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# Predicting Parkinson's Disease using Extreme Learning Measure and Principal Component Analysis based Mini SOM

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## ABSTRACT

Parkinson's Disease (PD) is one of the most common neurological disorders, affecting the age group of 40-60 Years mostly, occurs due to impairment of motor function of brain and thus early PD diagnosis is an important task for treatment initialization. The existing clustering techniques failed to group the data clusters properly during training and testing the models that failed to improve the efficiency of during classification. The present research work uses Extreme Learning Machine (ELM) with Self-Organizing Map (SOM) improves the precision and scalability validated the results during training and testing the models failed to group the cluster data properly. Because of the high-dimensional datasets tend to be unstructured that showed uncertainties for big datasets. Such noisy data can become more challenging to process. Therefore, the proposed method is evaluated for real-world PD dataset that uses Principal Component Analysis (PCA) to perform predictive analytic that learns only the most relevant variables responsible for the highest variation in that dataset and MiniSOM will improve the effectiveness and efficiency during training and testing for the obtained data clusters and are fed to the classification process. The results revealed that the proposed PCA-MiniSOM based approached obtained accuracy of 93.33% better when compared with the existing SOM model.

**Keywords:**
Extreme Learning Machine, Parkinson's Disease, Principal component analysis, Deep Neural Network, Self-Organizing Map, MiniSOM.

## Introduction

According to the latest statistics obtained from World Health Organization (WHO) has stated that around 10 million people worldwide are living with PD and men are having chances of 1.5 times more than that of a woman for disease cause [1]. The developed model performs self-diagnosis and allows the self-treatment of the disease using various technological advancement have led to rise in a greater number of people experiencing the disease [2]. There are various techniques under the neurology field that are used as a combination or individually for supporting the diagnosis clinically. However, there is burden for both health care systems as well as patients due to delay shown during diagnosis [3]. Usually, the binary diagnosis will focus on the validating the digital biomarkers distinguished the disease control as it failed to offer differential diagnosis from a variety of PD disorders [4]. The present research will focus on providing a promising step for providing decision support algorithm among the PD patients who are under screening [5]. The several different machine learning with AI models were utilized for classifying PD by using various PD datasets. The machine algorithms such as Naïve Bayes, decision tree, and support vector machine (SVM) were utilized for PD detection that evaluated with the standard metrics. The medical data were utilized for giving the structural information that monitored the symptoms for these functional insights.

The medical images that are utilized for the research has the anatomical body structure that is important for data mining application for Computer Aided Diagnosis (CAD) and physiology [7]. The extraction and analysis of pertinent information from the noisy medical data is a critical issue using these medical data [8]. The clinical diagnosis by using of original medical images is often insufficient so data clustering is required. The existing models used data clustering techniques for these unlabelled data and K-means algorithm has been used as it is easy for implementation and is simple [9]. The KMC is only dependent on the initial search and would lead to local and sub optima solutions. Therefore, a global search algorithmwas needed to be adapted for the cluster context analysis that will overcome the optimization problems [10]. In order to overcome such an issue, proposed Improved PCA based Mini Self- Organizing Map (SOM) for the data clustering to predict the diseases such as Parkinson’s disease, kidney related disease, heart disease etc.

The organization of the research paper are as follows: The section 2 focusses on the existing models developed for Parkinson’s disease detection. The section 3 introduces the proposed PCA based MiniSOM technique and elaborates its functionality in prediction the Parkinson’s disease. The section 4 provides the results and discussion section that consists of quantitative analysis and comparative analysis. The section 5 briefs the conclusion of the current research and its future scope

## Literature Review

The existing models that were used for disease prediction using Machine learning algorithms are as follows:

Nithya et.al.[11] used Artificial Neural Network (ANN) along with the multiple kernel k-means clustering to develop a method for kidney disease detection and segmentation for ultrasound images. Initially, the noise that was present in an input image was eliminated using pre-processing technique. The noise free data were now undergone for feature extraction using GLCM from the image and classified the image data as normal or abnormal using ANN. The abnormal image data obtained were now undergone for segmentation that segmented the tumor and stone parts using Kernel K-means clustering algorithms. However, the classified data includes incomplete information due to which the performance of disease detection decreased.

