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A Modified Approach of Early Prediction of Heart Disease Using Advanced Kernel Support Vector Machine with Genetic Algorithm

Mr. H. Ramprasanth[1], Dr. N. Kamalraj[2]
[1]Research Scholar, Department of Computer Science, Park's College (Autonomous), Tirupur. ramprasanth1408@gmail.com.
[2]Research Supervisor, Associate Professor and Vice Principal, Park's College (Autonomous), Tirupur. tpkamal@gmail.com.

Abstract - *These days, heart disease may be a leading cause of death and despair. Deaths from heart disease are rising faster than those from other diseases everywhere in the world. It is quite difficult to foresee the likely consequences related to heart disease in advance. Several techniques are developed that use clinical knowledge sets for identifications in order to identify the likely problems. Several of the methods forecast risk variables associated with heart conditions. Numerous obvious risk indicators that are prevalent in people with heart conditions will be successfully employed for identification. In addition to aiding medical examiners in making predictions, system-supported risk factors also alert patients in advance of the likely existence of heart conditions. These techniques are helpful in preventing time and money waste. In light of this, a genetic algorithm is used in conjunction with a support vector machine, which is mostly based on intelligent systems, for identification purposes in this investigation. To determine what kind of cardiac issue a patient may have, whether or not it is a heart attack, clinical symptoms backed by a knowledgeable system are used. The genetic algorithm-based support vector machine is mostly used to analyze patient knowledge in India. It has been suggested to use the Advanced Kernel Support Vector Machine (AKSVM) technique to repeatedly and incredibly quickly confirm the support vectors. Genetic algorithms, which also optimize SVM's classification accuracy, are used to choose the relevant and essential options and eliminate the unnecessary and redundant ones. The findings indicate that, in contrast to current techniques, support vector machines will be successfully used for the identification of cardiac conditions. The results highlight the importance of accurate identification and the advantages of knowledge coaching for machine learning-based autonomous diagnosis systems.*
Keywords: Heart Disease, Support Vector Machine, Heart Disease, Clinical Dataset, Genetic algorithm.

1 INTRODUCTION

The use of machine learning techniques in the medical field is currently the focus of extensive research, which mainly focuses on modeling various human behaviors or thought processes and identifying illnesses from a variety of input sources (e.g. patient knowledge cardiograms, CAT/MRI/Ultrasound scans, photomicrographs, etc.) [1]. Data discovery and medical specialty systems, which include biological science and DNA analysis, are two distinct application fields [2, 3]. According to a recent report, cardiopathy has become the leading cause of death among Indians. According to a recent study conducted by the Indian Council of Medical Research (ICMR) and the Registrar General of India (RGI), cardiac disorders account for 25% of mortality in the 25–69 age range. About 19% of all deaths are caused by cardiac problems, if all age groups are included. According to the survey, it is the primary cause of mortality in all of India's regions for both men and women. With a population of more than 1.2 billion, India is estimated to be responsible for 60% of cardiopathy cases globally [4]. Time is vitally important to ensure accurate diagnosis in the early stages of cardiopathy. Patients who complain of chest pain may receive excessive care or be admitted to the hospital. It appears that there aren't many professionals available for diagnosis in the majority of developing nations. Therefore, such a machine-driven approach will improve the medical field by assisting doctors in making accurate diagnoses much earlier [5, 6].
A group of characteristics or instances that are indicative of all the different forms of the illness may be necessary in a diagnosis drawback. If the system is to function reliably and effectively, the examples should be carefully selected. One significant advantage over applying machine learning techniques to current problems is the fact that there is no need to provide a specific method for identifying the illness.

Nevertheless, creating computer systems for medical decision-making is a difficult undertaking. Obtaining, gathering, and organizing the data that will be utilized to coach the system are challenges. This turns into a significant disadvantage, especially when the system requires extensive knowledge sets over extended periods of time, which are typically unavailable due to a lack of a financially stable system. The appearance of a decision support system (DSS) may be influenced by more than just the previously listed problems or the current practices involved in the medical task. Additionally, rather than the overall performance, the design may be impacted by the necessary performance on one or many of the matter's specific categories. This is frequently the case for the majority of medical jobs because each category may require a unique level of relevance for the system to function.

