Modified Artificial Bee Colony Optimization with SVM for Optimize the Selection and Classification of Heart Disease

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ABSTRACT

Medical guidance systems make extensive use of machine learning methods. A medical diagnostic aids in obtaining several characteristics that correspond to the various illness variants. It is probable to have redundant, irrelevant, and relevant aspects that reflect a disease with the use of various diagnostic techniques. The illness may be incorrectly classified due to redundant characteristics. Consequently, the amount of the data & computational complexity is decreased by eliminating the superfluous characteristics. Finding a suitable feature subset for efficient classification is a challenging problem. This calls for a thorough search over the dataset's sample space. This paper's primary goal is to identify the best feature subset with higher classification accuracy for the diagnosis of cardiovascular diseases using a metaheuristic algorithm. The best traits for illness detection are found using the Artificial Bee Colony (ABC) method, which is based on swarm intelligence. Support Vector Machine (SVM) categorisation is employed to assess ABC's capability. Dataset of Indian Heart Disease is used to verify the suggested algorithm's performance. According to the experimental findings, ABC-SVM performs well when compared with feature selection via reverse ranking. In addition, the results show that with only eight characteristics, the proposed approach accomplished maximum classification precision.

INTRODUCTION

The healthcare industry produces a significant volume of intricate data regarding patients, hospitals, disease diagnosis, electronic patient records, and medical devices. The significant quantities of data are a critical resource that must be processed and analysed to extract knowledge that facilitates decision-making and cost savings. In order to diagnose and treat diseases, it is imperative to extract valuable knowledge and make scientific decisions based on the data. Healthcare professionals are provided with a further resource of knowledge to make decisions by information mining in the medicinal ground, which introduces a set of instruments & methods which could be implemented to the processed data to uncover concealed designs. It is feasible for biological research to generate substantial datasets. The abundance of feature selection techniques that have been introduced in this field is a result of the multidimensional character of numerous modelling task of bioinformatics, which range from categorization investigation to spectral evaluation.

It is a group of diseases that affect the heart, blood systems, or both. It is also known as heart disease. Single photon emission computed tomography (SPECT) as well as electrocardiogram (ECG) are the main tests used. To get a SPECT imaging of the heart, one doesn't have to do anything risky. To make pictures of the heart, radioactive tracers are introduced into the blood. SPECT scans help doctors find coronary artery disease as well as figure out how likely it is that someone will have a heart attack. An ECG recording is looked at to find heart rate problems or abnormal heartbeats. Since an ECG is easy to record, it is often the first thing used to find out what is wrong with the heart. The ECG gives doctors important information about people whose hearts aren't beating

normally. Doctors can figure out what kind of abnormality the problem is by looking at the ECG record. Most of the time, though, the ECG is taken over a long period of time. This process takes a lot of time and is inconvenient for the doctor because he has to be alerted all the time.

The process of choosing a workable set of attributes from the initial collection of potential features is known as feature selection. The feature selection approach is used on datasets with known features, as opposed to feature extraction. From the initial collection of characteristics, these techniques will try to determine which ones are important and eliminate those that are redundant or unnecessary. Based on the methodology of the selection and search process, feature selection techniques may be divided into three main groups: heuristic, stochastic, and comprehensive search.

Finding the best feature subset for enhanced cardiovascular disease classification accuracy is the primary goal of this research, which employs a metaheuristic algorithm. The optimal characteristics for illness detection are discovered using an Artificial Bee Colony (ABC) method that is based on swarm intelligence. Use of Support Vector Machine (SVM) classification allows for the evaluation of ABC Fit.

This is the structure of the remainder of the paper: Section 2 highlights the literature survey and the outline of feature selection techniques is provided in Section 3. A suggested algorithm for artificial bee colonies (ABC) is covered in Section 4. The experimentation process using the dataset is then covered in Section 5. Results from experiments are contrasted with those from current methods in section 6. In Section 7, final conclusions are made.

