Voice Biomarkers for Parkinson's Disease Prediction with Enhanced Feature Reduction Methods in Machine Learning Models

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Abstract: As a chronic and life-threatening condition, Parkinson's disease (PD) causes patients to become stiff and lethargic and have unsteady voices. There is a claim that existing PD detection approaches are useless because to their high latency and poor accuracy. To boost the accuracy of PD detection, speech recordings were employed as biomarkers in combination with the synthetic minority oversampling method (SMOTE). Three machine learning (ML) models namely support vector machine (SVM), K-nearest neighbors (KNN), and random forest (RF) were employed to calculate the prediction accuracy. By implementing an unsupervised dimensional reduction strategy, the produced model reduces unnecessary data and speeds up training and testing. Model performance is evaluated by three factors, including accuracy, F1 score, and area under the curve (AUC) values. Experimental findings revealed that the RF model outperforms other models with 97.4% of classification accuracy. This sort of study seeks to analyze patient speech recordings to estimate the illness severity.

Keywords: Parkinson's disease, machine learning, SMOTE, accuracy, AUC

Introduction

Over 1% of persons over 50 worldwide suffer from Parkinson's disease (PD), a neurodegenerative condition (Bloem et al., 2021). As the world's population has grown older, this issue has become increasingly common in recent years. Tremors, bradykinesia, stiffness, and other motor symptoms are caused by Parkinson's disease (PD), along with cognitive problems (Hayes, 2019; Tolosa et al., 2021). 12.9 million individuals are predicted to have Parkinson's disease (PD) in 2040, about twice as many as in 2015 (Feigin et al., 2021). It is regrettable that 25% of PD patients are misdiagnosed and mistreated due to the lack of an accurate diagnostic test (Chia et al., 2020; Elsworth, 2020).

Early diagnosis and treatment may lower death rates and enhance quality of life. It is challenging to identify Parkinson's disease (PD) early and accurately due to a lack of resources and expertise (Weintraub et al., 2022). Even though Parkinson's disease is incurable, early therapy may lessen its symptoms and make them more inexpensive. Conventional methods such as positron emission tomography (PET) (Weber, 2020), magnetic resonance imaging (MRI) (Hemond & Bakshi, 2018), and dopamine transporter (DAT) (Bröm & Bröm, 2021) are available to identify Parkinson's disease (PD). These methods do have some accuracy issues, despite their notable advancements in PD identification and prevention. The primary drawbacks of imaging scans are their high cost and preparation time. Because machine learning (ML) may provide accurate results using new data taxonomies and algorithms, it has attracted a lot of interest in recent years (Esteva et al., 2019; Jayatilake & Ganegoda, 2021). Scientists used machine learning (ML) approaches to effectively forecast illness because of its significant influence on enhanced disease diagnostics. PET, MRI, and DAT scanned pictures may be used to forecast diseases using machine learning algorithms (Ohana et al., 2018; De Wachter et al., 2020). Classification algorithms cannot provide trustworthy models with a huge dataset. These datasets are incorrectly classified by the classifiers due to several duplicate or unnecessary characteristics. The categorization method tends to favor the majority class since many big datasets contain an unequal distribution of classes. By examining hand drawing and vocalization features in the existing datasets, Parkinson's disease (PD) may be identified (Arora et al., 2015; Papadopoulos et al., 2019). Voice issues are often experienced by PD patients in the beginning of the illness. Using several feature selection techniques and the voice biomarkers dataset, a supervised support vector machine (SVM) model was

