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Application of K-Means and Genetic Algorithms for Dimension Reduction by Integrating

SVM for Diabetes Diagnosis

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**Abstract**

Vast amount of data available in health care industry is difficult to handle, hence mining is necessary to find the necessary pattern and relationship among the features available. Medical data mining is one major research area where evolutionary algorithms and clustering algorithms play a vital role. In this research work, K-Means is used for

removing the noisy data and genetic algorithms for finding the optimal set of features with Support Vector Machine

(SVM) as classifier for classification. The experimental result proves that, the proposed model has attained an average accuracy of 98.79 % for reduced dataset of Pima Indians Diabetes from UCI repository. It also shows that the proposed method has attained better results compared to modified K-Means clustering based data preparation method with SVM classifier (96.71 %) as described in the literature

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*Keywords:* Diabetes Diagnosis; Feature Selection; Genetic Algorithms; K-Means; Support Vector Machine.

1. **Introduction**

# Extracting knowledge and patterns for the diagnosis and treatment of disease from the medical database becomes more important to promote the development of telemedicine and community medicine. The methods and applications of medical data include artificial neural network, genetic algorithms, fuzzy

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system, rough set, and support vector machine 1. One important application of medical mining is genetic algorithms. Dimension reduction is the mapping of data to a lower dimensional space such that

uninformative variance in the data is removed, such that a subspace in which the data lives is detected 2. It can be divided into instance selection or reduction and feature selection techniques. Instance reduction is reducing the irrelevant instances from the dataset to increase the classification accuracy. Selecting a subset of relevant features to be used in model construction is called feature Selection.

Genetic Algorithms (GAs) are intrinsically parallel. GAs have multiple offspring, they can explore the solution space in multiple directions at once. If one path has reached its end, then eliminate it and continue work on other paths, giving them a greater chance each run of finding the optimal solution 3. There is a greater scope for GAs in future for machine learning and optimization techniques. The K-Means clustering partitions the data into groups which contain similar objects. The instances which do not belong to any cluster (or) a cluster with fewer data points (or) forced to fit into a cluster are removed 4. Clustering when

cascaded with classification considerably increases the accuracy of the model. SVMs are set of related supervised learning methods used for classification and regression. It is a powerful machine method developed from statistical learning and has made significant achievement in the field of image classification, bioinformatics, text categorization, hand-written categorization, etc 5. Several recent studies have reported that the SVM generally are capable of delivering higher performance in terms of

classification accuracy than the other data classification algorithms including, statistical algorithms,

decision tree based algorithms and instance based learning methods 6.

K-Means clustering based outlier detection

This research work proposes followed by GA for feature

selection with SVM as classifier to classify the dataset. The rest of the paper is organized as follows: Section 2 shows the literature review. The preliminaries used is given in section 3 followed by data source description in section 4. The proposed model is described in section 5. Section 6 reports the experimental analysis and the final section deals with a conclusion.

## Literature Review

Ravi et al 7 proposed a method using GAs to find an appropriate feature subset and SVM classifier on

different datasets, to improve classification accuracy. Rajdev et al 8 used a method for selecting optimal

feature subset based on correlation using GA algorithm, where GA is used as optimal search tool for selecting subset of attributes. Aishwarya et al 9 proposed a medical decision support system based on GA

for feature subset selection and Least Square SVM for diagnosis of diabetes. Shruti et al 10 used GA to find

the optimal reduced set of attributes genetic search method and naïve bayes classifier to diagnose the

presence or absence of heart disease. Sumeet et al 11 presented a decision support system for heart disease classification based on SVM and integer-coded GA for selecting the important features in diagnosis of heart disease. Sarah Behnam Aziz 12 proposed a method for diagnosis of thyroid diseases using GAs and Neural

Networks. The GA was used to find the optimum network structure with high classification accuracy Mehdi et al 13 adopted a hybrid procedure using wrapper subset evaluation and genetic search. Information gain is used to find the optimal feature space and it is proved to be the best method with a lower cost. Ahmad et al 14 applied an improved GA for feature selection and multi-layer perceptron network to classify the medical datasets. Asha et al 15 used clustering and SVM for reducing datasets in the diagnosis of

tuberculosis.

Hemant et al 16 involved K-Means cluster to reduce datasets with different classification algorithms for

liver disorder and breast cancer datasets.

diabetes.

predicting

A hybrid model was proposed by Chin-Yuan Fan et al 17 by integrating a case based

data clustering method and a fuzzy decision tree to classify the

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Nihat et al 18 proposed modified K-Means for removing noisy data and SVM for classification of the

reduced datasets. Yuan et al 19 has modeled an objective function which is based on the leave-one-out cross-

validation, and the SVM parameters are optimized by using GA and PSO (particle swarm optimization). Patil et al 20 proposed a hybrid K-Means followed followed by naïve bayes and SVM classification, in which SVM achieved high accuracy percentage.