2. Review Of Literature:

Because data processing takes a lot of time and additional computer resources, overload of data is a big issue. Therefore, in order to save time and resources, the feature selection procedure is utilised to eliminate the noise or unnecessary characteristics from the data. The accuracy of identifying the illness shouldn't be lowered by fewer characteristics. Thus, the classification approaches are combined with feature selection. The various feature selection techniques and categorisation procedures are covered in the sections that follow.

Classification and clustering feature selection techniques are covered in detail. Researcher went on to provide an example of how to combine many feature selection algorithms into one meta-algorithm that makes use of each approach. An organising framework and a unified platform were the two designs they put out. The unified platform facilitates the integration of different approaches. Any newcomer to feature selection may use the provided examples of real-world applications to their advantage when deciding which algorithms to use for data mining and other specific applications.

An approach for classifying arrhythmias was put out that uses SVM-based classifiers and Linear Discriminant Analysis (LDA) to reduce feature dimensionality. Wavelet transform was used to retrieve 17 original input features from preprocessed signals, then LDA was used to compress those features to four features. Even with the original set of features, the SVM classifier performs better when its features are reduced using LDA than when it uses Principal Component Analysis (PCA). This SVM-based classifier has been contrasted with FIS classifiers and MLP as part of a cross-validation process. The SVM classifier performed better overall than the others, even though all of the classifiers employed the same reduced features.

The SA-SVM strategy used the Simulated Annealing (SA) technique to choose features and determine parameters. Selecting the kernel's function & its parameter values present the most challenges when configuring the SVM model. The categorisation results will be inadequate if the values of the parameters have not been entered correctly. Accuracy serves as the assessment criterion for the wrapper strategy. The goal of building a classifier is to maximise predicted accuracy. The best features are then chosen from among those used by the classifier. Several datasets from the University of India were tested using the Simulated Annealing-SVM technique without including feature selection, and the results were contrasted with the Support Vector Machine. The

findings unequivocally show that SA-SVM is very beneficial for choosing the attributes values.

Each forward choosing phase was simplified by employing the linear forward choosing system, which decreased the quantity of feature developments. Experiments have shown that this method is more efficient, identifies fewer subsets, and can even enhance the higher precision than conventional forward selection. This method yields competitive outcomes, as indicated by the findings. The outcome has a shorter runtime and less overfitting than fully execute the forward selection. Numerous projects have been implemented. This was done in earlier times to expedite the wrapping process. Two distinct linear variants fixed-width and fixed-set-width forward selection wurden vorgestellt. These are more advantageous than conventional forward. Primary reason for selection is the substantial decrease in their ability to generate reduced subsets, but also because of their latency accuracy is not significantly diminished.

For the feature selection issue, an enhanced metaheuristic built upon the GRASP has been created. GRASP-FS technique offers a successful wrapper-filter hybridisation strategy. GRASP components such as Sonar, Ionosphere, SpamBase, Audiology, and Arrhythmia were validated using five benchmark datasets from the VCI repository, each of which included 61, 35, 58, 70, and 280 characteristics, respectively. They looked at the GRASP component layout and how it was modified to address the feature selection issue. The hybridisation schemata's robustness was validated by the results.

To choose features for support vector machine (SVM) classification, researcher developed a hybrid filter-wrapper technique that uses Particle Swarm Optimisation (PSO). The filter model evaluates the relevance and redundancy of features in relation to the chosen feature subset; it is based on the mutual data. An approach for discrete PSO that has been modified is the wrapper model. The phrase "maximum relevance minimum redundancy PSO" describes this hybrid method. Additionally, the suggested method's performance has been contrasted with that of a hybrid filter-wrapper approach that combines genetic algorithm with PSO-based wrapper. According to the findings, the PSO system surpasses its competitors in performance.

