

Mathematical Modeling of Nonlinear Vocal Biomarker Dynamics for Early Detection of Parkinson's disease Using Hybrid Ensemble Learning

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Abstract: Parkinson's disease is a progressive neurodegenerative disorder characterized by motor impairment, vocal instability, and neuromuscular dysfunction affecting speech production. Early diagnosis remains clinically challenging because conventional neurological assessment and imaging procedures are often expensive, time-consuming, and inaccessible in resource-limited healthcare environments. Recent advances in speech signal analysis have demonstrated that nonlinear acoustic perturbations can serve as effective biomarkers for early Parkinsonian abnormalities. However, many existing artificial intelligence-based diagnostic systems primarily emphasize predictive performance without incorporating quantitative modeling of vocal biomarker dynamics. This study presents a mathematical modeling framework for analyzing nonlinear vocal biomarker dynamics using hybrid ensemble learning for early Parkinson's disease detection. A combined dataset consisting of 895 voice recordings and 22 clinically relevant acoustic features was utilized for experimental evaluation. The proposed framework integrates speech signal processing, statistical feature modeling, and ensemble-based machine learning to characterize disease-associated vocal perturbations. Acoustic biomarkers including jitter, shimmer, harmonic-to-noise ratio (HNR), recurrence period density entropy (RPDE), and detrended fluctuation analysis (DFA) were modeled to represent instability in vocal fold dynamics. The nonlinear vocal perturbation behavior was mathematically represented as:

$V(t) = \alpha J + \beta S + \gamma H + \delta R$, where J, S, H, and R correspond to jitter, shimmer, HNR, and RPDE-derived perturbation measures, respectively. To improve predictive robustness, a stacking ensemble framework integrating Random Forest, Gradient Boosting, Support Vector Machine, K-Nearest Neighbors, Logistic Regression, and Multilayer Perceptron classifiers was developed using a meta-learning strategy:

$y \approx f_m(f_1(x), f_2(x), \dots, f_n(x))$. Experimental findings demonstrated that the proposed framework achieved a classification accuracy of 97.77%, outperforming conventional standalone machine learning approaches. Statistical distribution analysis further revealed substantial nonlinear deviations in acoustic perturbation biomarkers among Parkinson's disease patients compared with healthy individuals. The proposed framework demonstrates the potential of mathematical modeling and hybrid ensemble intelligence for developing scalable, non-invasive, and computationally interpretable diagnostic systems for early Parkinson's disease screening and digital healthcare applications.

Keywords: Parkinson's disease, nonlinear vocal biomarkers, mathematical modeling, ensemble learning, speech signal processing, computational biomathematics

Introduction

Parkinson's disease is a chronic and progressive neurodegenerative disorder that primarily affects motor coordination, speech production, and neuromuscular control mechanisms. The disease is associated with degeneration of dopaminergic neurons in the substantia nigra region of the brain, resulting in symptoms such as tremors, rigidity, bradykinesia, postural instability, and progressive vocal impairment. Recent neurological health studies indicate that Parkinson's disease affects millions of individuals worldwide, and its prevalence continues to increase due to aging populations and improved clinical awareness [1], [2]. Early diagnosis is critically important because timely clinical intervention can significantly slow disease progression and improve patient quality of life. However, conventional diagnostic approaches generally rely on neurological examination, imaging modalities, and long-term monitoring of motor symptoms, which are often expensive, time-consuming, and inaccessible in resource-limited healthcare environments [3], [4]. Consequently, there is a growing need for computationally efficient and non-invasive diagnostic frameworks capable of supporting early-stage Parkinson's disease screening through quantitative biomarker analysis.

In recent years, artificial intelligence and machine learning techniques have emerged as powerful tools for identifying neurological abnormalities using biomedical data. Researchers have investigated several modalities including neuroimaging, gait analysis, wearable sensors, electroencephalography, and speech signal analysis for Parkinson's disease detection [5], [6]. Among these modalities, speech-based biomarkers have gained considerable attention because vocal abnormalities frequently appear during the early stages of Parkinsonian progression. Patients affected by Parkinson's disease commonly exhibit irregular pitch variation, reduced vocal intensity, unstable vocal fold vibration, and abnormal speech perturbation patterns caused by impaired neuromuscular control [7], [8]. Acoustic biomarkers such as jitter, shimmer, harmonic-to-noise ratio (HNR), recurrence period density entropy (RPDE), and detrended fluctuation analysis (DFA) therefore provide important quantitative indicators of neurological degradation associated with Parkinsonian speech disorders [9], [10].

From a computational biomathematics perspective, speech production may be represented as a nonlinear dynamical system influenced by biomechanical oscillations of vocal folds and neuromuscular regulation. The vibration behavior of vocal folds can be mathematically represented using a second-order dynamical system:

$$m\ddot{x} + c\dot{x} + kx = F(t)$$

where m denotes the mass of the vocal folds, c represents damping, k corresponds to stiffness, and $F(t)$ defines the external excitation force generated during phonation. Neuromuscular degradation associated with Parkinson's disease introduces instability into this oscillatory system, resulting in nonlinear perturbations in speech production. These perturbations can be quantitatively characterized using acoustic biomarkers derived from speech signals.

Among the most significant perturbation measures, jitter represents cycle-to-cycle frequency instability in speech production and can be mathematically expressed as:

$$Jitter = \frac{1}{N-1} \sum_{i=1}^{N-1} |T_i - T_{i+1}|$$

where T_i represents the duration of the i^{th} vocal cycle. Similarly, shimmer quantifies amplitude instability in successive speech cycles and is defined as:

$$Shimmer = \frac{1}{N-1} \sum_{i=1}^{N-1} |A_i - A_{i+1}|$$

where A_i denotes the amplitude of the i^{th} speech cycle. Increased values of jitter and shimmer are commonly associated with impaired vocal stability in Parkinson's disease patients [11], [12].

To represent the collective nonlinear behavior of vocal perturbation dynamics, the overall vocal instability function can be modeled as:

$$V(t) = \alpha J + \beta S + \gamma H + \delta R$$

where J , S , H , and R correspond to jitter, shimmer, harmonic-to-noise ratio, and RPDE-based perturbation measures, respectively. The coefficients α , β , γ , and δ define the contribution of individual biomarkers toward nonlinear speech degradation. Such mathematical representations enable computational analysis of Parkinsonian speech dynamics and facilitate the interpretation of disease-associated vocal instability patterns.

Although several studies have demonstrated promising predictive performance using machine learning and deep learning techniques for Parkinson's disease detection, many existing approaches primarily focus on maximizing classification accuracy without incorporating interpretable mathematical modeling of biomarker interactions [13], [14]. Standalone machine learning classifiers often fail to capture the complex nonlinear relationships among acoustic perturbation features, while many prediction systems lack computational frameworks capable of integrating statistical analysis, nonlinear biomarker dynamics, and ensemble intelligence within a unified diagnostic architecture. Consequently, there remains a significant research gap in the development of computational biomathematics frameworks that combine quantitative speech modeling with robust predictive learning systems for neurodegenerative disease screening.

To address these limitations, this study proposes a mathematical modeling framework for early Parkinson's disease detection using hybrid ensemble learning and nonlinear vocal biomarker analysis. The proposed framework integrates speech signal processing, acoustic perturbation modeling, statistical feature analysis, and ensemble-based machine learning to characterize disease-associated vocal abnormalities. A stacking ensemble architecture consisting of Random Forest, Gradient Boosting, Support Vector Machine, K-Nearest Neighbors, Logistic Regression, and Multilayer Perceptron classifiers is utilized to improve predictive robustness and generalization capability. The ensemble prediction mechanism is mathematically formulated as:

$$\hat{y} = f_m(f_1(x), f_2(x), \dots, f_n(x))$$

where $f_1(x), f_2(x), \dots, f_n(x)$ denote the predictions of individual base classifiers and f_m represents the meta-learning function generating the final prediction outcome. This hybrid modeling strategy enables the framework to capture both linear and nonlinear dependencies among acoustic biomarkers while improving predictive performance.

The major contribution of this work lies in integrating nonlinear mathematical modeling of vocal perturbation dynamics with hybrid ensemble intelligence for interpretable Parkinson's disease screening. Unlike conventional speech-based diagnostic systems that primarily emphasize algorithmic prediction accuracy, the proposed framework focuses on quantitative representation of disease-associated speech instability and computational interpretation of vocal biomarker behavior. The framework therefore contributes toward computational biomathematics and digital healthcare by demonstrating how nonlinear speech dynamics can be utilized to develop scalable, non-invasive, and cost-effective neurodegenerative disease screening systems.