## Preliminaries

* 1. *K-Means Clustering*

K-Means clustering algorithm was developed in 1976 by MacQueen. It is a unsupervised clustering algorithm generates a specific number of disjoint, flat (non-hierarchical) clusters The procedure follows a

simple and easy way to classify a given data set through a certain number of clusters (assume k clusters) fixed apriori 21, 22. K-Means algorithms randomly choses k objects, representing the k initial cluster center. The next step is to take each point belonging to a given data set and associate it to the nearest center based

Euclidean distance.

on the closeness of the object with cluster center using After all the objects are

distributed, recalculate new k cluster centers. The process is repeated until there is no change in k cluster centers. This algorithm aims at minimizing an objective function known as squared error function given by the following.

𝐽(𝑣) = ∑𝑐

∑𝑐i

(||𝑥

− 𝑣 ||)2

(1)

i=1

j=1 i j

where,

‘*||xi - vj||’* is the Euclidean distance between *xi* and *vj.*

*‘ci’* is the number of data points in *ith* cluster.

*‘c’* is the number of cluster centers.

The steps of K-Means Algorithm is given below:

* + 1. Randomly partition the dataset into k
    2. For each data point in the dataset:
       - *Calculate the distance from the data point to each cluster.*
       - *If the data point is closest to its own cluster, leave it where it is. If the data point is not closest to its own cluster, move it into the closest cluster*.
    3. Repeat the above step until a complete pass through all the data points’ results in no data point moving from one cluster to another. At this point the clusters are stable and the clustering process ends.
    4. The choice of initial partition can greatly affect the final clusters that result, in terms of inter- cluster and intra-cluster distances and cohesion.
  1. *Genetic Algorithms*

GA is based on Darwin’s theory of natural selection and ‘survival of the fittest’ 23. It is one important search method used for feature selection. It represent feasible solutions to the particular problem that evolves over successive iterations (generations) through a process of competition and controlled variation. The process of selection is to select the chromosomes in the population which satisfy the associated fitness to form new ones in the competition process. The genetic operators such as crossover and mutation are used to create the new chromosomes. The classical model of GAs consists of three operations:

* + 1. Evaluation of individual fitness.
    2. Formation of a gene pool (intermediate population) through selection mechanism.
    3. Recombination through crossover and mutation operators.

The selection mechanism produces a new population ***P(t)*** with copies of chromosomes in ***P(t-1)***. The number of copies received for each chromosome depends on its fitness; chromosomes with higher fitness usually have a greater chance of contributing copies to ***P(t)***. Then, the crossover and mutation operators are applied to ***P(t)***. Crossover takes two individuals called parents and produces two new individuals called the offspring by swapping parts of the parents. In its simplest form, the operator works by exchanging substrings after a randomly selected crossover point. The crossover operator is not usually applied to all pairs of chromosomes in the new population. A random choice is made, where the likelihood of crossover being applied depends on probability defined by a crossover rate. Mutation serves to prevent premature loss of population diversity by randomly sampling new points in the search space. Mutation is applied by flipping one or more random bits in the bit string with a probability equal to the mutation rate. Termination may be triggered by reaching a maximum number of generations or by finding an acceptable solution by some criterion.

* 1. *Support Vector Machines*

SVM is a classier that performs classification tasks by constructing hyperplanes in a multidimensional space that separates cases of different class labels. The SVM method 24 provides an optimally separating hyperplane in the sense that the margin between two groups is maximized. “Support Vectors” are defined as subset of data instances used to define the hyperplane. The distance between the hyperplane and the nearest support vector is called as margin 25. SVM supports both regression and classification tasks and can handle multiple continuous and categorical variables. There are two types of SVMs, (a) Linear SVM is used to separate the data points using a linear decision boundary and (b) Non-linear SVM separates the data points using a nonlinear decision boundary 7.

Traditional SVM training algorithms require quadratic programming (QP) package. Solving a quadratic programming problem is slow and requires a lot of memory as well as in depth knowledge of numerical analysis. Consider a binary classification problem with a dataset (*x*1, *y*1), ..., (*xn*, *yn*), where *xi* is an input vector and *yi* ∈ {-1, +1} is a binary label corresponding to it. The dual form of representing quadratic programming problem is given below 11:

˛𝑚\_𝑎¸𝑥 ∑𝑛 𝛼 − 1 ∑

∑𝑛 𝑦 𝑦 𝐾(𝑥 , 𝑥 )𝛼 𝛼 , (2)

i=1 i

𝛼

2 i=1

j=1 i j

i j i j

Subject to

0 ≤ 𝛼i ≤ 𝐶, fo𝑟 i = 1,2, … 𝑛, ∑𝑛

i=1

𝑦i 𝛼i = 0

(3)

