A Medical Expert System based on Genetic Algorithm and Extreme Learning Machine for Diabetes Disease Diagnosis

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Abstract— **An accurate diagnosis of diseases like diabetes, is a challenging and tedious task for physicians. This problem in diagnosis, has attracted researchers to design medical decision support systems with higher accuracy. In this paper, a clinical decision support system, based on Genetic Algorithm and Extreme Learning Machine (ELM) is proposed for the diagnosis of diabetes disease using Pima Indian Diabetes dataset of UCI machine learning repository with improved accuracy. Genetic Algorithm (GA) are used for the selection of the most significant feature set of the dataset. Classification is performed using ELM. The performance of the proposed system is analyzed based on several parameters such as classification accuracy, sensitivity and specificity using 10-fold cross-validation and confusion matrix. The accuracy of the proposed system is found to be superior to that of the other existing systems in the literature.**

Index Terms—**Extreme Learning Machine, Genetic Algorithm, Diabetes, Accuracy.**

I. INTRODUCTION

Diabetes is one of the major health challenges which is highly complex and complicated to diagnose for the past few decades. It is caused due to the improper production of insulin in the human body. Insulin is the key parameter responsible to regulate glucose. It leads to many other risks, including kidney disease, blindness, heart disease and never damages. Diagnosis of Diabetes can be done through routine blood checkup. Diabetes can be controlled by proper food habits and exercise program in order to reduce the given risks. Still there is no permanent cure for Diabetes. Diagnosis of diabetes needs special effort for any physician with prior knowledge of the symptoms and deep analysis of the patient's history. Thus to make the diagnosis easier and faster, many machine learning techniques are designed for the automatic diagnosis of Diabetes. Artificial Intelligence (AI), also known as Synthetic Intelligence, is a branch of engineering associated with the computational behavior or intelligent behavior. Essential part of AI in recent years is to simulate human intelligence. Machine Learning is a branch of AI which aims in providing knowledge to such intelligent systems. Machine learning consists of a huge number of algorithms to design and analyze any kind of datasets. Machine Learning can be either supervised or unsupervised. In Supervised learning, data are trained and predicted based on the training. Here, the function is created based on training samples and test on unknown samples. In unsupervised learning, system remains untrained. Decision support systems in the field of medical diagnosis have increased in recent decades. Design of medical expert systems has created more interest among researchers all over the world. Medical expert systems use machine learning techniques for the prediction of any disease based on their existence. Pattern recognition and data mining provide useful retrieval of medical data with the combination of such techniques. Most common data mining technique for decision making from real world data is classification. Usage of data directly could affect the system performance. Features or the attributes have much influence on the performance. Selection of best features will have more impact on the accuracy of the diagnosis system in prediction.

II. RELATED WORK

Fayssal et al [8] has designed a diagnosis system for diabetes using fuzzy classifier and modified Artificial Bee Colony algorithm. Still the Accuracy of this system is inferior and has paved the way for further research to increase the accuracy. Cheng-Lung Huang et al [9], proposed a general adaptive optimization search methodology and Grid Algorithm combined with SVM classifier. Several real-world datasets such as Diabetes, Heart disease, breast cancer, Contraceptive were validated using the Genetic Algorithm based approach and the Grid algorithm. Average AUC for datasets with two classes using Grid algorithm Diabetes with 0.7647.Hasan et al [10] have used Levenberg–Marquardt (LM) algorithm for training a multilayer neural network structure in order to diagnose diabetes. The obtained accuracy was 82.37%, which is low compared to other existing diabetes diagnosis systems. Yuan ren [11] have proposed two SVM parameter optimization approaches, i.e. GA-SVM and PSO-SVM, adopt an objective function which is based on the leave-one-out cross-validation, and

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the SVM parameters are optimized by using GA (genetic algorithm) and PSO (particle swarm optimization) respectively. Our proposed system uses the Pima Indian Diabetes (PID) datasets of UCI machine learning repository [8]. The feature selection using Genetic Algorithm is explained in Section 4. Section 5 is dedicated to the classification of PID dataset using Least Square Support Vector machine. The performance of the system on diabetes dataset and other medical datasets are analyzed in Section 6.

