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IMPROVED EVOLUTIONARY SUPPORT VECTOR MACHINE CLASSIFIER FOR CORONARY ARTERY HEART DISEASE PREDICTION AMONG DIABETIC PATIENTS

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Abstract

Soft computing paves way many applications including medical informatics. Decision support system has gained a major attention that will aid medical practitioners to diagnose diseases. Diabetes mellitus is hereditary disease that might result in major heart disease. This research work aims to propose a soft computing mechanism named Improved Evolutionary Support Vector Machine classifier for CAHD risk prediction among diabetes patients. The attribute selection mechanism is attempted to build with the classifier in order to reduce the misclassification error rate of the conventional support vector machine classifier. Radial basis kernel function is employed in IESVM. IESVM classifier is evaluated through the performance metrics namely sensitivity, specificity, prediction accuracy and Matthews correlation coefficient (MCC) and also compared with existing work and our earlier proposed works.

Keywords: Soft computing, machine learning, support vector machine, neural networks, radial basis function, attribute selection, sensitivity, specificity, Matthews correlation coefficient (MCC), decision support system.

1. Introduction

Normally, the basic considerations of conventional computing are precision, sureness, and carefulness. We perceive this as hard computing. Strikingly, the critical idea in soft computing is that precision and sureness pass on a cost; sand that estimation, thinking, and essential initiative should abuse (wherever possible) the opposition for imprecision, vulnerability, inexact thinking, and deficient truth for getting insignificant exertion game plans. This prompts the great human limit of understanding ruined talk, interpreting untidy handwriting, valuing the nuances of trademark language, gathering content, seeing and orchestrating pictures, driving a vehicle in thick surge hour gridlock, and, even more generally, settling on typical decisions in an area of vulnerability and imprecision. The test, by then, is to abuse the strength for imprecision by creating procedures for count that lead to a recognize competent plan expecting practically zero exertion. This, for the most part, is the fundamental belief of soft computing. There are consistent undertakings to join artificial neural networks (ANNs), fuzzy set theory, genetic algorithms (GAs), rough set theory and different methodologies in the soft computing perspective. Hybridization abusing the properties of these theories consolidate neuro-fuzzy, rough-fuzzy, neuro-genetic, fuzzy-genetic, neuro-rough, rough-neuro-fuzzy strategies. In any case, among these, neuro-fuzzy computing component has picked up may analysts' consideration in nowadays. Coronary illness remains the main source of death throughout the world for as far back as decades. In 2015, the World Health Organization (WHO) has evaluated that 17.7 million passing's have happened worldwide because of heart ailments. Heart maladies are the essential driver of death universally: a larger number of individuals bite the dust every year from CAHD than from some other causes. In the event that we can anticipate the CAHD and give cautioning in advance, a bunch of passing's can be forestalled. The utilization of soft computing conveys another measurement to CAHD risk prediction.

2. Related Works

Hybrid Intelligent Modeling Scheme [1] was proposed to find the various set of descriptive variables in order to classify the diseases related to heart. It is an ensemble of (i) logistic regression, (ii) artificial neural network, (iii) multivariate adaptive regression splines, and (iv) rough set method. Initially, it has eliminated the descriptive variables which were considered as important feature, and utilizes the other variables as input. Due to this the classification accuracy became low.

An attempt to classify and predict the heart disease using the networks of protein to protein interaction in human body. Disease gene classification method [2] was proposed with the utilization of metagraph representation method, where it has integrated the terms which describe the protein. The result showed the method is not suitable to predict the heart disease only by the gene, where the result came with increased false positive and false negative.

Deep Learning based Convolutional Neural Network [3] was proposed to classify the heartbeat to predict the level of heart disease. It utilized the function of batch-based weight loss to measure the loss and overcome the problem of imbalance which occur between classes. The accuracy has become low due to the dynamic change of class and batches.