developed with an accuracy of 97.57% (Aich et al., 2019). Al-Fatlawi et al. (2016) claimed a 94% testing accuracy for a deep belief network-based system designed for effective Parkinson's framework to categorize PD patients and healthy controls, and found that regression and SVM models yielded the best accuracy of 70% (Ali et al., 2019). Another research predicted the ideal deep brain stimulation settings for Parkinson's disease (PD) with 88% accuracy using functional MRI and machine learning. According to the authors, the model may be used in previously unexplored datasets to predict PD patients with a priori clinically optimum stimulation settings and those who have never undergone stimulation (Boutet et al., 2021). The training dataset is made easier to visualize with the use of dimensionality reduction methods. Principal component analysis (PCA), a dimensionality reduction approach, was used to condense and remove unnecessary features (Jolliffe & Cadima, 2016). 95% accuracy was observed by a PD diagnosis system based on PCA and ML algorithms employing voice characteristics (Rao et al., 2022). Additionally, the class distribution was balanced and the sample range was expanded by using the synthetic minority oversampling method (SMOTE) resampling (Fernández et al., 2018). Using SMOTE techniques and cascaded deep learning frameworks, PD was detected with 99% accuracy (Chintalapudi et al., 2022). According to reports, ML-based PD diagnosis had good classification rates; however, the literature either employed a large number of features, which increased computation time, or the extraction of the features was challenging even with a small number of features. Consequently, indirect calculation time is likewise high. Studies on the use of PCA and SMOTE feature selection methods are few. As a result, we combined the two methods of PD diagnosis utilizing machine learning algorithms and speech biomarkers. Using patient voice recordings, a speech processing approach was used to assess and estimate the persistence of Parkinson's disease. Tiny dimensions in the data boost the effectiveness of machine learning models since they are easier to calculate and visualize. The model is made more accurate by eliminating unnecessary data and decreasing the number of variables. Following data preparation, three distinct machine learning classifiers—k-nearest neighbors (KNN), SVM, and random forest (RF) disease detection. Another research suggested utilizing a multimodel approach to evaluate speech samples linked to Parkinson's disease.

algorithms—are used to train the dataset. The particular issue and the properties of the data you have determine the machine learning model to use. SVM is a supervised learning technique for regression analysis and classification. It classifies the data according to which side of the hyperplane it falls on after identifying the hyperplane that optimizes the margin between the two classes. When there are fewer characteristics than samples, SVM may work well. Furthermore, power is clearly divided among the classes. RF is an ensemble learning technique that builds a more reliable and accurate model by combining many decision trees. The final prediction is produced by integrating the predictions of many decision trees that are created by randomly choosing subsets of attributes and data. When working with high-dimensional data and datasets that include a lot of noise or missing data, RF might be useful. KNN is a nonparametric technique for regression analysis and classification. Finding the KNN for the current data point is how it works. It forecasts using the weighted average of those neighbors or the majority vote. When the link between the characteristics and the target variable cannot be clearly described by a functional form, KNN may be useful. Furthermore, the data is grouped together in certain areas of the feature space. To choose the model that best suits your needs, it's always a good idea to test a few different models and evaluate their performance.Three accepted models were evaluated for accuracy, precision, recall, false-positive rate, and F1 score. In this study, we generate the differences in ML model performance with and without feature reduction strategies by extrapolating the potential of data resampling techniques in voice recordings during Parkinson's disease diagnosis.