III. DATASET

The Pima Indian diabetes data set was obtained from the UCI Repository of Machine Learning Databases [12]. There are 268 (34.9%) cases in class '1' and 500 (65.1%) cases in class '0', Where '1' means a positive test for diabetes and '0' is a negative test for diabetes [9].
Diabetes Attribute information is given below:

1. Number of times pregnant
2. Plasma glucose concentration at 2 hours in an oral glucose tolerance test
3. Diastolic blood pressure (mm Hg)
4. Triceps skin fold thickness (mm)
5. 2-Hour serum insulin (mu U/ml)
6. Body mass index (weight in kg/ (height in m) ^2)
7. Diabetes pedigree function
8. Age (years)
9. Class variable (0 or 1)

IV. FEATURE SUBSET SELECTION

Selecting appropriate features are important for most data mining methods. Elimination of unimportant features assists in better classification. Usage of the complete and correct dataset will make the system more reliable. The dataset is normalized within a numerical range. The proposed system is shown in Figure.1.

A. Scaling

Pima Indian Diabetes dataset [12] consists of attributes with different range of values. Usage of these values directly could affect the system stability. In order to avoid any complications in computation the numerical values are linearly transformed to a fixed range using min-max normalization method. The values of the Features from the dataset are normalized between the ranges -1 to 1. The formula used for scaling is given in equation (1).

$$D_{normalized} = \frac{D - D_{min}}{D_{max} - D_{min}} (upperbound - lowerbound) \quad (1)$$

where D is the original data, D_{max} is the maximum value of D, D_{min} be the minimum value in D and $D_{normalized}$ be the normalized valued within the given upper and lower bound. Once scaling is done on the whole dataset feature selection is done to find the most discriminant features. Every feature provides some useful information that could reduce the accuracy of the classifier when the training data is less [5-7]. In order to extract such optimal features Genetic Algorithm is used.

B. Genetic Algorithm

Genetic Algorithm is an evolutionary algorithm which offers multi criterion optimization for higher dimensional pace problems. It's a popular stochastic search method used for feature selection. It is based on Darwin's theory of natural selection and 'survival of the fittest' [4].