Computer Aided Diagnosis System [4] was proposed to predict the valvular heart disease by utilizing the signals of impedance cardiography. It uses the concepts of selecting features by using the support vector machine and k-nearest neighbors' algorithms. The result came with very low true positive which affecting the accuracy.

Extreme Gradient Boosting based Classifier [5] was proposed to detect the heart disease by analyzing the electrocardiogram signals. It extracts the features from six broad categories and finds the best feature by utilizing the recursive feature elimination concept. During the feature extraction phase, important features were discarded leading to misclassification.

Robust Algorithm [6] was proposed to localize the heart beats and classify by utilizing the variables and threshold values. During the process of classification, dataset labels were utilized to find the variations in heartbeat. Localization errors in the results shows that the algorithm is not suitable large datasets.

Multistage Classification [7] was proposed to classify and provide diagnose to the patient of congestive heart failure. It performs the analysis based on variation in heart rate, and computes the features related to heart rate. For computing the features, it uses the domains of time and frequency. The result provided a ineffective result regarding the true negative which cannot be used to provide treatments or medications to the patients.

Mobile Health Service Platform [8] was proposed to analyze and classify the sounds of heart in order to predict the heart disease. It aims to monitor the patients from remote location by using the wireless technology. The service platform is built by integrating the Hidden Markov Model and Mel Frequency Cepstral Coefficient. The result provides inaccurate results varying with different mobile devices.

Firefly Classifier [9] was proposed to predict the heart disease by utilizing the attributes that are filtered by rough sets concept. Fuzzy concept was used to filter the attributes even more. Clustering concept was applied before filtering the attributes for heart disease prediction. The result showed that the results were having very high true positive and zero false positive, which was unacceptable to proceed with decision support system.

Binary Classifier [10] was proposed predict the risk level of coronary artery disease. It used Binomial Boosting algorithm integrated with the maximum likelihood and the logistic regression models, in order to choose the better fit value towards prediction. Hence there arise mismatches between maximum likelihood and the logistic regression models leading towards providing the inaccurate results.

3. Proposed Work

This research work is an extension of the previous works [12] – [15]. Among the earlier works by us the maximum of 91% prediction accuracy is reached and this work aimed to attain even better.

Improved Evolutionary Support Vector Machine (IESVM)

In general, SVM based classifiers falls under the category of supervised learning which is based on statistical learning theory (particularly kernel based). When compared with other machine learning algorithms, the advantage of SVM is to evade local optima. The process in IESVM identifies input patterns into a higher-dimensional attribute space in which linear parting is achievable. In a dataset that are having L diabetes patient's sets $\{(x_i, y_i) | x_i \in R^v, y_i \in R\}$, where x_i is an input vector of dimensionality v and y_i is the output vector corresponding to x_i. The fundamental building block of IESVM classifier is to map the input vector x_i into an N-dimensional attribute space. Once it is done, IESVM then then build the optimal decision-making function in the attribute space as described below:

$$\min\left(\frac{1}{2}\|\omega\| + C\sum_{i=1}^{L}\left(\xi_i + \xi_i^*\right)\right) \ldots (1)$$

$$y_i - f(x_i) \le \varepsilon + \xi_i$$

Such that, $f(x_i) - y_i \le \varepsilon + \xi_i^*$

$$\xi_i, \xi_i^* \ge 0, i = 1, 2, ..., L$$

where $\omega = (\omega_1, \omega_1, \omega_1, ..., \omega_N)^T$ is the weightage vector; C is the boundary stricture (or penalty); ε is the impervious forfeit coefficient that is capable enough to manage the number of support vectors; ξ_i and ξ_i^* are two baggy variables. The first equation is converted to a twofold delinquent and is mathematically modelled as,

$$f(x) = \sum_{i=1}^{L}\left(\alpha_i + \alpha_i^*\right)K(x, x_i) + b \ \ldots (2)$$

