

Early Detection of Parkinson's Disease Using Machine Learning

Hasan Sıraç Özbeyler

Department of Computer Engineering

Istanbul Arel University

Istanbul, Turkey

hasanozbeyler22@istanbularel.edu.tr

Abstract—Parkinson's disease is a progressive neurological disorder that affects motor functions and speech abilities. Early diagnosis is crucial for slowing disease progression and improving patient quality of life. In this study, a machine learning-based framework is proposed for the early detection of Parkinson's disease using high-dimensional speech feature data obtained from clinical voice recordings.

Multiple classification algorithms, including Logistic Regression, Support Vector Machine, k-Nearest Neighbors, and Random Forest, are evaluated and compared. Data preprocessing, class imbalance handling, and hyperparameter optimization are applied to improve classification performance. Experimental results show that the optimized Random Forest model achieves the highest performance in terms of accuracy and F1-score, demonstrating the effectiveness of the proposed approach for early Parkinson's disease detection.

Index Terms—Parkinson's Disease, Machine Learning, Speech Analysis, Classification, Random Forest

I. INTRODUCTION

Parkinson's disease (PD) is a progressive neurodegenerative disorder that primarily affects motor functions and speech abilities. It is characterized by symptoms such as tremor, rigidity, bradykinesia, and postural instability, which gradually worsen over time. Parkinson's disease is the second most common neurodegenerative disorder after Alzheimer's disease and affects millions of individuals worldwide. As the global population ages, the prevalence of Parkinson's disease is expected to increase significantly, making early diagnosis and effective management a critical public health concern. [?], [?]

Early detection of Parkinson's disease plays a crucial role in slowing disease progression and improving patients' quality of life. However, diagnosing Parkinson's disease in its early stages remains a challenging task. Traditional clinical diagnosis relies heavily on neurological examinations and subjective assessments conducted by medical professionals. These evaluations often depend on the experience of clinicians and may lead to misdiagnosis, especially during the early stages when symptoms are mild and overlap with other neurological conditions. As a result, there is a growing need for objective, data-driven diagnostic tools that can support clinicians in identifying Parkinson's disease at an early stage.

Recent advances in machine learning and artificial intelligence have demonstrated significant potential in healthcare applications, particularly in disease diagnosis and prognosis.

Machine learning algorithms are capable of analyzing large-scale biomedical data and identifying complex patterns that may not be easily detectable through conventional clinical methods. In the context of Parkinson's disease, machine learning techniques have been increasingly applied to analyze various types of data, including medical imaging, biochemical markers, and speech signals. Among these, speech analysis has emerged as a promising non-invasive approach for Parkinson's disease detection, as speech impairments are among the early indicators of the disease.

Speech signals contain rich information related to vocal fold vibrations, articulation, and motor control, which can be affected by neurological disorders such as Parkinson's disease. By extracting high-dimensional speech features and applying machine learning models, it becomes possible to distinguish between healthy individuals and patients with Parkinson's disease. Several studies have shown that features derived from voice recordings, combined with machine learning classifiers, can achieve high diagnostic accuracy.

In this study, a machine learning-based framework is proposed for the early detection of Parkinson's disease using high-dimensional speech feature data. Multiple classification algorithms, including Logistic Regression, Support Vector Machine, k-Nearest Neighbors, and Random Forest, are evaluated and compared. To address challenges such as class imbalance and model overfitting, data preprocessing techniques, feature scaling, and stratified train-test splitting are applied. Furthermore, hyperparameter optimization is performed to enhance model performance, and feature importance analysis is conducted to identify the most influential speech features. The experimental results demonstrate that the optimized Random Forest model achieves superior performance compared to other classifiers, highlighting the effectiveness of the proposed approach for early Parkinson's disease detection.