Qianyi Zhan et.al.[12] have worked on multi-view clustering algorithm and deep features to develop epilepsy detection method. The developed Electro-Encephalo-Gram (EEG) detection firstly utilized a multi view Fuzzy C-Means (FCM) that was used for training the samples. The weight of each view was obtained trained calculated the value of view weighted membership for new prediction samples. The classification label was given during prediction of the disease automatically. However, the time domain deep feature classification performance was lesser.

Mehrbakhsh Nilashi et.al.[13] developed a remote tracking for PD progression using Support Vector Regression (SVR) and Deep Belief Network (DBN) that utilized SOM for performing data clustering. The DBN was developed for ELM performed supervised learning in using SVR that obtained better predictions of disease. The hybrid model developed using clustering and DBN was aid for SVR to perform the ensemble, making better predictions using Motor PD prediction. However, the better features were not selected due to which the PD disease accuracy was decreased.

Haolin Wang et.al.[14] developed Kawasaki disease assessment method based on feature clustering and CNN. The developed method addresses the insufficiency for the clinical data and uses matrix-based representation extracting the essential features using Convolutional Neural Network that determines the Kawasaki disease. However, the noise that exists in the data, forms bias and single data collection is unable to improve the performance for KD as it lacked the publicly available datasets concerned the ethics and patient’s privacy.

Chunyan Guo et.al.[15] developed a online method that uses recursive enhanced random forest technique along with an enhanced linear regression for heart disease. The developed model used better level of precision performance for heart disease prediction. However, the larger number of data used made the model to be operated slow which was ineffective during disease prediction.

Pooja Rani1 et al [2] developed decision support system for heart disease prediction based upon machine learning. The developed model utilized hybridized features by combining the recursive feature elimination and Genetic Algorithm was utilized for feature selection from the available data. However, further preprocessing of data was required using SMOTE (Synthetic Minority Oversampling Technique that failed to diagnosed the disease with this system.

Afzal Hussain Shahid et al [5] developed a deep learning approach for PD prediction using PCA. The PCA was employed for addressing the featured dataset addressed the multi collinearity problems reduced the input featured dimension. The reduced input features were fed to the DNN model that tuned the parameters norm penalty analyzed the performance during prediction diagnosed the PD. However, the independent feature space that were reduced fed to the DNN model showed complexity and showed difficulty for generalizing the proposed technique.

## Proposed Methodology

The block diagram of the proposed method explains the steps involved in the proposed PCA with MiniSOM Technique and is shown in the figure 1.

### Data collection

The Parkinson’s disease datasets are used in the present research, are taken from the University of California, Irvine the dataset is obtained and is widely used for PD prediction. The dataset consists of 5875 records that belongs to 14 women and 28 men that has approximately 200 records for each patient and approximate data per each of the patient is provided in the below table.

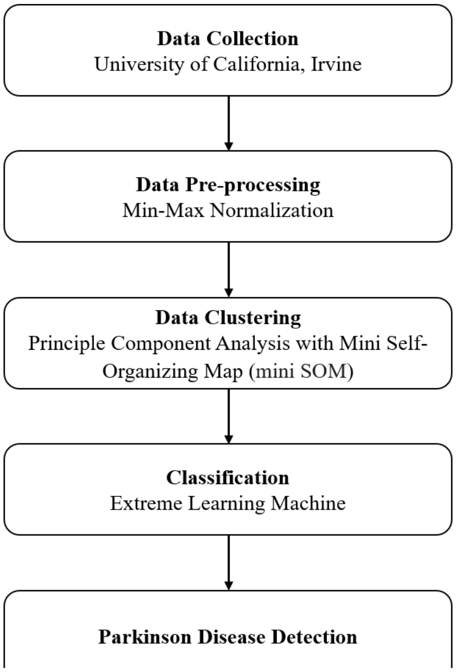

Figure 1: Block diagram of the proposed PCA with MiniSOM

Table 1 : Parkinson Disease Dataset Description

| | | | | | |
|---|---|---|---|---|---|
| Data Set Characteristics: | Multivariate | Number of Instances: | 197 | Area: | Life |
| Attribute Characteristics: | Real | Number of Attributes: | 23 | Date Donated | 26-06-2008 |
| Associated Tasks: | Classification | Missing Values? | N/A | Number of Web Hits: | 300088 |

