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Genetic algorithm and principal components analysis in speech-based parkinson's early diagnosis studies

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Abstract

Parkinson's Disease (PD) is a neurodegenerative disorder that affects predominantly neurons in the brain. The main purpose of this paper is to define a way in detecting the PD in its early stages. This has been achieved through the use of recorded speech, a biomarker in the natural environment in its original state. In this paper, the Mel-Frequency Cepstral Coefficients (MFCC) method is utilized to extract features from the recorded speech. The principal component analysis (PCA) and Genetic algorithm (GA) are then applied for feature extraction/selection. Once the features are selected, multiple classifiers are then applied for classification. Performance metrics such as accuracy, specificity, and sensitivity are measured. The result shows that Support Vector Machine (SVM) along with the GA has shown optimal performance.

Keywords: Parkinson's Disease, Support Vector Machine, Mel Frequency Cepstral Coefficient, Principal Component Analysis, Accuracy, Sensitivity, Specificity, Genetic algorithm.

1. Introduction

Parkinson's disease is a neurological issue that influences motor and non-motor actions in the human body. For the provision of customized patient care, monitoring, and diagnosis using smart gadgets there is a requirement for a framework that works in indigenous habitats just a controlled condition was proposed by Bocklet et al. [3] Gupta B et al. [5], and Gupta K [6] in their paper proposed a very important statistic highlighted in Mumbai, the Parsi Community most affected in

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the world with a PD with a prevalence rate of 328/100000 population. Prosodic features can be seen as speech highlights related to huge units. For example, syllables, words, expressions, and sentences naturalization speech signal is obtained from the pitch, time, and audibility level by Al-Ali et al. [1]. Fundamental frequency (F0), pitch, and power spectrum depict prosodic features in a speech signal. To analyze aperiodic vibrations in the speech signal, acoustic tools are used by Cernak M et al. [4] Speech signal can be utilized as a biomarker for the early introduction of the ailment. Matrices for PD advance incorporate the Unified PD Rating Scale: motor subscale (UPDRS-III) by Qian L et al. [11] and Wicks P et al. [15] UPDRS can then reveal the existence of sever nature gravity of PD symptoms. The programmed discovery of Parkinson's infection from the speech is a fundamental advancement towards the smart technology-aided apparatuses supporting the diagnosis and determination of the sickness Arora et al. [2]. Although others have proposed limited strategies, the results of their implementation in real life circumstances is yet unknown.

Furthermore, the utilization of acoustic conditions in diagnosing PD from speech is not yet a very well-known approach proposed by Vasquez et al. [13]. Among the thought about conditions, foundation commotion creates the most noticeably awful impact, while dynamic pressure or some discourse codecs can even have a negligible positive effect by Correa [13]. PD progression based on its manifestations on the vocal system using UPDRS standardized speech signal characteristics and evaluating the performance of GMM and SVM classifiers to estimate PD severity from UPDRS was investigated by Verma et al. [14]. This study focuses on tele-diagnosis but leaves out the period at which it is critical to identify a disease, especially PD with no known cure, which needs control measures to be taken care of as early as possible.

An insight was done by Wenhai Ji et al. [16] into the advanced stages of PD and classification challenges. Kruger R et al. [9] in their methodologies require strengthening of patients and coordination into treatment choices, by introducing correspondence techniques and choice help in light of new advances to modify the treatment of PD as per patient requests and wellbeing. Vocal impairments are prodromal for PD. They argue that most studies for the detection of PD using acoustic tend to consider universal characteristics. Jeancolas et al. [7] work is based on analyzing speech and speaker recognition by using the MFCC feature extraction method and a GMM classifier. They carried automatic analysis using: vowels, syllables, and sentences. They concluded that their method was inconclusive and better performance can be achieved by a combination of more classical methods to improve classifier efficiency and effectiveness by Jeancolas L et al [7].

In another work by Mirarchi et al. [10] on PD, it was found that PD is highly affected by challenges with respect to vowel pronunciation. Problems in phonation are associated with PD effects and the condition is called Parkinsonian. Dysarthria was highlighted by the vocal analysis. The focus in that research work was placed on biomarker discovery. This was then utilized in different methodologies to streamline building a machine learning arrangement models for the early diagnostic of the PD by Soliman A et al. [12] and Wenhai Ji et al. [16]. The objective was to sort the therapeutic estimations and select the most significant parameters to construct a quicker and more exact model utilizing highlight determination procedures. In that work the clinical measurements were utilized to point out UPDRS, which is a standard measure in PD clinical analysis. The filter method had shortfalls on the provision of comprehensive information on the correlation of data sets, it analyses attributes individually was proposed by Jancovic J et al. [8] and Bocklet T et al. [3].