where α_i and α_i^* are Lagrange coefficients representing the two baggy variables, $b \in R$ is the bias, and $K(x, x_i)$ is the kernel function

$$K(x, x_i) = \langle \Phi(x), \Phi(x_i) \rangle \ \ldots (3)$$

In the Eqn. 3, $\Phi(.)$ denotes the mapping function to the attribute space. The kernel function is employed in order to calculate the dot product of two diabetes patient's points in the high-dimensional space. IESVM is having several kernel functions namely radial basis kernel function, polynomial kernel function, sigmoidal

member function and many more. In this research work radial basis kernel function is used and α, β and are kernel strictures.

Formulation of Conformation

It is fixed as Θ is the search space of the probable IESVM conformations that includes C, radial basis kernel function and its corresponding strictures, D is the distribution of the set of patient records, C is the cost function, and S is the statistical information.

$$\theta^* \in \arg\min_{\theta \in \Theta} I(\Theta) \quad \ldots (4)$$

In the proposed work, the aim is to optimize the cost function $C : \Theta \times D \mapsto R$ of the IESVM over a set of patient records $\pi \in D$ to find

$$\theta^* \in \arg\min_{\theta \in \Theta} \frac{1}{|D|} \sum_{\pi \in D} C(\theta, \pi) \quad \ldots (5)$$

Each $\theta \in \Theta$ denotes one possible conformation of the IESVM. The cost function C denotes the single execution of the IESVM using θ to solve a problem instance $\pi \in D$. The statistical information S (which is the mean value) encompasses the output of C which is got during testing the IESVM classifier over a set of patients' records. The main role of the proposed improved context is to find a $\theta \in \Theta$ such that $C(\theta)$ is optimized.

In this research work two objective functions are subject to be applied for optimization using evolutionary approach and the same is mathematically modelled as

$min\, F\,(X) = [F_1(x), F_2(x)] \ldots (6)$

where $f_1(x) = err$ and $f_2(x) = NSV$

Here err denotes the misclassified patient's dataset and NSV denotes the number of support vectors.

The main role of the improved context is to generate a conformation (C, kernel type and kernel strictures) and direct the same to the IESVM. The IESVM uses the generated conformation to solve a given problem instance and then sends the cost function (mean values of err and NSV) to the improved context and the above-mentioned procedure is carried out several times. In this research, 1000 iterations are set.

In order to address the bi-objective optimization problem, in this research work population-based improved context that operates on a population of class labels and uses a store to save the non-dominated class labels. The decomposition approach operates on the population of class labels, whereas the dominance approach uses the store. The improved context stimulates a new population of class labels using the existing population, the store, or both the old population and the store. This allows the search to achieve a proper balance between convergence and diversity.

Class label Representation

In this research work, each class label represents one conformation $(\theta \in \Theta)$ of the IESVM, which is represented in the form of a one-dimensional array, KF is the radial basis kernel function, and $k_1, k_2, \ldots\ldots, k_{KF}$ are the strictures of that kernel function.

Population Initialization

The population of class labels (PCL) is randomly initialized. The following equation is employed to allocate a random value to each decision variable in a given class label (x):

$$x_i^p = l_i^p + Rand_i^p(0,1) \times (u_i^p - l_i^p), p = 1,2,\ldots,|PCL|, i = 1,2,\ldots,d \quad \ldots (7)$$

where i is the index of the decision variable, d is the total number of decision variables, p is the index of the class label, |PCL| is the population size, $Rand_i^p(0,1)$ returns a random value in the range [0,1] for the i^{th} decision variable, l_i^p is the lower bound on the value of that decision variable, and u_i^p is the upper bound.