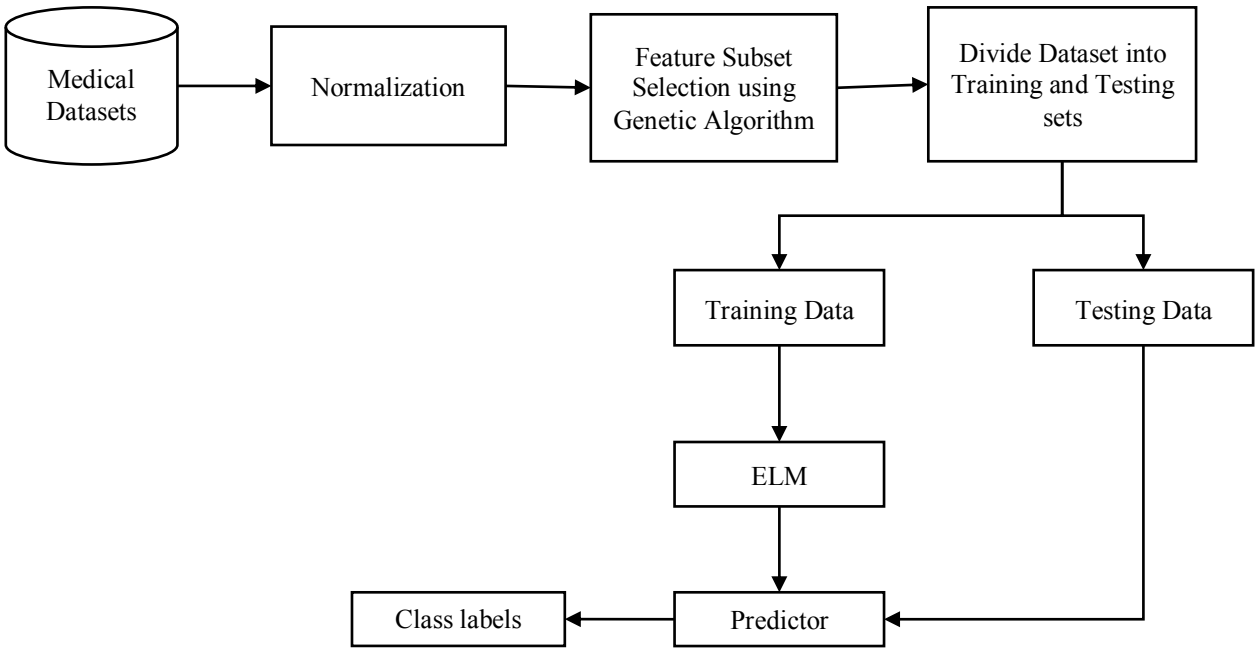

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Fig. 1: Proposed System

Genetic algorithm search initially starts with the least number of attributes. Every set of individuals are called population and each individuals are called as chromosomes. These chromosomes are constituted of many genes which are most binary value indicating the presence of the element in the set. The search of the best result is based on the objective function called as Fitness Function.
Fitness function can be calculated using the formula (2)

$$\text{Fitness}=\frac{\text{Total No of Correctly Classified Intances}}{\text{Total No of Training Samples}} \quad (2)$$

The selected solutions with highest fitness value have more influence than that of the new solutions with less fitness value. This function plays a key role in the selection of the best solution of the problem. In Genetic algorithm, each iteration is known as generation. Fittest individuals are selected from each generation and pooled out to form base for new populations. A new population is created based on the compliance to the fitness function. Offspring's are generated based on the genetic operator's crossover and mutation. Threshold for fitness function will be the maximum accuracy at which the system converges. This process continues till the Fitness threshold is met. GA procedure of the parameters is as follows,

Step 1: Read the data and define Fitness function.
Step 2: Determine population size, crossover and mutation.
Step 3: Evaluate fitness for each member of the generation
Step 4: With the crossover rate, generate offspring, in which the ranking mechanism is used for selection of chromosomes.
Step 5: With the mutation, generate offspring.
Step 6: Select the members of the new generation from the parents in the old generation and the offspring in Step 5 and Step 6 according to their fitness values.
Step 7: Repeat the procedure in Step 5 through Step 7 until the number of generations reaches a prescribed value.

V. EXTREME LEARNING MACHINE

Huang et al., have proposed a new learning algorithm called the ELM; it is a single-hidden layered feed forward neural networks (SLFNs). Hanang, G.B., et.al. [18] Says that ELM may randomly choose and fix all the hidden node parameters and then analytically determine the output weights.Once the weights of the SLFNs have been randomly assigned, then SLFNs is to be considered as a linear system then the output weights can be obtained analytically through a generalized inverse operation of the hidden layer output matrices. The activation functions used in ELM are any nonlinear activation function used in neural network (sigmoid, hyperbolic function etc.,), radial basis function, complex activation function [19], and so on.The proposed SLFN can have P hidden nodes and it can be approximated through the given N pairs of input / output values, namely,$(x_i,t_i) \in R^n \times R^m$ with zero error, then we have

$$\sum_{i=1}^{p} \beta_i G(a_i, x_j, b_i) = t_j \text{ for } j= 1, 2, \ldots. P \quad (3)$$

where (a_i, b_i) is the parameter associated with i^{th} hidden node and β_I is the output weight linking the i^{th} hidden node to the output node.