Medical expertise fuelled to pick out relevant characteristics, researcher used Feature Selection (MFS) in conjunction with the widely used AI-based feature selection technique. A combination of MFS and CFS has also been studied, and promising outcomes have been seen, especially for Naive Bayes and Sequential Minimal Optimisation (SMO). The implementation was evaluated using the VCI Heart Disease dataset. Four performance parameters is taken into account to compare the common categorisation methods. The four factors are time, F-measure, accuracy, and true positive rate (TP). In this instance, TP was the positive groups' correct classification rate, efficiency was the total prediction accuracy, and the F-measure indicates the way an algorithm performs when accounting for the accurate prediction rates of both classes. The computational complexity for learning was also compared with training time. Selecting features using medical

To classify high-dimensional cancer microarray data, a new feature selection method was suggested, which makes use of particle swarm optimisation (PSO) and SNR scores. Prior to ranking genes, the data collection is grouped via k-means cluster. In order to create a new feature subset, we collect the genes with the highest scores from each cluster. Next, the created optimised feature subset is made by feeding the generated subset to PSO. Researcher employ probabilistic neural network (PNN), support vector machine (SVM), and k-nearest neighbour (k-NN) classification algorithms with a leave one out cross validation strategy to evaluate the feature subsets. According to the findings, the suggested method that makes use of PSO outperforms the others.

In classification tasks, BC was suggested as a way to reduce the number of data dimensions. In the original high-dimensional data, it is used to pick the best group of dimensions. Based on the ABC scheme, the k-NN technique is employed to measure suitability. There is an effective method to reduce the number of dimensions that uses ABC and k-NN that has been changed and put together. Employed bees, observer bees, as well as scout bees are the three

kinds of bees that ABC uses. ABC wrapper and a k-NN classifier are used in the suggested technique. The k-NN is utilized to figure out how fit the ABC food sources are. k-NN is used to test how well the newly identified food sources are classified after the hired bees and the spectator bees come up with them using a subset of the chosen features. For choosing the best set of traits, the accuracy is employed as a barometer. A lot of time is wasted on interviews and watching people's behaviour, which is how the current diagnosis tools work. Data on gene expression and data on autism were used in the studies. Researcher found that the ABC-k-nearest neighbour technique can successfully lower the information size though keeping maximum classification precision in the gene expression analysis.

The feature selection process was made more efficient by combining the Revised Binary Particle Swarm Optimisation (MBPSO) approach with the optimisation of SVM kernel parameters. That was then used to forecast the death rate of patients with septic shock. In order to prevent the BPSO method becoming convergent too soon, an improved version of the algorithm has been developed. Using swarm speed and best-swarm-solution similarity, MBPSO controls swarm variability. By optimising the kernel parameters concurrently, this technique employs SVM within a wrapper way. One major area of medicine is the development of representations to evaluate the risk of death in affected person with illness. The method has been used to forecast whether septic shock patients would survive or not. Several benchmark datasets have been used to evaluate MBPSO, and it has been compared to other Genetic methods (GA) and PSO based methods. Experiments validated that the suggested method not only gets high accuracy in differentiating input feature selection, but also precision in classification, in contrast to competing algorithms that rely on PSO. There are several similarities between GA and MBPSO in with respect to precision, however, fewer solutions from the subset features.

To improve classification performance for the diagnosis of cardiovascular illness, a hybrid model that incorporates filter and wrapper approaches has been developed. SVM classifiers and hybrid models are used to construct three methods. They are Backelimination Feature Selection, Forward Attribute Selection & Forward Attribute Inclusion. After ranking the attributes according to the separation criteria, the classification model is assessed using the wrapper model. All attributes are ranked according to their significance for target class identification using these criteria.

Biological processes may generate enormous datasets. In order to diagnose a certain ailment, several studies need additional characteristics or aspects to be examined. However, because of irrelevant, noisy, and duplicated features in the dataset, computational cost and classification accuracy are both impacted by a large dimensionality feature space. Using the feature reduction methods is one such option. There have been several approaches to feature selection. Their similarities have prompted comparisons. Combinations of filter, wrapper, and embedding techniques are used. Wrapper approaches were extensively employed in biological research and produced the best classification accuracy, according to the assessment. A wrapper strategy is suggested to improve the precision of heart disease estimation by categorisation.