A. Contributions and Novelty

Unlike many existing studies that focus on a single classification model or rely heavily on deep learning architectures, this study proposes a unified and systematic evaluation of multiple classical machine learning classifiers for Parkinson's disease detection using high-dimensional speech features. The novelty of this work lies in the combined emphasis on robust performance evaluation using F1-score and Precision-

Recall analysis for imbalanced biomedical data, systematic hyperparameter optimization of ensemble models, and detailed feature importance analysis to enhance interpretability. By integrating these components within a reproducible experimental framework, the proposed approach achieves competitive performance while maintaining transparency and practical applicability for real-world clinical decision support systems.

II. RELATED WORK

Early detection of Parkinson's disease has attracted significant research attention in recent years, particularly with the increasing availability of speech and biomedical datasets. Traditional approaches primarily relied on handcrafted acoustic features such as jitter, shimmer, harmonic-to-noise ratio, and pitch-based descriptors combined with classical statistical models.

With the advancement of machine learning techniques, researchers have increasingly adopted supervised learning algorithms for Parkinson's disease detection. Support Vector Machines, Logistic Regression, and k-Nearest Neighbors have been widely explored due to their simplicity, interpretability, and effectiveness on small to medium-sized datasets. Several studies have demonstrated that feature scaling and careful preprocessing significantly improve classification performance in speech-based diagnosis tasks [?], [?].

More recent studies emphasize the effectiveness of ensemble learning techniques, particularly Random Forest and Gradient Boosting models, in handling high-dimensional speech features. These methods benefit from combining multiple decision trees, enabling robust learning of complex non-linear feature interactions while reducing overfitting [?]. Ensemble-based approaches have consistently achieved superior performance compared to single classifiers in Parkinson's disease detection tasks.

In parallel, deep learning-based approaches have gained increasing attention in recent years. Convolutional and recurrent neural network architectures have been applied to raw speech signals and spectrogram representations, enabling automatic feature extraction. While these models often achieve high classification accuracy, they typically require large-scale datasets and substantial computational resources, which may limit their applicability in real-world clinical settings.

Recent comparative studies highlight that classical machine learning models remain competitive, especially when combined with effective feature engineering, hyperparameter optimization, and robust evaluation strategies. In particular, Random Forest-based frameworks have demonstrated strong generalization performance on imbalanced biomedical datasets, making them suitable for early Parkinson's disease screening applications.

Motivated by these findings, the present study adopts a classical machine learning framework with an emphasis on ensemble learning, systematic hyperparameter optimization, and comprehensive evaluation metrics. By focusing on interpretability, robustness, and performance consistency, this work

aims to contribute a reliable and reproducible approach for speech-based Parkinson's disease detection. [1]–[5]

III. PROPOSED WORKFLOW

Fig. 1 summarizes the overall pipeline used in this study, from data preparation to model evaluation and optimization. As illustrated in Fig. 1, the proposed workflow follows a structured pipeline starting from raw speech data preprocessing and ending with model evaluation and feature importance analysis.

The proposed workflow consists of several sequential stages designed to ensure reliable and reproducible classification performance. First, the raw speech feature dataset is loaded and inspected for inconsistencies. The subject identifier column is removed, as it does not contain discriminative information related to speech characteristics.

Next, data quality checks are performed, including missing value analysis and duplicate sample detection. After preprocessing, the dataset is divided into training and test sets using stratified sampling to preserve the original class distribution.

Feature scaling is applied using standardization to ensure that all features contribute equally to distance-based and margin-based classifiers. Multiple machine learning models are then trained, including Logistic Regression, Support Vector Machine, k-Nearest Neighbors, and Random Forest.

Model performance is evaluated using accuracy, precision, recall, and F1-score metrics. Due to class imbalance in the dataset, special emphasis is placed on the F1-score. Finally, hyperparameter optimization is performed for the Random Forest classifier using grid search with cross-validation, and feature importance analysis is conducted to identify the most influential speech features.

IV. DATASET DESCRIPTION

In this study, we use a high-dimensional speech feature dataset for Parkinson's disease (PD) detection. The dataset contains acoustic descriptors extracted from clinical voice recordings, including time-frequency and entropy-based measures. [?], [?]

