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Diagnosis of Diabetes Using an Intelligent Approach Based on Bi-Level Dimensionality Reduction and Classification Algorithms

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Abstract

Objective: Diabetes is one of the most common metabolic diseases. Earlier diagnosis of diabetes and treatment of hyperglycemia and related metabolic abnormalities is of vital importance. Diagnosis of diabetes via proper interpretation of the diabetes data is an important classification problem. Classification systems help the clinicians to predict the risk factors that cause the diabetes or predict people who are at risk of developing diabetes.

Materials and Methods: In this study, Pima Indian diabetes dataset taken from the UCI machine learning repository was used which contains 786 samples of normal and diabetes with 8characteristics.Selection of efficient features of this dataset was analyzed using correlation criterion, information gain and CfsSubsetEval. Then diagnosis of diabetes diseases on Pima dataset was considered using proposed by-level dimensionality reduction method and classification algorithms. Classification algorithms used in this study are KNN, quadratic, Naïve Bayes, nearest mean classifier, non-parametric Gaussian and Mahalonobis kernel and linear discriminant.

Results: In all feature selection methods, plasma glucose concentration a 2-hours in an oral glucose tolerance test, body mass index and age have been selected as the top-ranked features in intelligent diagnosis of diabetes. Proposed method has achieved the accuracy of 82.09 using KNN and quadratic methods and bi-level dimensionality reduction on Pima dataset. The best performance has been achieved by performing PCA algorithm on the features, namely, number of pregnancy, plasma glucose concentration a 2 hours in an oral glucose tolerance test, body mass index, diabetes pedigree function and Age.

Conclusion: The results of this study showed that bi-level dimensionality reduction and classification algorithm scan be very helpful in assisting the physicians to diagnosis diabetes.

Key words: Diabetes, Data mining, Classification, Dimensionality reduction, Feature selection, Feature extraction.

Introduction

Diabetes mellitus is a group of metabolic diseases characterized by abnormal high levels of plasma glucose or hyperglycemia in the fasting state or after administration of glucose during an oral glucose tolerance test (1). It causes by a

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combination of insulin resistance and impaired insulin secretion by pancreatic *B* cells (2-3). Diabetes increases the risks of developing kidney disease, blindness, nerve damage, blood vessel damage and it contributes to heart disease (4). Today, more than 200 million people in the world have type-2 diabetes (1). The total number of people with diabetes is expected to reach 370 million worldwide in 2030 (1). The Pima Indians of Arizona have the highest prevalence and incidence of Type-2 diabetes of any population in the world (4).

Early detection of diabetes, treatment of hyperglycemia and related metabolic abnormalities is of vital importance (4). Evaluation of data taken from patient and decisions of experts are the most important factors in diagnosis of diabetes, but in modern medicine large amounts of data taken from patient are stored in the diabetes database and there is a widening gap between data collection and data comprehension (4-6). It is often impossible to process all of the available data and making a rational decision on basic trends. Thus, there is a great need for intelligent data analysis such as data mining to extract the useful knowledge from these data to help the experts in decision making. Data mining is the search for relationships and patterns that exist in large databases but are hidden among the vast amount of data, such as a relationship between patient data and their medical diagnosis. Data mining techniques on diabetes data help to predict the risk factors that cause the diabetes or predict people who are at risk of developing diabetes (4-9).

Classification is one of the data mining techniques which have been successfully applied for medical diagnosis (7). Classification systems make medical data to be examined in shorter time and more detailed. The classification derives the class of an object based on its features while prediction means an indication in advance based on observations, experiences, or scientific reasons. The goal of classification is to maximize predictive accuracy; therefore, predictive accuracy is generally accepted and widely used as the primary measure by researchers and practitioners (4).

The aim of this paper is to propose a method based on bi-level dimensionality reduction and classification algorithms to improve the diagnostic accuracy of diabetes. Dimensionality reduction is very crucial for improving classification performance, especially in the case of high-dimensional data classification (10). There are two main methods for dimensionality reduction: (i) feature selection, and (ii) feature extraction (11). Feature selection is an essential pre-processing method to remove irrelevant and redundant features (11).Feature extraction is a process to create a new set of *k* features that are combinations of the original *d* features. When the original feature sets transform to a new smaller feature space, it called feature extraction. The feature transformation may be a linear or nonlinear combination of original features (12). Bi-level dimensionality reduction of the proposed method in this study is based on feature selection followed by feature extraction. Correlation Criterion (CC), Information Gain (IG) and CfsSubsetEval method are used for feature selection and Principal Component Analysis (PCA) is used for feature extraction.