3. Methods For Feature Selection:

The four fundamental phases of the typical feature selection procedure are resulting validation, stopping criteria, subset assessment, and subset creation. In addition to reducing the number of features, feature selection heavily relies on the correctness of the chosen feature subset. Therefore, it is used to model and understand the fundamental mechanisms in bioinformatics in combination with classification algorithms. Combining feature selection with classification techniques may be done in a number of ways. Filter, embedding, and wrapper techniques are the three most often used feature selection approaches.

3.1. Integrated approach:

Embedded approaches are often tailored to individual learning machines and carry out selection of features as part of the learning process. One way to think about the classifier building involves an examination in the integrated region of feature subset & hypotheses, which includes searching for an optimum subset of features. Examples include regularization-based approaches, random forests, classification trees, and feature selection utilising Support Vector Machines' (SVM) weight vector. These approaches use less computing power than wrapper approaches. It is necessary to create embedded feature selection strategies especially for learning algorithms. Nevertheless, developing a mathematical model for an embedded classifier that uses feature selection is quite challenging.

3.2. Sorting Algorithms:

To assess and choose feature subsets, the filter model does not use a mining method but rather depends on the data's overall qualities. Two distinct processes, feature selection and classification, are carried out autonomously. When deciding which features to use, several feature selection algorithms use statistical functions to rank them. An ideal subset of characteristics, free of noise and redundancy, is the result. After that, the characteristics that were chosen are fed into classification algorithms and their performance is assessed. While this method is quick and can handle many high-dimensional issues, it isn't very good at classifying data.

3.3. Envelope Method:

Feature selection is not embedded inside a classifier but rather wrapped around it. To choose the workable subset of characteristics, the feature selection techniques rely on the classifier's accuracy. Consequently, the sets of characteristics that are ultimately chosen will vary depending on the classification method and the selection mechanism used. Compared to the embedded approaches, this method needs greater computational time. Filter techniques do not rely on classification methods, yet this one is easy to install and works in tandem with them.

4. An Algorithm for Artificial Bee Colonies:

The suggested feature selection method makes use of the ABC algorithm to enhance the classifier's predicted performance by optimising the attribute selection process & producing the finest possible attribute subset. A classifier is utilised to assess every attribute subset generated from the observers, whereas ABC acts as a feature choice & produces the feature subsets. Therefore, a wrapper-based system is what the suggested solution is. Here is the suggested algorithm in action:

i. Phase = 1
ii. Set up the ABC parameters
iii. Assess each feature's fitness separately
iv. Reiterate
v. Make use of the worker bees to build solutions

- Give each worker bee a binary bit string with a feature subset setting
- Create new subgroups of features
$$Upsilon_{kl} = Phi_{kl}[Y_{kl} - Y_{mn}]$$
- Send SVM classifier the generated feature subset

vi. Assemble answers from spectators

- Choose a characteristic by considering its likelihood L_i
- Calculate V_k by Y_k and Y_l
- Make use of greedy selection to choose between V_k and Y_k

vii. Find the answer that was left behind and the scout bee.
viii. Determine the cycle's optimal feature subset.
ix. Commit to memory the ideal subset of features
x. Phase = 1 + Phase
xi. every cycle till the end of the set time
xii. Create the ideal feature subset by using the same bee-searching process.

4.1. SVM Based Classification:

SVM are frequently employed in computational biology because of its high accuracy, capacity to handle big, high-dimensional datasets, and adaptability in modelling a variety of data sources. Binary classification is the most basic kind of prediction issue, including attempting to distinguish between items that fall into

either the positive (+1) or negative (-1) categories. SVMs address this issue by using two fundamental ideas: kernel functions and high margin separation. Classifying points in two dimensions may serve as inspiration for the concept of broad margin separation. Making a straight line & designating points on one sideways as positive & points on the other side as negative is a straightforward method of classifying the points. Nonlinear categorisation makes use of kernels. Classifying more than two classes is necessary for many real-world challenges.

