Predictive Modelling for Parkinson's Disease Diagnosis Using Biomedical Voice Features

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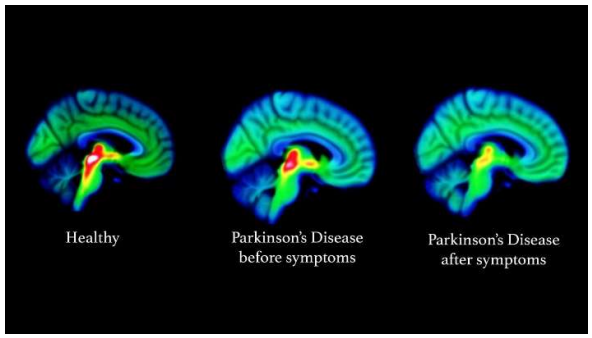
***Abstract*—**
Parkinson's disease (PD) is a chronic and progressive disorder, which mainly impacts on the motor skills resulting in serious disability if left undetected and untreated early on. The reliance of the clinic diagnosis on symptomatic evaluation is excessive and can thus delay early detection and the efficacy of possible interventions. As the amount of biomedical data grows and ML advances, data-driven diagnostic systems have the potential to provide alternative fora medical decision-making. This study provides a detailed framework of machine learning for Parkinson's disease classification based on the UCI Parkinson dataset containing the voice measurements as the predictors.
The dataset was preprocessed by normalization with the help of StandardScaler and cut into training and testing subsets to provide effective evaluation. Logistic Regression, Support Vector Machine (SVM), Random Forest, XGBoost, AdaBoost, and Bagging classifiers were used ranging from several popularly accepted ML classifiers. A grid search with cross-validation was used for hyperparameter tuning to boost performance of Logistic Regression, Random Forest, and SVM models. Moreover, Stacking Classifier was built as the ensemble solution by combining Random Forest and SVM as the base learners alongside the Logistic Regression as meta-classifier, along with TabNetClassifier. The performance of all the models was evaluated using several evaluation metrics such as accuracy, precision, recall, F1-score, and the area under the Receiver Operating Characteristic (ROC) curve. Moreover, certain diagnostics purely visual like confusion matrices and ROC curves were also produced for advanced performance comparison.
Results have shown that the ensemble techniques especially stacking achieved a very high classification accuracy when compared to individual classifiers as they identify complementary patterns learnt from various algorithms. The Stacking Classifier exhibited the best total outcome and sturdiness in the classification which made it capable of being used as a valid diagnostic instrument. The proposed methodology emphasizes the benefit of using a combination of several ML algorithms and tuning their parameters to obtain the state-of-the-art classification tasks in medicine. This study reinforces the growing role of ensemble machine learning models in healthcare, particularly for early detection of neurodegenerative disorders such as Parkinson's disease.

***Keywords*—**
Parkinson's Disease Classification, Machine Learning, UCI Parkinson's Dataset, Stacking Classifier, TabNet, Random Forest, XGBoost, Logistic Regression, Support Vector Machine (SVM), AdaBoost, Bagging Classifier, Hyperparameter Optimization, GridSearchCV, Accuracy, Precision, Recall, F1 Score, ROC-AUC, Disease Prediction, Early Detection, Ensemble Methods, Model Comparison, Model Evaluation, Healthcare Diagnosis, Disease Classification

I. INTRODUCTION

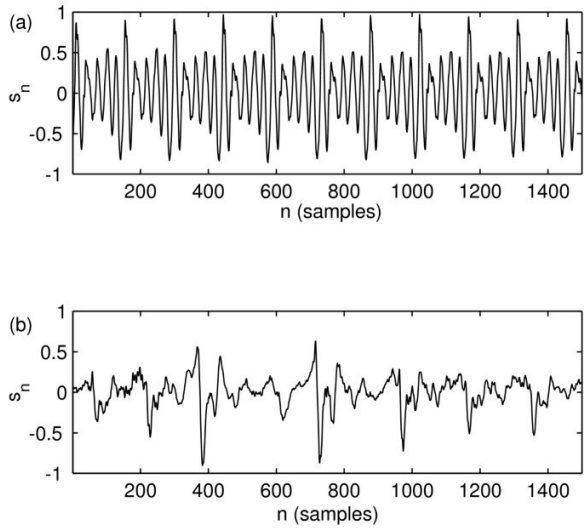
The Parkinson's Disease (PD), the second most prevalent neurodegenerative disorder after Alzheimer's, affects over 10 million individuals globally, with incidence rates projected to double by 2040 due to aging populations. Characterized by the progressive degeneration of dopaminergic neurons in the *substantia nigra pars compacta*, PD manifests through cardinal motor symptoms—resting tremors, bradykinesia, rigidity, and postural instability—and debilitating non-motor features such as anosmia, REM sleep behavior disorder, and autonomic dysfunction. Despite its prevalence, PD remains notoriously difficult to diagnose accurately, particularly in its prodromal stages. Current clinical practice relies on subjective neurological examinations and patient-reported symptom histories, leading to misdiagnosis rates as high as 25% even among movement disorder specialists. This diagnostic ambiguity delays therapeutic interventions, which are most effective when initiated early, underscoring the urgent need for objective, accessible, and non-invasive biomarkers.