Materials and Methods

Sample selection

In this study, Pima Indian diabetes dataset (13) taken from the UCI machine learning repository was used. This dataset was selected from a larger dataset held by the National Institutes of Diabetes and Digestive and Kidney Diseases. Since Pima Indians are the most intense population with type-2 diabetes in the world, data from this population is widely used in diabetic studies. The diagnostic, binary-valued variable investigated is whether the patient shows signs of diabetes according to World Health Organization criteria (i.e., if the 2 hour post-load plasma glucose was at least 200 mg/dl at any survey examination or if found during routine medical care). All patients in this dataset are Pima-

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Indian women at least 21 years old and living near Phoenix, Arizona, USA. The binary response variable takes the values '0' or '1,' where '1' means a positive test for diabetes and '0' is a negative test for diabetes.

The dataset has 768 instances with two class problems to test whether the patient is positive or negative for diabetes. There are 500 (65.1%) instances in class '0' (normal) and 268 (34.9%) instances in class '1' (Pima Indian diabetes). All instances have eight features. These features are:

- Features 1: Number of pregnancy
- Features 2:Plasma glucose concentration after 2 hours oral glucose tolerance test
- Features 3: Diastolic blood pressure (mm Hg)
- Features 4: Triceps skin fold thickness (mm)
- Features 5: 2-Hours serum insulin (mu U/ml)
- Features 6: Body mass index (weight in kg/(height in m)^2)
- Features 7: Diabetes pedigree function
- Features 8: Age (years)

Proposed method based on bi-level dimensionality reduction

To classification of Pima Indian diabetes dataset, we randomly split the original dataset into training and test sets. The proposed method to classify instances of the Pima into two classes relies on five operational steps. The steps of proposed classification structure are shown in Figure 1. These steps are explained in the following subsections:

Pre-Processing step

Pre-Processing is the first step of proposed method. In this step, data are normalized between 0 and 1. Normalization is applied where data are scaled to fall within a smaller range. Normalizing the data attempts to give all features an equal weight. The data normalization has a significant impact on the performance of many learning algorithms. This can improve the accuracy and efficiency of mining algorithms involving distance measurements (14).

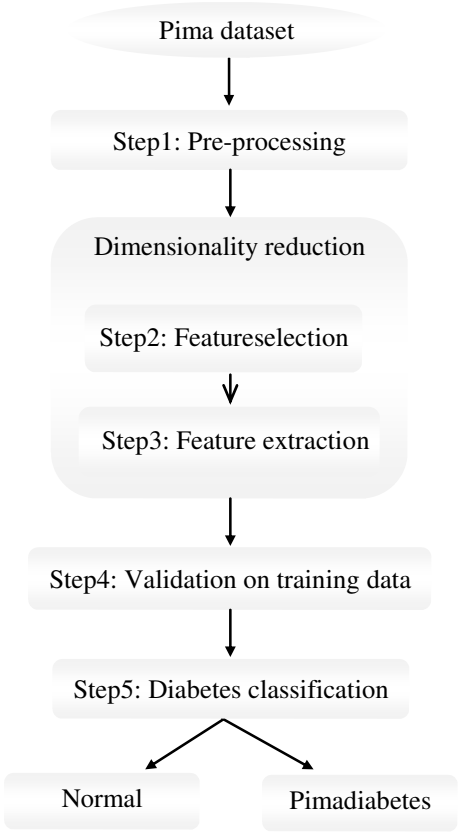


Figure 1. Diagram of the proposed method for diabetes diagnosis

Dimensionality reduction

In the proposed method, dimensionality reduction consists of two steps, feature selection and feature extraction. Initially, feature selection is applied on the original feature set to reduce its dimension and determine important features and then feature extraction is applied on the reduced feature set to further reduce its dimensions. In this study, we use three combinations of feature selection and feature extraction methods:

- Feature selection based on correlation criteria followed by PCA.
- Feature selection based on information gain followed by PCA.
- Feature selection based on CfsSubsetEval method followed by PCA.