## Pre-processing technique using Min Max Normalization

The examination of a large number of patient’s data for the current research is is taken into account in order to accurately detect PD. Human error, database failure, or device malfunction all contribute to missing data in large datasets. To prevent this, the structured data would be used to fill in the missing data. As these missing data are incomplete or uncertain medical data, they can be updated by deleting unwanted data to improve their accuracy. Data pre-processing is then used to complete the data integration process. The Min-Max normalisation method is critical for data normalisation as well as integration. Every feature value with a minimum value is set to 0 and every feature value with a maximum value is set to 1. The values obtained will be converted to decimals in the range 0 to 1. Normalization process expressed in the form of an equation is given in Eq. (1).

$$X_{norm} = \frac{X_i - X_{min}}{X_{max} - X_{min}} \qquad \text{Eq. (1)}$$

Where, $X_i$ is the $i^{th}$data point, $X_{min}$ is the data point minimum value, $X_{max}$ is thedata point maximum value or instances of the batch $D = \{X_0, \dots . X_{n-1}\}$. $X_0, \dots . X_{n-1}$ variables determine normalized value given by $X_{norm}$ thereby uses structured data to fill the missing values.

## Data clustering using PCA based Mini SOM

After collecting the data improved SOM is applied to Parkinson disease data to divide the experimental data into several groups comprising cases that are similar. The clustering process is mainly used for dimensionality reduction and grouping the similar data belonging to similar classes thereby forms the data to clusters. The SOM works similar to the neural network technique and could be used both for unsupervised and supervised learning. The unsupervised learning focusses on the data dimension reduction and data clustering is considered for distinct sizes of SOM. The present research uses SOM having the size of 3X3 that provided better clustering results when compared with the other SOM sizes such as SOM 2 * 2, SOM 2 * 3, and SOM 3 * 4. The present research uses 3 * 3 nine clusters for analysis furtherly by using PCA approach. The present research uses Improvised SOM is done for clustering indications aimed separated different classes with exact boundaries built the unlabeled units. The unlabeled units are used that reveal the distances among the label grid units apart from illustrating the units from the neighbors calculated by using the Manhattan distance. Manhattan distance is sum of all the real distances between initial source point to destination point and each distance are always the straight lines.

$$\text{manhattan distance} = |a - c| + |b - d|$$

where $a$ and $b$ are minimum latitude and longitude and c and d are maximum latitude and longitude respectively.

The SOMs will be different from that of ANN as it is applied for competitive learning which is opposed with error correlated learning as well uses the backpropagation networks. The training data is usually not consisting of labels and the map will learn to distinguish and different features based on the similarities. Therefore, in the exisitng models that used SOMs for clustering showed misclassification for disease detection. The proposed model will implement into two process one is training the random data and testing the random data. The SOMs are different from ANN as it is applied a competitive learning that opposed to learning related to error that involves gradient descent and back propagation. In competitive learning, the nodes compete towards the right for responding towards the input data subset. The data which is trained usually do not have labels but the map will learn the distinguished and differentiated features based on the similarities. There are two types of training and testing the random batch samples using the MiniSom. The model is trained randomly by picking up the random data samples are picked and stored. Thee random weights are initialized with the weights by random samples of data by picking.

### MiniSom

The MiniSOM is an implementation performed using minimalistic Numpy package that converts high dimensional data which are statistical, non-linear, and complex data into a a low-dimensional data for simple geometric relationship. The Principal Component Analysis (PCA) algorithm acts as a statistical algorithm that sets up the possible correlated variables to uncorrelated based upon the linear re-combinations. The recombination components obtained are known as principal components. These principal components perform recombination of all these linear variables for all the dataset present and the weights derived are obtained from the correlation or co-variance matrix from the dataset available. Initial principal component is present on the linear line which reduces the distance between data points after performing the squared distances between the data points. A single line can be used to represent the least squares approximation on the dataset. Initial principal component has the maximum variance for a single line and therefore the highest variance amount is explained from the dataset. The remaining principal components are extracted from the data in next stage. There is successive component that explains less variance and requires to be sufficient for selecting the principal components where the amount of variance principal components is more than that of the threshold which reduces the dimensional problem from the variables provided the principal components. The algorithm is sensitive for scaling the variables for the dataset and hence, it is required to compute the mean centering and data training usually do not have labels and has no labels learned to distinguish and differentiate the features based on their similarities. The MiniSom implemented trained and training random samples trained batch. The trained random samples are trained with the model picked the random samples from the data and trained the batch samples are picked stored the order.