A misclassification during this class could result in a healthy patient receiving therapy without cause, therefore for instance, in a severe cardiopathy diagnosis task, the accuracy on healthy patients must be as high as possible. The system's performance balance across all areas may differ and is mostly focused on the medical disadvantage itself as well as the body of information. Additionally, the death rate for patients with a wide range of illnesses has increased in the majority of countries due to a shortage of doctors. It has been found that in numerous instances, incorrect diagnosis or a trial-and-error diagnostic process compromises the patient's health. Computer programs or machine learning techniques are used to decrease the death rate, increase the accuracy of illness diagnosis, and, most importantly, shorten the time needed for diagnosis. Health care providers are encouraged to use telemedicine technology via the internet as a result of communication and technological advancements [7, 8]. This research presents a victimization support vector machine decision support system for cardiopathy categorization. The Cleveland Heart database, which Detrano provided from the UCI learning data set repository, is the knowledge set that was employed [9], [10].

Five categories are used to categorize the dataset: 0 represents no illness, and 1, 2, 3, and 4 represent four distinct disease kinds. To the best of our knowledge, every work that has been made public has utilized the dataset to distinguish between the presence (1, 2, 3, or 4) and absence (0) of a disease. Sort the information in the current work into five categories, including the type of illness. To find the support vectors for the SVM, we often employ a fast reiterative computational approach known as the Support Vector Machine algorithm (SVM). Furthermore, in order to avoid the curse of dimensionality, a reasonable call web should be incredibly time-efficient. It also tends to employ a genetic algorithmic rule to choose the optimum feature set that maximizes the SVM classification accuracy with a less number of possibilities. The rest of the document is structured as follows: A few earlier studies on machine learning methods for diagnosis are briefly reviewed in Section II. The anticipated call web and the methods employed are briefly described in Section III. Section VI presents the findings of the experiment. The paper is concluded in Section VII.

2. RELATED WORK

Heart conditions receive a great deal of attention in medical study among the many potentially fatal illnesses. It has a significant effect on human health as well. Many cardiac conditions were listed and discussed, but they all lead to heart attacks [11]. Anger was cited as the primary cause of death in industrialized nations. Not only do vessel diseases significantly affect people's regular quality of life, but they also have an impact on public health costs and the economics of the nations. Polygenic disorder, smoking, case history, obesity, high steroid alcohol consumption, and other characteristics are risk factors for these diseases [12]. Health data calls were made possible by a thorough understanding of the center's structure and operations. An infant born via replacement may even develop heart problems. People with cardiac conditions often experience weariness and chest pain. It happened when the heart is unable to meet the body's circulation needs [13].

Arunachalam, S. (2020) examine the study of cardiovascular diseases can often be prevented by leading a healthy lifestyle and addressing behavioural risk factors such as unhealthy diet and obesity, tobacco use, harmful use of alcohol and physical inactivity using population-wide strategies. Predicting cardiovascular illness can be aided by machine learning, and if done well in advance, this knowledge can give physicians valuable insights that they can use to modify their diagnosis and treatment plans for individual patients. It is suggested to use a prediction model that can determine if a person has heart disease and, if so, diagnose them or discuss the findings. This is achieved by applying rules to the individual outcomes of classification algorithms that were applied to the dataset, including the Multi-Layer Perceptron (MLP) Classifier, Logistic Regression, Support Vector Machine, Extremely Randomized Trees Classifier (Extra Trees Classifier), Random Forest Classifier, and Gradient Boosting Classifier. [15]. In their 2020 study, Marbaniang, I. A., et al. analyze six supervised machine learning algorithms—K-Nearest Neighbors Classifier, Naïve Bayes Classifier, Decision Tree Classifier, Random Forest Classifier, Support Vector Machine Classifier, and Linear Discriminant Analysis—to predict cardiovascular disease (CVD). Additionally, two health risk factors (feature extraction) have been added to the dataset: body mass index and blood pressure. This has been shown to improve accuracy. To identify the key risk indicators, feature selection was done. Finding the best CVD prediction outcomes from the provided dataset is our primary objective. [14].

According to Patil, P. B., et al. (2020), the primary cause of death for humans is cardiovascular disease (CVD). In addition to environmental and genetic variables, gut microbiota has become a novel factor influencing CVD in recent years. Changes in gut microbiota have been linked to cardiovascular disease (CVD), yet cause-and-effect interactions are not well defined. Therefore, it was anticipated that gut microbiome-based diagnostic screening for CVD may make use of machine learning (ML). Five supervised machine learning algorithms—random forest, support vector machine, decision tree, elastic net, and neural networks—were used to evaluate fecal 16S ribosomal RNA sequencing data from 478 CVD and 473 non-CVD human participants that were gathered through the American Gut Project in order to test our hypothesis. Thirty-nine differential bacterial taxa were identified between the CVD and non-CVD groups [16].