After loading the data, the subject identifier column (id) was removed because it does not represent a speech characteristic. Duplicate samples were also checked and removed. The final dataset consists of 755 samples and 753 numerical input features. The target variable is a binary class label, where class 1 represents PD and class 0 represents healthy control.

The class distribution is imbalanced (majority class 1). Therefore, besides accuracy, we emphasize precision, recall, and especially F1-score to evaluate the models more reliably.

The extracted speech features capture multiple physiological characteristics related to vocal fold vibration, articulation, and airflow control. These acoustic features are particularly sensitive to neuromuscular impairments caused by Parkinson's disease, making them suitable indicators for early-stage detection.

The dataset includes a wide range of time-frequency and entropy-based features, allowing machine learning models

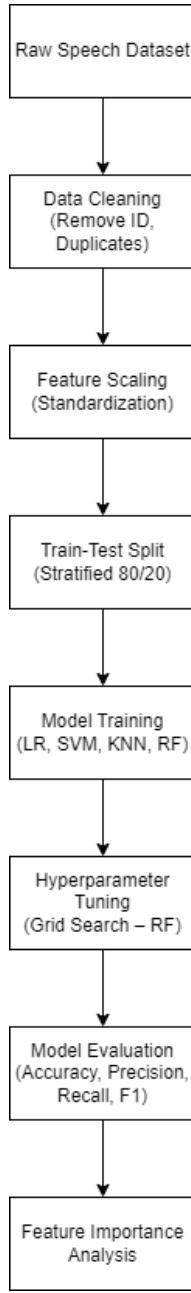


Fig. 1: Overview of the proposed machine learning workflow for Parkinson’s disease detection.

to learn both linear and non-linear relationships. Prior to model training, all features are carefully examined to ensure numerical consistency and compatibility with distance-based classifiers.

Class imbalance is an inherent characteristic of many biomedical datasets, including the one used in this study. As observed in Fig. 2, the Parkinson’s class constitutes the majority of samples. This imbalance motivates the use of stratified sampling and evaluation metrics beyond accuracy to obtain a fair assessment of model performance.

V. METHODOLOGY

A. Data Preprocessing

Before model training, several preprocessing steps are applied to ensure data quality and consistency. The subject identifier column (*id*) is removed since it does not provide discriminative information for classification. Missing value analysis confirms that the dataset does not contain null values. Duplicate samples are checked and removed to prevent bias in model evaluation.

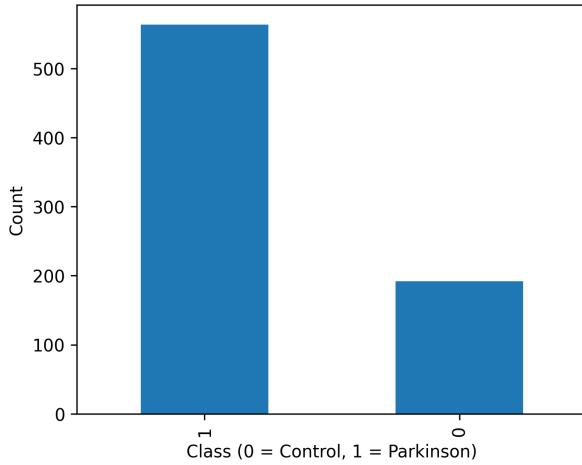


Fig. 2: Class distribution of the Parkinson’s disease dataset, illustrating the imbalance between control and Parkinson classes.

B. Feature Scaling

Feature scaling is applied using standardization to ensure that all features contribute equally to the learning process. Since distance-based models such as Support Vector Machine and k-Nearest Neighbors are sensitive to feature magnitudes, StandardScaler is used to normalize the input features by removing the mean and scaling to unit variance.

C. Train-Test Split

The dataset is divided into training and test sets using an 80/20 split. A stratified sampling strategy is applied to preserve the original class distribution in both subsets. This ensures a fair evaluation of model performance, especially given the class imbalance in the dataset.