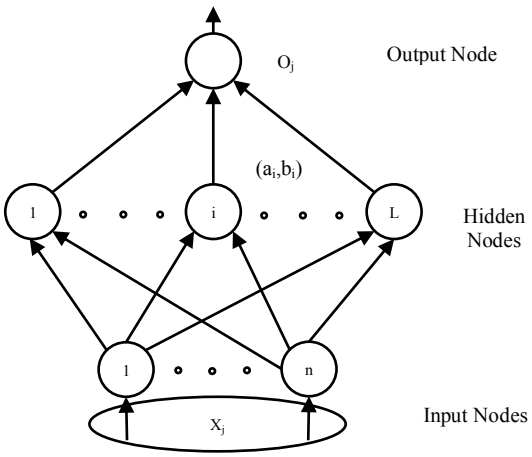

Fig. 2: Single Hidden Layer Feed Forward Network

In this paper, non-linear activation function, called sigmoid function (Eq.4) is used. That is,

$$G(a_i, x_j, b_i) = \frac{1}{1+e^{-(-a_i.x_j+b_i)}} \quad (4)$$

Hence, equation (*) can be rewritten as $H\beta = T$
Where

$$H = \begin{pmatrix} G(a_1,x_1,b_1) & G(a_2,x_1,b_2) & \ldots\ldots & G(a_p,x_1,b_p) \\ G(a_1,x_2,b_1) & G(a_2,x_2,b_2) & \ldots\ldots & G(a_p,x_2,b_p) \\ & & \vdots & \\ G(a_1,x_N,b_1) & G(a_2,x_N,b_1) & \ldots\ldots & G(a_n,x_N,b_n) \end{pmatrix}$$

$$\beta = [\beta_1^T, \beta_2^T, \beta_3^T \ldots \beta_p^T]^T$$

$$T = [t_1^T, t_2^T, t_3^T \ldots t_N^T]^T$$

While computing, $\tilde{\beta} = H^{\#}T$ is used as the estimated value of β, where $H^{\#}$ is the Moore-Penrose generalized inverse of the hidden layer output matrix H [20]. The following is the formal ELM algorithm proposed by Huang et. Al.[21].

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ELM Algorithm

Given a training set of input / output Values, $(x_i,t_i) \in R^n x R^m$ for i = 1, 2, …, N; the activation function $G(a_i, x_j, b_i) = \frac{1}{1+e^{-(-a_i.x_j+b_i)}}$ and the number of hidden nodes P.

Step 1: By using continuous sampling distribution, assign random hidden nodes by randomly generating parameters (ai, bi) for i = 1,2, …, N

Step 2: Compute the hidden layer output matrix H

Step 3: Compute the output weight $\tilde{\beta}$, by using the relation $\tilde{\beta} = H^{\#}T$

VI. PERFORMANCE EVALUATION

The proposed System is examined by 10 fold cross validation methodology. The performance of the system is evaluated using four measures: Confusion Matrix, Sensitivity, Specificityand Classification Accuracy.

Confusion Matrix

Confusion matrix [3] (COM) is a 2×2 matrix which shows the predicted and actual classification given in Table 1.

Table. 1 Confusion Matrix

Predicted	**Actual**	
	Positive	*Negative*
Positive	TP (true positive)	FP (false positive)
Negative	FN (false negative)	TN (true negative)

- TN is the *correct* predictions of an instance as *negative*.
- FNis the *incorrect* predictions of an instance as *positive*.
- FP is the *incorrect* of predictions of an instance as *negative*.
- TPis the *correct* predictions of an instance as *positive*.

Classification Accuracy

Performance of classifier is commonly measured using classification accuracy (CA). It provides the rate of correctly predicted instances to the overall instances in the dataset. CA can be calculated from Confusion Matrix [3] using the equation (5).

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (5)$$

Sensitivity and Specificity

Sensitivity is the true positive rate of prediction, and specificity is the true negative rate [3]. They are defined as in (6) and (7)

$$\text{Sensitivity} = \frac{TP}{TP+FN} \quad (6)$$

$$\text{Specificity} = \frac{TN}{TN+FP} \quad (7)$$

VII. EXPERIMENTAL SETUP

The Proposed System for the diagnosis of diabetes disease is divided into two stages as shown in figure. In the first Stage the Feature selection on the disease dataset is done to reduce the feature space dimension and at this stage different sets of features are obtained. In the second stage, ELM classifier is used to classify these feature subsets and the classification accuracy is evaluated. The fittest set of feature subsets with the best classifier parameters are chosen to get an optimal system. The range of neurons is fixed from 1 to 200.