Aptness Calculation

The aptness calculation assigns a value to each class label in the population that indicates how apt the corresponding class label is when compared with those in the current population. In this research work a scalarization function is employed to decompose a given problem into a number of scalarized single-objective sub-problem. It is mathematically modelled as:

$$g^{te}(x, \lambda) = \max_{i \in m} (\lambda_i | z_i^* - f_i(x) |) \quad \ldots (8)$$

where g^{te} is the decomposition approach, x is a given class label, m is the number of objectives, $\lambda = (\lambda_1, \lambda_2, ..., \lambda_m)$ is a weight vector such that $\lambda_i \geq 0, \forall i \in m$. f_i is the aptness value for the i^{th} objective calculated using Equation (6).

$z^* = (z_1^*, z_2^*, ..., z_m^*)$ is the idea or the reference point, i.e., $z_i^* = \min\{f_i(x) | x \in \Omega\}$ for each i=1, 2, …, m

Selection

Each data with class label is associated with two variables: the observed recompense q_i and the sureness grade n_i. The observed recompense q_i represents the average recompense obtained during the search process using this heuristic. A higher value of the observed recompense is better. The sureness grade n_i is the number of times that the i^{th} heuristic has previously been applied using the following Equation (9),

$$\arg \max_{i=LLH_1 \ldots LLH_n} \left(q_{i(t)} + c\sqrt{\frac{2\log \sum_{i=LLH_1}^{LLH_n} n_{i(t)}}{n_{i(t)}}} \right) \quad \ldots (9)$$

The collection of empirical dimensions is denoted by $\{LLH\_1, ..., LLH\_n\}$, where n is the total number of empirical decisions. The index t is the time step or the number of the current iteration of the search. c is a scaling factor that adjusts the balance between the influence of the observed recompense and the sureness grade to ensure that the confidence interval will not be excessively biased by either of these indicators.

Application

Two mechanisms are incorporated in the application step namely class label selection and heuristic application. Class label selection recognizes the corresponding class labels to form the mating collection. In order to cartel decomposition and dominance, each sub-problem is optimized using information from only its neighbouring sub-problems. A fixed set of neighbouring class labels for each sub-problem is determined using the Euclidean distances between any two class labels based on their weightage vectors. In the Heuristic application, the chosen heuristic is applied to the generated mating pool to advance a new set of class labels.

Class Label acceptance

This step checks whether the newly generated class labels need to be accepted. In this work, we first compare each class label x with its neighbouring sub-problems y. x will replace y if it is superior in terms of the scalarization function, $g^{te}(x, \lambda) < g^{te}(y, \lambda)$. After that, the store using non-dominated class labels is updated.

Stopping Criterion

In this step the total number of iterations is checked for reaching the maximum number. In this research work, the iteration count is checked as 1000. Once when the maximum iteration is met, the search process will be terminated and returns the set of non-dominated class labels.

The heuristics are depicted as follows

Stricturized Gaussian Mutation

$$x = x + N(Mean, \sigma 2) \quad \ldots (10)$$

where Mean D=0 and $\sigma 2 = 0.5$ is the standard deviation.

Differential Mutation

$$x = x_1 + F \times (x_1 - x_2) + F \times (x_3 - x_4) \quad \ldots (11)$$

Where x_1, x_2 are the two different class labels selected from the mating pool in accordance with the class label selection process. F is a scaling factor, whose value is fixed to 0.5 in this research work.

Arithmetic Crossover

$$x = \lambda \times x_1 + (1 - \lambda) \times x_2 \quad \ldots (12)$$

Where λ is a randomly generated number, whose value is within the range $\lambda \in [0,1]$. x_1 is the current sub-problem, and x_2 is the best class label in its neighbourhood.

Store

The store saves the set of class labels and is updated in each iteration. In this research work, the newly generated class labels are first added to the store. Sorting is performed to split the store into two class labels.

The list of attributes is shown in Table 2. The list of chosen attributes by IESVM is given in Table 3.