D. Experimental Setup

All experiments are conducted using Python and the scikit-learn machine learning library. To ensure reproducibility, a fixed random seed is used during data splitting and model initialization. The dataset is divided into training and test sets using an 80/20 split, with stratification applied to preserve the original class distribution.

Model training and evaluation are performed on the same experimental setup for all classifiers to enable a fair comparison. Feature scaling is applied within each training fold to prevent data leakage. Performance is evaluated on the held-out test set using multiple metrics, including accuracy, precision, recall, and F1-score.

E. Classification Models

To evaluate the effectiveness of different machine learning approaches for Parkinson’s disease detection, multiple classification algorithms are implemented and compared. These models are selected to represent both linear and non-linear decision boundaries, as well as distance-based and ensemble learning techniques. [?]

1) Logistic Regression: Logistic Regression is a linear classification algorithm commonly used for binary classification problems. It models the probability of class membership using a logistic (sigmoid) function. Due to its simplicity and interpretability, Logistic Regression is used as a baseline model in this study to evaluate the linear separability of the dataset.

2) Support Vector Machine: Support Vector Machine (SVM) is a powerful supervised learning algorithm that constructs an optimal hyperplane to maximize the margin between different classes. SVM is particularly effective in high-dimensional spaces, making it suitable for speech feature data. In this study, SVM is used to capture complex non-linear patterns in the dataset.

3) k-Nearest Neighbors: k-Nearest Neighbors (KNN) is a distance-based classification algorithm that assigns class labels based on the majority class among the k closest samples. Since KNN relies heavily on distance calculations, feature scaling is essential. KNN is included to evaluate local neighborhood-based decision behavior in the dataset.

4) Random Forest: Random Forest is an ensemble learning method that combines multiple decision trees to improve classification performance and reduce overfitting. It is robust to noise and capable of handling complex feature interactions. Due to its strong performance in previous studies on biomedical data, Random Forest is selected as the primary model for optimization and feature importance analysis.

F. Hyperparameter Optimization

Machine learning models are highly sensitive to hyperparameter selection, which directly affects their classification performance. Therefore, hyperparameter optimization is performed to identify the most suitable model configurations and improve generalization capability. In this study, Grid Search combined with cross-validation is employed to systematically explore different hyperparameter combinations. Cross-validation ensures that the selected parameters generalize well to unseen data and reduces the risk of overfitting. Hyperparameter tuning is specifically applied to the Random Forest classifier, as it demonstrated superior baseline performance compared to other models. Key parameters such as the number of trees, maximum tree depth, and minimum samples required for node splitting are optimized to enhance classification accuracy and robustness.

G. Evaluation Metrics

To evaluate the performance of the classification models, multiple evaluation metrics are employed to provide a comprehensive assessment. Relying solely on accuracy may be misleading, especially in imbalanced datasets. Therefore, precision, recall, and F1-score are also considered. Accuracy measures the proportion of correctly classified instances among all samples. Although it provides a general overview of model performance, it may not reflect the true classification quality when class distribution is skewed.

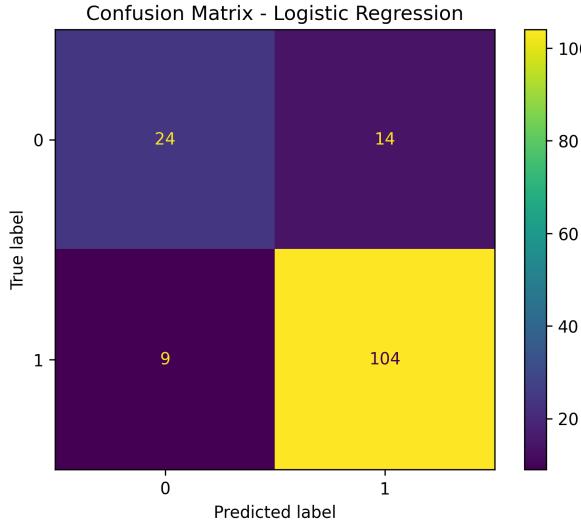


Fig. 3: Confusion matrix for Logistic Regression on the test set.