1. **Methods**

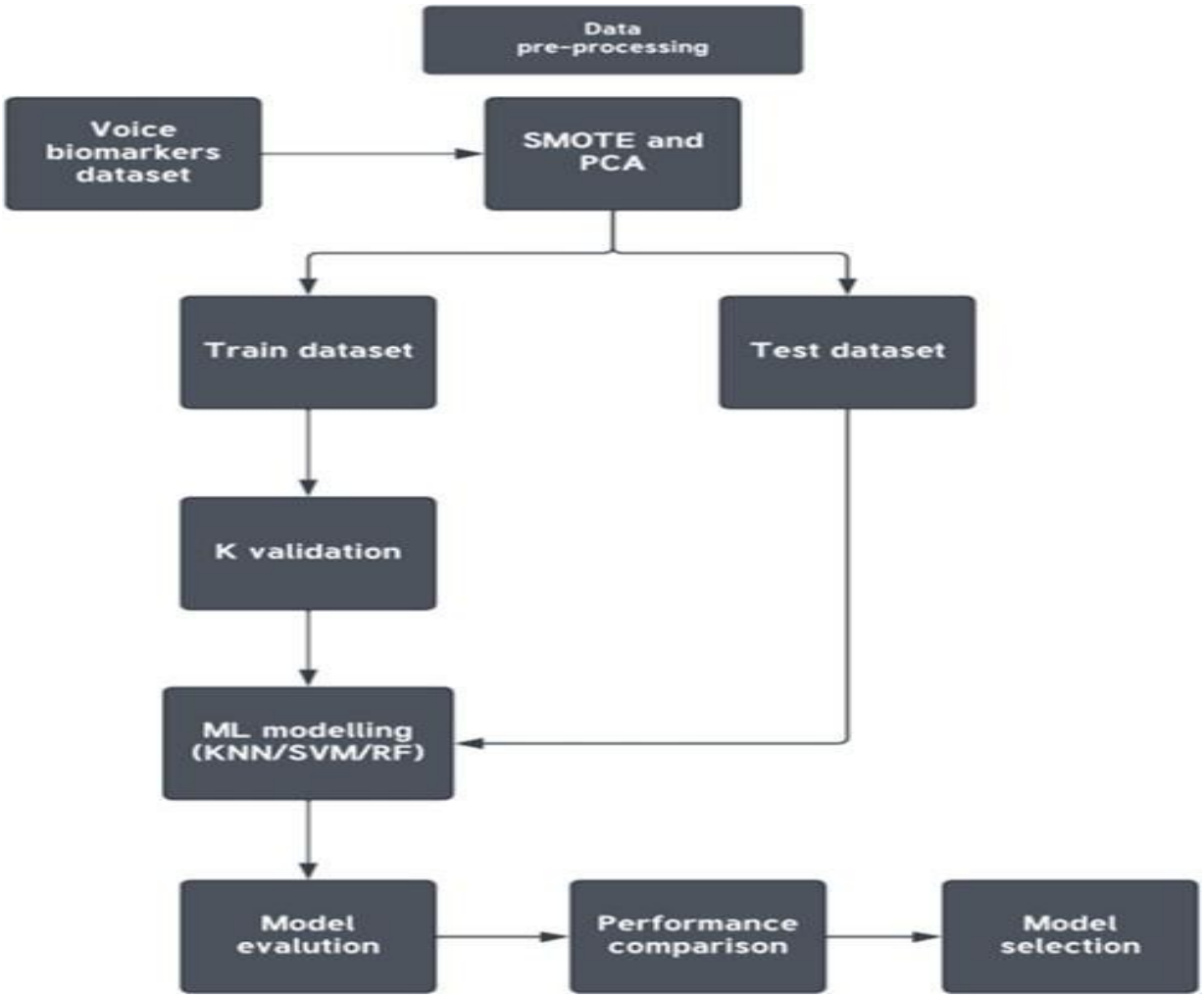
The experimental framework for PD classification using feature reduction methods in conjunction with machine learning modeling is shown in Figure 1. The PD dataset was first taken from the UCI ML repository. PCA and SMOTE techniques were used as data preparation methods after data gathering. The final dataset is separated into training and testing

datasets after data preparation. Metrics such as accuracy, precision, sensitivity, and F1 score are used to calculate the three-model performance with k-fold validation. The ultimate goal of the comparison study is to choose the best model for more accurate PD patient categorization.

1.1. **Dataset**

A dataset from the UCI collection on PD was considered (UCI ML Repository: Parkinsons Data Set n.d.). These data included 195 voice recordings data of 31 PD subjects who were categorized as 23 with PD and the remaining eight are healthy characteristics (HC). There is a special voice measurement applied to each column that pertains to a voice recording of each subject who attended at least

Figure 1 Experimental framework

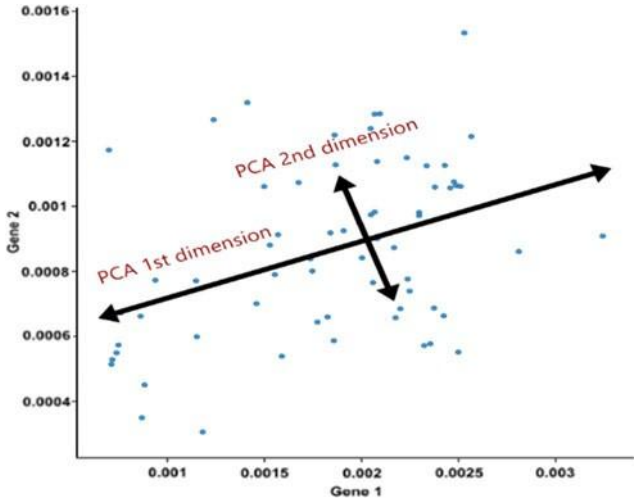


six speaking sessions. Table 1 presents a vocal feature along with the acoustic features that were extracted. Each column represents a special voice measurement based on voice recordings from at least