In section 2 of this paper the proposed methodology for feature extraction is explained and in section 3 the classifiers used have been discussed. Results for various classifiers and comparison of performance metrics are then discussed in section 4.

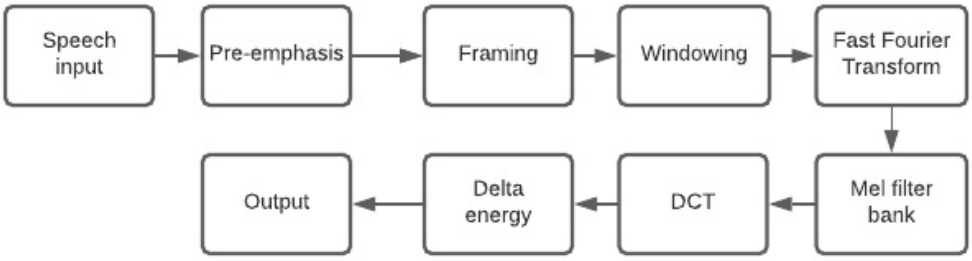

Figure 1: Block diagram of MFCC

2. Proposed Methodology

The methodology of feature extraction in this paper will be based on the Mel frequency cepstral coefficient (MFCC) with successive separations of high and low-frequency components. First, the recorded speech is pre-processed and the features are extracted and normalized. After extracting the features, certain features are then selected using methods like PCA and GA. Once the features are selected they will be given to the classifiers which will identify whether the sample is normal or abnormal.

2.1. MFCC Feature Extraction

MFCCs are essential parameters of voice. Feature extraction involves gathering of MFCCs and organizing their components into vectors of comparative measurements shown in figure 1. The predicted vectors are extracted from each frame of the sample voice signal under test. In this context, the subjects recite sustained vowels "a", "o", and "u" as part of their medical examinations. The features that are analysed are prosodic features F0, jitter, shimmer and PPE, formants, etc [1]. The MFCCs are figured over Hamming window frames with 30ms size and 10ms overlap speech signal. Equation (2.1) represents the computation of the Hamming window.

$$Hamm(X) = [0.54 - 0.460^{*} \cos(\frac{\cos 2\pi(x-1)}{(X-1)})] \tag{2.1}$$

where the number of samples in one frame ($X = 160$) and x is from 1 to X. FFT process represents the time domain into the frequency domain. By applying FFT the output is a spectrum or periodogram .The MFCC features are obtainable through the use of 32 channel Mel filter banks, continued by transformation to the Cepstral domain with 13 coefficients. Then the Cepstral coefficients are affixed to the MFCC features. Feature warping is conducted on obtained MFCC features. MFCC computation is shown in Equation (2.2).

$$\sum_{b=1}^{C} \log(Mb) \cos[2\pi/C(b+1/2)p] = mfcc \tag{2.2}$$

where 'p' is the coefficients and 'C' is the channel number. The positive value range only used for the calculations.