Feature selection step

The objective of feature selection is to identify important features in the dataset and discard the unimportant features. Redundant features can be eliminated by feature selection without

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losing essential classificatory information (10). In this study, we perform feature selection for selecting the more relevant features prior to derivation of classification predictors. This process involves removing irrelevant features. In this step, features are ranked depending on their importance for the classification in decreasing order using the information gain (15,16) or correlation criterion (17) There by, features of less importance are ignored, and feature extraction method is applied on highest important features.

Feature extraction step

The objective of feature extraction is finding a new set of k features that are combinations of the original d features. Feature extraction is a process through which a new set of features is created (11). Principal Components Analysis (PCA) is a well-known and most widely used feature extraction method (15,18-19).PCA algorithm consists of the following main steps:

1. Compute the mean vector.
2. Subtract the mean: subtract the mean from each of the data dimensions. This produces a dataset whose mean is zero.
3. Calculate the covariance matrix.
4. Calculate the eigenvectors (u_1,u_2, …,u_N) and eigenvalues (λ_1,λ_2 , …,λ_N)of the covariance matrix.
5. Sort the eigenvectors by decreasing eigen values.
6. Choose k eigenvectors with the largest eigen values: We take into account the k components that explain more than, for example, 90 percent, of the variance. When λ_i are sorted in descending order, the proportion of variance explained by the k principal components is:

(1) $$T = \frac{\lambda_1+\lambda_2+\cdots+\lambda_k}{\lambda_1+\lambda_2+\cdots+\lambda_k+\cdots+\lambda_d}$$

7. Transform the samples to the new subspace.

Validation step

In addition to the feature reduction, in some classification methods such as KNN, non-parametric Gaussian kernel and non-parametric Mahalonobis kernel, proper parameters setting can improve the classification accuracy. The values of the parameters in these classification have to be chosen carefully in advance. For this purpose, we use 10-fold cross-validation on the training set to find out the optimal parameter values of these classification by maximizing the accuracy. Then, the classifiers were validated against the test set. Some classification algorithms may not need this validation step.

In 10-fold cross validation, the training set is divided into 10subsets, and each time, one of the 10subsets is used as the test set and the other 9 subsets are put together to form a training set. Then the average error across all 10trials is computed. The advantage of this method is that it is not important how the data is divided. Every data point appears in a test set exactly once, and appears in a training set 9 times.

Classification step

In this step, the diabetes patient in the test set is predicted. The prediction of diabetes patient is done by a classifier using the features extracted in the feature extraction step and the optimal parameters of the classifier obtained in validation step. Classification algorithms used in this study are KNN, quadratic, Naïve Bayes, nearest mean classifier, non-parametric Gaussian and Mahalonobis kernel and linear discriminant.

Results

To evaluate the effectiveness of the proposed method, we conducted experiments on the Pima Indian diabetes dataset. The experiment is carried out via Matlab software and Weka data mining tool. We perform 10-fold cross-validation on the training set to choose the best values of parameter *K* for KNN classifier from the set {15,17,19,…,101} and the parameter *h* for non-parametric Gaussian kernel and non-parametric Mahalonobis kernel from the set {0.1,0.2,0.5,1,1.5,2,2.5,5,10, 20,30,40,50,100} and choose the parameter with the best 10-fold cross-validation accuracy as the parameter of these classifiers.

For evaluation of the performance of proposed method, we define and compute the

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classification accuracy, recall, precision and F-measure. The formulations are as follows (21):

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

(3)$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}}$

(4)$\text{Precision} = \frac{\text{TP}}{\text{TP+FP}}$

(5)$F = \frac{2\times\text{precision}\times\text{recall}}{\text{precision+recall}}$

TP is the number of true positives; FN, the number of false negatives; TN, the number of true negatives; and FP, the number of false positives.

For experiments, we used the following methods:

- Feature selection using Correlation Criterion (CC) followed by feature extraction using PCA.
- Feature selection using Information Gain (IG) followed by feature extraction using PCA.
- Feature selection using CfsSubsetEval evaluator and Greedy Stepwise search method followed by feature extraction using PCA.

In the experiments, two values {0.9, 0.8} are considered for parameter *T* in PCA algorithm and three values {0.9, 0.8, 0.7} are considered for threshold parameter in feature selection using Correlation Criterion (CC).

