AI in Neurology: Speech-Based Detection of Parkinson's Disease using Machine Learning Models

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***Abstract*—Parkinson's Disease (PD) is a progressive neurodegenerative disorder that affects motor and speech functions. Early and accurate detection of PD is crucial for timely medical intervention. This study uses machine learning techniques to develop a non-invasive classification model based on vocal biomarkers extracted from the UCI Parkinson's Disease dataset that includes jitter, shimmer, fundamental frequency, recurrence period density entropy (RPDE), and pitch period entropy (PPE), which have been previously identified as indicators of PD. To classify PD patients from healthy individuals, ten machine learning models were evaluated, including LightGBM, XGBoost, Random Forest, AdaBoost, Bagging, Decision Tree, Logistic Regression, Support Vector Machine (SVM), K-Nearest Neighbor (KNN), and Naïve Bayes. Feature selection techniques were employed to enhance model efficiency by reducing redundancy while maintaining classification performance. Experimental results demonstrated that LightGBM achieved the highest accuracy of 98.00% with an AUC of 97.00%, outperforming other classifiers. This study highlights the potential of machine learning-based speech analysis for early, cost-effective, and scalable PD detection, providing a foundation for future clinical applications in non-invasive neurological assessments.**

***Index Terms*—Parkinson's Disease, Vocal Biomarkers, Health Care, Machine Learning, Speech Analysis.**

I. Introduction

Parkinson's Disease (PD) is a chronic and progressive neurodegenerative disorder that affects millions of individuals worldwide [1]. It is primarily characterized by the degeneration of dopaminergic neurons in the substantia nigra, leading to motor symptoms such as tremors, bradykinesia, rigidity, and postural instability [2]. While these motor impairments are the most visible indicators of PD, vocal impairments are also prevalent, affecting nearly 90% of PD patients at some stage of the disease [3]. These vocal abnormalities include dysphonia, reduced loudness, breathy or hoarse voice, imprecise articulation, and monotonic speech, all of which significantly impact the patient's communication abilities and quality of life. Given that these vocal impairments often manifest before severe motor dysfunction, they offer a unique opportunity for early and non-invasive detection of PD through computational analysis [4].

Traditionally, PD diagnosis is based on neurological examinations, clinical assessments such as the Unified Parkinson's Disease Rating Scale (UPDRS), and imaging techniques such as MRI and PET scans [5]. However, these diagnostic approaches are often costly, time-consuming, and require specialized medical infrastructure, limiting their accessibility, particularly in resource-constrained settings. Consequently, automated and non-invasive diagnostic approaches based on vocal biomarkers and machine learning have gained increasing attention as potential alternatives for early PD detection.

Machine learning (ML) techniques have demonstrated remarkable advancements in speech and signal processing, enabling the automated extraction and classification of disease-related patterns in vocal signals. The ability to analyze vocal biomarkers computationally provides a scalable and efficient way to screen for PD with minimal patient burden. By leveraging acoustic and speech features such as jitter, shimmer, fundamental frequency variations, recurrence period density entropy (RPDE), noise-to-harmonic ratio (NHR), and pitch period entropy (PPE), ML algorithms can distinguish PD patients from healthy individuals with high accuracy [6]. These approaches have the potential to revolutionize early-stage PD diagnosis, disease progression monitoring, and treatment evaluation.

Despite the promise of ML-based PD detection, challenges remain in developing robust, interpretable, and scalable models that can generalize across diverse patient populations. This

study aims to enhance the performance of Parkinson's disease detection using machine learning models trained on vocal biomarkers. By integrating all features and machine learning techniques, we seek to improve classification accuracy, model interpretability, and clinical applicability.

This paper presents a comprehensive analysis of PD detection using machine learning models applied to the UCI Parkinson's dataset, which contains 195 vocal samples from 31 individuals [7]. The experimental results highlight the effectiveness of machine learning in accurately extracting meaningful representations from vocal features while maintaining high diagnostic accuracy. The findings contribute to advancing automated, non-invasive, and scalable diagnostic frameworks for Parkinson's Disease, with the potential for future clinical implementation [8].