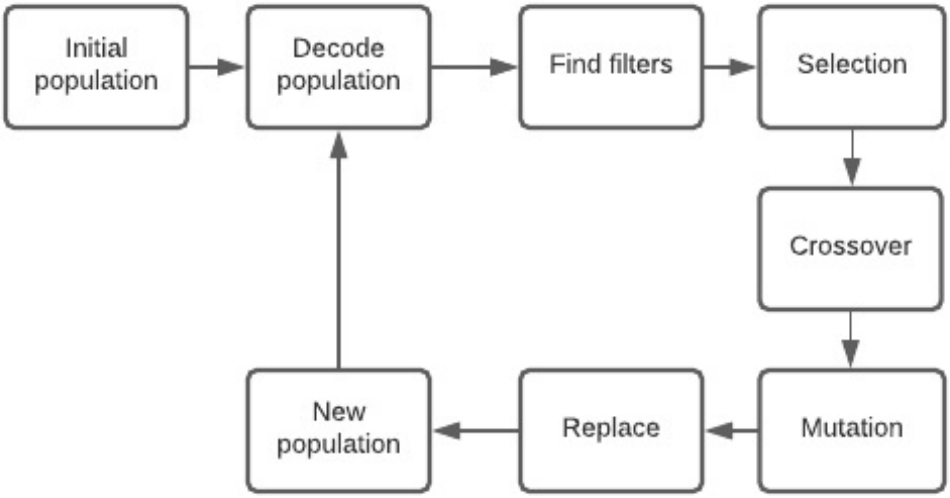

Figure 2: Block diagram of a genetic algorithm

2.2. Principal Component Analysis

Principal Component Analysis is a dimensionality reduction technique that is frequently used to diminish the dimensionality of enormous informational indexes. The technique involves exchanging a huge arrangement of factors into a smaller one which contains the majority of the data in the larger set. Diminishing the number of factors of an informational index normally comes to the detriment of exactness; however, the trap in dimensionality decrease is to exchange a little precision for straightforwardness. Having a simpler informational collection can result in an easier investigation and quicker computation time for the machine learning algorithms as there won't be any superfluous factors to process in the data. In this work, PCA=10 is implemented and also tested for different components. There is no increase in accuracy when the components are decreased.

2.3. Genetic algorithm

A genetic algorithm is a feature reduction technique that is used to select the most powerful features ramous hunt spaces productively, and thus has less opportunity to get local optimal solution than other algorithms.

The basic block diagram is shown in figure 2. The initial population of GA is created haphazardly utilizing $200 \times n$ chromosomes; where n is the number of features that should be chosen for acceptable precision. Then a fitness value for each chromosome is obtained. The chromosomes are then rearranged according to their fitness values. At that point Crossover and Mutation is applied. A new population is then developed. At last, the chromosome with the most noteworthy wellness is picked and the number of features in that chromosome assessed as chosen features.

3. Classifiers

Multiple classifiers such as Linear Regression (LR), Linear Discriminant Analysis (LDA), k-Nearest Neighbourhood (KNN), Decision Tree (DT), Neural Network (NN), Naive Bayes (NB), Gradient Boost (GB), Random forest (RF), Support Vector Machine (SVM) and their performance parameters (sensitivity, specificity, accuracy, Mathew's correlation coefficient) are gathered and compared.

3.1. Logistic Regression (LR)

Uses the sigmoid logistic equation with weights (coefficient values) and biases (constants) to model the probability of a certain class for binary classification. An output of 1 represents one class, and an output of 0 represents the other. Training the model will learn the optimal weights and biases.

3.2. Linear Discriminant Analysis (LDA)

Assumes that the data is Gaussian and each feature has the same variance. LDA estimates the mean and variance for each class from the training data and then uses properties of statistics (Bayes theorem, Gaussian distribution, etc) to compute the probability of a particular instance belonging to a given class. The class with the largest probability is the prediction.

3.3. k-Nearest Neighbours (KNN)

Makes predictions about the validation set using the entire training set. KNN makes an expectation about another example by looking through the entire set to discover the k "nearest" cases. "Closeness" is resolved to utilize a nearness estimation (Euclidean) overall features. The class that the majority of the k closest instances belong to is the class that the model predicts the new instance to be.

3.4. Decision Tree (DT)

Represented by a binary tree, where each root node represents an input variable and a split point, and each leaf node contains an output used to make a prediction.

3.5. Neural Network (NN)

Models the way the human brain makes decisions. Each neuron takes in 1+ inputs and then uses an activation function to process the input with weights and biases to produce an output. Neurons can be arranged into layers, and multiple layers can form a network to model complex decisions. Training the network involves using the training instances to optimize the weights and biases.

3.6. Naive Bayes (NB)

Simplifies the calculation of probabilities by assuming that all features are independent of one another (a strong but effective assumption). Bayes theorem is often used to calculate the probabilities that the instance to be predicted is in each class, and then finds the class with the highest probability.

3.7. Gradient Boost (GB)

Generally used when seeking a model with a very high predictive performance. Used to reduce bias and variance ("error") by combining multiple "weak learners" (not very good models) to create a "strong learner" (high-performance model). Involves 3 elements: a loss function (error function) to be optimized, a weak learner (decision tree) to make predictions, and an additive model to add trees to minimize the loss function. Gradient descent is used to minimize error after adding each tree (one by one).