When the threshold parameter in feature selection using correlation criterion was set to 0.9, the features {Number of pregnancy, Plasma glucose concentration after 2 hours oral glucose tolerance test, 2-Hours serum insulin, Body mass, Diabetes pedigree function, Age} were selected as important features in the Pima Indian dataset and two features {Diastolic blood pressure, Triceps skin fold thickness} were removed. Then PCA algorithm was performed on the features selected in this step. When parameter *T* in PCA algorithm was set to 0.9, a new dataset with 5 features was created. When parameter *T* was set to 0.8, another dataset with 4 features was created.

When the threshold parameter in feature selection using correlation criterion was set to 0.8, the features {Number of pregnancy, Plasma glucose concentration after 2 hours oral glucose tolerance test, Body mass, Diabetes pedigree function, Age} were selected as important features in the Pima Indian dataset and three features {Diastolic blood pressure, Triceps skin fold thickness, 2-Hours serum insulin} were removed. Then PCA algorithm was performed on the features selected in this step. When parameter *T* in PCA algorithm was set to 0.9 and 0.8, a new dataset with 4 features was created.

When the threshold parameter in feature selection using correlation criterion was set to 0.7, the features {Number of pregnancy, Plasma glucose concentration after 2 hours oral glucose tolerance test, Body mass, Age} were selected as important features in the Pima Indian dataset and four features {Diastolic blood pressure, Triceps skin fold thickness, 2-Hours serum insulin, Diabetes pedigree function} were removed. Then PCA algorithm was performed on the features selected in this step. When parameter *T* in PCA algorithm was set to 0.9, a new dataset with 4 features was created. When parameter *T* in PCA algorithm was set to 0.8, another dataset with 3 features was created.

We computed Information Gain (IG) for each features in Pima Indian dataset. Information gain for the features {Diastolic blood pressure, Triceps skin fold thickness, Diabetes pedigree function} was zero. In feature selection using information gain, we selected the features {Number of times pregnant, Plasma glucose concentration a 2 hours in an oral glucose tolerance test, 2-Hour serum insulin, Body mass, Age} as important features in the Pima Indian. Then we performed PCA algorithm on the features selected in this step. When parameter *T* in PCA algorithm was set to 0.9, a new dataset with 4 features was created. When parameter *T* was set to 0.8, another dataset with 3 features was created.

We also used Attribute Selection filter (package weka. filters. supervised. attribute) for feature selection. The Attribute Selection filter takes an evaluator and a search algorithm as parameter. The evaluator determines what method is used to assign a worth to each

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Table 1. New different diabetes datasets created by proposed method

Dataset number	Feature selection method	The features selected using feature selection method	Parameter *T* in PCA algorithm	Final number of features in dataset
1	Correlation Criterion ; Threshold=0.9	{1,2,5,6,7,8}	0.9	5
2	Correlation Criterion; Threshold=0.9	{1,2,5,6,7,8}	0.8	4
3	Correlation Criterion ; Threshold=0.8	{1,2,6,7,8}	0.9 or 0.8	4
4	Correlation Criterion; Threshold=0.7	{1,2,6,8}	0.9	4
5	Correlation Criterion; Threshold=0.7	{1,2,6,8}	0.8	3
6	Information Gain	{1,2,5,6,8}	0.9	4
7	Information Gain	{1,2,5,6,8}	0.8	3
8	CfsSubsetEval	{2,6,8}	0.9	3
9	CfsSubsetEval	{2,6,8}	0.8	2

subset of attributes. The search method determines what style of search is performed. In this study, we used CfsSubsetEval as evaluator and a backwards operating Greedy Step wise as search algorithm. CfsSubsetEval method selected the features {Plasma glucose concentration after 2 hours oral glucose tolerance test, Body mass index, Age} as the most important features in the Pima Indian dataset and removed remaining features. Then we performed PCA algorithm on the features selected in this step. When parameter *T*in PCA algorithm was set to 0.9, a new dataset with 3 features was created. When parameter *T* was set to 0.8, another dataset with 2 features was created.

After performing dimensionality reduction step on Pima dataset, 9 new different diabetes datasets were created and different classification methods were applied on new datasets in classification step.

Table 1 shows new different diabetes datasets created by proposed method. This table also indicates the number of features in new data sets and the factors which make these new datasets such as feature selection method and the value of parameter *T* in PCA algorithm.

For evaluating the performance of proposed method, we compared the performance of different classifiers on the Pima dataset, normalized Pima dataset and diabetes datasets created by proposed method respect to accuracy, recall, precision and F-measure.