The Process is carried out as below:

Step 1. Different feature subsets are obtained by Feature selection using Genetic Algorithm.

Step 2. Pima Indian Dataset is randomly divided into 10 fold of equal size using k fold cross validation methodology. This is done to maintain the class distribution in each and every fold in the same dataset.

Step 3. First feature subset is fed into ELM to get its Fitness value

Step 4. ELM parameters are initialized within the selected range.

Step 5. Classification is performed by using 10-fold cross validation

Table. 2 Feature Subsets using Genetic Algorithm and their accuracy

Set	**Size**	**Attributes**	**Accuracy**
R1	3	Tri Fold Thick, Serum Ins,DP Function	0.7337
R2	3	Diastolic BP,Tri Fold Thick,Age	0.8133
R3	3	Serum Ins,BMI,DP Function	0.7732
R4	4	Pregnancies,PGConcentration,BMI,AGE	0.8263

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R5	4	Pregnancies,PGConcentration,DPFunction,Age	0.8954
R6	4	Pregnancies,PGConcentration,DiastolicBP,Age	0.8534
R7	4	Pregnancies,DiastolicBP,SerumIns,BMI	0.8354
R8	5	Pregnancies,PGConcentration,DiastolicBP,Tri Fold Thick,Age	0.8234
R9	5	Pregnancies,PGConcentration,DPFunction,Tri Fold Thick,Age	0.8137
R10	6	PG Concentration,DiastolicBP,Tri Fold Thick,SerumIns,DPFunction,Age	0.7933

Table. 3: Comparison with existing system

Disease	Methodology	Accuracy (%)
DIABETES	GA - based approach	82.98
	Grid Algorithm	76.47
	ACO -SVM	67.11
	SVM	77.73
	GA-SVM	78.64
	PROPOSED GA-ELM	89.54

Step 6. Classification accuracy in each fold are calculated and the overall accuracy is obtained.
Step 7: Repeat Steps 3 to 6 for all feature subsets.
Step 8: The feature subset with the highest overall classification Accuracy is chosen as the best discriminating subset.

VIII. Simulation Results

The diabetes dataset from UCI repository consists of attributes with different numerical ranges and is a complete data set. There are no missing values in this dataset. The numerical ranges are made to be constrained within a fixed range of -1 to 1 using scaling concept. These scaled datasets are fed for feature selection using Genetic Algorithm. The genetic algorithm generates random sequences of subset combinations and uses the Fitness value to predict the fittest subset of features. Here, we have generated 10 Feature Subset from which one optimal subset can be obtained. Table 2 shows the list of all subsets generated. This fitness value depends on the classification accuracy of the system. Classification of these subsets is done by using ELM classifier as shown in Table 2.

Discussions

The proposed system shows a higher performance with feature subsets at an accuracy of 89.54%. The subset consists of Pregnancies,PG Concentration,DP Function and Age shows the highest fitness and selected as the optimal feature set. The ELMparameteris chosen to be 20. The feature subsets and its accuracy are shown in Table 2. Overall classification accuracy of the proposed system is computed by averaging the classification accuracies of tenfold, which is 89.54%. Sensitivity and specificity rates of the proposed expert system are obtained as 87.96% and 85.67%, respectively. Classification accuracies of the studies in the literature and our proposed expert system are given in Table 3 for comparison. Performances of all methods given in Table 3 were evaluated on the same Pima Indian Diabetes dataset taken from the UCI machine learning repository.

IX. Conclusion

In this paper, a decision support system based on GA-ELM is proposed for the diagnosis of the diabetes disease. A Gaussian radial basis function is used as a kernel of ELM.The robustness of the proposed system were analyzed with metrics like classification accuracy, using 10-fold cross-validation and confusion matrix. The accuracy of the system for the PID dataset was found to be 89.54% with GA as a feature selection method. In future, this system can be used for the diagnosis of real life medical data of patients.

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