3.8. Support Vector Machine (SVM)

SVM tends to be utilized for non-linear data by using a kernel function to first indirectly map the non-linear data into a linear feature space. The Support-vector machine constructs a set of hyperplanes in an infinite-dimensional space, which can be used for classification. Naturally, a decent division is accomplished by the hyperplane that has the biggest separation to the closest preparing information purpose of any class (purported utilitarian edge), since as a rule the bigger the edge, the lower the speculation blunder of the classifier.

3.9. Performance Metrics

The goal is to implement a machine learning model to diagnose Parkinson's disease given various features of a patient's speech with at least 90% accuracy and/or a Matthews Correlation Coefficient of at least 0.9. Performance parameters are calculated as shown in the equations below.

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN} \tag{3.1}$$

$$Sensitivity = \frac{TP}{TP + FN} \tag{3.2}$$

$$Specifity = \frac{TN}{TN + FP} \tag{3.3}$$

$$MCC = \frac{TP.TN - FN.FP}{\sqrt{((FN + TP)(FP + TN)(FP + TP)(FN + TN))}} \tag{3.4}$$

Accuracy represents the success of the classifier in distinguishing between normal and Parkinson patients. Detecting PD patients accurately represents the sensitivity and accuracy whereas detecting normal patients represents specificity. The quality of binary classification in machine learning represents Mathew's correlation coefficient (MCC). The MCC is in essence a correlation coefficient between the observed and predicted binary classifications; it returns a value between -1 and $+1$. A coefficient of $+1$ represents a perfect prediction, 0 is basically a random prediction and -1 indicates disagreement between prediction and observation.

3.10. Dataset

The dataset was created by Max Little of the University of Oxford, in collaboration with the National Centre for Voice and Speech, Denver, Colorado, who recorded the speeches. The data consists of 195 sustained vowel phonations from 31 male and female subjects. 23 of the subjects were diagnosed with PD. The data set mentioned above has 22 extracted features using the MFCC algorithm. As a part of feature selection to find the most powerful features, the dataset is fed to a genetic algorithm for feature selection and out of those 22 features 10 powerful features were selected. A description of those extracted and selected features is summarized in table 1. Among the extracted features 10 features were selected and they are MDVP: Flo (Hz), Jitter(%), Jitter (Abs), MDVP: RAP, MDVP: PPQ, Shimmer, Shimmer (dB), HNR, D 2, and DFA. The convergence and fitness curve for validation size of 70% is shown in figures 3 and 4.

4. Results and Discussion

The descriptions for all the features are listed in Table 1. Table 2 lists the performance metrics such as accuracy, sensitivity, and specificity. Using the MFCC feature extraction technique and without any feature selection technique for the various training and test data such as 80-20, 70-30, 60-40, and 50-50, the performance metrics were measured. SVM performed well under various test data when compared to other classifiers. For validation size of 0.2 SVM, LDA, KNN performed well, for 0.3 SVM, LDA, KNN performed well, for validation size of 0.4 SVM, GB, LDA, KNN performed well, for validation size of 0.5 SVM, LDA, GB performed well. Overall, SVM has shown the best performance when compared to all other classifiers and that was also evident in figure 5.
Table 3 also lists the performance metrics using the MFCC feature extraction technique and Genetic algorithm feature selection technique for the various training and test data as mentioned earlier.

