5	55.0	53.8	86.6
	SVM	57.9	53.8	51.1	57.9
	Adaboost	50.8	-	-	50.8
	LogitBoost	59.5	56.3	53.8	59.6
	Bagging	56.9	52.6	50.0	56.9
Cleveland (2 class)	Random Forest	80.5	80.4	80.6	80.5
	SVM	80.5	80.4	80.6	80.5
	Adaboost	81.5	81.5	81.5	81.5
	LogitBoost	81.8	81.8	81.9	81.8
	Bagging	81.1	81.2	81.2	81.2
Cleveland+ Statlog (2 Class)	Random Forest	97.1	97.2	97.2	97.2
	SVM	86.7	86.7	86.7	86.7
	Adaboost	83.4	83.4	83.4	83.4
	LogitBoost	84.4	84.5	84.5	84.5
	Bagging	88.1	88.1	88.3	88.2

When the results were compared, an average improvement of 0.026% was observed in **Table 4** and **Table 3** values. When each data set is compared within itself, the highest improvement was Cleveland (2 class), with an average increase of 0.71% between models. There was a 0.006% improvement between models in the Cleveland + Statlog combination. In the combined data set, the average success rate before the feature processing is 87.986%, and the average accuracy is 87.992%, which are very close to each other. Achieving

better performance with fewer features is essential for rapid diagnosis and reducing the use of data storage systems and testing costs. Our study has shown that a more stable structure can be achieved with fewer data.

4. Conclusions and Future Work

The study aims to assist in diagnosing heart disease by using a hybrid feature selection process based on genetic and Tabu search methods and an ensemble learning classification system based on heart disease datasets widely used in the literature. The proposed system includes three subsystems:

1. Consolidation and cleaning of datasets
2. Genetic algorithm - feature selection system with taboo search algorithm and Random Forest algorithm as the evaluation function
3. A classification system with SVM and ensemble learning methods.

Table 5. *Comparison with studies in the literature*

Study	Data set	Method	Acc.
[1]	Statlog	a new ReliefF and a Rough Set- (RFRS-)-based classification	92.59
[5]	Cleveland	Tiered Multivariate Analysis +MLP- NN	86.30
[6]	Statlog	Vote with Naïve Bayes and Logistic Regression	87.41
	Cleveland	SVM	86.87
[7]	Cleveland	a cluster-based DT learning (CDTL)	89.30
[8]	Cleveland	a genetic algorithm (GA) based on trained recurrent fuzzy neural networks (RFNN)	97.78
[9]	Cleveland	Majority vote with NB, BN, RF, and MP	85.48
This study	Statlog+Cleveland	Random Forest	97.55

Achievement metrics for each data set were compared with studies in the literature (see **Table 5**). This study outperformed five of the six compared studies. The study [8] separated the data as training and test set on the Cleveland data set. To evaluate the performance of the classifier more accurately, all data should be used in the testing and training phase [40]. Therefore, although there is a 0.23% difference between the study [8] and this study, this study is more stable and consistent.

There are different datasets for heart attack risk in the literature. The most frequently used data sets were examined both separately and in combination. The feature selection process was applied to all the analyzed data sets. A genetic algorithm, which is frequently used in the literature, was used in the feature selection process. On the other hand, the capabilities of the Tabu search algorithm, which is frequently used in the literature, have been added to the genetic algorithm. In this way, it is thought that the most appropriate solution is approached the fastest. The proposed approach is not specific to the dataset used in the study. It provides a general recommendation that can be used in optimization methods.

Declaration of interest

The authors declare that there is no conflict of interest. It was presented as a summary at the ICAIAME 2022 conference.

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