Table 1 Voice biomarkers

Attribute	Descriptions
name	ASCII subject name and recording number
MDVP	Average vocal fundamental frequency
MDVP	Fhi(Hz) - Maximum vocal fundamental frequency
MDVP	Flo(Hz) - Minimum vocal fundamental frequency

Figure 2
Selection of principal components



Several measures of variation in fundamental frequency

every variable contributes to providing the output uniformly. A variable with a range of 0 to 100 will predominate over a variable with a range of 0 to 1, producing a biased result. Thus, the input variables must be rescaled to be on the same scale such that they are in the same range. Mathematically, it was written as:

$$Z = \frac{\text{value} - \text{mean}}{\text{standard deviation}}; \quad (1)$$

NHR,HNR	Two measures of ratio of noise to tonal components in the voice
status	Health status of the subject (one) - Parkinson's, (zero) - healthy
RPDE, D2	Two nonlinear dynamical complexity measures
DFA	Signal fractal scaling exponent
spread1,spread2, PPE	Three nonlinear measures of fundamental frequency variation

six speech sessions. According to biomedical voice measurements, the 31 subjects are classified as healthy or having PD. The status variable was set to healthy (0), and the PD variable to 1. We use this variable as our target or dependent value.

1.2. Feature reduction techniques

1.2.1. Principal component analysis (PCA)

The PCA technique can be used to reduce data and denoise data by preserving the most relevant information while reducing the size of large datasets. By using PCA, we aimed to select the two principal components with the highest variances. The updated variables can be obtained by deleting components with less information. The selection of principal components can be explained in Figure 2. On PCA1, the largest variances are spread out, and on PCA2, they are spread out perpendicular to PCA1 and have the second-highest variances. To put it all together, we examined the absolute values of the eigenvector components corresponding to the k greatest eigenvalues.

PCA is particularly useful for data with high dimensions and highly associated variables and features. Before every variable can contribute to uniform output, it is important to standardize the input variable range. There will be a bias in the results if a variable with a range of 0 to 100 predominates over a variable with a range of 0 to 1. It is therefore necessary to rescale the input variables to keep them on the same scale. The range of continuous input variables must first be standardized to ensure after standardization, all input variables will have the same range.

Correlations are found by computing the covariance matrix. When the covariance is positive, it indicates that the two variables are increasing or decreasing in the same direction, meaning they are correlated. A negative covariance means that the variables are changing in opposite directions. There can be an increase in one variable, while a decrease in the other. To identify the primary components of the input data, we compute the eigenvalues and eigenvectors of the covariance matrix. Information is conveyed by eigenvectors. An eigenvalue is used to express the variance of a principal component. The proportion of information for each primary component can be determined by dividing each eigenvalue by the sum of all eigenvalues.

As a result, we have been able to determine what the differences are between the input datasets. Datasets with highly correlated variables tend to contain more redundant information. An M × M matrix which is symmetric called the 3 × 3 covariance matrix contains covariance values linked to the potential pairs:

$$COV_{Matrix} = \begin{bmatrix} cov(x;x) & cov(x;y) & cov(x;z) \\ cov(y;x) & cov(y;y) & cov(y;z) \\ cov(z;x) & cov(z;y) & cov(z;z) \end{bmatrix} \quad (2)$$

signs play an imperative role here. As part of the data retention process, Eigenvectors were constructed as a matrix consisting of eigenvalues but arranged in decreasing order.

1.2.2. Synthetic minority oversampling technique (SMOTE)

The process of making prediction models for datasets with significant class imbalances is known as imbalanced classification. Although performance in the minority class is frequently the most critical in unbalanced datasets, most ML

approaches ignore it. Based on the binary classification (healthy: 0 and PD: 1), the dataset contains information on

The binary values 0 and 1 correspond to 48 (no PD) and 147 (PD) individual records, respectively. The minority class can be oversampled to handle unbalanced datasets, but this will lead to subpar results. A type of data augmentation approach is to create synthesized examples by synthesizing previous ones. Oversampling is used in the SMOTE algorithm to rebalance the original training set (Blagus & Lusa 2013; Fernández et al., 2018). Rather than simply replicating minority class instances, SMOTE introduces synthetic examples. By interpolating between several minority class instances within a defined neighborhood, this new data is generated. The instructions to execute SMOTE methods presented in algorithm 1 are described as:

Algorithm 1: SMOTE algorithm

1. Input: minority class examples i.e., T; N; k.
   a. Output: synthetic minority class samples i.e., (N/100) *T
   b. Variables: Sample array of minority class
2. *If* N < 100
   a. *then* ensure that T minorities are randomly selected
   b. T= (N/100) *T5
   c. N = 100
3. Endif multiples of 100 are assumed to represent SMOTE
   a. N= (int)N/100
4. *For* i = 1 to T do Create an nn-array with the indices of k nearest neighbors for i
5. POPULATE(N,i,nnarray)
6. End for
7. End Function

1.3. ML modeling

Before model training, the given data is decomposed into an 80:20 2020 2020). There is “n” randomly chosen bushes in a forest with “k” randomly selected bushes. A decision tree

195 sustained vowel phonations.

will be built for each bush, which will generate an output. Using majority voting or averaging, the final output will be used for classification, which enhances prediction accuracy.

1.4. Model validation

We have applied cross-validation (CV) for model validation (Pal & Patel, 2020). The CV is a statistical model that has been used to estimate the model performance and is commonly applied to ML for any problem regarding predictions. This is selected as it is simple to implement and understand and also produces low bias when compared with other models. This is also known as k-fold validation and k represents randomly spilled dataset portions (Pal & Patel, 2020; Vabalas et al., 2019). This work adopted a 10-fold CV technique where the model has initiated with one dataset, further randomly split into 10 portions. Therefore, 90% of the data was used for model training, and 10% was used for testing purposes. Models can be described in terms of the likelihood of error functions for each data point, and discrepancies between expected and actual results can be clarified.

1.5. Performance metrics

Performance metrics can be used to evaluate a model’s ability. It is possible to compare model predictions with known values of dependent features in a dataset by using parameters such as accuracy, precision, recall, and receiver operating characteristic (ROC) curve. The prediction outcomes can be evaluated based on the confusion matrix that is presented in Table 2.

both before and after feature reduction techniques that were presented in Figure 5. It is evident that the RF model outperforms others in terms of accuracy. The highest PD classification accuracy was achieved at 97.4% for the RF model with the feature reduction approach followed by SVM (85.1%) and KNN (80.7%).

Figure 5
Model performance chart

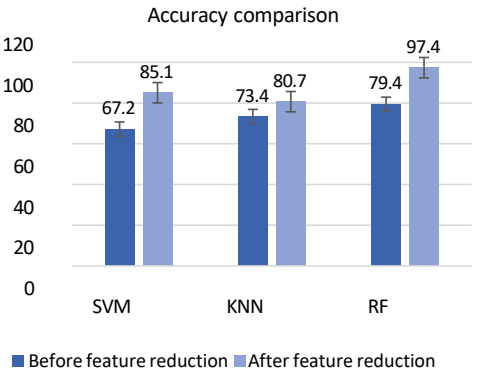
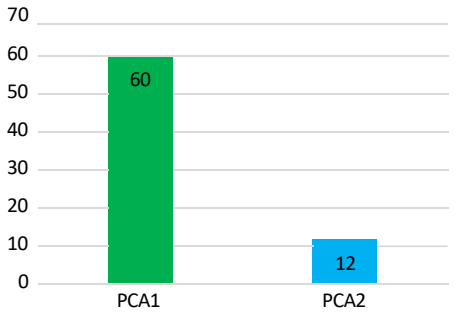


Figure 3
Information percentage in PCA1 and PCA2



Following feature reduction, the dataset was trained using k-fold CV (k = 10), using a different set of data for testing and training each time. For three different models, the confusion matrix for the test dataset can be visualized in Figure 4. My

Due to the distinct decision trees in the RF, the variance of the RF classifier as a whole is reduced. An RF classifier's final decision is an aggregation of the individual tree decisions, which allows it to generalize effectively. Without overfitting, the RF model is more accurate than others. Further, the RF model predicts 100% true positives, while SVM and KNN predict 0.92 and 0.84, respectively. In addition to the recall, F1 score, and area under the curve (AUC), RF also performed superiorly on other metrics. The performance metrics of the three models are presented in Table 3.