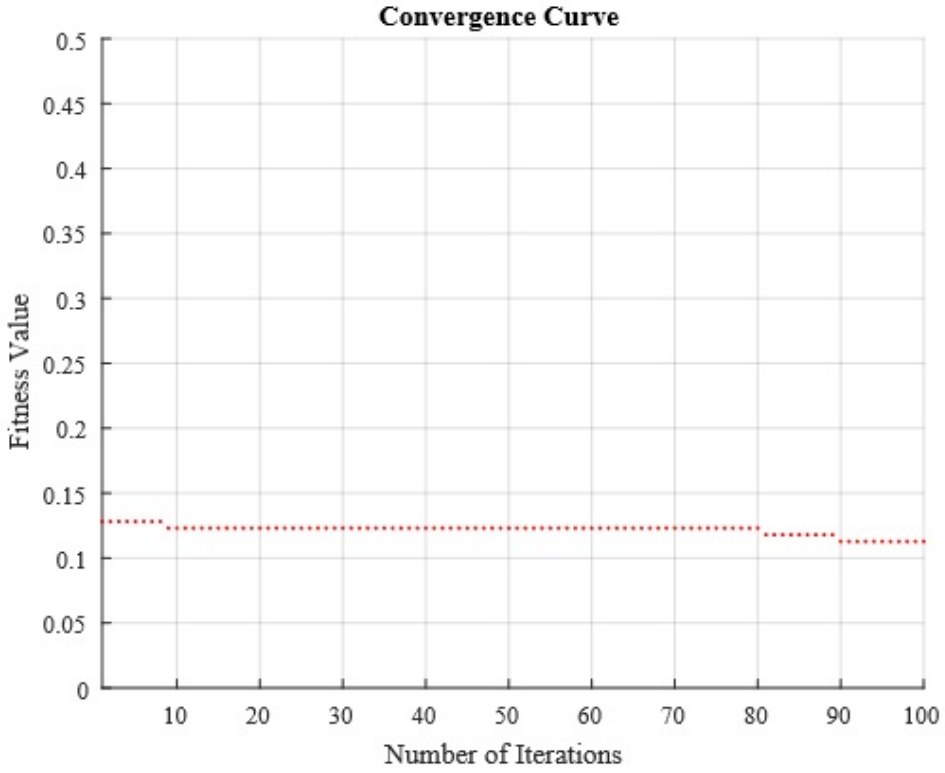

Figure 3: convergence curve for validation size of 70-30

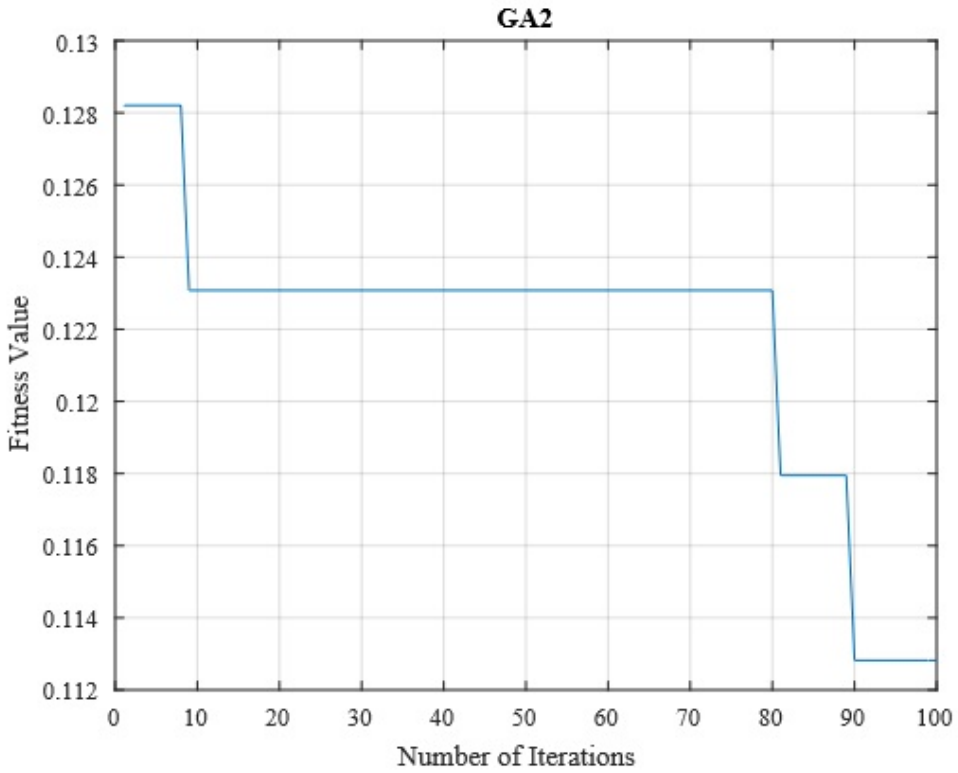

Figure 4: Fitness curve for validation size of 70-30

Table 1: Extracted and selected features [?]

Features	Description
MDVP: Fo (Hz)	The average vocal fundamental frequency
MDVP: Fhi (Hz	The maximum vocal fundamental frequency
MDVP: Flo (Hz)	The minimum vocal fundamental frequency
Jitter (%)	The measure of variation in fundamental frequency
Jitter (Abs)	A measure of variation in fundamental frequency
MDVP: RAP	A measure of variation in fundamental frequency
MDVP: PPQ	The measure of variation in fundamental frequency
Jitter: DDP	A measure of variation in fundamental frequency
Shimmer	The measure of variation in amplitude
Shimmer (dB)	The measure of variation in amplitude
Shimmer: APQ3	The measure of variation in amplitude
Shimmer: APQ5	The measure of variation in amplitude
MDVP: APQ	The measure of variation in amplitude
Shimmer: DDA	A measure of variation in amplitude
NHR	The measure of the ratio of noise to tonal components in the voice
HNR	The measure of the ratio of noise to tonal components in the voice
RPDE	The nonlinear dynamical complexity measure
D 2	A nonlinear dynamical complexity measure
DFA	The signal fractal scaling exponent
spread 1	The nonlinear measure of fundamental frequency variation
spread 2	The nonlinear measure of fundamental frequency variation
PPE	The nonlinear measure of fundamental frequency variation