5. About the Dataset

The dataset is obtained fromdiabetes care medical centers and cariology specialized clincal care centers. The obtained dataset is having 7525 records which includes 4329 male diabetic patients and 3196 female diabetic patients. Seventeen attributes (also class label). Out of 4329 male diabetic patients' records, 3911 patients owe the risk of CAHD and the remaining do not owe the risk of having CAHD. Out of 3196 female diabetic patients' records, 2808 patients owe the CAHD risk of developing CAHD and 388 female diabetic patients' do not have

the risk of having CAHD. Program implementations and experiments are carried out using Scilab 6.0.2 in the desktop personal computer with a 3.4 giga hertz Intel Core i7-6700 processor and 8 giga bytes RAM. Table - 1 shows the details of the dataset.

Table - 1. Dataset Details

Number of Attributes	Total Number of patients	Male – 4329		Female – 3196	
		Number of patients with risk of CAHD	Number of patients with no risk of CAHD	Number of patients with risk of CAHD	Number of patients with no risk of CAHD
17	Male 4329 + Female 3911 = 7525 patients	3911	418	2808	388

Table – 2. List of Attributes in the dataset

S.No.	Attribute Name	Specifications
1	Age	in years
2	Gender	Male / Female
3	Family history of Diabetes	1- Yes 0 – No
4	Family history of CAHD	1- Yes 0 – No
5	Chest pain	1 – typical angina 2 – atypical angina 3 – non – anginal pain 4 – asymptomatic
6	BP at rest	Resting blood pressure (in mm/Hg on admission to the hospital)
7	Cholesterol	Serum cholesterol in mg/dl
8	Fasting blood sugar	Fasting blood sugar in mg/dl
9	Postprandial blood sugar	Postprandial blood sugar in mg/dl
10	ECG	0 - normal 1 - having ST-T wave abnormality (T wave inversions and/or ST elevation or depression of > 0.05 mV) 2 - showing probable or definite left ventricular hypertrophy by Estes' criteria
11	Physical activity	0 – No physical activity 1 – Occasional physical activity 2 – Regular physical activity
12	BMI	Body mass index 0 – normal 1 – overweight 2 - obese
13	Sleep pattern	0 – Eight to 10 hours of sleep 1 – less than 6 hours of sleep 2 – less than 4 hours of sleep
14	Eating habits	0 – mixed diet 1 – more of unhealthy / junk foods
15	Smoking	0 – non smoker / occasional smoker 1 – heavy smoker
16	Alcoholic	0 – Non – alcoholic 1 – occasional alcoholic 2 – chronic alcoholic
17	Class label	1 – Having the risk of CAHD 0 – Not having the risk of CAHD

Table – 3. Chosen attributes by IESVM

S.No.	Attribute Name
2	Gender
3	Family history of Diabetes
4	Family history of CAHD
6	BP at rest
11	Physical activity

15	Smoking

6. Results and Discussions

Male patients and female patient's records are tested separately. Before that, 60% of the patient records (both male and female) are taken for training the classifier. 100% of the patient records are tested for performance evaluation in terms of sensitivity, specificity, prediction accuracy and Matthews's correlation coefficient (MCC). The results are portrayed in the Table – 4 and Table – 5 for male and female patients respectively.

Table – 4. Performance Results – Male Patients

Classifiers	TP	TN	FP	FN	Sensitivity (in %)	Specificity (in %)	Accuracy (in %)	Mathews correlation coefficient (in %)
Mamdani Fuzzy Classifier [12]	3156	339	392	442	87.72	46.37	80.73	33.21
ANN – GA Classifier [11]	3211	393	322	403	88.85	54.97	83.25	42.00
IFANN Classifier [13]	3352	385	266	326	91.14	59.14	86.32	48.51
ALC Classifier [14]	3416	376	255	282	92.37	59.59	87.60	51.07
ROA – IFANN Classifier [15]	3617	359	182	171	95.49	66.36	91.85	62.39
Proposed IESVM Classifier	3828	341	81	79	97.98	80.81	96.30	78.95