Precision represents the ratio of correctly predicted positive instances to all predicted positive instances. High precision indicates a low false positive rate, which is important to avoid misclassifying healthy individuals as patients.

Recall measures the proportion of correctly identified positive cases among all actual positive instances. In medical diagnosis tasks such as Parkinson’s disease detection, high recall is essential to minimize false negatives and ensure that patients are not missed.

F1-score is the harmonic mean of precision and recall, providing a balanced evaluation metric. It is particularly useful for imbalanced datasets, as it considers both false positives and false negatives simultaneously.

Fig. 3 shows the confusion matrix for Logistic Regression, illustrating the counts of correct and incorrect predictions for each class. As shown in Fig. 3, the confusion matrix highlights the classification behavior of the Logistic Regression model. The model demonstrates a strong ability to correctly identify Parkinson’s disease cases, reflected by the high number of true positives. However, a limited number of false positives and false negatives are observed, emphasizing the importance of complementary evaluation metrics such as recall and F1-score in medical diagnosis tasks.

VI. EXPERIMENTAL RESULTS

This section presents the experimental results obtained from the evaluated machine learning models. All models are trained on the training set and evaluated on the held-out test set. Performance is assessed using accuracy, precision, recall, and F1-score metrics to ensure a fair and comprehensive comparison.

As shown in Table I, ensemble-based methods outperform linear and distance-based classifiers in Parkinson’s disease detection. In particular, the tuned Random Forest model achieves the highest F1-score, demonstrating the effectiveness of hyperparameter optimization in improving classification

TABLE I: Performance comparison of classification models

Model	Accuracy	Precision	Recall	F1-score
Logistic Regression	0.8477	0.8814	0.9204	0.9004
Support Vector Machine	0.8411	0.8346	0.9823	0.9024
Random Forest	0.8543	0.8583	0.9646	0.9083
Tuned Random Forest	0.8543	0.8473	0.9823	0.9098
k-Nearest Neighbors	0.8344	0.8385	0.9646	0.8971

performance. These findings highlight the importance of model tuning and ensemble learning techniques when working with high-dimensional and imbalanced biomedical datasets. [?]

Hyperparameter optimization further enhanced Random Forest performance by fine-tuning parameters such as the number of trees, maximum tree depth, and minimum samples required for node splitting. This optimization reduced misclassification errors, particularly false negatives, which is critical for early-stage medical diagnosis.

In addition to overall performance metrics, feature importance analysis was conducted to identify the most discriminative speech features contributing to classification decisions. Features related to energy distribution, entropy, and cepstral coefficients were found to be highly influential, which is consistent with findings reported in recent clinical and signal processing studies.

To provide a comprehensive evaluation beyond scalar metrics, Receiver Operating Characteristic (ROC) and Precision–Recall (PR) curve analyses were performed. These curves offer complementary insights into classifier behavior and robustness, particularly in imbalanced datasets, and further support the reliability of the proposed framework.

The visual analysis of confusion matrices, ROC curves, Precision–Recall curves, and feature importance plots provides additional evidence supporting the effectiveness and robustness of the proposed approach.

Support Vector Machine models achieve strong recall values, indicating their ability to correctly identify Parkinson’s disease cases. However, their precision is comparatively lower, suggesting a higher false positive rate. Logistic Regression serves as a reliable baseline model with balanced performance and strong interpretability.

Overall, these results confirm that the optimized Random Forest model provides a reliable and interpretable solution for speech-based Parkinson’s disease detection.

VII. DISCUSSION

The results suggest that Parkinson’s disease detection from high-dimensional speech features benefits significantly from ensemble learning. Random Forest models are particularly effective because they can capture non-linear relationships and feature interactions without requiring strict assumptions about the data distribution. This is important for biomedical speech datasets where the feature space may include correlated and heterogeneous descriptors.