This rest of the paper is structured in the following way. Section 2 is a literature review of the current machine learning methods applied to the detection of Parkinson diseases and their limitations. Section 3 explains the methodology that is proposed, such as dataset description, data preprocessing, feature extraction mechanism, machine learning model architecture, and integration of the conversational AI assistant. Section 4 provides the experimental results and performance analysis together with the comparative analysis with the existing state-of-the-art models. Lastly, Section 5 gives a conclusion to the study, which summarizes the most important findings, talks about the applicability in the real world, and provides the possible future research directions.

Literature Review

Computational Modeling in Parkinson's Disease Detection

Parkinson's disease has become one of the most extensively studied neurological disorders in computational healthcare research due to its progressive impact on motor coordination, speech production, and cognitive functionality. Recent advancements in artificial intelligence and computational biomarker analysis have enabled the development of automated systems capable of identifying disease-associated abnormalities using biomedical data. Researchers have explored multiple modalities including neuroimaging, gait dynamics, wearable sensors, electroencephalography (EEG), handwriting analysis, and speech signal processing to improve the accuracy of Parkinson's disease screening and monitoring [1], [2].

Machine learning techniques have demonstrated considerable potential in distinguishing Parkinsonian patterns from healthy physiological behavior through quantitative analysis of biomedical signals. Several studies have proposed predictive models using supervised learning algorithms trained on structured clinical and biomedical datasets [3], [4]. Ensemble learning frameworks have also been investigated to improve robustness and reduce prediction variance in Parkinson's disease classification systems [5]. Although these approaches achieved promising classification performance, many existing systems primarily focus on predictive accuracy without integrating interpretable mathematical representations of disease-associated biological dynamics.

Recent research has also emphasized multimodal computational frameworks that combine multiple biomedical features for disease prediction. Neuroimaging-based machine learning systems have shown strong performance in identifying structural abnormalities associated with Parkinson's disease progression [6]. Similarly, wearable sensor-based frameworks and gait monitoring systems have been utilized to capture motor instability and tremor-related characteristics [7], [8]. Despite their effectiveness, these systems often require expensive medical infrastructure or specialized sensing hardware, limiting their applicability in large-scale and resource-constrained healthcare settings.

Speech Signal Analysis and Acoustic Biomarkers

Among various computational modalities, speech signal analysis has emerged as one of the most promising non-invasive approaches for Parkinson's disease detection because vocal impairments frequently appear during the early stages of neurological degeneration [9], [10]. Parkinsonian speech is commonly characterized by reduced vocal intensity, unstable pitch variation, breathiness, tremor, monotonic articulation, and irregular vocal fold vibration resulting from impaired neuromuscular regulation. These abnormalities can be quantitatively represented using acoustic perturbation biomarkers extracted from speech recordings.

Several studies have demonstrated that acoustic features such as jitter, shimmer, harmonic-to-noise ratio (HNR), recurrence period density entropy (RPDE), and detrended fluctuation analysis (DFA) are effective indicators of Parkinsonian vocal instability [11], [12]. Voice-based diagnostic systems using machine learning algorithms including Support Vector Machines, Artificial Neural Networks, Random Forest, and Gradient Boosting classifiers have reported promising prediction accuracy for distinguishing Parkinson's disease patients from healthy individuals [13], [14].

From a mathematical perspective, speech production can be interpreted as a nonlinear oscillatory system governed by biomechanical movement of vocal folds and neuromuscular excitation. Vocal fold vibration dynamics may be represented as:

$$m\ddot{x} + c\dot{x} + kx = F(t)$$

where m denotes vocal fold mass, c represents damping, k corresponds to tissue stiffness, and $F(t)$ defines external excitation forces during phonation. Neurological degradation associated with Parkinson's disease introduces perturbations within this oscillatory system, resulting in unstable vocal frequency and amplitude variations.

Jitter, which represents frequency perturbation between successive speech cycles, is mathematically expressed as:

$$Jitter = \frac{1}{N-1} \sum_{i=1}^{N-1} |T_i - T_{i+1}|$$

while shimmer, which measures amplitude instability in vocal signals, is defined as:

$$Shimmer = \frac{1}{N-1} \sum_{i=1}^{N-1} |A_i - A_{i+1}|$$

where T_i and A_i correspond to the duration and amplitude of the i 'th speech cycle, respectively. Increased perturbation values are commonly associated with Parkinsonian vocal instability caused by impaired neuromuscular coordination [15], [16].

Recent studies have further investigated deep learning and transformer-based architectures for extracting hierarchical speech representations associated with Parkinson's disease [17], [18]. Hybrid computational systems combining handcrafted acoustic biomarkers with deep neural networks have also demonstrated improved classification performance [19]. However, many of these approaches remain primarily data-driven and often lack mathematical interpretability of biomarker interactions and nonlinear speech dynamics.

Nonlinear Dynamics and Statistical Modeling of Vocal Biomarkers

The analysis of Parkinsonian speech dynamics has increasingly attracted attention within computational biomathematics because vocal perturbation behavior exhibits nonlinear and stochastic characteristics. Neuromuscular degradation in Parkinson's disease introduces irregularities into the oscillatory behavior of vocal folds, leading to instability in speech frequency, amplitude, and harmonic structure. These perturbations can be modeled quantitatively using nonlinear biomarker representations.

The collective vocal instability behavior may be mathematically formulated as:

$$V(t) = \alpha J + \beta S + \gamma H + \delta R$$

where $V(t)$ denotes overall vocal instability, while J , S , H , and R represent jitter, shimmer, harmonic-to-noise ratio, and RPDE-based perturbation measures, respectively. The coefficients α , β , γ , and δ define the contribution of individual biomarkers toward nonlinear speech degradation.

Several studies have utilized entropy analysis, nonlinear feature extraction, and statistical learning techniques to analyze the complexity of Parkinsonian speech patterns [20], [21]. Correlation-based biomarker analysis and statistical feature interaction studies have shown that perturbation features exhibit strong nonlinear dependencies associated with disease progression [22]. Furthermore, recurrence-based and fractal analysis methods such as RPDE and DFA have demonstrated effectiveness in identifying chaotic behavior and temporal irregularities in Parkinsonian speech signals [23].

Despite these advancements, many existing systems lack unified frameworks capable of integrating nonlinear biomarker modeling with interpretable ensemble learning strategies. Most traditional machine learning systems operate as standalone prediction models without incorporating quantitative mathematical representations of disease-associated vocal instability. Consequently, there remains a significant research gap in the development of computational biomathematics frameworks that combine nonlinear vocal dynamics, statistical biomarker analysis, and robust ensemble intelligence for Parkinson's disease screening.

Hybrid Ensemble Learning for Biomedical Prediction

Hybrid ensemble learning has emerged as an effective strategy for improving predictive robustness in biomedical classification tasks because it combines multiple learning models to minimize variance and improve generalization capability [24]. Ensemble approaches such as bagging, boosting, and stacking integrate predictions from diverse classifiers to generate more stable and accurate outcomes compared with standalone machine learning systems.

In Parkinson's disease detection, ensemble learning frameworks have demonstrated improved classification performance by combining complementary decision boundaries derived from multiple algorithms [25], [26]. Stacking ensemble architectures, in particular, utilize meta-learning strategies to

integrate outputs from base classifiers and generate optimized final predictions. Mathematically, the ensemble prediction process can be represented as:

$$\hat{y} = f_m(f_1(x), f_2(x), \dots, f_n(x))$$

where $f_1(x), f_2(x), \dots, f_n(x)$ denote the outputs of individual base classifiers and f_m represents the meta-learning function responsible for generating the final prediction.

Although ensemble systems have shown strong predictive capability in biomedical classification tasks, many existing studies focus primarily on performance optimization without integrating mathematical modeling of disease-associated biomarkers. Furthermore, several frameworks lack interpretability regarding the nonlinear interactions among acoustic perturbation features and their biological significance in Parkinsonian speech degradation.

Based on the analysis of the existing literature, it can be observed that there remains a substantial research gap in computational biomathematics frameworks capable of integrating nonlinear vocal biomarker modeling, statistical feature interaction analysis, and hybrid ensemble intelligence within a unified Parkinson's disease screening architecture. Therefore, the present study proposes a mathematical modeling framework that combines nonlinear speech perturbation analysis with hybrid ensemble learning to develop an interpretable and computationally robust diagnostic system for early Parkinson's disease detection.