Tables 2 to 5 show the performance of different classifiers on different diabetes datasets respect to accuracy, recall, precision and F-measure, respectively. In these tables, Full dataset1 represents Pima dataset with 8 features and full dataset2 represents normalized Pima dataset with 8 features. KNN+ Euclidean represents K-Nearest Neighbor classifies based on Euclidean distance and KNN+ Manhattan represents K-Nearest Neighbor classifier based on Manhattan distance.

As shown in Table 2, the performance of all classifiers has been improved in terms of accuracy measure on the different datasets created by the proposed method. It can also be seen from Table 2 that in classifiers such as

Table 2. Performance of different classifier respect to accuracy measure on different diabetes datasets

Method	Full dataset1	Full dataset2	Dataset1	Dataset2	Dataset3	Dataset4	Dataset5	Dataset6	Dataset7	Dataset8	Dataset9
KNN+ Euclidean	74.25	79.48	80.22	81.72	82.09	80.97	80.97	80.22	79.85	80.60	80.97
KNN+ Manhattan	76.12	79.85	80.60	80.60	82.09	78.73	78.73	79.48	80.22	81.34	81.72
Quadratic	76.49	76.49	77.61	78.73	81.72	79.48	79.48	79.85	77.24	80.22	82.09
NaiveBayes	78.36	78.36	76.87	75.37	78.73	78.73	78.73	79.48	74.63	79.48	79.85
Nearest mean	60.82	77.61	77.61	76.12	77.99	77.24	77.24	76.12	75.37	80.22	79.85
Gaussian kernel	73.88	78.36	77.24	77.61	80.60	79.10	79.10	78.73	78.36	79.85	81.34
Mahalonobis kernel	73.133	73.13	76.87	77.24	78.36	76.87	76.87	77.99	79.85	79.48	81.72
Linear discrimination	79.85	79.85	81.34	76.87	80.97	80.60	80.59	79.85	76.87	80.60	79.85

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quadratic, naïvebayes, nearest mean and non-parametric Gaussian and Mahalononbis kernels which work based on bayes theorem, feature selection using CfsSubsetEval method has the best performance in terms of accuracy measure. The comparison results of fulldataset1 and fulldataset2 show that data normalization in the classifiers such as KNN+ Euclidean, nearest mean and non-parametric Gaussian kernel which work based on euclidean distance significantly improves the performance of the classifiers in terms of accuracy measure.

The best performance in terms of accuracy measure has been achieved using KNN classifier and quadratic classifier on dataset3 and dataset9, respectively. Means that using KNN classifier on the features {Number of times pregnant, Plasma glucose concentration a 2 hours in an oral glucose tolerance test, Body mass index, Diabetes pedigree function, Age} and performing PCA algorithm, the best performance has been achieved in terms of accuracy measure. In addition, using quadratic classifier on the features {Plasma glucose concentration a 2 hours in an oral glucose tolerance test, Body mass index, Age} and performing PCA algorithm, the best performance has been achieved in terms of accuracy measure.

It is clear from Table 3 that the performance of all classifiers except naïvebayes classifier has been improved in terms of recall measure on the different datasets created by the proposed method. As shown in Table 3, nearest mean classifier has the best performance in terms of recall measure on dataset1 and dataset3. Means that using nearest mean classifier on the features {Number of times pregnant, Plasma glucose concentration a 2 hours in an oral glucose tolerance test, Body mass index, Diabetes pedigree function, Age} or on the features {Number of times pregnant, Plasma glucose concentration a 2 hours in an oral glucose tolerance test, 2-Hour serum insulin, Body mass index, Diabetes pedigree function, Age} and performing PCA algorithm, the best performance has been achieved in terms of recall measure.

It can be seen from Table 4 that the performance of all classifiers in terms of precision measure has been improved on the different datasets created by the proposed method. The comparison results of fulldataset1 and fulldataset2 indicate that data normalization in the classifiers such as KNN+ Euclidean, nearest mean and non-parametric Gaussian kernel which work based on Euclidean distance and in KNN+ Manhattan classifier which works based on Manhattan distance significantly improves the performance of the classifiers in terms of precision measure.