Table 3
Performance measurements

Algorithm	Precision	Recall	F1 score	AUC
SVM	0.92	0.88	0.86	0.91
KNN	0.84	0.91	0.92	0.93
RF	1.00	0.96	0.98	0.96

Figure 4
Confusion matrix outcome (A) SVM, (B) KNN, and (C) RF

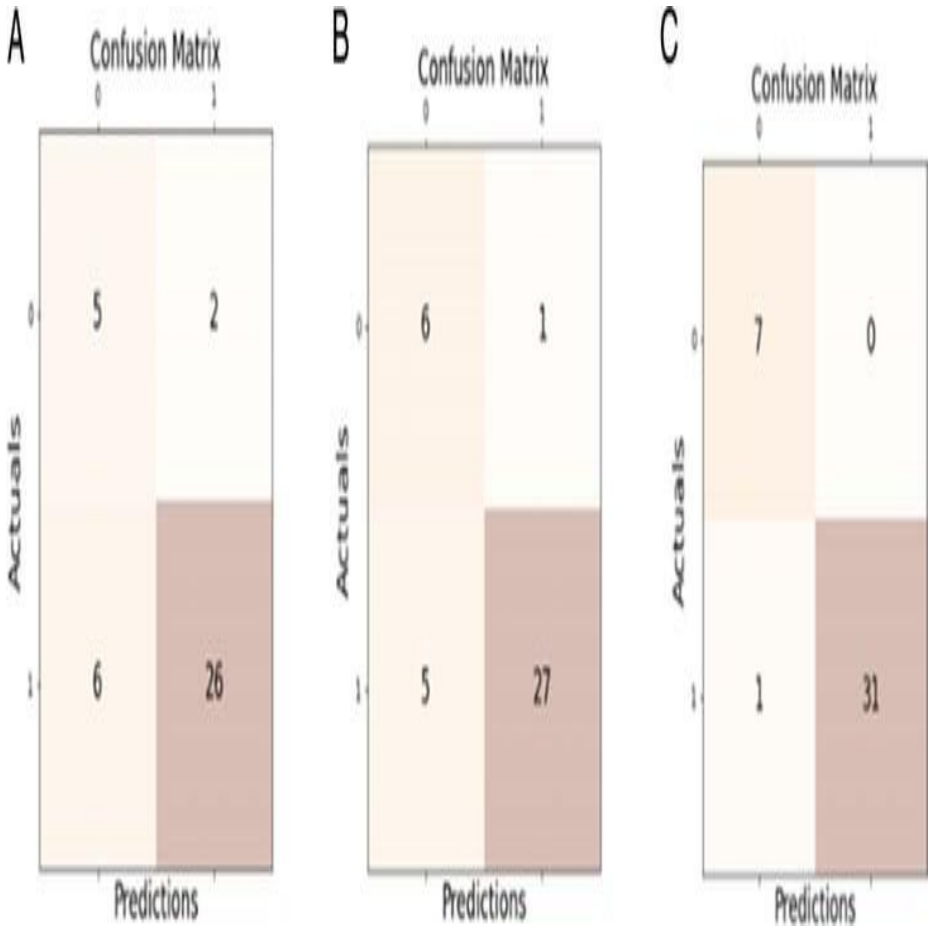
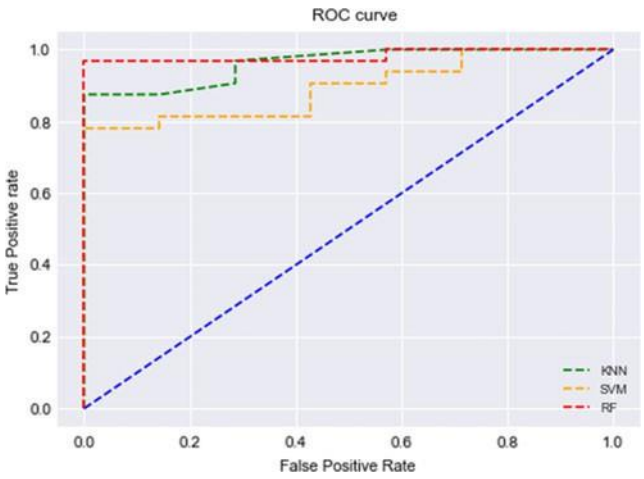


Figure 6
ROC curve outcome



Binary classification is largely based on ROC curves. The ROC curve in Figure 6 shows the RF value approaching near 1 when the ROC curve is visualized.