### Data Classification

Once the data clustering is performed the classification process has to be performed using ELM. ELM is a supervised learning algorithm that uses ELM for PD detection thereby sets up the hidden layers. The ELM are the feed forward neural networks utilized for classification that learns the features that were fed to the multiple layers of the hidden nodes. The features fed for the hidden nodes are nothing but the parameters present in the hidden nodes. The model randomly divides the data as training and testing set for each of the clusters and is fed to ELM as a feed forward Neural network that has one hidden layer, output layer and input layer. The parameters present in the hidden nodes are not only weights but that provides a connection from inputs to the hidden nodes. The hidden nodes are assigned randomly that never gets updated but has the possibility of inheriting from the ancestors without getting changed. The output weights present in the hidden nodes are learned in one step that amounts for learning an essentially a linear model. The learning models includes the matrices of weights such as $a$ and $b$ sets up a connection among the output obtained from the hidden and output neurons. Therefore, PD is detected and the FFNN and ELM consists of an input layer and hidden layer that are represented with k data samples having $X_j$ and $y_i$ the ELM's output is calculated using the following equation:

$$o_i = \sum_{j=1}^{l} \beta_j g(X_j) = \sum_{j=1}^{l} \beta_j g(a_j X_j + d_j) \qquad \text{Eq. (2)}$$

$$i = 1, \dots, k$$

The matrices are having the weights as a and b that are having the connection among the hidden input and output neurons. $l$ is known as bias vector consisting hidden neurons. Similarly, the difference obtained among o and y is represented as E which is calculated by using the below equation

$$E = \sum_{i=1}^{k} \left( \sum_{j=1}^{l} \beta_j g\left(a_j X_j + d_j\right) - y_i \right)^2 \qquad \text{Eq. (3)}$$

where $i = 1, \dots, k$

The least square solution $\hat{\beta}$ is obtained for the linear system which is represented as $H\beta = Y$

Therefore

$$H = \begin{pmatrix} g(a_l x_l + d_l) & \cdots & g(a_l x_l + d_l) \\ \vdots & \ddots & \vdots \\ g(a_l x_k + d_l) & \cdots & g(a_l x_k + d_l) \end{pmatrix}_{k*l} \qquad \text{Eq. (4)}$$

where $H$ is known as the Output Matrix for the Hidden Layers.

## Results (Times New Roman, bold, 12)

The proposed PCA-MiniSOM evaluates the results using the performance metrics accuracy, precision, specificity, sensitivity and F-score. The simulation setup for the proposed method is evaluated by using the following metrics by working on Python 3.6, Jupyter Notebook powered by Anaconda Navigator on Windows 10 Operating Systems. The proposed PCA-MiniSOM was implemented on system configured with RTX 2080 Ti GPU and i9 processor operating at 3 GHz and 1 TB HDD. In the proposed PCA-MiniSOM model performance is compared with a benchmark model to validated the overall performance for PD prediction.

### Performance Metrics

**Accuracy:** Accuracy is the ratio of number of correct predictions to the overall predictions and it is used for evaluating the classification of models. It is defined in equation (5).

$$Accuracy = \frac{Number\ \ of\ \ correct\ \ predictions}{overall\ \ predictions} \qquad \text{Eq. (5)}$$

**Sensitivity:** Sensitivity is the calculation that measures the ratio of positives that are correctly determined. It is defined in equation (6).

$$Sensitivity = \frac{TP}{TP+FN} \qquad \text{Eq. (6)}$$

**Specificity:** Specificity is the calculation that measures the ratio of negatives that are correctly determined. It is defined in equation (7).