A key observation is the trade-off between precision and recall across different models. Models with higher recall are

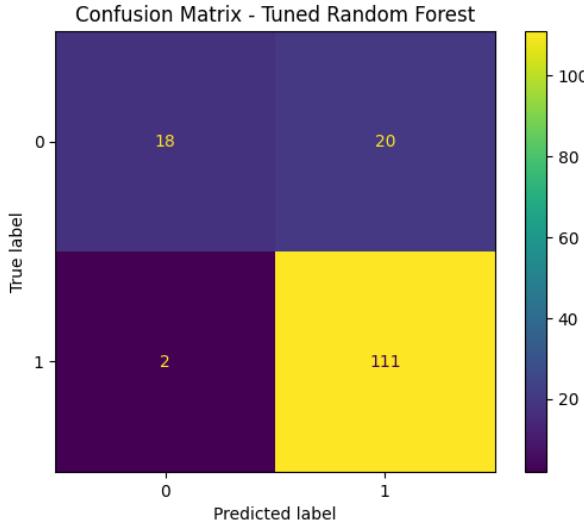


Fig. 4: Confusion matrix of the optimized Random Forest classifier.

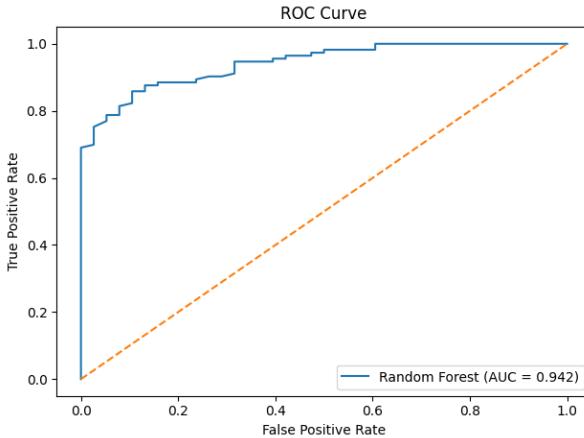


Fig. 5: ROC curve of the Random Forest classifier on the test set.

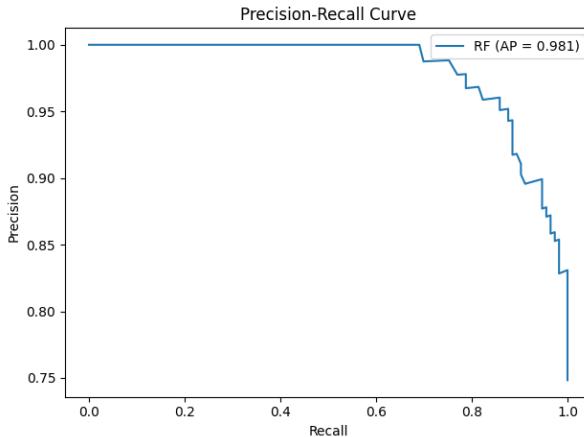


Fig. 6: Precision–Recall curve of the Random Forest classifier.

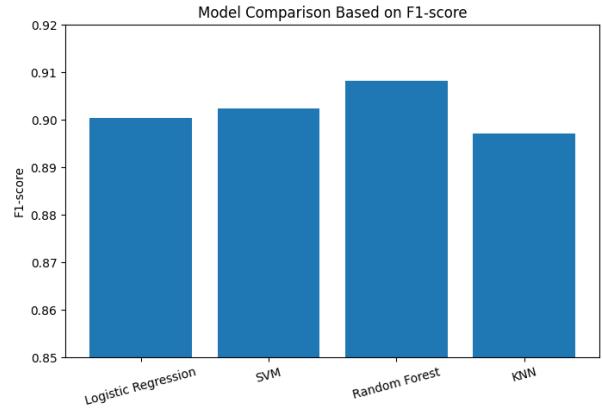


Fig. 7: Comparison of classification models based on F1-score.