II. Literature Review

The use of machine learning and deep learning for the detection of Parkinson's Disease (PD) through vocal biomarkers has gained significant attention in recent years. Numerous studies have explored various methodologies for speech-based PD classification, ranging from machine learning algorithms to deep learning architectures. In this section we review key contributions in this field, focusing on advances, challenges, and potential areas for improvement.

One of the earliest studies to apply machine learning techniques to PD detection was conducted by Little et al. [9], who analyzed dysphonia measures using the UCI Parkinson's dataset. They extracted vocal features such as jitter, shimmer, fundamental frequency (F0), and noise-to-harmonics ratio (NHR) and evaluated the performance of Support Vector Machines (SVM) and Decision Trees. Their results demonstrated that SVM achieved an accuracy of 91.4%, proving the feasibility of using vocal biomarkers for automated PD detection. However, their study was limited by the reliance on manually selected features, which may not fully capture complex vocal variations.

Building upon this work, Tsanas et al. [10] introduced additional dysphonia measures such as Recurrence Period Density Entropy (RPDE) and Detrended Fluctuation Analysis (DFA), improving classification accuracy. They demonstrated that ensemble models such as Random Forest and Gradient Boosting could outperform SVM in certain cases, reaching an AUC of 96%. Their study reinforced the importance of feature selection in improving classification performance but highlighted the challenge of dataset limitations, as the small sample size could lead to overfitting.

Further refinements in machine learning-based PD classification were explored by Gupta & Arora [11], who conducted a comparative analysis of multiple classifiers, including LightGBM, XGBoost, and K-Nearest Neighbors (KNN). Their results showed that LightGBM outperformed other models, achieving a classification accuracy of 95%. They also applied Recursive Feature Elimination (RFE) to optimize the feature set, reducing model complexity while maintaining high performance. However, their study, like previous ones, suffered from the constraint of small datasets, limiting the generalizability of their findings.

While traditional machine learning models have shown promise, deep learning approaches have emerged as powerful alternatives due to their ability to learn feature representations automatically. Arora et al. [12] applied 1D Convolutional Neural Networks (CNNs) to vocal data for PD classification, achieving a classification accuracy of 97%. Their study highlighted the effectiveness of CNNs in capturing spectral and temporal patterns in speech signals. However, CNNs alone are limited in modeling sequential dependencies in speech, necessitating the use of recurrent models.

To address this limitation, Mandrekar [13] explored the use of Long Short-Term Memory (LSTM) networks, which are well-suited for sequence modeling. Their results demonstrated that LSTMs could achieve a sensitivity of 98.2%, making them highly effective in classifying PD patients based on vocal biomarkers. However, LSTM models are computationally expensive and require large datasets, which remain a challenge in PD detection research.

A hybrid approach combining CNN and LSTM was proposed by Dua & Graff [14], where CNNs extracted spatial features from speech spectrograms, while LSTMs captured long-term dependencies in vocal patterns. Their model achieved an AUC of 98.5%, outperforming standalone CNN and LSTM models. Despite these improvements, the study noted the necessity of larger datasets and better interpretability to enhance clinical applicability.

A major issue in PD classification research is the limited availability of large-scale datasets. The widely used UCI Parkinson's dataset, containing only 195 samples from 31 individuals, presents a significant limitation in terms of model generalization. To mitigate this, Tsanas et al. [15] employed Synthetic Minority Oversampling Technique (SMOTE) to balance the dataset, reducing bias in classification. Similarly, Gupta & Arora (2022) explored transfer learning using Wav2Vec and Whisper models, showing that pretrained embeddings could enhance generalization when fine-tuned on small PD datasets.

While previous studies have made significant advancements, several challenges remain unaddressed. Deep learning models, despite their high accuracy, often function as black-box models, making it difficult for clinicians to interpret their predictions. Mandrekar [13] attempted to integrate Explainable AI (XAI) techniques such as SHAP and LIME to provide insights into feature importance, demonstrating that jitter, RPDE, and shimmer were among the most influential features for PD detection. However, the need for more interpretable models remains a critical area of future research.