Model Methodology

This section explains the entire architecture and the experiment process that was employed to come up with the proposed Parkinson disease prediction system. The approach combines the speech signal processing, classification using machine learning, and intelligent conversational assistant in a single framework. The suggested system has four key elements, including data acquisition, speech feature extraction, machine learning model training, and system implementation with an AI chatbot interface. The general architecture will facilitate automated prediction of Parkinson disease using vocal biomarkers and support user interaction and education in real-time using an intelligent conversational interface.

System Architecture Overview

The proposed system adheres to a multi-layer design, which includes frontend user interface, backend prediction engine, speech feature extraction module and machine learning model layer as shown in Figure 1. The system has a web interface that enables the users to capture voice samples or speech data to analyze them.

The speech signal processing methods are then applied to the audio signal in order to obtain acoustic biomarkers. They are normalized features that are forwarded to a stacking ensemble classifier that is trained to identify the risk of Parkinson disease.

As Figure 1 demonstrates, the architecture will also incorporate an AI-driven chatbot that can deliver information regarding the symptoms of Parkinson disease, interpret the results of prediction, and refer users to the relevant medical consultation in case of need.

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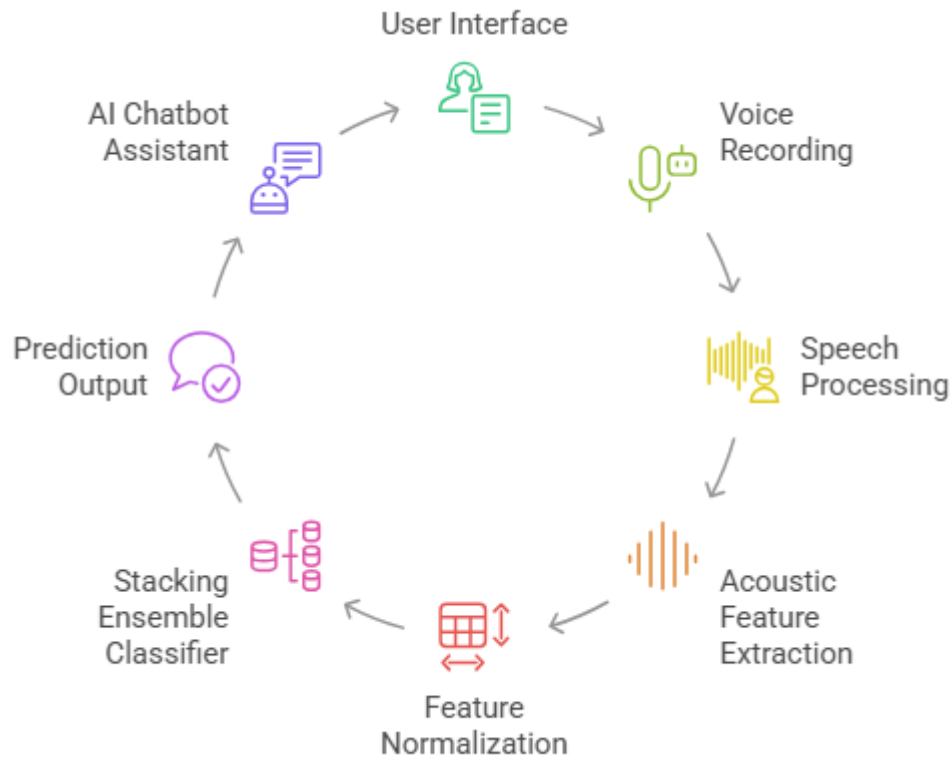


Figure 1: System Architecture Diagram

Dataset Description

There were two publicly available Parkinson disease datasets (speech-based biomedical attributes) that were used as the experimental assessment. These data sets were combined together to form one comprehensive data set that was utilized in the training and testing of the machine learning models.

The datasets involve a set of biomedical voice measures that were obtained by using continued recording of phonation of patients with Parkinson disease as well as normal control patients.

The combined dataset consists of:

Total Samples: 895

Number of features: 22

Target variable: Parkinson's disease status

The target variable is represented as a binary classification problem where

$$y = \{1 \text{ Parkinson's Disease}, 0 \text{ Healthy Individual}\} \quad (1)$$

The data set has a number of acoustic characteristics of the vibration of the vocal cords and signal distortions. The features are clinically relevant biomarkers that are related to Parkinson disease.

Some important features include:

Fundamental frequency measures (Fo, Fhi, Flo)

Jitter measures (Jitter %, RAP, PPQ)

Shimmer measures (Shimmer, APQ3, APQ5)

Harmonics-to-noise ratio

Nonlinear dynamic features such as RPDE and DFA

Overall, these acoustic characteristics represent various dimensions of vocal stability, noise

elements, and nonlinear speech dynamics which in many patients with Parkinson's disease are disturbed.

Table 1: Acoustic Voice Features Used in Parkinson's Disease Detection

Feature	Description
MDVP:Fo	Average fundamental frequency
MDVP:Fhi	Maximum fundamental frequency
MDVP:Flo	Minimum fundamental frequency
Jitter	Frequency variation in speech
Shimmer	Amplitude variation
HNR	Harmonics-to-noise ratio
NHR	Noise-to-harmonics ratio
RPDE	Recurrence period density entropy
DFA-	Detrended fluctuation analysis

Data Preprocessing

Preprocessing of data is relevant in enhancing the performance of machine learning models. The preprocessing phase had a number of steps that included the aspects of data cleaning, feature alignment, dataset merger, and feature scaling.

To prepare the datasets, it was first loaded and then combined into one dataframe. Some of the non-predictive attributes like patient identifiers were dropped so as to make the model learn only clinically relevant features.

As the datasets were slightly dissimilar in terms of the column arrangement, there was feature alignment to guarantee the similarity of features prior to merging.

An 80-20 split was then used to split the dataset into training and testing sets. The stratified sampling was used to ensure that the classes were distributed in both subsets.

$$X_{train}, X_{test}, y_{train}, y_{test} = TrainTestSplit(X, y) \quad (2)$$

Normalization of features was done through StandardScaler technique to make sure that all the features play an equal part in learning.

The features are changed in accordance with the following equation as a result of the standardization process:

$$Z = \frac{x - \mu}{\sigma} \quad (3)$$

Where:

x represents the original feature value,

μ represents the mean of the feature,

σ represents the standard deviation.

Normalization of features is particularly significant to machine learning models that are sensitive to differences of the magnitude of features (e.g. Support Vector Machines and K-Nearest Neighbors).

Speech Feature Extraction

The speech feature extraction module is based on audio recordings processed through the Parselmouth speech analysis library that gives Python access to the Praat speech analysis toolkit.

The voice recordings are first changed into the WAV file and then processed to determine acoustic biomarkers of pitch variation, stability of vocal fold vibration, and perturbation of the signal.

The fundamental frequency of speech is calculated as:

$$F_o = \frac{1}{T} \quad (4)$$

where T represents the vibration period of the vocal folds.

Jitter measures are measurements of cycle-to-cycle variations in frequency and are calculated as below.

$$Jitter = \frac{1}{N-1} \sum_{i=1}^{N-1} \left| \frac{T_i - T_{i+1}}{T_i} \right| \quad (5)$$

Shimmer measures are the amplitude variations in the speech signal and they are defined as shimmer measures.

$$Shimmer = \frac{1}{N-1} \sum_{i=1}^{N-1} \left| \frac{A_i - A_{i+1}}{A_i} \right| \quad (6)$$

The Harmonics-to-Noise Ratio (HNR) is used to quantify the percentage of periodic energy in comparison to noise in the voice signal and is determined as

$$HNR = 10 \log_{10} \left(\frac{P_{harmonic}}{P_{noise}} \right) \quad (7)$$

These acoustic data offer valuable data on the vocal abnormalities that are usually seen in patients of Parkinson disease. Figure 2 shows the general algorithm of the speech biomarker extraction of raw audio samples.