By creating an n-dimensional hyperplane that divides the data into two groups as efficiently as possible, VM carries out classification.

The hyper plane with greatest distance to the closest data points within the training set achieves a decent separation (highest margin). The SVM hyper planes as well as support vectors are shown in Fig 1. With the aid of the kernel function, Support Vector Machine can effectively execute for non-linear classification. Typical kernels include:
- Equational kernel
- Structured Kernel
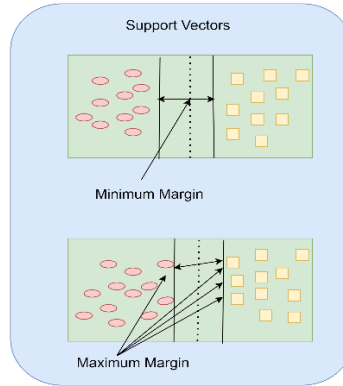- Curved kernel
- RBF kernel

Fig 1, illustrates the SVM Hyper Plane & Support Vectors.

5. Experimental Method:

MATLAB, which runs on an Intel Core i3 CPU with 4 GB of RAM & a 320 GB hard drive, is used to implement the suggested model. The dataset is from India. Table 1 lists the characteristics associated with the Indian dataset along with an explanation of each.

Attributes	Explanation
Age of the patient	Age is taken in years.
Sex	Female or Male
H_P	Various types of chest pain Type 1 – Normal Angina Pectoris Type 2 - Unusual Angina Pectoris Type 3 - Angina Pectoris that is not normal Type 4 - Symptom-Free
T_{r_bp}	Hospitalised patients resting blood pressure measured in millimetres of mercury.
Co	Level of serum cholesterol in milligrammes per decilitere
F_{bp}	Boolean function represents whether fasting blood sugar is higher than 120 mg/dl (1 = Correct; 0 = Incorrect)
$Rest_{ECG}$	ECG result at rest
Thalach	High heart rate reached
Old_{peak}	Exercise-induced ST depression as compared to resting state
Slope	For peak activity, the ST segment's slope
Co	Count of main vessels (0-3) shown via fluoroscopy
Thal	The condition of the heart (reversible, fixed, or normal)
Class	Class features

5.1. Evaluation Parameters:

The confusion matrix is provided in Table 2. It is a great tool for evaluating classifier performance. Researcher can identify whether the classifier is correct using CP and CN, and when it is incorrect using IP and IN. The extreme specialisation of the learning process might cause inaccurate estimations when classifiers are derived from training data and the precision of the learnt design is estimated. The precision of the classifier should instead be evaluated using a separate test set that contains tuples with labels the fact that weren't utilised during training.

Table 2, demonstrates the confusion matrix.

	Prediction	
	0	1
Actual	CN	IP
	IN	CP

Four categories may be formed from a population of people who have been screened for heart disease:

➢ Correct Positive - People who have a disease and test positive for it (CP).
➢ Incorrect Positive - Individuals who provide positive test results but are really negative (IP).
➢ Correct Negative - Those who do not have a positive test result (CN).
➢ Incorrect Negative - People who are positive yet test negative (IP).

Identifying Subjects One measure of performance is the precision or recognition rate, which is the proportion of properly identified test dataset tuples. The formula provides it.

$$Accuracy = \frac{CP + CN}{Total\_Input}$$

6. Results And Discussion:

The subsequent variables are used to assess the suggested method's performance.