III. DATASET INFORMATION

The dataset used in this study is sourced from the UCI Machine Learning Repository [16]. It was originally developed by Max Little at the University of Oxford in collaboration with the National Centre for Voice and Speech in Denver, Colorado, where the speech recordings were collected. The

dataset was designed to analyze vocal characteristics associated with Parkinson's Disease (PD) and has been widely used for machine learning-based diagnosis models. The feature extraction techniques applied in this dataset were introduced in the original study on general voice disorders [17].

The dataset consists of 195 voice samples collected from 31 individuals, including 23 Parkinson's Disease patients and 8 healthy controls. Each row in the dataset represents a single voice recording, while each column corresponds to a specific vocal feature. The target variable, "status", indicates whether the speaker is healthy (0) or diagnosed with PD (1). The primary goal of this dataset is to differentiate between PD patients and healthy individuals based on biomedical voice measurements.

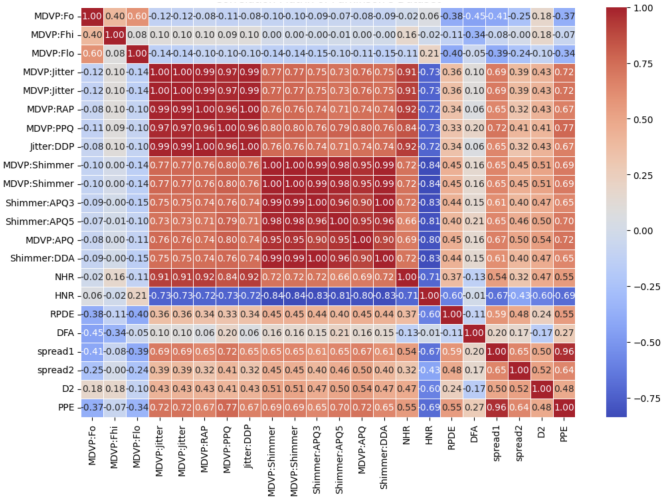

Fig. 1: Co-relation Matrix of Variables.

This dataset includes 24 clinical attributes, capturing various vocal characteristics that are known to be affected by Parkinson's Disease. These features are categorized into: Fundamental Frequency Measures: MDVP:Fo(Hz) – Average fundamental frequency, MDVP:Fhi(Hz) – Maximum fundamental frequency, and MDVP:Flo(Hz) – Minimum fundamental frequency. Frequency Variation (Jitter) Measures: MDVP:Jitter(%), MDVP:Jitter(Abs), MDVP:RAP, MDVP:PPQ, Jitter:DDP, Amplitude Variation (Shimmer) Measures: MDVP:Shimmer, MDVP:Shimmer(dB), Shimmer:APQ3, Shimmer:APQ5, MDVP:APQ, Shimmer:DDA Noise-to-Tone Ratio Measures: NHR (Noise-to-Harmonic Ratio), HNR (Harmonic-to-Noise Ratio). Nonlinear Dynamical Complexity Measures: RPDE (Recurrence Period Density Entropy), D2 (Correlation Dimension). Signal Fractal Scaling and Frequency Spread: DFA (Detrended Fluctuation Analysis), Spread1, Spread2, PPE (Pitch Period Entropy)

This dataset contains one dependent variable (status) and 23 independent variables used as predictors. These features have been extensively studied as biomarkers for Parkinson's Disease, making this dataset a valuable resource for developing predictive models.

To further explore the relationships between different vocal features, a correlation matrix is used to identify strongly correlated variables. The correlation matrix helps understand how these attributes interact and contribute to PD classification. This visualization aids in feature selection and dimensionality reduction, improving the efficiency of machine learning models [18].

IV. METHODOLOGY

This study follows a structured approach to analyze the Parkinson's Disease dataset using machine learning models. The methodology consists of three key stages: dataset collection, data preprocessing, and validation. Each step showed in figure 2 ensures that the dataset is well-prepared for model training and evaluation.

A. Data Collection

In this study, we utilized a publicly available dataset from the UCI Machine Learning Repository that contains vocal biomarkers for Parkinson's Disease (PD) detection [16]. The dataset was originally compiled through a collaboration between the University of Oxford and the National Centre for Voice and Speech, Denver, Colorado. The data acquisition process involved recording sustained phonations of the vowel sound $/a/$ from individuals, ensuring consistency in vocal characteristics across participants. These recordings were then analyzed to extract relevant speech features associated with PD symptoms.