Table 2: Performance comparison of various classifiers

Classifier/Training & Test Data		LR	LDA	KNN	DT	NN	NB	GB	SVM
Training and Test Data(80-20)	Accuracy	84.6	92.3	89	76.9	87.12	64.1	84.6	92
	Sensitivity	0.97	0.97	0.94	0.85	0.1	0.65	0.91	0.85
	Specificity	0	0.6	0.6	0.2	0	0.6	0.4	0.62
	MCC	-0.06	0.62	0.54	-0.12	0	0.16	0.31	0.68
Training and Test Data(70-30)	Accuracy	76.12	84.3	86.1	79.6	86.2	72.8	83.05	90
	Sensitivity	0.88	0.94	0.94	0.84	1	0.78	0.82	0.96
	Specificity	0	0.25	0.37	0.5	0	0.37	0.5	0.56
	MCC	-0.13	0.24	0.36	0.27	0	0.13	0.35	0.51
Training and Test Data(60-40)	Accuracy	80.1	84	84	85.8	87.1	70.5	84.18	88
	Sensitivity	0.89	0.88	0.92	0.91	1	0.75	0.89	0.94
	Specificity	0.2	0.6	0.3	0.5	1	0.4	0.5	0.58
	MCC	0.101	0.42	0.25	0.27	0	0.11	0.37	4.46
Training and Test Data(50-50)	Accuracy	79.3	82.56	82.56	81.4	81.1	73.1	83	89
	Sensitivity	0.9	0.89	0.91	0.88	0.91	0.77	0.89	0.95
	Specificity	0.07	0.38	0.23	0.38	0.15	0.46	0.38	0.53
	MCC	-0.02	0.27	0.17	0.19	0.4	0.19	0.29	0.39

Table 3: Performance of various classifiers implementing Genetic algorithm

Classifier/Training & Test Data		LR	LDA	KNN	DT	NN	NB	GB	SVM
Training and Test Data(80-20)	Accuracy %	77.12	89.7	85	77.1	77.12	59.9	83.1	92
	Sensitivity	0.88	0.97	0.91	0.88	0.88	0.59	0.88	1
	Specificity	0	0.4	0.4	0	0	0.6	0.4	0.5
	MCC	-0.12	0.46	0.31	0.17	0	0.12	0.31	0.68
Training and Test Data(70-30)	Accuracy %	77.12	88.23	83.1	75.12	87.2	63.33	84.7	88
	Sensitivity	0.84	0.98	0.88	0.83	1	0.66	0.88	0.96
	Specificity	0	0.25	0.5	0.37	0	0.37	0.5	0.44
	MCC	0.13	0.35	0.35	0.15	0	0.03	0.35	0.48
Training and Test Data(60-40)	Accuracy %	80.1	88.81	84	80.1	88.81	66.3	84.18	87
	Sensitivity	0.82	0.94	0.88	0.86	1	0.69	0.89	0.95
	Specificity	0.1	0.4	0.5	0.3	0	0.4	0.4	0.33
	MCC	-0.03	0.38	0.34	0.22	0	0.06	0.29	0.44
Training and Test Data(50-50)	Accuracy %	80.16	88.56	86.1	84.23	87.1	70.1	84	85
	Sensitivity	0.9	0.96	0.91	0.9	1	0.73	0.9	0.94
	Specificity	0.07	0.3	0.46	0.38	0	0.46	0.83	0.33
	MCC	-0.02	0.35	0.38	0.29	0	0.15	0.29	0.32