The best performance in terms of precision measure has been achieved using KNN+ Euclidean classifier on dataset3which consists

Table3. Performance of different classifiers respect to recall measure on different diabetes datasets

Method	Full dataset 1	Full dataset 2	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5	Dataset 6	Dataset 7	Dataset 8	Dataset 9
KNN+ Euclidean	50	43.02	47.67	58.14	54.65	63.95	63.95	56.98	59.30	63.95	60.47
KNN+ Manhattan	54.65	46.51	54.65	54.65	58.14	62.79	62.79	55.81	59.30	67.44	62.79
Quadratic	63.95	63.95	62.79	70.93	75.58	67.44	67.44	66.28	62.79	66.28	67.44
NaiveBayes	61.63	61.63	48.84	48.84	56.98	56.98	56.98	55.81	50	52.33	52.33
Nearest mean	43.02	77.91	80.23	76.74	80.23	77.91	77.91	75.58	74.42	77.90	76.74
Gaussian kernel	46.51	61.63	44.19	50	53.49	60.47	60.47	53.49	54.65	61.63	60.47
Mahalonobis kernel	25.58	25.58	48.84	48.84	51.16	41.86	41.86	51.16	58.14	62.79	61.63
Linear discrimination	50	50	52.33	45.35	52.33	55.81	55.81	55.81	47.67	53.49	52.33

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Table4. Performance of different classifiers respect to precision measure on different diabetes datasets

Method	Full dataset 1	Full dataset 2	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5	Dataset 6	Dataset 7	Dataset 8	Dataset 9
KNN+ Euclidean	62.32	86.05	83.67	79.37	83.93	73.33	73.33	75.38	72.86	72.37	75.36
KNN+ Manhattan	65.28	83.33	78.33	78.33	80.65	68.35	68.35	73.84	73.91	72.50	76.06
Quadratic	63.22	63.22	65.85	65.59	69.89	68.24	68.24	69.51	65.06	70.37	74.36
NaiveBayes	67.95	67.95	70	65.63	71.01	71.01	71.01	73.85	63.24	76.27	77.59
Nearest mean	39.75	62.04	61.61	60	62.16	61.47	61.47	60.19	59.26	66.34	66
Gaussian kernel	62.50	67.95	74.51	71.67	79.31	70.27	70.27	73.02	71.21	71.62	76.47
Mahalonobis kernel	73.33	73.33	70	71.19	73.33	75	75	72.13	73.53	70.13	76.81
Linear discrimination	79.63	79.63	83.33	72.22	81.82	77.42	77.42	75	70.69	79.31	77.59

of performing PCA algorithm on the features {Number of pregnancy, Plasma glucose concentration after 2 hours oral glucose tolerance test, Body mass index, Diabetes pedigree function, Age}.

As shown in Table 5, the performance of all classifiers except naïvebayes classifier has been improved in terms of F-measure on the different datasets created by the proposed method. The comparison results of fuudataset1 and fulldataset2 indicate that data normalization in the classifiers such as KNN+ Euclidean, nearest mean and non-parametric Gaussian kernel which work based on Euclidean distance significantly improves the performance of the classifiers in terms of F-measure. Quadratic classifierhas the best performance in terms of F-measure on dataset 3 compared with other classifiers.

Discussion

Nowadays huge amounts of data about diabetic patients are captured by the healthcare information systems in healthcare organizations. Traditional manual data analysis isn't able to analyze the huge amount of data. Data mining methods can be applied in medical research in order to analyze large volume of medical data and get useful clinical knowledge from medical databases. In this study, a method was proposed for diagnosis of diabetes on Pima Indian diabetes dataset

Table5. Performance of different classifiers respect to F-measure on different diabetes datasets

Method	Full dataset 1	Full dataset 2	Dataset 1	Dataset 2	Dataset 3	Dataset 4	Dataset 5	Dataset 6	Dataset 7	Dataset 8	Dataset 9
KNN+ Euclidean	62.32	86.05	83.67	79.37	83.93	73.33	73.33	75.38	72.86	72.37	75.36
KNN+ Manhattan	65.28	83.33	78.33	78.33	80.65	68.35	68.35	73.84	73.91	72.50	76.06
Quadratic	63.22	63.22	65.85	65.59	69.89	68.24	68.24	69.51	65.06	70.37	74.36
NaiveBayes	67.95	67.95	70	65.63	71.01	71.01	71.01	73.85	63.24	76.27	77.59
Nearest mean	39.75	62.04	61.61	60	62.16	61.47	61.47	60.19	59.26	66.34	66
Gaussian kernel	62.50	67.95	74.51	71.67	79.31	70.27	70.27	73.02	71.21	71.62	76.47
Mahalonobis kernel	73.33	73.33	70	71.19	73.33	75	75	72.13	73.53	70.13	76.81
Linear discrimination	79.63	79.63	83.33	72.22	81.82	77.42	77.42	75	70.69	79.31	77.59