Unlike the dataset description section, which details the dataset structure, this section emphasizes the data acquisition methodology and its significance in the context of machine learning applications. The dataset consists of 195 vocal samples collected from 31 individuals, including 23 diagnosed PD patients and 8 healthy controls. The extracted vocal biomarkers include fundamental frequency variations, amplitude perturbations, noise-to-harmonics ratio, and nonlinear dynamic measures, all of which serve as potential indicators of neurodegenerative changes [19].

The choice of this dataset aligns with our objective of developing a non-invasive and scalable approach for PD detection. By emphasize this well-structured dataset, we aim to enhance predictive accuracy using machine learning techniques while ensuring the applicability of our model in clinical and telemonitoring settings.

B. Data Preprocessing

Before training machine learning models, data preprocessing is performed to enhance model performance and reliability. The dataset does not contain missing values, as it was preprocessed in its original study [17]. However, an initial data integrity check is conducted to ensure consistency. Since the dataset contains features with different scales, such as frequency (Hz) and amplitude ratios, Min-Max Scaling is applied to normalize all values between 0 and 1. The normalization formula is expressed as follows:

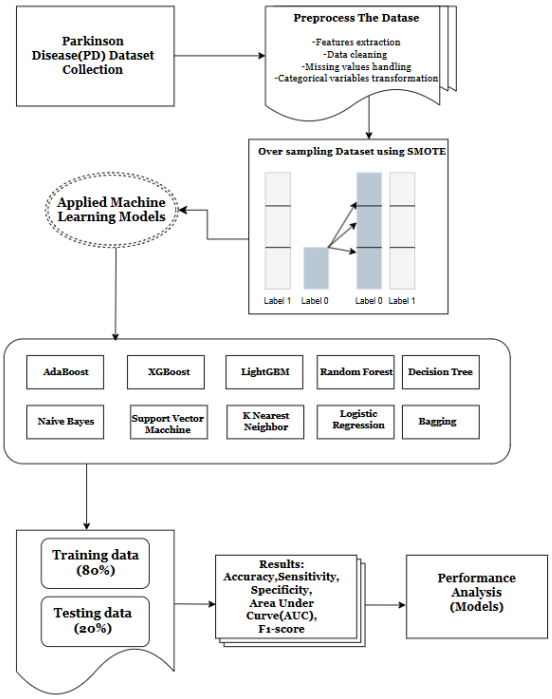

Fig. 2: Flow Chart Diagram.

$$X_{\text{scaled}} = \frac{X - X_{\min}}{X_{\max} - X_{\min}} \tag{1}$$

This step ensures that models relying on distance-based metrics, such as Support Vector Machines (SVM) and k-Nearest Neighbors (KNN), perform optimally. To analyze the relationships between features, a correlation matrix is computed. Features with high correlation (above 0.85) are considered for removal to reduce redundancy and improve generalization [15]. Additionally, Recursive Feature Elimination (RFE) is applied to retain only the most relevant predictors. Finally, the dataset is split into training (80%) and testing (20%) subsets using stratified sampling, ensuring that the proportion of PD and healthy samples remains balanced across sets.

C. Validation Process

To ensure model reliability, k-fold cross-validation is applied to mitigate overfitting and improve generalization [20]. A 10-fold cross-validation strategy is used, where the dataset is split into 10 equal parts. Each model is trained on 9 folds and tested on the remaining fold, with the process repeated until every sample has been used in validation. The final model performance is reported as the average accuracy across all folds.

To evaluate the classification performance, several performance metrics are computed [21]. Accuracy measures the proportion of correctly classified samples, while precision and recall assess the model's ability to correctly identify PD patients. The F1-score, which is the harmonic mean of precision and recall, provides a balanced evaluation of the classifier's effectiveness. Additionally, the AUC-ROC curve is used to analyze the model's ability to distinguish between PD and healthy individuals. These validation steps ensure the robustness, reliability, and clinical applicability of the proposed Parkinson's Disease detection models [22].