$$Specificity = \frac{TN}{TN+FP} \qquad \text{Eq. (7)}$$

**Precision:** Precision is the ratio of overall number of truly classified positives to the overall number of predicted positives. It is defined in equation (8).

$$Precision = \frac{TP}{TP+FP} \times 100 \qquad \text{Eq. (8)}$$

**F-score:** F-score calculates the accuracy of the model and it is the combination of precision and recall. It is defined in equation (9)

$$F - score = \frac{TP}{TP+1/2(FP+FN)} \qquad \text{Eq. (9)}$$

Where,
$TP$= True Positive
$TN$ = True Negative
$FP$= False Positive
FN = False Negative

**Quantitative Analysis:**

While evaluating the performance measures, the metric Precision measures the number of positive class predictions for disease prediction which belongs to positive class. Recall measures the number of positive class predictions for PD disease detection has made out of all positive examples in the dataset. The F-Measure provides a single score that balances both the concerns of precision and recall in one number. The results obtained for the proposed PCA-MiniSOM data clustering technique evaluates the results in terms of accuracy, precision, recall and F-score. The results evaluation is done for the existing SVM, MLP, KNN classifiers that obtained accuracy of 72.88%, 77.97 %, 79.66%, whereas the proposed PCA-MiniSOM has obtained accuracy of 93.33% for Parkinson disease detection. The SVM uses the hyper plane parameters for tuning and fails to perform well, when the dataset has more target classes overlapped for Parkinson's dataset. Therefore, the efficiency of the model was lowered whereas the proposed PCA with MiniSOM on a low-dimensional display, transforms complex, nonlinear statistical relationships between high-dimensional data items into simple geometric relationships which improves the efficiency of the model. Similarly, due to the hard-limit transfer function, the output values of a perceptron can only take one of two values (0 or 1) and can only classify linearly separable sets of vectors. Similarly, The accuracy of the KNN model is determined by the data quality, and for large data, the prediction stage can be slow due to the data's size and irrelevant features, whereas the size of the variables in the data set affects the PCA algorithm, therefore in the present research it perform mean centering and the map learns to differentiate and distinguish features based on similarities and therefore improves the performances when compared to the existing models. The precision values obtained for the existing methods such as SVM, MLP, and K-NN are 74 %, 61% and 84 % whereas the proposed PCA-MiniSOM clustering has obtained precision of 92.95 %. The Recall values obtained for the existing SVM, MLP, and KNN for PD disease detection has obtained 73%, 78 % and 80 % whereas the proposed PCA-MiniSOM has obtained Recall of 93.33 %. The F-score values obtained for the exisitng methods such as SVM, MLP, and SVM are 74 %, 68% and 72 % whereas the proposed PCA-MiniSOM clustering has obtained Recall of 95.71%.

Table 1: The values obtained for the proposed PCA-MiniSOM in terms of Accuracy, Precision, Recall and F-score are as follows

| **Methods** | **Accuracy(%)** | **Precision(%)** | **Recall(%)** | **F1-Score(%)** |
|---|---|---|---|---|
| SVM | 72.88 | 74.00 | 73.00 | 74.00 |
| MLP | 77.97 | 61.00 | 78.00 | 68.00 |
| KNN | 79.66 | 84.00 | 80.00 | 72.00 |
| **Proposed** | **93.33** | **92.95** | **93.33** | **95.71** |