2. Discussion

People with PD have a dynamic sensory system problem that affects their development. A slight tremor may be the first PD symptom, and diagnosis of this disease should be done at an early condition providing the opportunity for disease treatment and getting adopted with a new lifestyle with positive outcomes. In this work, we proposed a combined approach of PCA and SMOTE. Auditory features have been used to test three supervised ML methods for PD detection. The SVM, KNN, and RF confusion matrices derived from the testing data are used to compare each classification model after feature selection with SMOTE sampling.

A proteomic biomarker, ideally one that accurately represents the disease process, should be available for investigation in diseased tissues, such asthose impacted. There isanobstaclethatprevents causal or disease-modifying medicines for PD from being developed. To achieve the most favorable clinical outcome, each PD case must be diagnosed and treated individually. With Ml techniques, it is possible to identify complex data patterns, automate data analysis, and make inferences and classifications based on individual patient data. This could be useful for precision medicine for PD.

Over the past few years, ML has become increasingly popular for diagnosing PD. It is reported that deep learning models like artificial neural networks help to do PD diagnosis with 94.4% of accuracy (Vabalas et al., 2019). It would be possible to screen large populations of patients for PD using such approaches on an affordable basis. Another study highlighted the gradient-boosting technique for PD diagnosis from voice samples and achieved an AUC of 0.951 (Karabayir et al., 2020). Other experiments showed that boosted decision trees, an ensemble model made from gradient-boostedregression trees, hadthehighest accuracyscoreonthe datawith 91–95%. By filter-based feature detection, it was also determined that spread1, spread2, and PPE are among the strongest nonlinear measures of fundamental frequency variation (Dinesh & He, 2017).

An analysis of the role of cascaded deep learning frameworks in detecting PD with voice biomarkers was explained, and a loss function curve was presented to demonstrate the relevance of good-fitting models for PD identification (Chintalapudi et al., 2022). Our study is in line with the work (Abdullah et al., 2020) where the authors introduced the feature selection method of Least Absolute Shrinkage and Selection Operator (LASSO) with multimodel ML approaches, including RF, SVM, deep neural networks (DNN), and gradient boosting. An accuracy of 96.67% was achieved for binary classification based on prediction over the UCI speech recording dataset. To improve data quality, other researchers have proposed data standardization, multicollinearity diagnosis, and dimensionality reduction techniques (Pramanik & Sarker, 2021). Their model achieved 95.1% of accuracy after they applied KNN, SVM, RF, AdaBoost, and logistic regression.

However, the above-mentioned studies have not sufficiently discussed the quality of true PD classification done by given ML models. Our updated RF model is more comprehensive than the values of previous works, as we can classify 100% of true PD subjects. We also achieved 97.4% classification accuracy with our proposed model with a combination of PCA and SMOTE algorithms. K-fold validation was used to test the model's performance and achieve maximum classification accuracy depending on the AUC parameter. Voice biomarkers are both cheap and easy to obtain compared to MRIs and motion-based diagnosis methods. Based on the findings of these studies, the maximum classification accuracy for PD subjects was achieved by RF with SMOTE oversampling. The models we propose can be implemented in neurological studies by using biomarker datasets.

The application of ML algorithms to PD diagnosis and treatment has the potential to make a significant difference in the future. Our ability to diagnose and manage this disease will become more sophisticated with the growing availability of data and the advancement of algorithms. In the future, by identifying new biomarkers for PD, ML algorithms could help diagnose and track the disease. By analyzing data from wearable devices, an algorithm could identify changes in movement patterns or physiological changes related to the disease.

3. Conclusion

The paper proposed an ML framework for PD detection at its early stages. Three models namely KNN, SVM, and RF were meticulously analyzed for performance and accuracy. In terms of model performance, RF outperforms the rest of the models with 98% of accuracy. This investigation reported an increase in recall value from 0.9 to 0.989 at an early stage.

From speech recordings of healthy and PD patients, this model aims to identify the real positives. With the suggested model, recall increased from 0.95 to 0.989. The availability of a large amount of clinical data can further enhance the accuracy of the proposed model, which can assist future PD researchers. It is straightforward to collect samples using this model, since it is noninvasive. PD prediction by periodic voice recordings reduces the patient's hospitalizations.

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