V. Results and Discussion

Table I presents the performance comparison of various machine learning models, including LightGBM, Random Forest, XGBoost, AdaBoost, Bagging, Decision Tree, Logistic Regression, Support Vector Machine, K-Nearest Neighbor, and Naïve Bayes for Parkinson's Disease (PD) detection. The models are evaluated based on Accuracy, Sensitivity, Specificity, AUC (Area Under the Curve), and F1-score. Figures 3 and 4 further illustrate the model performance through visual comparisons.

TABLE I: Performance Comparison of Machine Learning Models for Parkinson's Disease Detection.

Model	Accuracy (%)	Sensitivity (%)	Specificity (%)	AUC (%)	F1-score (%)
LightGBM	98.00	100.00	95.50	97.00	91.00
Random Forest	93.50	100.00	90.32	99.00	85.50
XGBoost	92.00	90.00	90.00	98.00	82.00
AdaBoost	90.00	80.00	92.87	95.00	84.80
Bagging	85.62	80.00	90.00	98.00	85.50
Decision Tree	85.80	82.00	91.00	95.00	78.50
Logistic Regression	85.20	85.71	84.38	95.00	70.00
Support Vector Machine	84.00	70.00	85.10	95.00	68.70
K-Nearest Neighbor	78.00	73.30	81.25	89.00	65.60
Naïve Bayes	68.30	60.70	92.00	96.00	62.00

From Table I, it is evident that LightGBM demonstrates the best overall performance, achieving an accuracy of 98%, sensitivity of 100%, specificity of 95.50%, AUC of 97%, and an F1-score of 91%. This indicates that LightGBM effectively distinguishes between PD patients and healthy individuals while maintaining a high balance between precision and recall.Random Forest also achieves strong results, closely following LightGBM. It achieves an accuracy of 93.50%, sensitivity of 100%, specificity of 90.32%, AUC of 99%, and an F1-score of 85.50%. These results suggest that ensemble learning techniques like LightGBM and Random Forest are particularly effective for PD classification due to their ability to handle complex relationships in the dataset.On the other hand, Naïve Bayes exhibits the lowest performance among all classifiers. It achieves an accuracy of 68.30%, sensitivity of 60.70%, specificity of 92%, AUC of 96%, and an F1-score of 62%. The lower sensitivity suggests that Naïve Bayes struggles to correctly identify PD cases, likely due to its assumption of feature independence, which does not hold well for biomedical data [23].To provide a clearer comparison, Figure 3 presents a bar chart visualization highlighting the accuracy and AUC of different models. These metrics are crucial as they provide insight into both the overall correctness of classification (accuracy) and the model's ability to distinguish between PD and non-PD cases (AUC) [24].