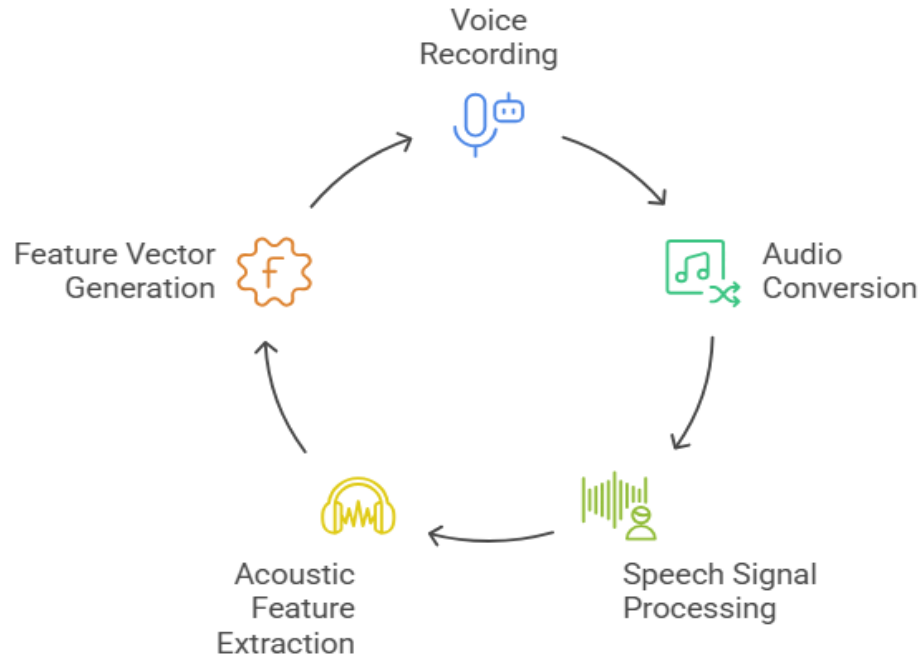


Figure 2: Voice Signal Processing Pipeline

Nonlinear Mathematical Modeling of Vocal Biomarkers

The nonlinear behavior of Parkinsonian speech signals was modeled using acoustic perturbation dynamics associated with neuromuscular degradation in vocal fold activity. Speech production can be represented as a nonlinear oscillatory system where neurological impairment introduces instability in frequency, amplitude, and harmonic structures of speech signals. To mathematically characterize this instability, a composite vocal perturbation function was defined using clinically relevant acoustic biomarkers.

The nonlinear vocal instability model is represented as:

$$V(t) = \alpha J + \beta S + \gamma H + \delta R$$

where $V(t)$ denotes the overall vocal instability function, while J , S , H , and R represent jitter, shimmer, harmonic-to-noise ratio (HNR), and recurrence period density entropy (RPDE), respectively. The coefficients α , β , γ , and δ define the contribution of individual biomarkers toward speech degradation associated with Parkinsonian progression.

To model temporal instability in speech dynamics, the variation of vocal perturbation over time was further represented using a nonlinear differential formulation:

$$\frac{dV}{dt} = \alpha V - \beta V^2 + \gamma N + \epsilon$$

where N represents neuromuscular degeneration intensity and ϵ denotes stochastic perturbation noise associated with speech variability. This formulation enables quantitative representation of nonlinear deterioration patterns observed in Parkinsonian vocal behavior.

The mathematical representation of acoustic perturbation dynamics provides a computational framework for analyzing instability in speech production and facilitates interpretation of disease-associated vocal abnormalities.

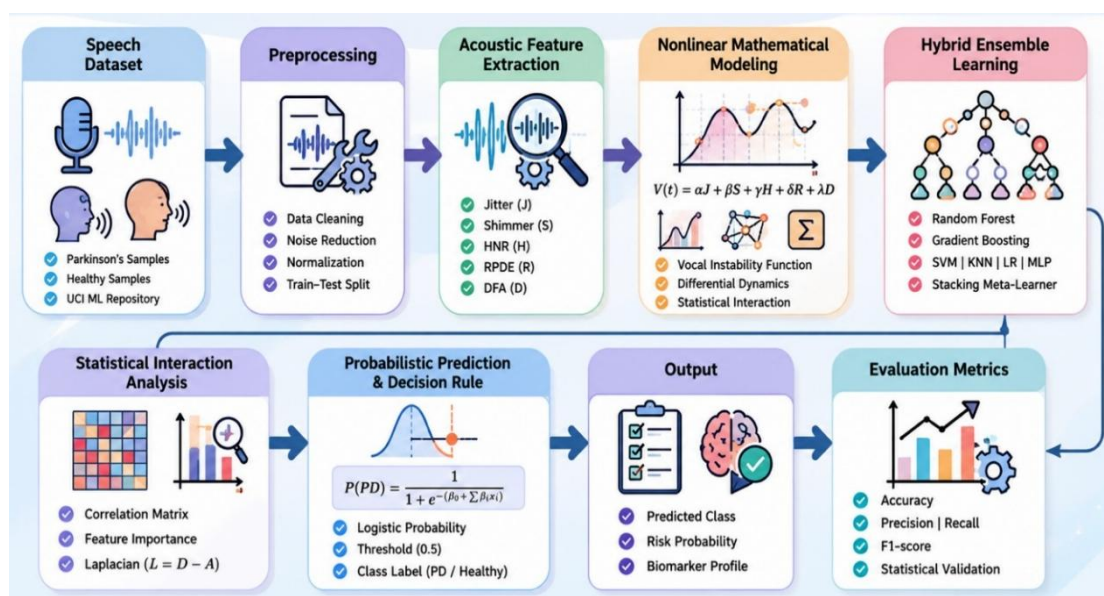


Figure 1 Proposed computational biomathematical framework for early Parkinson's disease detection using nonlinear vocal biomarker modeling, statistical interaction analysis, and hybrid ensemble learning.

Hybrid Ensemble Learning Framework

To improve predictive robustness and generalization capability, a hybrid ensemble learning framework was developed using multiple machine learning classifiers integrated through a stacking-based meta-learning architecture. Ensemble learning enables the combination of diverse decision boundaries generated by individual classifiers, thereby improving classification stability in biomedical prediction tasks.

Let the dataset be represented as:

$$D = \{(x_i, y_i)\}_{i=1}^N$$

where x_i represents the acoustic feature vector and y_i denotes the corresponding disease label.

The proposed framework integrates the following base classifiers:

Random Forest

Gradient Boosting

Support Vector Machine

K-Nearest Neighbors

Logistic Regression

Multilayer Perceptron Neural Network

The outputs generated by these classifiers are combined through a meta-learning function formulated as:

$$\hat{y} = f_m(f_1(x), f_2(x), \dots, f_n(x))$$

where $f_1(x), f_2(x), \dots, f_n(x)$ denote the outputs of individual base classifiers and f_m represents the Logistic Regression-based meta-classifier responsible for generating the final prediction.

The stacking ensemble architecture improves predictive performance by reducing bias and variance while capturing both linear and nonlinear relationships among acoustic perturbation biomarkers.

Statistical Feature Interaction Analysis

To investigate relationships among acoustic biomarkers, statistical interaction analysis was performed using correlation-based dependency modeling. The correlation coefficient between acoustic features was calculated as:

$$r_{xy} = \frac{\sum (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum (x_i - \bar{x})^2 \sum (y_i - \bar{y})^2}}$$

where x_i and y_i represent paired acoustic feature observations.

Feature interaction analysis enables identification of nonlinear dependencies among perturbation biomarkers including jitter, shimmer, HNR, RPDE, and DFA. These statistical relationships provide insight into the collective behavior of Parkinsonian speech abnormalities and support interpretation of disease-associated vocal instability.

To represent the interaction structure among biomarkers, a graph-based dependency formulation was also considered:

$$L = D - A$$

where A represents the adjacency matrix of biomarker interactions and D denotes the degree matrix. The Laplacian matrix L provides a quantitative representation of acoustic biomarker connectivity and nonlinear interaction behavior.

Model Evaluation Metrics

The proposed framework was evaluated using multiple statistical performance metrics including accuracy, precision, recall, and F1-score. Classification accuracy was computed as:

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

Precision and recall were determined as:

$$Precision = \frac{TP}{TP + FP}$$

$$Recall = \frac{TP}{TP + FN}$$

while the F1-score was calculated using:

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

To validate statistical significance of predictive improvement, paired t-test analysis was conducted across cross-validation accuracy scores obtained during model training.

Proposed Mathematical Algorithm

Algorithm 1: Nonlinear Vocal Biomarker-Based Parkinson's Disease Detection

Input: Acoustic feature matrix X , class label Y

Output: Predicted class label $\hat{Y}$

Initialize acoustic feature vector:

$$X = \{J, S, H, R, D\}$$

where J , S , H , R , and D denote jitter, shimmer, HNR, RPDE, and DFA, respectively.

Normalize each feature:

$$X' = \frac{X - \mu}{\sigma}$$

Compute nonlinear vocal instability score:

$$V = \alpha J + \beta S + \gamma H + \delta R + \lambda D$$

Generate base learner outputs:

$$P_i = f_i(X'), i = 1, 2, \dots, n$$

Combine base predictions using meta-learning:

$$\hat{Y} = f_m(P_1, P_2, \dots, P_n)$$

Assign final class:

$$\hat{Y} = \begin{cases} 1, & \text{if } P(PD) \geq 0.5 \\ 0, & \text{if } P(PD) < 0.5 \end{cases}$$

Evaluate prediction performance using accuracy, precision, recall, and F1-score.