Sequential Minimal Optimization does a way with the need for quadratic programming. The Sequential Minimal Optimization (SMO) algorithm (Platt, 1999a) avoids working with numerical QP routines by analytically solving a large number of small optimization sub-problems that involves only two Lagrange multipliers at the time. For any two multipliers 𝛼1 and 𝛼2, the constraints are reduced to the following:

0 ≤ 𝛼1, 𝛼2 ≤ C (4)

𝑦1𝛼1 + 𝑦2 𝛼2 = 𝐾 (5)

This reduced problem can be solved analytically by finding a minimum of a one-dimensional quadratic function. The value of 𝐾 is fixed in each iteration, it is the negative of the sum over the rest of terms in the equality constraint. The algorithm proceeds as follows:

1. Find a Lagrange multiplier 𝛼1 that violates the Karush–Kuhn–Tucker (KKT) conditions for the optimization problem.
2. Pick a second multiplier 𝛼2 and optimize the pair (𝛼1, 𝛼2).
3. Steps 1 and 2 are repeated until convergence.

The quadratic programming problem has been solved, when KKT 26 is satisfied by the Lagrange multipliers. The above algorithm guarantees convergence and heuristic measures are used to choose the pair of multipliers so as to increase the rate of convergence.

## Data Source

Pima Indian Diabetes 7, 9, 18 contains female patients with at least 21 years old. It is used to diagnose the presence of diabetes in pregnant women. There are 768 records, out of which 268 cases in class ‘positive test for diabetes’ and 500 cases for “negative test for diabetes” with 376 records contain missing values. It contains 8 numerical attributes as input and one output variable. The attribute information present in the dataset is as follows:

* 1. Number of times pregnant
  2. Plasma glucose concentration a 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 – Absence of disease / 1 – Presence of disease)

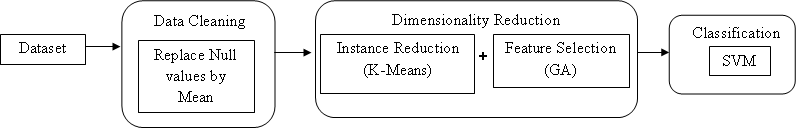


Fig.1 Block Diagram of the Proposed Method

## Proposed Method

The working principle of proposed system shown in Fig.1, comprises of 3 steps: (1) Data cleaning is done by replacing the missing values with mean (as the dataset lies under a normal distribution curve). (2) The cleaned datasets is clustered using K-Means to remove outliers, inconsistent and noisy data and the reduced data is used for selecting the optimal features with genetic algorithm. (3) The reduced dataset is classified using SVM classifier to achieve better accuracy compared to existing methods in literature. In order to increase the reliability of classifier performance 10-fold cross-validation method is used

*5.1. Evaluation Metrics*

To visualize the performance of supervised machine learning algorithms, confusion matrix is used. The four classification performance indices present in confusion matrix is given in Fig. 2. The evaluation metrics used are: Sensitivity, Specificity, Positively Predicted and Negatively Predicted value. Sensitivity

and Specificity is the proportion of actual positives and negatives which are correctly identified as such. The Positive and Negative predictive values are the proportions of positive and negative results, which are predicted.

𝑆e𝑛𝑠i𝑡i𝑣i𝑡𝑦 (%) = 𝑇𝑃

𝑇𝑃+𝐹𝑁

𝑆e𝑐ifi𝑐i𝑡𝑦 (%) = 𝑇𝑁

𝑇𝑁+𝐹𝑃

× 100 (6)

× 100 (7)

𝑃o𝑠i𝑡i𝑣e𝑙𝑦 𝑃𝑟e𝑑i𝑐𝑡e𝑑 𝑉𝑎𝑙𝑢e (%) = 𝑇𝑃

𝑇𝑃+𝐹𝑃

𝑁e𝑔𝑎𝑡i𝑣e𝑙𝑦 𝑃𝑟e𝑑i𝑐𝑡e𝑑 𝑉𝑎𝑙𝑢e (%) = 𝑇𝑁

𝑇𝑁+𝐹𝑁

× 100 (8)

× 100 (9)

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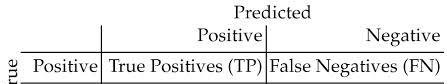
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*Fig 2.Confusion Matrix*

## Experimental Results

After replacing the missing values by mean, outliers, noisy and inconsistent samples / cases were removed using simple K-Means clustering algorithm. Then, GA was used as a feature selection tool and its

# output was fed to SVM using 10-fold cross validation technique for classification.

selected different features from the original set of features and the classification accuracy was recorded.

During each run, GA

To

# achieve consistent result, the experiment was repeated 50 times and the outcomes were listed in table 1. The average classification accuracy was 98.79 %.