Dimension count = 15
Number of bees working and bees watching = 13
Upper limit on the number of cycles = 100
Boundary = 10

Bar graph 1 compares the outcomes obtained from the advanced feature selection method with the recommended ABC-SVM strategy. The results show that ABC-SVM works better than reverse ranking feature selection. The results also show that the proposed method obtained good classification accuracy using just eight variables.
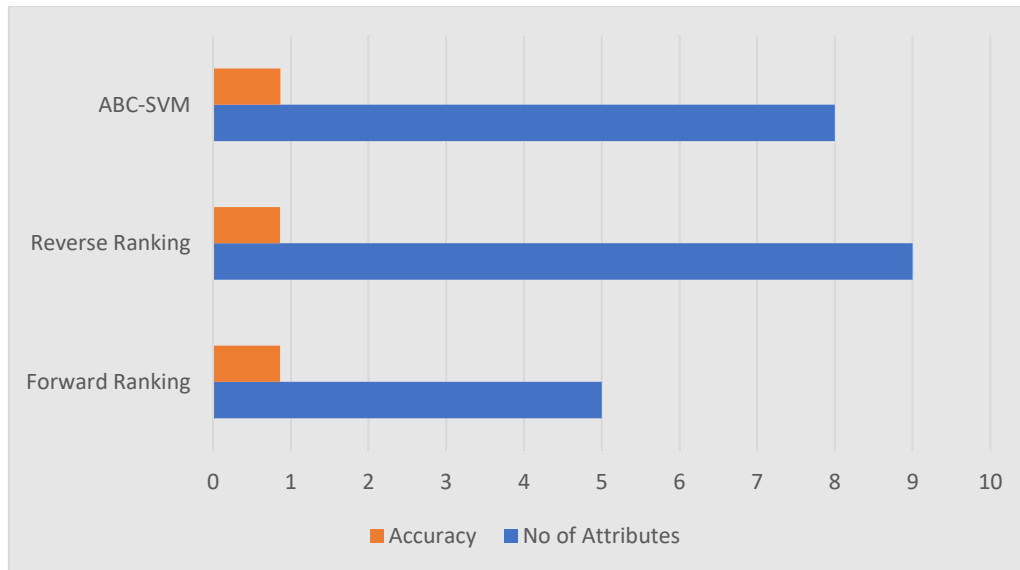
Graph 1, illustrates the result comparison of the forward and reverse selection with the suggested ABC-SVM approach.

Information on specific properties acquired by the ABC-SVM approach is provided in figure 2. In the first test, ABC-SVM achieved a five-feature accuracy of 85.30 percent. The second experiment used the same dataset and yielded an accuracy of 86.77% using eight characteristics. The most notable characteristics of cardiovascular disease are age & fasting blood sugar levels.
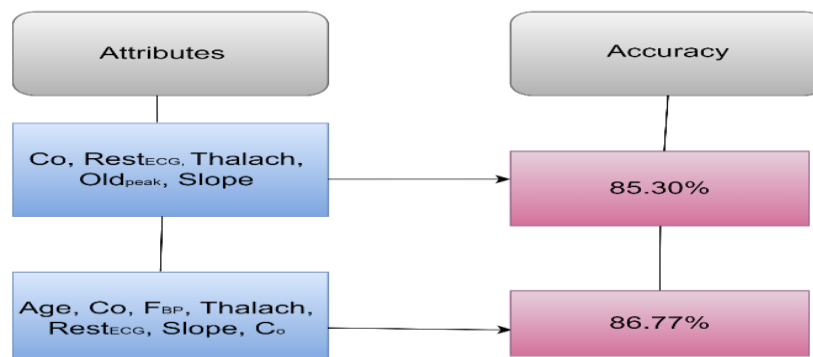

Figure 2, shows the specific properties acquired by the ABC-SVM approach.

CONCLUSION

The primary purpose of feature selection is to choose the best characteristics from the available data, particularly for medical diagnosis. The challenge of choosing the best characteristics is addressed by heuristic approaches. ABC is an algorithm known as metaheuristic that selects workable solutions that meet the established requirements by exchanging information among the bees within the population. The findings may rapidly converge to the ideal solution because to ABC's special solution updating process, which updates in two parts. Additionally, since there are less control parameters to establish, it is straightforward and simple to implement.

Experimental findings using the heart disease data shown that ABC-SVM, which utilized the wrapping approach to categorising, outperformed the usual forward selection & reverse feature selection algorithms in terms of accuracy. Eight characteristics for illness detection were found by the algorithm.

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