Table – 4. Performance Results – Female Patients

Classifiers	TP	TN	FP	FN	Sensitivity (in %)	Specificity (in %)	Accuracy (in %)	Mathews correlation coefficient (in %)
Mamdani Fuzzy Classifier [12]	2372	205	321	298	88.84	38.97	80.63	28.32
ANN – GA Classifier [11]	2263	360	303	270	89.34	54.30	82.07	44.48
IFANN Classifier [13]	2385	341	255	215	91.73	57.21	85.29	50.29
ALC Classifier [14]	2471	318	205	202	92.44	60.80	87.27	53.37
ROA – IFANN Classifier [15]	2632	279	155	130	95.29	64.29	91.08	61.10
Proposed IESVM Classifier	2843	235	57	61	97.90	80.48	96.31	77.90

Performance metrics namely sensitivity (percentage of sick people those are prone for CAHD are correctly identified as having the condition), specificity (percentage of healthy people who are correctly identified as not having the condition), prediction accuracy and Matthews correlation coefficient (MCC) are taken for comparing the proposed IESVM classifier with the existing classifiers. The obtained results are presented in Table 3 (for

male patients) and Table 4 (for female patients). As far as the male patients are concerned, it is clearly understood that IESVM is having maximum of 97.98 % sensitivity percentage and outperformed than the other chosen machine learning classifiers. The specificity of 80.81 % is achieved by IESVM and it is also better than that of other chosen classifiers. The prediction accuracy of CAHD is 96.30% is attained by IESVM which is also better than other classifiers. The remarkable performance metric MCC is 77.90% is attained by IESVM which is better than other classifiers [11] – [15].

Taking into account of female patients, sensitivity of 97.90%, specificity of 80.48%, CAHD risk prediction accuracy of 96.31% and MCC of 77.90% is attained by IESVM classifier which is better than that of chosen machine learning classifiers. The obtained results are displayed pictorially in the Figures [Fig 1 to Fig 8].