Table 4: Performance metrics for various classifiers with PCA

Classifier/Traing & Test Data		LR	LDA	KNN	DT	NN	NB	GB	SVM
Training and Test Data(80-20)	Accuracy %	76.9	84.61	82.05	82.05	82.05	58.97	89.74	85
	Sensitivity	0.93	1	0.93	0.93	1	0.53	1	1
	Specificity	0	0.14	0.28	0.28	0	0.85	0.42	0
	MCC	-0.1	0.35	0.29	0.29	0	0.29	0.61	0.1
Training and Test Data(70-30)	Accuracy %	79.6	84.07	83.05	86.4	83.05	59.3	84.74	90
	Sensitivity	0.95	0.98	0.93	0.93	1	0.53	0.93	1
	Specificity	0	0.2	0.3	0.5	0	0.9	0.4	0
	MCC	-0.08	0.3	0.3	0.49	0	0.32	0.39	0.1
Training and Test Data(60-40)	Accuracy %	82.05	84.6	78.02	75.64	83.3	60.25	78.2	85
	Sensitivity	0.96	0.96	0.89	0.84	1	0.55	0.97	1
	Specificity	0.07	0.23	0.23	0.3	0	0.84	0.15	0
	MCC	0.09	0.3	0.14	0.15	0	0.3	0.07	0.1
Training and Test Data(50-50)	Accuracy %	83.5	85.5	80.4	74.2	81.4	56.7	79.3	90
	Sensitivity	0.98	0.95	0.92	0.82	0.97	0.49	0.92	1
	Specificity	0.06	0.38	0.18	0.31	0	0.93	0.12	0
	MCC	0.13	0.4	0.14	0.13	-0.06	0.32	0.07	0.1

Table 5: Performance Metrics for SVM Classifier using Genetic Algorithm

Parametric measures	Training and Test data (80-20)	Training and Test data (70-30)	Training and Test data (60-40)	Training and Test data (50-50)
Accuracy (%)	**92.00**	88.00	87.00	85.00
Sensitivity	**1.00**	0.96	0.95	0.94
Specificity	**0.50**	0.44	0.42	0.33

Table 6: Performance Metrics for SVM Classifier using PCA

Parametric measures	Training and Test data (80-20)	Training and Test data (70-30)	Training and Test data (60-40)	Training and Test data (50-50)
Accuracy (%)	85.00	85.00	**90.00**	**90.00**
Sensitivity	1.00	1.00	**1.00**	**1.00**
Specificity	0.00	0.00	**0.00**	**0.00**

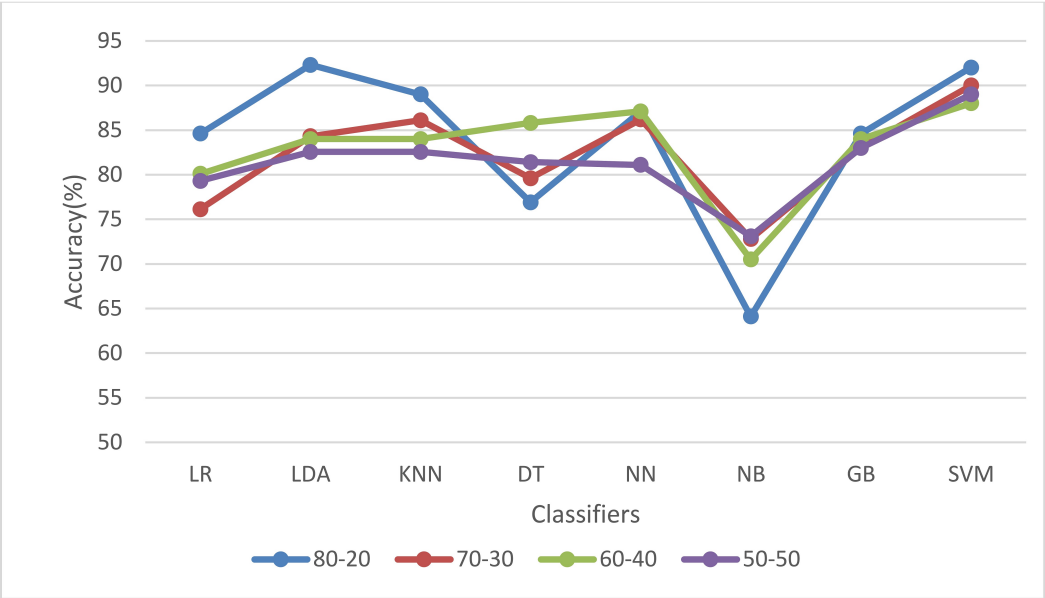

Figure 5: Comparison of accuracy for multiple classifiers for various validation sizes without feature selection