Results And Discussion

This part provides the experimental analysis of the suggested scheme to predict Parkinson disease. Several machine learning models were trained and tested on the obtained acoustic features, such as the Logistic Regression, Random Forest, Support Vector Machine, K-Nearest Neighbors, Gradient Boosting, and a Stacking Ensemble classifier. The findings indicate that learning as an ensemble can be used to a great effect in order to enhance prediction by utilizing the capability of individual classifiers.

The stacking ensemble model had the most overall accuracy of 97.77 which was better than all the individual machine learning models. Gradient Boosting and Random Forest also proved to have good predictive power above 96 percent, whereas simple models like the Logistic Regression and the K-Nearest Neighbors had relatively poor predictive power.

The confusion and model comparison chart above depicts the effectiveness of the proposed system in classification. Besides predictive accuracy, further analysis was done in order to find out the statistical significance of the results and the role of acoustic features in the classification process.

Statistical Significance Analysis

Several machine learning models were trained and tested to obtain the best predictive model. The models that were taken into consideration in the given study are Logistic Regression, Random Forest, Support Vector Machine, K-Nearest Neighbors, Gradient Boosting, and a Stacking Ensemble classifier.

The outcomes of the experiment show that there is a high degree of differences in the performance of various algorithms. The classic models like the Logistic Regression and the K-Nearest Neighbors showed moderate predictive accuracy because they have less capability to explain nonlinear relationships among biomedical speech characteristics. More sophisticated ensemble algorithms like Random Forest and Gradient Boosting exhibited a significant enhancement in classification accuracy since they are a combination of more than one decision tree and less variance in a model.

The stacking ensemble classifier was the best performing model in the overall performance that was evaluated. In ensemble approach, multiple predictions of base classifiers are combined and a meta-learning model is used to come up with the final prediction. The method enables the model to take the advantages of the various algorithms and minimize the individual model biases.

Table 2 summarizes the performance of each evaluated machine learning model.

Table 2: Performance Comparison of Machine Learning Models

Model	Accuracy	Precision	Recall	F1 Score
Logistic Regression	0.8380	0.7612	0.7969	0.7786
Random Forest	0.9665	0.9833	0.9219	0.9516
Support Vector Machine	0.8994	0.8710	0.8438	0.8571
K-Nearest Neighbors	0.8268	0.7143	0.8594	0.7801
Gradient Boosting	0.9721	0.9836	0.9375	0.9600
Stacking Ensemble (Proposed)	0.9777	0.9839	0.9531	0.9683

The findings show that the stacking ensemble classifier has the highest accuracy of 97.77 percent compared to all other models and this shows that ensemble learning is effective in predicting Parkinson disease.

Statistical Significance Analysis

To confirm the statistical significance of the performance enhancement of the stacking model over the traditional classifiers, paired t-test was done using the cross-validation accuracy scores achieved during training as shown in Figure 9.

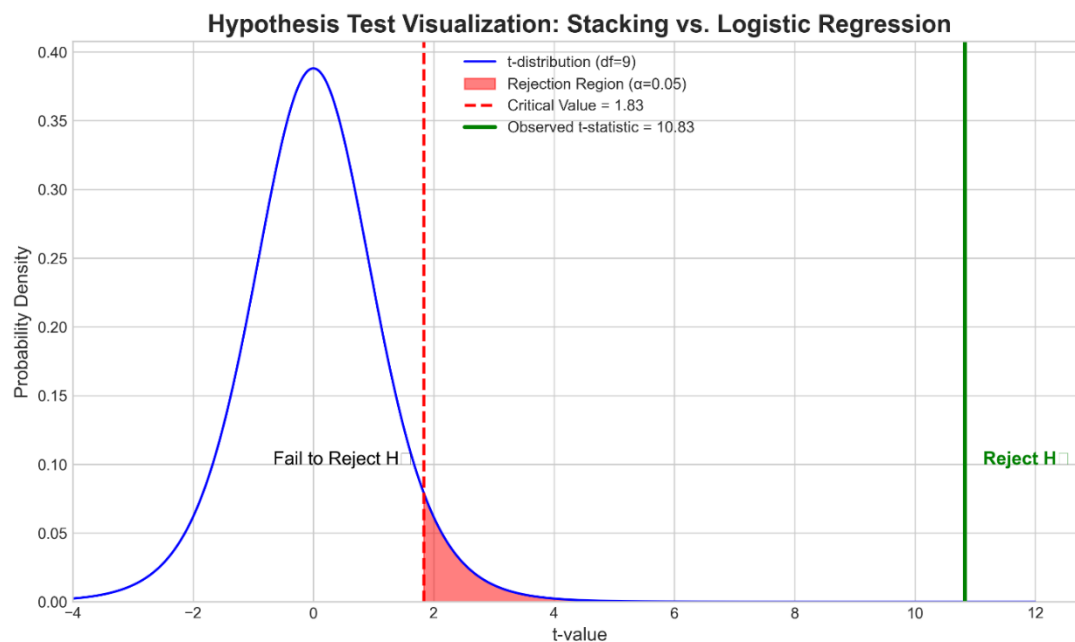


Figure 9: Paired T-Test Distribution Showing Statistical Significance of the Stacking Ensemble Model Compared to Logistic Regression

The hypothesis test is performed to compare the stacking ensemble classifier to the logistic regression as the baseline model.

Null hypothesis (H_0) There is no notable distinction in the performance of the stacking model and the logistic regression.

Alternative hypothesis (H_1): The stacking model is far more effective as compared to logistic regression.

The t-statistic value calculated was around 10.83, which is much greater than the level of significance of criterion value of 1.83 at the level of significance, $\alpha = 0.05$.

The observed statistic is much in the rejection region of the t-distribution as indicated in Figure 9. Thus, the null hypothesis is dismissed, and the fact that the performance improvement of the stacking ensemble classifier is statistically significant and, therefore, does not happen due to random variation, has been proved.

Confusion Matrix Analysis

The confusion matrix of the stacking classifier was examined to gain a deeper insight into the behavior of the proposed model in prediction. The confusion matrix gives a breakdown of the classification results in detail, which indicates the number of samples that were correctly or incorrectly classified.

The experimental evaluation produced the following classification results:

- True Negatives: 114
- False Positives: 1
- False Negatives: 3
- True Positives: 61

These findings suggest that the model rightly categorized most of the Parkinson and normal samples and had very low misclassification values.

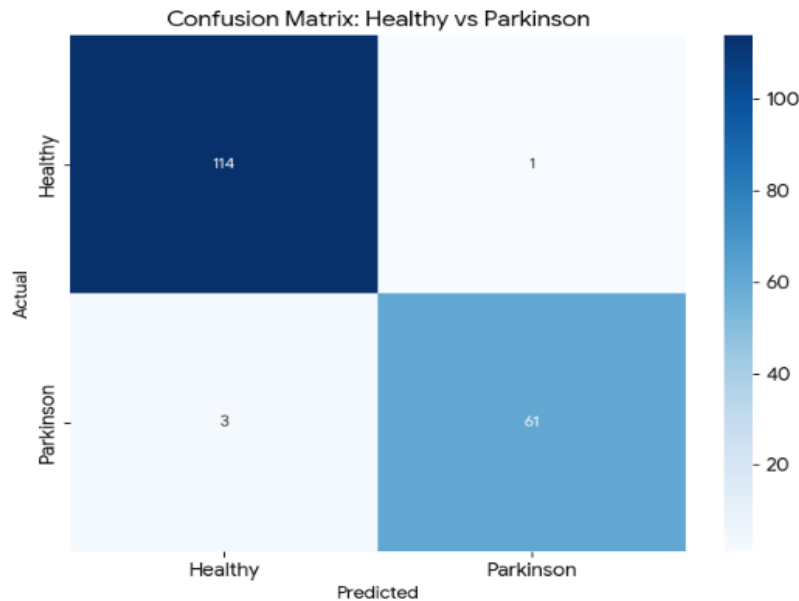


Figure 10: Confusion Matrix of the Proposed Stacking Model

Figure 10 indicates that the confusion matrix indicates that the proposed model has high sensitivity in the detection of the Parkinson disease and a high specificity in healthy individuals. The few false positives and false negatives also prove the stability of the stacking ensemble classifier on predicting Parkinson disease.