The main causes of cardiovascular illnesses are high blood pressure, family history, stress, age, gender, cholesterol, body mass index (BMI), and an unhealthy lifestyle, according to Rahim, A., et al. (2021). Researchers have put up a number of methods for early diagnosis based on these considerations. For the efficient and highly accurate prediction of cardiovascular disorders, a MaLCaDD (Machine Learning based Cardiovascular Disease Diagnosis) framework is suggested. In particular, the approach initially addresses data imbalance (using the Synthetic Minority Over-sampling Technique, or SMOTE) and missing values (using the mean replacement technique). The feature selection process then employs the Feature Importance approach. Lastly, for a more accurate prediction, a combination of KNN classifiers and logistic regression is suggested. The validation of framework is performed through three benchmark datasets (i.e. Framingham, Heart Disease and Cleveland) and the accuracies of 99.1%, 98.0% and 95.5 % are achieved respectively. [19].

Ten conventional machine learning methods were investigated by Abdar, M., et al. (2019), who then employed the top three algorithms (three varieties of SVM). An early and precise diagnosis of CAD lowers mortality by enabling prompt delivery of the right medication. Data pre-treatment and normalization was done to enhance these algorithms' performance. Additionally, stratified 10-fold cross-validation was employed twice, once for parallel feature selection and once for classifier parameter tuning using a genetic algorithm and particle swarm optimization. Experiments showed that N2Genetic-nuSVM predicted CAD outcomes among patients in a well-known Z-Alizadeh Sani dataset with an accuracy of 93.08% and an F1-score of 91.51%. These outcomes are competitive and on par with the industry's top outcomes. [26].

You can include a brief analysis of published material that is theoretically related to your planned work, unlike most of these publications. A brief summary of what ought to be included in the Relevant Works section is as follows: Work that presents a fresh method for resolving the same issue.

3. THE PROPOSED SCHEME

Because it entails erroneous assumptions during uncertain effects, early detection of heart disease from many circumstances or symptoms has become challenging. This study suggests using a genetic algorithm in conjunction with an Advanced Kernel Support Vector Machine (AKSVM) to retrieve data from patient medical records. The suggested system's block diagram is shown in Figure 1.

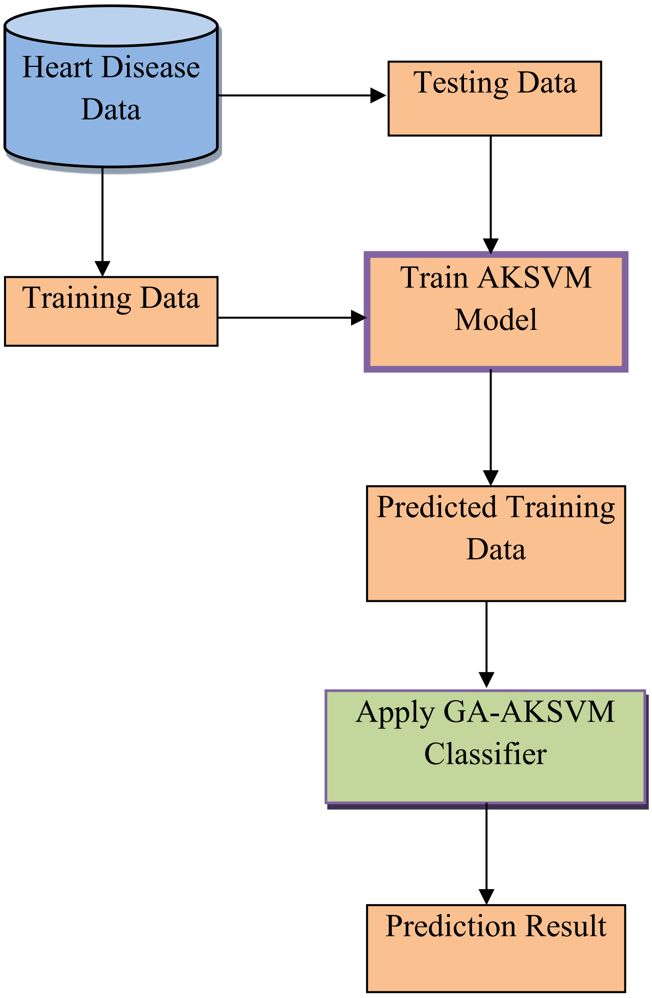

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Figure 1: Proposed Architecture Diagram