Among the 50 test runs done, one trail / run which is closer to the average classification accuracy value is chosen to determine the various performance metrics. The evaluation metrics obtained by SVM for classifying the reduced dataset is shown in table 2 and confusion matrix in table 3. From table 4, it is proven that the classification accuracy percentage of the proposed work is better than the existing work.

Table 1. Experimental Outcome for 50 runs.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Test No. of  Run Attributes | | SVM Test No. of SVM  Accuracy Run Attributes Accuracy | | | |
|  | Selected | (%) |  | Selected | (%) |
| 1 | 5 | 98.63 | 26 | 6 | 98.43 |
| 2 | 3 | 98.43 | 27 | 5 | 98.82 |
| 3 | 4 | 99.21 | 28 | 4 | 98.43 |
| 4 | 5 | 99.21 | 29 | 5 | 99.02 |
| 5 | 4 | 99.21 | 30 | 4 | 98.43 |
| 6 | 5 | 99.02 | 31 | 5 | 98.63 |
| 7 | 6 | 99.02 | 32 | 4 | 98.43 |
| 8 | 3 | 98.43 | 33 | 4 | 99.21 |
| 9 | 5 | 98.43 | 34 | 4 | 98.43 |
| 10 | 5 | 99.21 | 35 | 4 | 98.82 |
| 11 | 4 | 98.82 | 36 | 4 | 99.21 |
| 12 | 5 | 98.82 | 37 | 5 | 99.02 |
| 13 | 6 | 98.43 | 38 | 5 | 98.63 |
| 14 | 4 | 99.21 | 39 | 5 | 99.02 |
| 15 | 3 | 98.43 | 40 | 4 | 99.21 |
| 16 | 4 | 98.43 | 41 | 4 | 98.82 |
| 17 | 4 | 98.43 | 42 | 4 | 98.82 |
| 18 | 4 | 98.63 | 43 | 3 | 98.43 |
| 19 | 4 | 98.82 | 44 | 5 | 98.82 |
| 20 | 5 | 99.21 | 45 | 5 | 99.02 |
| 21 | 3 | 98.43 | 46 | 5 | 99.02 |
| 22 | 4 | 99.21 | 47 | 4 | 98.82 |
| 23 | 5 | 98.82 | 48 | 5 | 98.63 |
| 24 | 3 | 98.43 | 49 | 4 | 99.21 |
| 25 | 5 | 98.82 | 50 | 3 | 98.43 |

Table 2. Evaluation Metrics obtained from SVM classifier

|  |  |
| --- | --- |
| Performance Measures | Reduced Dataset |
| No. of Attributes Used | 5 |
| Sensitivity (%) | 96.40 |
| Specificity (%) | 99.73 |
| Positively Predicted value (%) | 99.25 |
| Negatively Predicted value (%) | 98.67 |
| **SVM Accuracy** | **98.82** |

Table 3. Confusion Matrix obtained from SVM

Absent Present

Absent 134 5

Present 1 371

Table 4. Comparison of the proposed work with the existing works in terms of Accuracy. Author (Year) Method Accuracy (%)

Isa and Mamat (2011) 27 Clustered-HMLP 80.59

Aibinu et al (2011) 28 ARI+NN 81.28

Chikh M.A et al (2012) 29 AIRS2 82.69

MAIRS2 89.10

Ozcift A. (2012) 30 RBF+eACC, LADTree+eACC 76.30

Ahmad F. et al (2013) 14 Improved GA 80.4

Anuja Kumari et al, 2013 31 SVM 78

Ravi et al (2014) 7 GA + SVM 77.3

Nihat Yilmaz et al (2014) 18 K-Means + SVM 93.65

Modified K-Means + SVM 96.71

## Proposed Method K-Means+GA+SVM 98.82

The Research Findings are:

* 1. The minimum no. of attributes selected using GA is 3 and maximum is 6.
  2. The minimum and maximum classification accuracy using SVM is 98.43% and 99.21% and the average accuracy is 98.79 %
  3. Out of 768 instances, K-Means selected 511 samples as correctly classified and 257 samples were detected as outliers. The outlier detection percentage is 33.46.

critical attributes

* 1. Pregnancies, PGConcentration and Age are considered as dataset.

## Conclusion

for Pima diabetes

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Medical mining is one major application area where accuracy is important. This study has implemented K-Means and GA for dimensionality reduction and SVM to classify the diabetes dataset. The SVM classification accuracy of the proposed method has an increase of 2.08 % over the Modified K-Means and SVM reported in the literature. The future work will concentrate on use of standard deviation to replace

missing values, box plot for outlier detection, algorithms like SVM / PCA for feature selection and to

experiment classifiers from statistical, neural, fuzzy and tree families to enhance the resulting accuracy.

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