Comparative Visualization of Model Performance

In order to further breakdown the performance of various machine learning algorithms a comparative visualization was created to show the accuracy of classification of each model as in Figure 11.

Figure 11 compares the accuracy of the prediction of a number of machine learning algorithms applied in the research.

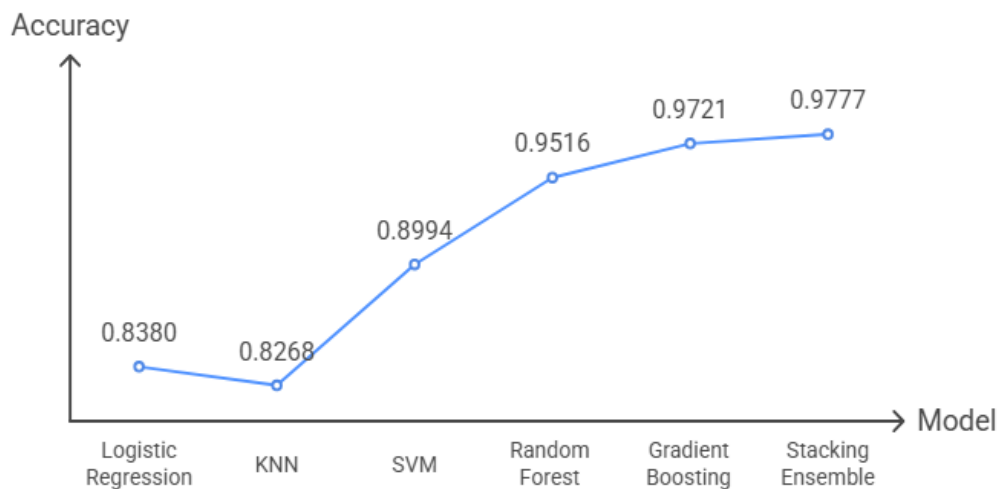


Figure 11: Accuracy Comparison of Machine Learning Models

The figure indicates clearly that ensemble based methods are more efficient than conventional classifiers. Specifically, the stacking model has always been the most predictive due to its combination of various learning strategies into one single framework that enables the meta-classifier to exploit the

advantages of each single model while minimizing the flaws of each.

Acoustic Feature Distribution Analysis

In addition to the classification performance, one should be able to learn the difference between the acoustic features in Parkinson patients and healthy people. To investigate the behavior of a number of valuable vocal biomarkers, extracted out of speech recordings, distribution analysis was conducted.

These characteristics are able to record anomalies in the vibration of vocal folds and changes in amplitude that are usually related to Parkinson disease.

Jitter Feature Distribution

Jitter (%) as shown in Figure 12 is the variation of the vocal frequency cycle to cycle.

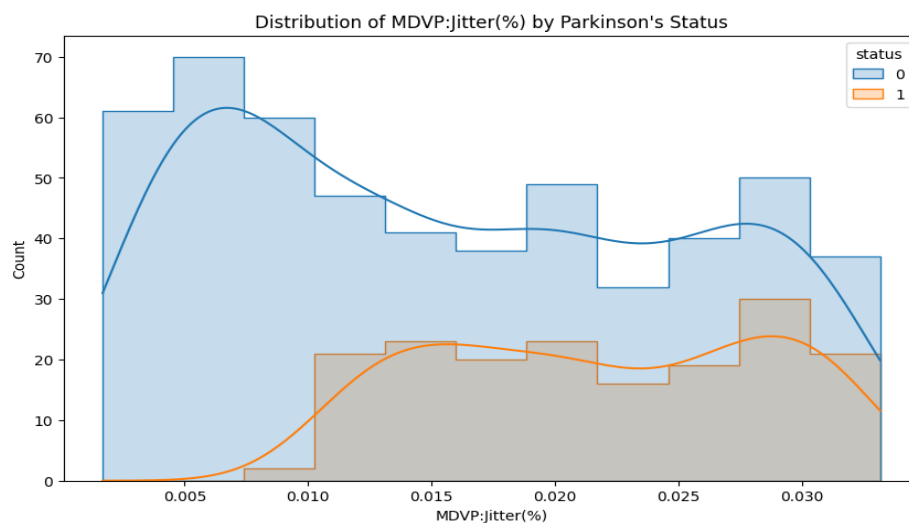


Figure 12: Distribution of Jitter (%) Values for Parkinson's Patients and Healthy Individuals

Jitter is the cycle to cycle fluctuation in vocal frequency. The patients of Parkinson are more likely to have a greater jitter value because they have poor neuromuscular control of the vocal folds. As Figure 12 illustrates, the distribution of Parkinson patients is skewed to the right side of the distribution than the case of healthy individuals, which means that vocal instability and abnormal vocal fold vibrations are more likely to occur in patients with Parkinson disease.

Jitter Feature Distribution

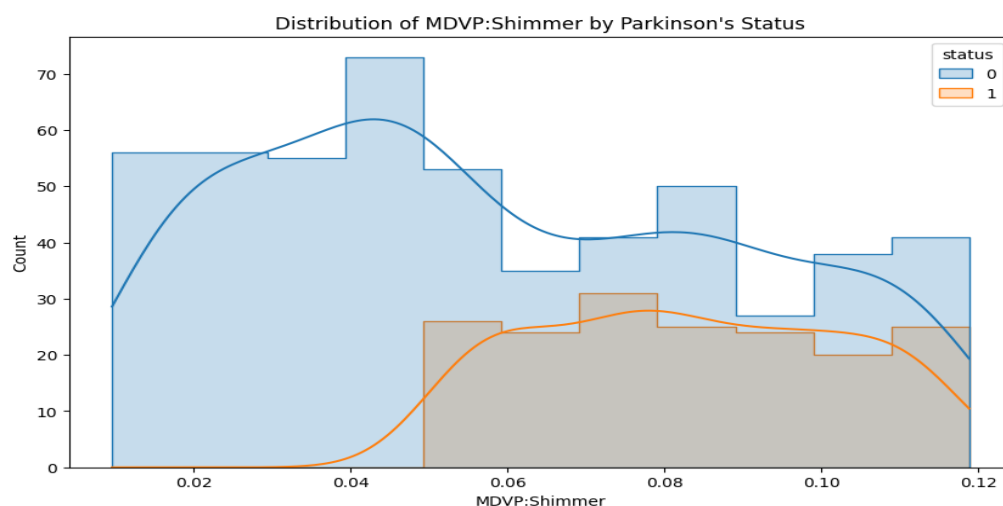


Figure 13: Distribution of Shimmer Values for Parkinson's Patients and Healthy Individuals

Shimmer is used to assess change in amplitude between successive speech cycles. Higher shimmer values imply the instability of the vocal intensity due to the lack of control over the speech apparatus using the motor control. Parkinson patients are more likely to have high amplitude fluctuations than healthy people as demonstrated in Figure 13, which shows that the vibration patterns of the vocal folds are irregular as is common in patients with the Parkinson condition.

Shimmer:APQ5 Feature Distribution

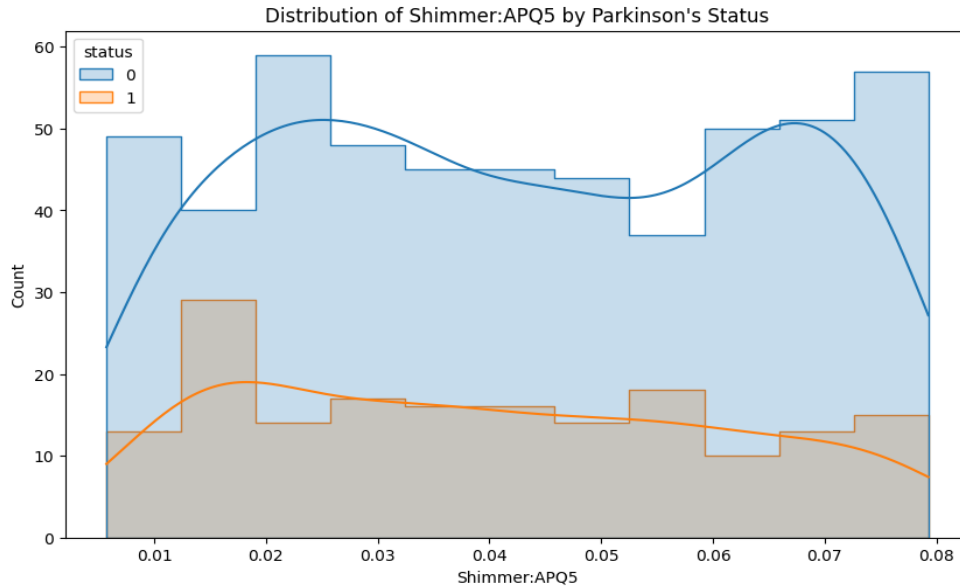


Figure 14: Distribution of Shimmer:APQ5 Values for Parkinson's Patients and Healthy Individuals

Shimmer:APQ5 records short-term changes in speech intensity based on the analysis of amplitude perturbations across five consecutive vocal cycles. Perturbations in vocal fold vibration are usually large because of decreased vocal fold stability in patients with Parkinsonism. Figure 14 demonstrates that the distribution of the patients with Parkinson is skewed to a higher range than that of healthy individuals, which implies that there is more irregularity in the amplitude of speech in cases of the Parkinson disease.