3.1. Input Data Collection

The records of 271 patients with fourteen dimensions were gathered based on the expert opinions of the physicians. Table I frequently lists and illustrates this. While the sample of data was being collected, the body state and, consequently, the eating habits of a median Indian were kept intact. The information was gathered from the Cardio Department of Apollo Hospitals in Chennai. The computer's patient observation system, which records data in structured form, was linked to the hospital's testing apparatuses. Since there was no risk of a heart issue, the heart diagnosis of 0 meant that the diameter was less than 500th. If the value of one was established, it meant that narrowing of the >500th diameter had occurred, indicating a high risk of heart disease. The pre-processing was performed on knowledge using Orange tool box.

Table 1: Input Dataset

S. No	Name of the Dataset	No. of Patients	No. of Images
1.	PROMISE12	50	1250
2.	ACDC-MICCAI (Workshop 2017)	150	150
3.	LASC STACOM 2018	20	100
4.	ACDC STACOM 2017	100	100

3.2. Advanced Kernel Support Vector Machine

Let M m-dimensional training inputs x_i $(i = 1, \ldots, M)$ belong to Class 1 or 2 and the associated labels be $y_i = 1$ for Class 1 and -1 for Class 2. If these data are linearly separable, the decision function is given by

$$y_i \left(w^T x_i + b \right) \geq 1 \text{ for } i = 1, \ldots, M.$$

The decision boundary can be found by solving the following constrained optimization problem

Minimize $\frac{1}{2} ||W||^2$

Subject to $y_i \left(w^T x_i + b \right) \geq 1$

In non-linearly separable problem, introduce a slack variableξ. If error is between$0 \leq \xi \leq 1$, then data can be properly classified, but if $\xi \geq 1$ then the data is misclassified. So, ξ should be minimized. The hyperplanes are computed as

$$y_i \left(w^T x_i + b \right) \geq 1 - \xi_i, \text{for } y_i = 1.$$

$$y_i \left(w^T x_i + b \right) \leq -1 + \xi_i, \text{for } y_i = -1.$$

The decision boundary can be found by the following optimization problem

Minimize $\frac{1}{2} ||W||^2 + C \sum_{i=1}^{M} \xi_i$

Subject to $y_i \left(w^T x_i + b \right) \geq 1 - \xi_i$ for $\xi_i > 0$

The function ̧ maps the training vectors x_i into a higher (perhaps infinite) dimensional space. Next, SVM locates a linear separating hyperplane, and the error term's penalty parameter is C > 0, which is the maximum margin in this higher dimension space. Furthermore, the kernel function is denoted as K(x_i,x_j) ≡ ̣(x_i)T ̣(x_j). The Fisher kernel, so named in honor of Sir Ronald Fisher, is a statistical classification function that calculates how similar two items are based on sets of measurements for each object and a statistical model. The class of a new item whose actual class is unknown can be inferred in a classification process by minimizing the average Fisher kernel distance between the new object and every known member of the class across classes. The 1998 introduction of the Fisher kernel combines the benefits of discriminative techniques (such as support vector machines) and generative statistical models (such as the Hidden Markov Model): discriminative techniques can have flexible criteria and produce better results, while generative models can process data of variable length (adding or removing data is well-supported). The Fisher Score, which is defined as U_X=∇_θ log⁡〖P(X┤|θ)〗, with θ being a collection (vector) of parameters, is used by the Fisher kernel. The function taking θ to $\log P(X|\theta)$ is the log-likelihood of the probabilistic model. The Fisher kernel is defined in equ. (2) with I the Fisher information matrix as

$$K\left(X_i, X_j\right) = U_{x_i}^T I^{-1} U_{x_j}$$

3.3. Genetic Optimization Algorithm

Genetic algorithms are frequently used to find the best range of risk variables for each input and to optimize control parameters like weight and learning rate in order to improve the AKSVM's performance and speed up training. Because redundant variables are eliminated, this method also helps identify the most important properties of the training data and allows for flexibility when generalizing to newly provided data. The GA looks for the best solution to a problem by combining selection, crossover, and mutation operators until the necessary criterion is satisfied. A chromosome, which is made up of a collection of genes, is the solution to a problem. The GA creates an initial population and so evaluates this population by training a network for everybody.