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which used a bi-level approach for dimensionality reduction. Different classifiers such as KNN, quadratic, naïvebayes, nearest mean classifier, non-parametric Gaussian kernel, non-parametric Mahalonobis kernel and linear discriminant were applied to classify and analyze the diabetes data. The performance of all classifier son the datasets created by the proposed method has been significantly improved with respect to accuracy, recall, precision and F-measure. Proposed method consists of five steps. The first step is data normalization which significantly improves the performance of the classifiers which are based on Euclidean distance in terms of different measures.

In the experiments, the correlation of each feature in the Pima dataset with the decision attribute was computed. Feature 1 (Number of times pregnant), Feature 2 (Plasma glucose concentration after 2 hours oral glucose tolerance test), Feature 6 (Body mass index) and Feature 8 (Age) were the top-ranked four features which have shown strong relevancy with the decision attribute.

In all feature selection methods used in this study, Feature 2 (Plasma glucose concentration after 2 hours oral glucose tolerance test), Feature 6 (Body mass index) and Feature 8 (Age) have been selected as the top-ranked features. It is suggested an important clue for the physicians to pay much more attention to these features, namely, Plasma glucose concentration after 2 hours oral glucose tolerance test, Body mass index and Age for diabetes diagnosis. We believe that the proposed method can be very helpful in assisting the physicians to make the accurate diagnosis on the patients and can show great potential in the area of clinical diagnosis. In all feature selection methods, the features, diastolic blood pressure and Triceps skin fold thickness are removed and indicated as the least important features in diagnosis of diabetes diseases.

The best performance with respect to accuracy, recall, precision and F-measure has been achieved on dataset3 which consists of performing PCA algorithm on the features {Number of pregnancy, Plasma glucose concentration after 2 hours oral glucose tolerance test, Body mass index, Diabetes pedigree function, Age}.

A hybrid model was proposed by Karegowda et al. (23) that integrates Genetic Algorithm and Back Propagation network (GA-BPN) for predictions of medical data where GA is used to initialize and optimize the connection weights of BPN. GA- BPN method has achieved the accuracy of 77.707 on Pima dataset.

Balakrishnan and Narayanaswamy (8) applied a method to derive the optimal feature subset for the Pima dataset that improves the performance of the Libsvm classifier. They achieved the accuracy of 77.9948 on Pima dataset.

Rakotomamonjy et al. (24) proposed an approach for solving the multiple kernel learning problem in support vector machines. Their approach uses aweighted 2-norm regularization. This method obtained the accuracy of 75.8 ± 1.6 on Pima dataset.

A comparative study on diabetes disease diagnosis using neural networks was proposed by Temurtas et al. (4). They reported 79.62 classification accuracy using MLNN with LM (10x FC) algorithm, 78.05 classification accuracy using PNN (10x FC) algorithm and 80.21 accuracy using GRNN (conventional valid) method.

Polat and Gunes (6) reported classification accuracy between 59.5 and 77.7 on Pima datasetand Watkins and Boggess (25) reported accuracy between 73.0 and 77.7 on this dataset.

Yin and Han (26) presented classification based on predictive association rules (CPAR) which obtained 73.8 classification accuracy on Pima dataset. They also reported 75.5, 73.1, 72.9, 75.1 classification accuracy using C4.5, Ripper, CBA and CMAR methods, respectively.

A Classwise k-Nearest Neighbor (CKNN) method for classification of diabetes dataset has been presented by Angeline and

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Sivaprakasam (14). CKNN obtained accuracy of 78.16 on Pima dataset. They also reported that accuracy of KNN method is 71.84, naïvebayes is 73.8 and logdisc is 77.7.
BOZKURT et al. (27) compared the performance of different neural networks on Pima dataset. They obtained accuracy between 65.97 and 73.6 on these data.
Our proposed method has achieved accuracy of 82.09on Pima dataset using KNN and quadratic classifiers and bi-level dimensionality reduction based on feature selection followed by PCA.

Conclusion

The results of this study showed that proposed method have achieved better performance compared with other methods (6,8,14,23-27).

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