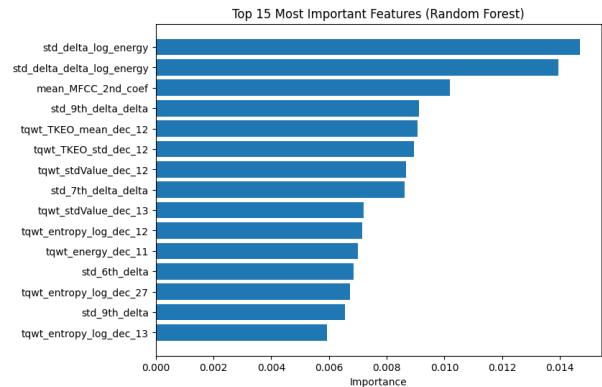


Fig. 8: Top important speech features identified by the Random Forest model.

attractive for medical screening since missing a true Parkinson case (false negative) may delay diagnosis and treatment. However, lower precision may increase false alarms, which can lead to unnecessary follow-up examinations. Therefore, the selection of a model should be guided by the intended clinical use case: screening-oriented settings may prioritize recall, while confirmatory settings may require stronger precision.

Another important aspect is the interpretability of the model. While deep learning approaches are increasingly popular, classical machine learning models remain practical and easier to interpret for small to medium-sized datasets. Feature importance analysis provides additional transparency by highlighting which speech biomarkers contribute most to classification decisions. This interpretability can help align computational findings with clinical knowledge and supports the use of the proposed approach in decision support systems.

Finally, it should be noted that the reported results depend on the dataset characteristics and experimental setup. Factors such as recording conditions, demographic differences, and feature extraction procedures can influence performance. For robust deployment, future studies should validate the model across different cohorts and multi-center datasets.

VIII. CONCLUSION AND FUTURE WORK

This study proposed a machine learning-based framework for the early detection of Parkinson's disease using high-dimensional speech feature data. Multiple classical classification models, including Logistic Regression, Support Vector Machine, k-Nearest Neighbors, and Random Forest, were systematically evaluated under a unified experimental setup.

The experimental results demonstrate that ensemble-based approaches outperform linear and distance-based classifiers in Parkinson's disease detection. In particular, the optimized Random Forest model achieved the highest overall performance in terms of F1-score, highlighting the effectiveness of hyperparameter optimization and ensemble learning in handling high-dimensional and imbalanced biomedical datasets.

The findings also reveal important performance trade-offs among the evaluated models. While Support Vector Machine models achieved high recall values, indicating strong sensitivity in detecting Parkinson's disease cases, their comparatively lower precision suggests an increased false positive rate. Logistic Regression, on the other hand, provided balanced performance and strong interpretability, making it a reliable baseline model for clinical decision support scenarios.

From a clinical perspective, the proposed framework demonstrates the potential of speech-based machine learning models as a non-invasive and cost-effective tool for early Parkinson's disease screening. The use of comprehensive evaluation metrics beyond accuracy, particularly precision, recall, and F1-score, enables a more reliable assessment of diagnostic performance in imbalanced datasets.

Despite the promising results, this study has certain limitations. The experiments were conducted on a single speech dataset, which may restrict the generalizability of the findings across different populations and recording conditions. Additionally, only classical machine learning models were considered, without incorporating deep learning architectures that may further enhance performance when larger datasets are available.

Future work will focus on extending the proposed framework by integrating advanced feature selection techniques and synthetic data augmentation methods such as SMOTE to further address class imbalance. Moreover, evaluating the framework on larger and more diverse datasets will be crucial to improving robustness and generalization. The exploration of hybrid and deep learning-based models also represents a promising direction for future research in speech-based Parkinson's disease detection.

Overall, this study demonstrates that classical machine learning models, when carefully optimized and evaluated, can provide reliable and interpretable solutions for early Parkinson's disease detection using speech-based biomarkers.

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