In order to find the best weight parameters, it then evolves the population across several generations. GAs because the original population will gradually change into a population that should include the best solution [7]. and frequently employ the ensuing cycle of copy analysis for each iteration, which is known as a generation. A certain probability is used to elect chromosomes (persons) from the current population, and copies of those individuals are produced. The selection of chromosomes is based on how suitable they are to the current population; the more robust chromosomes have a better probability of being found. The response from the AKSVM model could be used for fitness. Elect chromosomes are susceptible to crossing and mutation. Quasi-genetic mechanisms of crossing and mutation can manipulate these mathematical chromosomes. Chromosomes were paired at random, and parts of the paired chromosomes between two randomly chosen breakpoints were switched in order to perform crossovers. In order to invert altered genetic material before it is integrated into the recipient's body, inversions can even be sculpted. By slightly flipping a binary locus, mutations were imposed so that a "0" bit would regenerate to a "1" or a "1" bit would reincarnate to a "0." The serial methodology of binary type, roulette-wheel within the choice operator, tow-point crossover within the crossover operator, and boundary within the mutation operator were employed by GA in this study to develop the AKSVM model.

4. PERFORMANCE EVALUATION

Out of the fourteen features in the cardiac data, the algorithm was used to select the top N features. It should be mentioned that adding recent options from the previous set results in the new best feature set since the value of N is increased. This demonstrates that adding a feature has an impact on that particular subset's classification capacity, either positively or negatively. As a result, there is an optimal feature set where accuracy is maximized. The heart disease dataset is subjected to a variety of machine learning techniques in order to evaluate the suggested implementation. In this case, the dataset was evaluated using AKSVM and neural networks.

4.1. Dataset Details

- **PROMISE12**

One of the 50 training cases in Promise12 (Litjens, G., et al, 2014) is a transversal T2-weighted MR image of the prostate. About 1250 photos with matching labels (only the voxel values 0 and 1) make up the training set. After resizing each 2D MRI slice to 256 x 256 pixels, contrast limited adaptive histogram equalization (CLAHE) is used to equalize the histogram. Ten validation examples and forty training cases make up the training dataset. A variety of prostate shapes and sizes are shown in the set. Every case in the training package uses reference segmentation.

- **ACDC-MICCAI**

The suggested approach will be assessed using data from the Automatic Cardiac Diagnosis Challenge (ACDC-MICCAI Workshop 2017). Thirty individuals with normal heart function, thirty with myocardial infarction, thirty with dilated cardiomyopathy, thirty with hypertrophic cardiomyopathy, and thirty with irregular right ventricular function (RV) comprise the 150 cine-MR images in this dataset. The remaining 50 cine-MR images were used for research, and the first 100 were used for processing. Using an SSFP series in short axis in breath hold (with gating), cine MR images were obtained. The LV is covered by a sequence of short axis slices that are 5 mm thick (or occasionally 8 mm) and have a 5 mm gap between them from base to apex. The spatial resolution ranges from 1.37 to 1.68mm2/pixel, and 28 to 40 volumes cover the cardiac cycle fully or partially.

- **LASC STACOM 2018**

This dataset was submitted as part of the STACOM 2018 challenge for the job of left atrium (LA) segmentation. It comprises 100 LGE-MRIs taken from individuals suffering from atrial fibrillation (AF). The resulting data measures 88 x 640 × 640 and 88 x 576 x 576 voxels, with a resolution of 0.625 x 0.625 x 0.625 mm3.

- **ACDC STACOM 2017**

The ACDC dataset was created using actual medical examinations from the University Hospital of Dijon and made public as part of the MICCAI 2017 Challenge on Automated Cardiac Diagnosis. One hundred patients with heart failure with infarction, hypertrophic cardiomyopathy, dilated cardiomyopathy, or right ventricular abnormalities were included in this dataset's cardiac Cine-MR pictures (CMRI). Every grade level is represented equally in the photographs that are displayed. For every 100 samples, experts manually created ground truth segmentations for the MYO, RV endocardium, and LV cavity at end-systole (ES) and end-diastole (ED).