Shimmer:DDA Feature Distribution

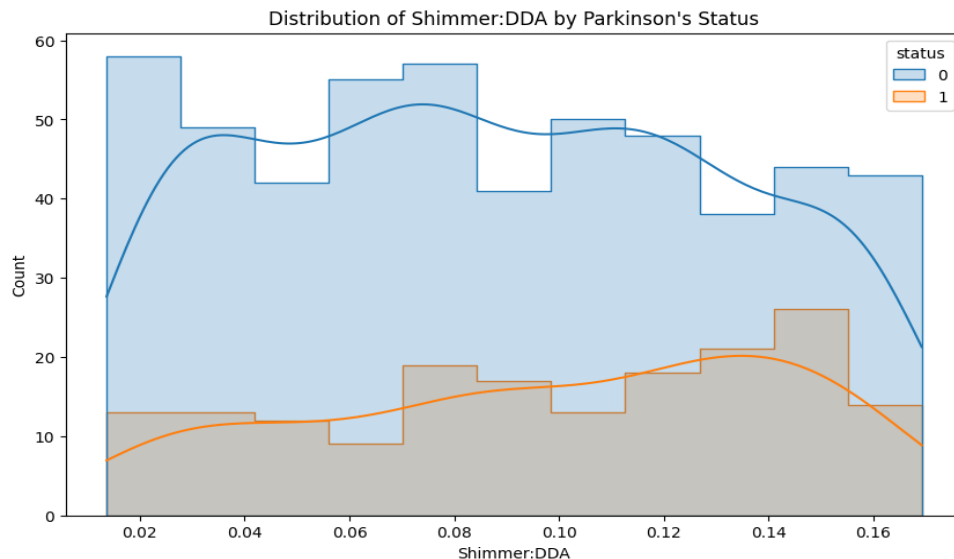


Figure 15: Distribution of Shimmer:DDA Values for Parkinson's Patients and Healthy Individuals

Shimmer:DDA records amplitude perturbation of speech signals by computing the mean absolute difference between consecutive vocal cycle amplitudes. The increase in values is a sign of an increase in instability of the vocal intensity, which is typical of the patients with Parkinson disease. Figure 15 demonstrated that the amplitude fluctuations of the patients with Parkinson are usually larger than those of healthy subjects indicating that the amplitude perturbation features can be useful in enhancing the prediction models of Parkinson disease.

Feature Correlation Analysis

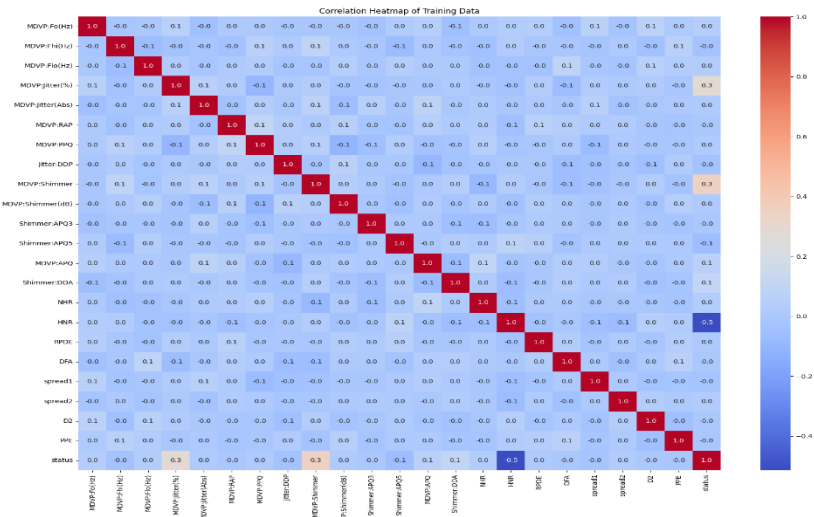


Figure 16: Correlation Heatmap of Acoustic Voice Features

The heatmap in Figure 16 demonstrates the relationship between various speech features and the level of their connection with each other and the variable of the Parkinson’s disease status. Some of the features of perturbation, especially those concerning jitter and shimmer, are moderately correlated with the disease status, which validates these features as diagnostic ones.

Also, the heatmap indicates inter-feature correlations between acoustic variables that reflect comparable speech properties, e.g. frequency perturbation and amplitude variation. This discussion justifies the suitability and usefulness of the chosen acoustic characteristics in machine learning-based detection of Parkinson disease.

Feature Importance Analysis

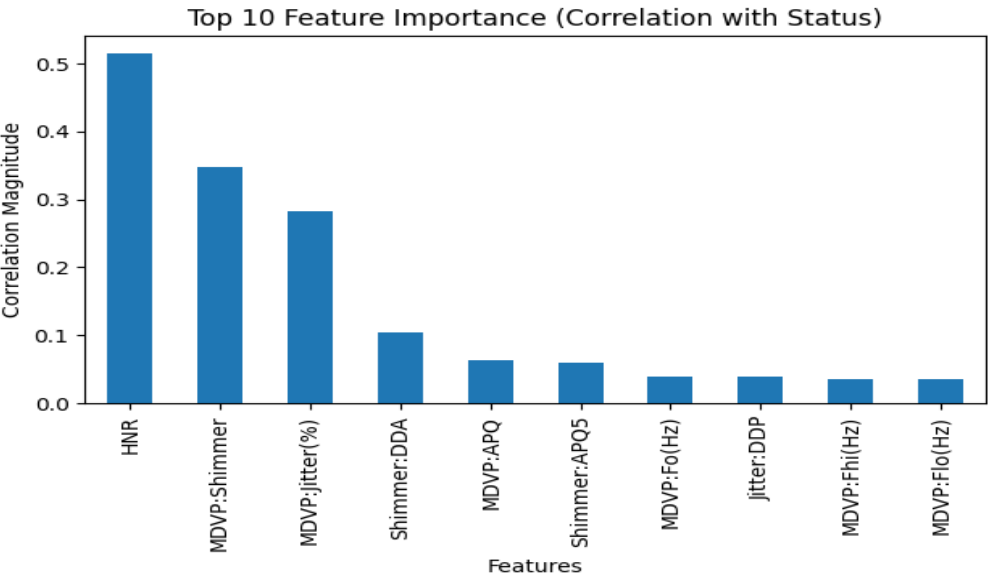


Figure 17: Top acoustic features contributing to Parkinson’s disease prediction.

In order to determine which features are the most useful in the classification process, the feature importance analysis was carried out based on correlation-based ranking. These findings suggest that some of these acoustic perturbation indices, including the jitter, shimmer, harmonic/noise ratio, and nonlinear dynamic attributes, have high discriminative predictive power of the presence of Parkinson disease. These results are comparable to past studies that identified vocal instability as a critical biomarker of Parkinson disease (Figure 17).

System-Level Evaluation

Other than model accuracy, a system architecture view was also considered in the proposed system. The proposal of the framework that incorporates automated feature extraction of speech and a conversational AI assistant makes the proposed framework more realistic than fully algorithmic solutions.

The speech signal analysis module was able to extract acoustic features of voice recordings through the use of speech signal analysis. The machine learning pipeline then used these features to make real-time predictions. A FastAPI backend was used to deploy the prediction system, and the system was able to communicate effectively between the machine learning model and the web interface.

The AI chatbot feature also makes the system more effective as the system can offer contextual explanations and educate the users on the topic of Parkinson disease. This interaction layer will assist the users in having a better idea of the prediction results and motivate them to consult medical specialists in case of need. This type of machine learning prediction systems integration with conversational interfaces is indeed a significant move towards user-friendly healthcare technologies.