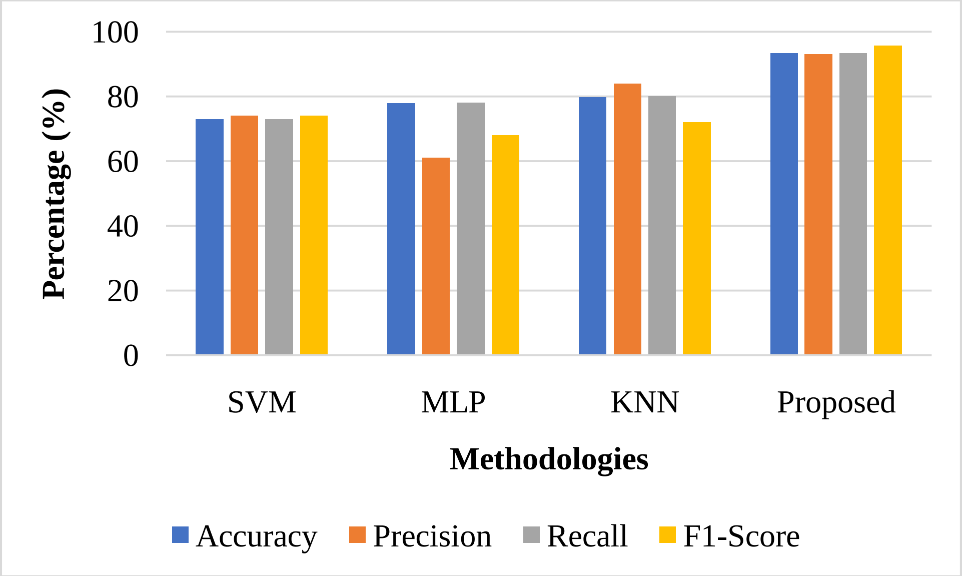

Figure 3 : Results obtained for the proposed PCA-MiniSOM

The results for the proposed method obtains MAE values for SVM, MLP and KNN as 0.27118, 0.22034, and 0.20339, whereas the proposed PCA-MiniSOM has obtained MAE as 0.06667. The existing models obtained MSE value as 0.27118, 0.22034, and 0.20339, whereas the proposed PCA-MiniSOM obtained MSE value lower of 0.06667 error values when compared with the existing models. The existing models obtained RMSE as 0.52075, 0.46940, and 0.45099, whereas the proposed model obtained lower error values of 0.25820 which was having lesser error values when compared with the existing models.

Table 2 : Evaluation of the proposed PCA-MiniSOM in terms of Error Values

| Methods | MAE | MSE | RMSE |
|---|---|---|---|
| SVM | 0.27118 | 0.27118 | 0.52075 |
| MLP | 0.22034 | 0.22034 | 0.46940 |
| KNN | 0.20339 | 0.20339 | 0.45099 |
| **Proposed** | **0.06667** | **0.06667** | **0.25820** |

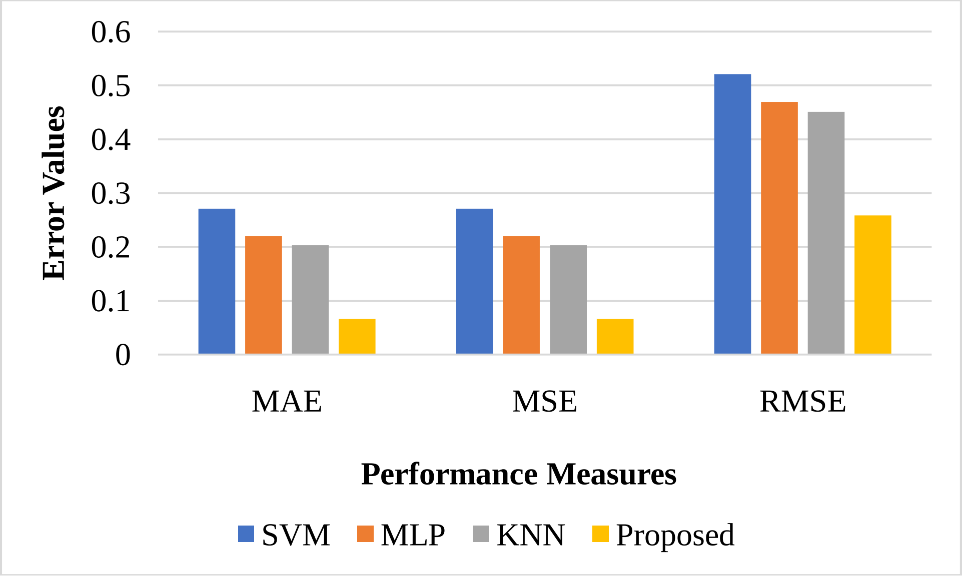

Figure 4 : Results evaluation for the proposed PCA with MiniSOM in terms of error values