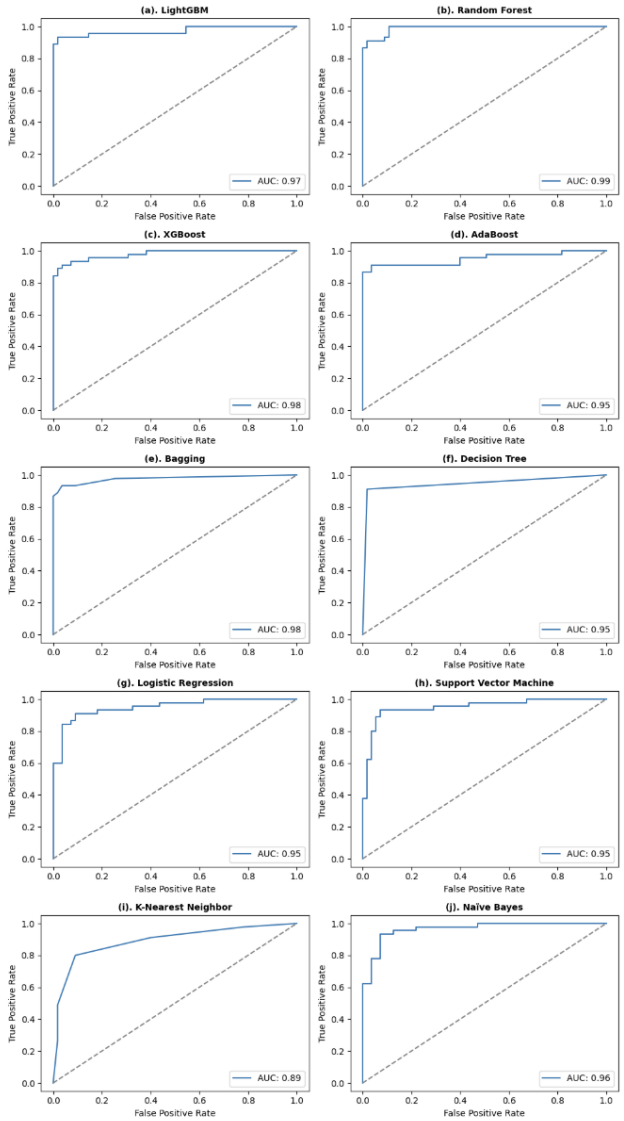

Fig. 3: Output grap for AUC: a. LightGBM, b. Random Forest, c. XGBoost, d. AdaBoost, e. Bagging, f. Decision Tree, g. Logistic Regression, h. Support Vector Machine, i. K-Nearest Neighbor, and j. Naïve Bayes.

The AUC (Area Under the Curve) metric plays a crucial role in evaluating classification models for Parkinson's Disease (PD) detection. Unlike accuracy, which simply measures the proportion of correctly classified instances, AUC assesses a model's ability to distinguish between positive (PD) and negative (healthy) cases across various classification thresholds. A higher AUC score indicates a stronger discriminative ability and a more reliable classification model [25]. According to Hanley & McNeil (1982), an AUC of 0.5 suggests no discrimination (random classification), whereas a score between 0.7 and 0.8 indicates acceptable performance. AUC values ranging from 0.8 to 0.9 signify good classification ability, while models with $AUC \geq 0.9$ demonstrate excellent performance in distinguishing PD cases. Based on this scale,

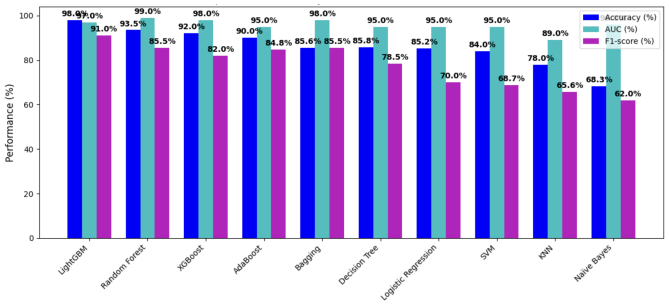

Fig. 4: Models Comparison among Accuracy, AUC, and F1-score.

LightGBM and XGBoost, which achieved AUC scores of 97% and 99%, respectively, exhibit outstanding classification performance. Figure 3 presents AUC plots for the tested models, illustrating their ability to differentiate between PD-positive and PD-negative cases.

VI. CONCLUSION

Parkinson's disease (PD) is a progressive neurodegenerative disorder that significantly impacts motor function, speech, and cognition. Early detection plays a crucial role in effective disease management and improving patient outcomes. In this study, we utilized machine learning algorithms to classify PD patients using vocal biomarkers from the UCI Machine Learning Repository dataset. Since the dataset was imbalanced, we applied SMOTE for oversampling and evaluated ten machine learning models, including LightGBM, Random Forest, XGBoost, AdaBoost, Bagging, Decision Tree, Support Vector Machine, Logistic Regression, K-Nearest Neighbor, and Naïve Bayes.Among these models, LightGBM outperformed the others, achieving an accuracy of 98%, sensitivity of 100%, specificity of 95.50%, AUC of 97%, and F1-score of 91%. These results demonstrate that ensemble learning methods are highly effective in detecting PD from vocal features and could serve as non-invasive diagnostic tools for early-stage PD screening.For future work, we aim to explore deep learning techniques, such as Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), to improve feature extraction and classification accuracy. Additionally, integrating larger and more diverse datasets from real-world clinical sources can enhance the model's generalization and robustness. Finally, developing an interpretable AI framework will help increase trust and adoption in clinical applications, facilitating early and automated PD diagnosis.

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