4.2. Performance Analysis

4.2.1. Accuracy Comparison

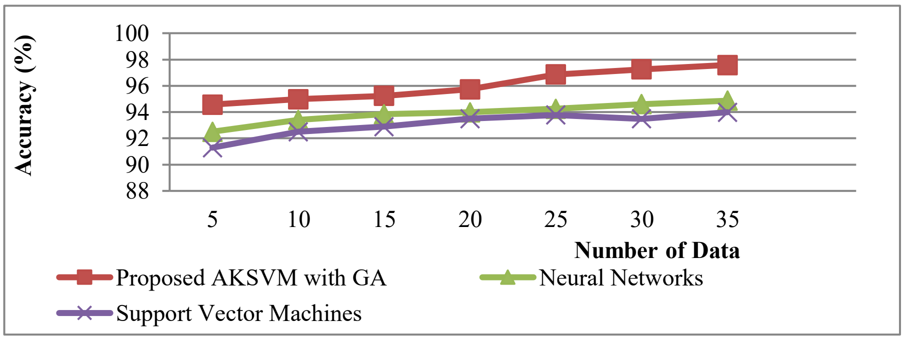

Figure 2:- Prediction and Detection accuracy Comparison

Since the suggested methods pick the key features in the dataset, the prediction and detection accuracy of the suggested AKSVM with GA based method achieves higher classification accuracy than the current classification methods like SVM and Neural Network. The accuracy result is shown in Figure 2. Perform the fisher kernel provided in the suggested work to lower the errors.

4.2.2. Error rate Comparison

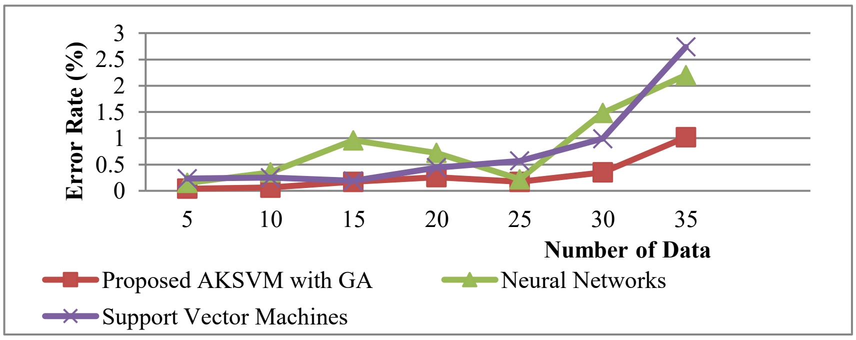

Figure 3: - Error Rate Comparison Results

The data's classification error rates are shown in Figure 3. According to the graph, the suggested AKSVM with GA method produces generally low error rates. The reason is that the GA algorithm, which is used in the proposed work for feature subset selection, allows a group of concurrent distributed agents to jointly identify the best features for a given dataset. Additionally, compared to current techniques like SVM and neural networks, the classification methodology is far more effective.

4.2.3. Execution Time comparison

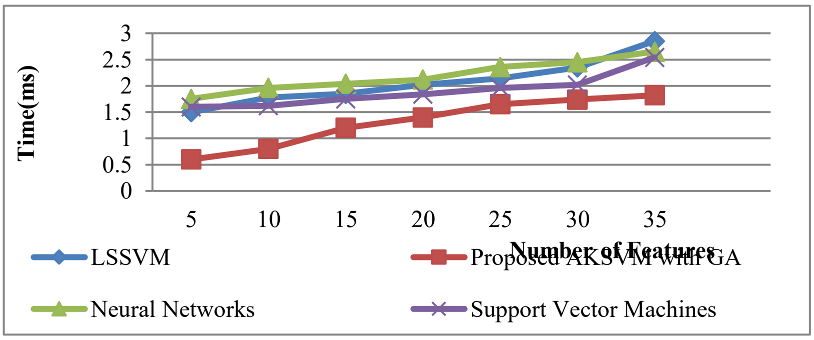

Figure 4: - Execution Time comparison

The results of comparing the execution times of the suggested AKSVM with GA approach and the current techniques, including SVM and Neural Network, are displayed in Figure 4. Since the suggested method can accurately predict heart illness at an early stage, the suggested AKSVM with GA methodology has a shorter execution time for diagnosing heart disease.

5. CONCLUSION

Lastly, AKSVM is used to define a decision support system for classifying cardiac disease. The best feature subset to maximize AKSVM's classification accuracy with less characteristics is found using a genetic algorithm. Support vectors are found quickly and iteratively using the AKSVM technique. The AKSVM's performance was greatly improved by using genetic algorithms for feature selection, and a high accuracy of 97.55% was attained. In the future, the system can be improved to diagnose heart disease more accurately by employing a better optimization algorithm to build a model that produces an effective outcome and by adding more categorization techniques and algorithms.

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