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## Comparative Analysis

The proposed PCA-MiniSOM is compared with the exisitng methods that are shown in the table 3. The existing ANN and Muti Kernel K-Means Clustering Algorithm included incomplete information due to which the performance of disease detection decreased. Similarly, The GA and RFE were in charge of parameter tuning, which could be more automatic. In the sense of precision medicine, the incorporation of multi-omics data should be done as part of a full work flow to ensure that the data is analysed properly. Similarly, the PCA + Deep Learning was utilized for classification problems showed imbalanced data for fraud detection and recommendation. Whereas the proposed PCA with MiniSOM performed better parameter tuning ensured the optimal data Analysis and overcame the problem of imbalance data for disease detection. The Existing ANN-KKMC obtained accuracy of 84.61%, GA-RFE obtained accuracy of 86.6% and the PCA with Deep Learning obtained accuracy of 86.8%. The proposed PCA with MiniSOM showed better accuracy values of 93.33 % better when compared with the existing methodologies. The graphical representation for the proposed PCA-MiniSOM with the existing method is shown in the figure 5.

Table 3: Comparison of the performances of the proposed PCA-MiniSOM with respect to exisitng models

| **Author** | **Methods** | **Accuracy (%)** |
|---|---|---|
| Pooja Rani [2] | Genetic Algorithm (GA) and Recursive Feature Elimination | 86.6 |
| Afzal Hussain Shahid [5] | PCA + Deep Learning | 86.8 |
| A.Nitiya [11] | Artificial neural network and Muti Kernel K-Means Clustering Algorithm | 84.61 |
|  | **Proposed PCA based Mini SOM** | **93.33** |

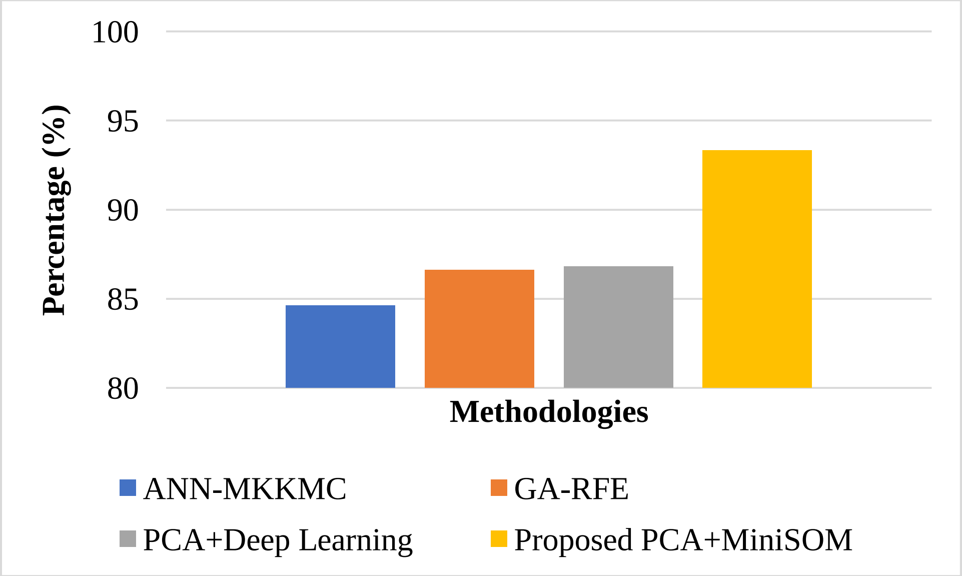

Figure 5: Graphical representation for the proposed and the exisitng methods in terms of Accuracy.

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## Conclusion

The present research developed a new model that monitored the PD prediction based on the supervised and unsupervised learning techniques that was employed for developing a method. The importance of the proposed method research are that the deep learning and the clustering approaches utilized showed improvement in the performances during prediction. The SOM helped to learn the mapped features by using ELM for performing the prediction tasks. The clustering technique includes the data from the PD dataset for the results prediction. The results showed that the superiority aided by the deep learning with respect to the clustering techniques addressed the existing model problems thereby improved the efficiency of the system. The present research work utilized Mini-SOM that included sufficient number of features for the evaluation and secondly the ELM which is supervised learning technique considered the top layers also for parameter evaluation and therefore suggest that it improved the stability of the present research as it showed improvement in the accuracy. However, the feature selection process was required to select best features needed to be addressed in developing the PD diagnosis.

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