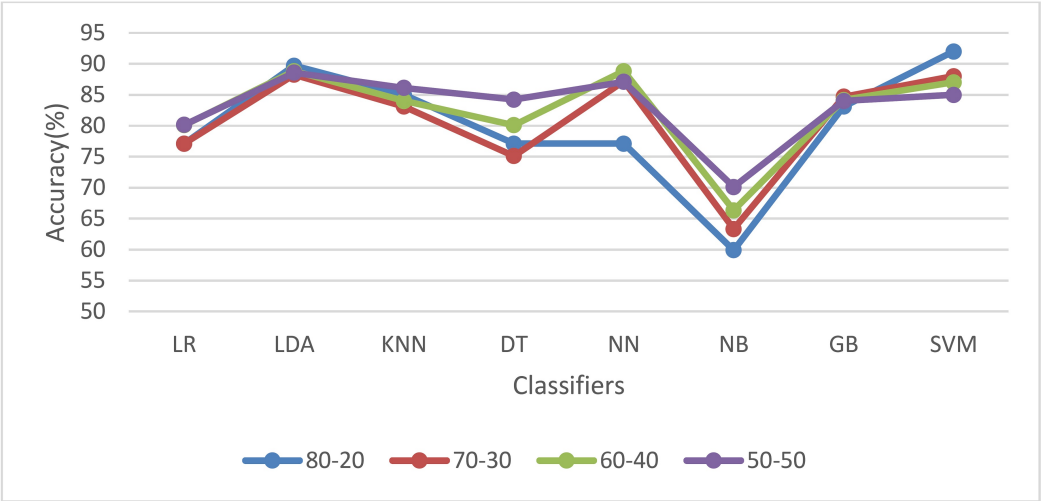

Figure 6: Comparison of accuracy for multiple classifiers for various validation sizes with genetic algorithm

SVM performed well under various test data when compared to other classifiers. LDA and KNN was also found to provide good results. For validation size of 0.2 SVM,LDA,KNN performed well, for 0.3 SVM,LDA,KNN,GB performed well, for validation size of 0.4 SVM,GB,LDA,KNN performed well, for validation size of 0.5 SVM,LDA,KNN performed well and is depicted in figure 6.
Table 4 lists the performance metrics when MFCC feature extraction technique is used along with the PCA feature selection technique for various training and test data such as 80-20, 70-30, 60-40, 50-50,. For validation size of 0.2 LDA, KNN performed well, for 0.3 GB, LDA, KNN performed well, for validation size of 0.4 LDA, LR performed well, for validation size of 0.5 LDA, LR, KNN performed well.
Judging from the above results, it is evident that the performance metrics have shown better results when appropriate features were selected.
Table 5 shows the performance metrics for the SVM classifier using the Genetic algorithm. For validation size of 0.2, the classifier has achieved 92% accuracy along with 100% Sensitivity and 50% specificity. This is relatively the best result when compared with all other validations.
Table 6 shows the performance metrics for the SVM classifier using Principal Component Analysis. For validation size of 0.4 and 0.5, the classifier has achieved 90% accuracy along with 100% Sensitivity and 0% specificity.

5. Conclusion

The future is headed towards real-time as well as smart diagnosis and monitoring of pathological and non-pathological clinical features for PD patients. When implementing Principal component analysis, LDA, SVM, KNN, and GB performed well for the fusion of the MFCC feature extraction technique for a validation size of 0.2. When the validation size is increases to 0.3, LDA, KNN, GB, and SVM showed better accuracy of around 86%, 84%, 85%, and 90% respectively. LDA, LR, and SVM also performed well having an accuracy of around $80-87\%$ for 50-50 validation data. Overall, LDA and SVM performed well for the fusion of MFCC feature extraction for various validation sizes. When implementing Genetic algorithm LDA, SVM, KNN performed well for the fusion of the MFCC feature extraction technique for a validation size of 0.2. For validation size of 0.3, LDA, KNN, GB, and SVM showed better accuracy of around 88%, 83%, 84%, and 88%. LDA, KNN, GB, and SVM performed well having an accuracy of around $84-88\%$, for 50-50 validation data. Overall, SVM

performed well for the fusion of MFCC feature extraction, and especially for 0.2 validation size the sensitivity was 100% and the accuracy was 92%. When comparing all the feature selection algorithms and various classifiers Genetic algorithm along with SVM classifier have yielded the best results.

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