Comparison with State-of-the-Art Methods

However, recent development in artificial intelligence has contributed to a tremendous enhancement of the automated recognition and tracking of Parkinson disease based on diverse biomedical measurements and computational systems. The modalities studied by researchers include motion analysis, imaging, wearable sensors, and voice-based biomarkers to identify the symptoms of diseases and their progression. Although such approaches have yielded high potential results, most of the current research centers on the performance of the algorithms, but they lack an end-to-end diagnostic system that can readily interface with the users or provide real-time decision support.

A number of studies have explored the motion-based analysis in the detection of Parkinson disease. Indicatively, a comparative model could be suggested on the basis of 2D webcam shots and 3D motion sensors that assess hypokinesia in Parkinson patients by analyzing their hand-movements [1]. Though the experiment proves the practicability of the low-cost video-based detection, its accuracy is restricted and the system is not capable of handling natural speech input but controlled movement activities. Similarly, machine-learning methods on neuroimaging data have demonstrated possible results in distinguishing between Parkinson's disease and other neurological disorders as well as enhancing the accuracy of the diagnosis in the eyes of radiologists [2]. Nonetheless, imaging-based methods demand costly infrastructures in medicine and are not readily adaptable in massive screening over a distance.

The other studies have been conducted on wearable sensors and gait monitoring of Parkinson disease. Two-stage machine learning model based on vertical ground reaction force signals of foot sensors has shown good abilities to identify Parkinson disease and determine the levels of severity [3]. On the same note, deep learning architectures have been investigated to be used in wearable sensor-based monitoring systems to detect motor states like tremor and dyskinesia during day-to-day activities [6]. Although these methods allow tracking the movement of patients constantly, they need specialized hardware equipment and cannot be used to screen the general population without difficulty.

The most promising non-invasive methods that have been identified to detect Parkinson disease include speech analysis. A number of studies have shown that the differences in the vocal qualities, including jitter, shimmer and harmonic to noise ratio, could be used to effectively differentiate the Parkinson patients and the healthy people. Voice-based machine learning systems have demonstrated promising results in detecting patterns of the disease of Parkinson based on audio patterns [7]. Later

studies have continued to enhance the voice-based detection systems through the use of machine learning algorithms on voice recording and testing a variety of classifiers to predict disease [8]. It has also been suggested that advanced acoustic feature extraction methods and state-of-the-art machine learning models can be used to enhance the reliability and interpretability of the classification [9].

There has also been a study on feature optimization and acoustic feature weighting methods to enhance accuracy in prediction in voice based Parkinson detection systems. The combination of machine learning classifiers and Particle Swarm Optimization (PSO) has been found to improve the performance of the classification by determining the most significant speech characteristics that related to Parkinson's disease [10]. Moreover, deep learning techniques have been used to work with other biomedical data such as voice data, MRI images and handwriting patterns to automatically identify disease-related features [11], [12]. The recent surveys highlight that artificial intelligence and deep learning methods have become critical to the analysis of complicated biomedical data and enhancing the frameworks of early detection of Parkinson's disease [13].

In addition to the diagnostic classification, machine learning has also been used in other clinical areas of the management of Parkinson disease. As a case in point, long-term biomarker analysis coupled with machine learning has been considered to forecast cognitive deterioration in early patients with Parkinson using blood biomarkers [14]. Equally, other voice-based machine learning works have shown that non-invasive screening by sustained vowel phonation and acoustic analysis methods can be achieved [15]. Deep learning models based on images have also been applied to spiral drawings created by patients in order to determine the patterns of motor impairment related to Parkinson's disease [16]. Moreover, smart gloves as wearable devices have been invented to track the intensity of tremors and analyze the motor activity of a patient in a real-time setting [17].

Other new studies have also used sophisticated ensemble learning algorithms and gradient boosting techniques to perform vocal biomarkers analysis in the detection of Parkinson disease [18]. Recurrent neural networks (RNNs) have been suggested to have hybrid deep learning architectures that would enhance the performance of prediction by capturing the temporal dependency in the speech signals [19]. Extensive surveys of the use of artificial intelligence in Parkinson disease underscore the need to have scalable and accessible diagnostic platforms that can combine multiple data modalities and facilitate clinical decision-making systems [20].

Despite the fact that these studies have played an important role in enhancing the accuracy of detection of the Parkinson disease, majority of them invest much on individual machine learning algorithms or on particular biomedical modalities. Table 3 provides a comparative analysis of these methods and their weaknesses.

Comparatively, the suggested framework involves the presentation of a full diagnostic ecosystem, which incorporates automated feature extraction of speech, ensemble machine learning prediction, and conversational AI assistant into a single platform. The system allows users to record voice samples, automatically extract clinically relevant acoustic biomarkers, create prediction results with a stacking ensemble model, and communicate with an AI chatbot that gives educational advice about Parkinson's disease. The combination of predictive modelling and conversational AI with web-based diagnostic interface makes the proposed system unique among a number of existing methods that merely work with algorithmic assessment.

Table 3: Comparison with State-of-the-Art Parkinson's Disease Detection Methods

Study	Data Modality	Technique	System Capability	Key Limitation
[1]	Hand movement video	ML models (SVM, RF, LR)	Motion analysis for PD detection	Requires controlled hand-movement tasks
[2]	Neuroimaging data	ML-based imaging analysis	Improved radiological diagnosis	Requires expensive imaging infrastructure

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[3]	Gait sensor data	Random Forest + Ensemble regression	Detects PD and severity levels	Requires specialized foot sensors
[6]	Wearable sensors	CNN deep learning	Continuous motor state monitoring	Requires wearable hardware
[7]	Voice recordings	ML classifiers (SVM, ANN, KNN)	Voice-based PD detection	Limited system integration
[8]	Voice recordings	ML classification models	Non-invasive PD detection	Small dataset size
[9]	Vocal features	ML models with advanced feature extraction	Improved acoustic feature modeling	Focused mainly on algorithm accuracy
[10]	Voice features	PSO optimized ML classifiers	Acoustic feature optimization	No interactive diagnostic platform
[11]	MRI images	YOLOv5 deep learning	Image-based PD classification	Requires medical imaging data
[12]	Voice signals	Autoencoder + DNN	Deep learning feature extraction	Computationally intensive models
Proposed System	Voice recordings	Stacking Ensemble + AI Chatbot	Automated feature extraction, prediction, and conversational AI assistance	Designed primarily for voice-based screening

Conclusion And Future Work

This study presented a computational biomathematical framework for early Parkinson's disease detection using nonlinear vocal biomarker dynamics and hybrid ensemble learning. The proposed framework integrated speech signal processing, acoustic perturbation analysis, statistical interaction modeling, and stacking-based ensemble intelligence to characterize Parkinsonian speech abnormalities through quantitative computational analysis. Acoustic biomarkers including jitter, shimmer, harmonic-to-noise ratio (HNR), recurrence period density entropy (RPDE), and detrended fluctuation analysis (DFA) were utilized to model instability in vocal fold dynamics associated with neuromuscular degeneration.

The nonlinear perturbation behavior of speech biomarkers was mathematically represented using a composite vocal instability formulation:

$$V(t) = \alpha J + \beta S + \gamma H + \delta R$$

which enabled quantitative interpretation of Parkinsonian speech degradation patterns. Furthermore, the hybrid stacking ensemble framework successfully captured complex linear and nonlinear relationships among acoustic biomarkers, thereby improving predictive robustness and classification stability.

Experimental evaluation performed on 895 speech recordings demonstrated that the proposed framework achieved a classification accuracy of 97.77%, outperforming conventional standalone machine learning approaches. Statistical interaction analysis further revealed substantial nonlinear deviations in acoustic perturbation biomarkers among Parkinson's disease patients compared with healthy individuals, confirming the biological significance of the extracted vocal features. The ensemble prediction mechanism also demonstrated strong discriminative capability in separating Parkinsonian speech perturbations from normal vocal dynamics.

The findings of this study demonstrate the effectiveness of integrating mathematical modeling and hybrid ensemble intelligence for computational analysis of neurodegenerative speech disorders. Unlike conventional artificial intelligence-based prediction systems that primarily emphasize classification accuracy, the proposed framework contributes toward computational biomathematics by incorporating interpretable nonlinear vocal dynamics into the disease prediction process. The framework therefore provides a scalable, non-invasive, and computationally interpretable approach for early Parkinson's disease screening and digital healthcare applications.

Future work may focus on incorporating temporal speech sequence modeling, multimodal neurological biomarkers, stochastic dynamical systems, and deep learning-based nonlinear representation techniques to further enhance computational interpretability and predictive generalization in neurodegenerative disease analysis.

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