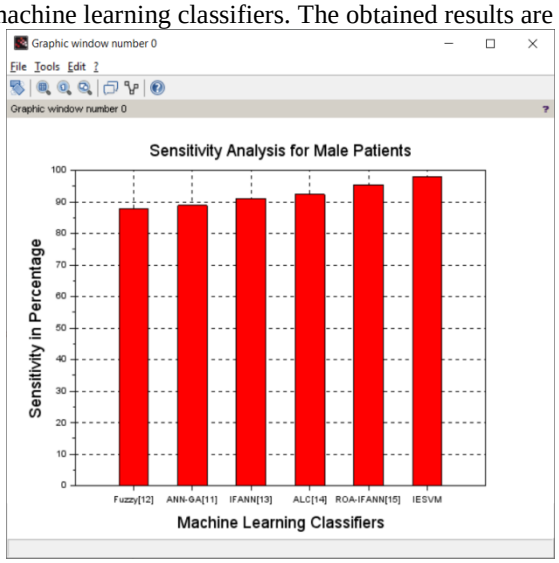

Fig.1. Sensitivity Analysis for Male Patients

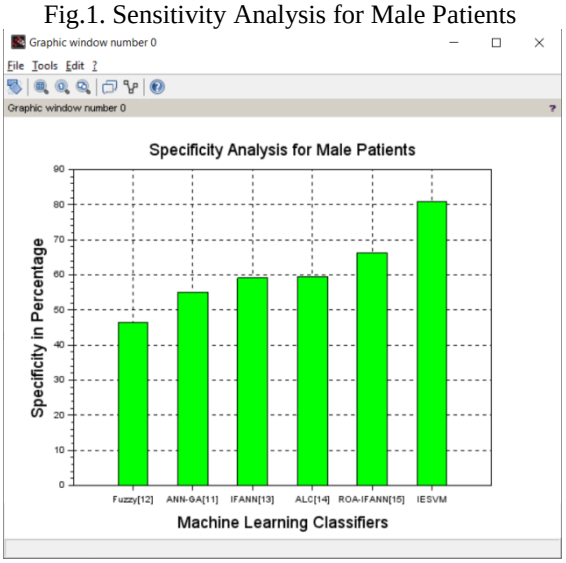

Fig.2. Specificity Analysis for Male Patients

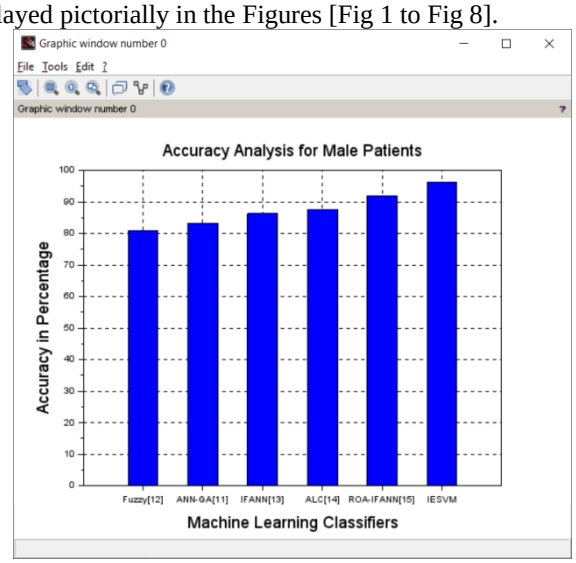

Fig.3. Accuracy Analysis for Male Patients

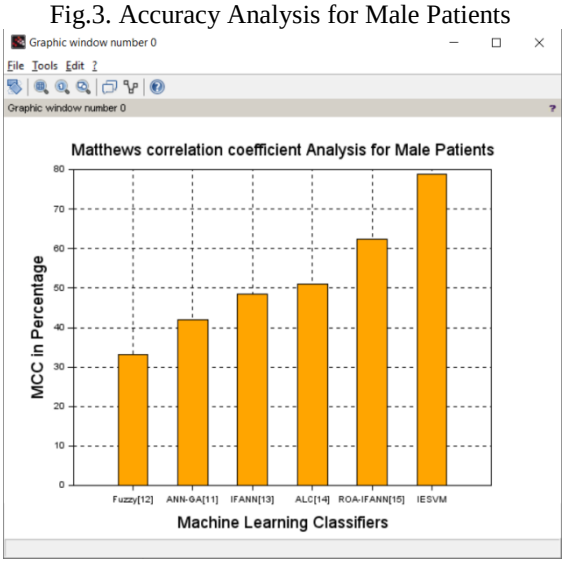

Fig.4. MCC Analysis for Male Patients

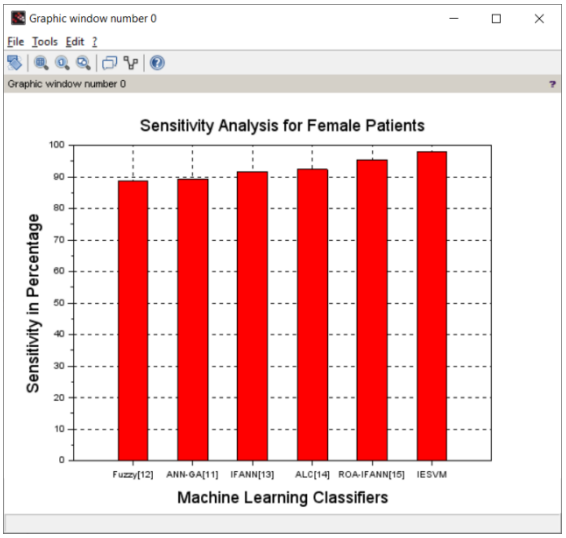

Fig.5. Sensitivity Analysis for Female Patients

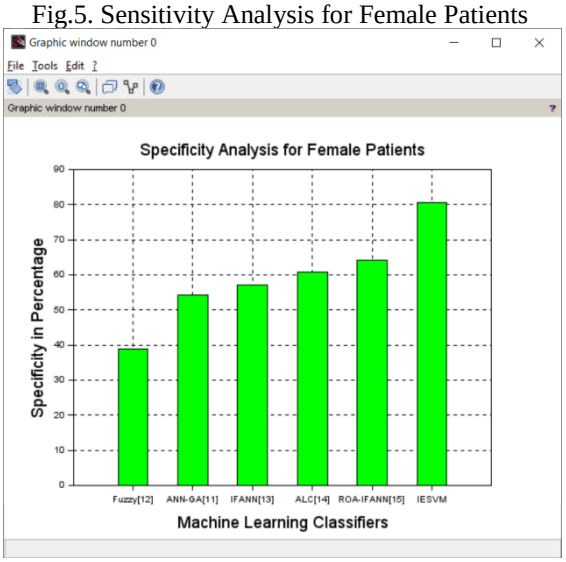

Fig.6. Specificity Analysis for Female Patients

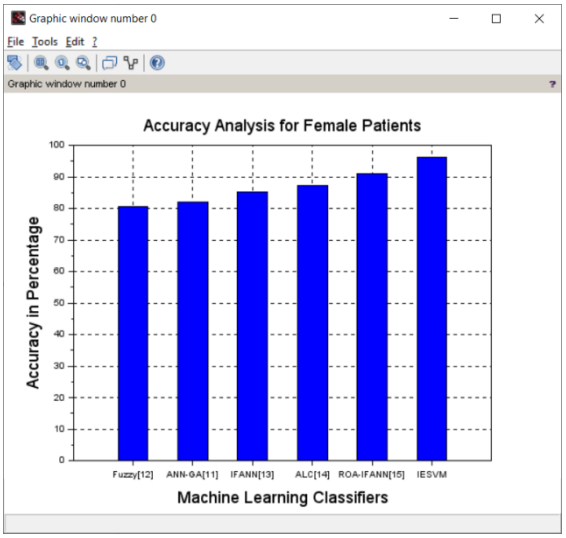

Fig.7. Accuracy Analysis for Female Patients

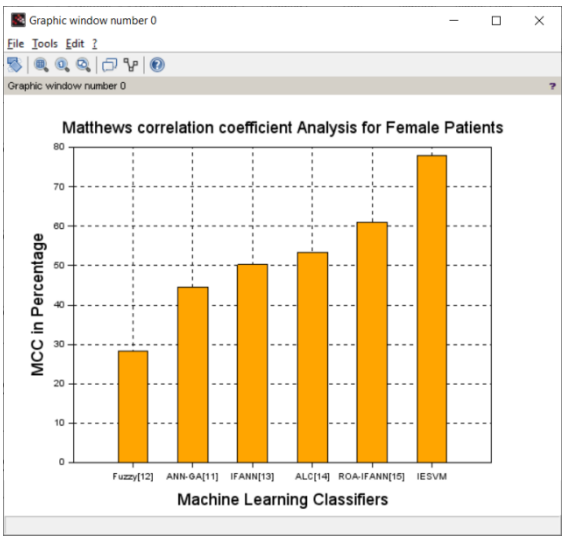

Fig.8. MCC Analysis for Female Patients

7. Conclusion

This research work aimed to propose a machine learning classifier to attain maximum MCC and accuracy for CAHD risk prediction among diabetic patients. The classifier is in having the inbuilt capability of choosing attributes in the available dataset. The proposed classifier namely Improved Evolutionary Support Vector Machine shortly IESVM is modeled in such a way that mimics the evolutionary behavior of biological species. Performance metrics such as sensitivity, specificity, prediction accuracy and MCC are taken into account for IESVM classifier to compare with other machine learning classifiers. From the results it is evident that IESVM outperforms that that of other chosen machine learning classifiers.

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