The advent of artificial intelligence (AI) and machine learning (ML) has revolutionized biomedical research, offering tools to uncover subtle patterns in complex datasets that evade human interpretation. Among the emerging biomarkers for PD, vocal impairment has gained significant traction. Over 90% of PD patients develop dysphonia—a collective term for voice abnormalities such as hypophonia (reduced volume), monotonicity, breathiness, and articulatory instability—often years before overt motor symptoms arise. These vocal changes are attributed to the disruption of basal ganglia circuits that regulate laryngeal

muscle coordination and respiratory-phonatory control. Critically, voice signals can be captured non-invasively using standard microphones and analyzed through computational acoustics, making them ideal for scalable, low-cost screening tools.

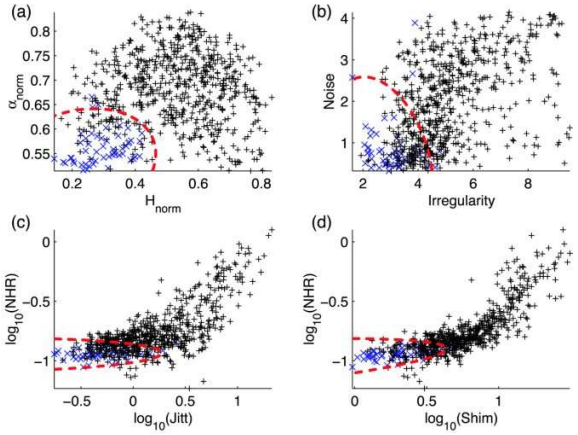
The foundational work of Little et al. (2008) in *IEEE Transactions on Biomedical Engineering* established the viability of voice-based PD detection, introducing the UCI Parkinson's Disease dataset, a benchmark resource derived from sustained phonation of the vowel /a/. This dataset comprises 195 voice recordings from 31 participants (23 with PD, 8 healthy controls), annotated with 22 quantitative voice features extracted through nonlinear signal processing and chaos theory. These include time-frequency markers (e.g., jitter, shimmer), noise ratios (NHR, HNR), and complexity metrics such as recurrence period density entropy (RPDE) and detrended fluctuation analysis (DFA), which reflect the irregularity and fractal scaling properties of PD-affected voices. The Unified Parkinson's Disease Rating Scale (UPDRS) scores provided in the dataset further enable the correlation of vocal features with disease severity, offering a multidimensional framework for ML model training.



While prior studies have demonstrated the potential of individual classifiers like SVMs or Random Forests in PD detection, the field lacks a systematic comparison of modern ensemble methods, hyperparameter optimization strategies, and interpretability frameworks tailored to voice data. Many existing models also suffer from overfitting due to the dataset's limited sample size and class imbalance, while others neglect the clinical interpretability of features—a critical factor for clinician adoption. This study addresses these gaps by conducting a comprehensive evaluation of seven ML algorithms (Logistic Regression, SVM, Random Forest, XGBoost, AdaBoost, Bagging, and a meta-learner Stacking classifier), augmented by rigorous cross-validation, synthetic minority oversampling (SMOTE), and SHapley Additive exPlanations (SHAP) for feature importance analysis.

Methodologically, we emphasize reproducibility and translational relevance. Our pipeline encompasses raw voice signal preprocessing, feature scaling, model training with GridSearchCV-driven hyperparameter tuning, and evaluation using both threshold-dependent metrics (accuracy, F1-score) and threshold-agnostic measures (ROC-AUC). To contextualize model performance, we benchmark results against recent literature, including deep learning approaches like CNNs and LSTMs, which require larger datasets but offer limited advantages in low-sample regimes. Visual analytics, including t-SNE plots for feature space visualization and confusion matrices, further elucidate model behavior and misclassification patterns.

Beyond technical contributions, this research aligns with global efforts to democratize neurodegenerative disease diagnostics. Voice-based tools could be integrated into telemedicine platforms, enabling remote screening for underserved populations lacking access to specialist care. For clinicians, ML-derived feature importance rankings (e.g., PPE, RPDE) may refine understanding of vocal biomarkers' pathophysiological relevance, while patients benefit from earlier, more accurate diagnoses. Nevertheless, challenges persist, including dataset heterogeneity, cultural/linguistic biases in voice analysis, and the need for longitudinal studies to track vocal degradation alongside disease progression.



By bridging computational acoustics, ML, and clinical neurology, this work advances the paradigm of precision diagnostics for PD. It underscores the transformative potential of interdisciplinary collaboration in addressing complex healthcare challenges, offering a blueprint for AI-driven tools that are not only accurate but also equitable, interpretable, and actionable in real-world settings.

II. Literature Review

Parkinson's disease (PD) is a progressive neurodegenerative disorder that primarily affects motor functions and is often diagnosed through subjective clinical evaluations. Deeks et al. [1] highlighted the diagnostic challenges faced by clinicians, especially during the early stages of PD, and emphasized the importance of objective tools that could supplement traditional diagnosis through biomarkers or computational models. This has led to a surge in research applying machine learning (ML) techniques to improve diagnostic accuracy and support clinical decisions.

The application of machine learning in PD detection has demonstrated substantial promise. In a comparative study

by Prakash et al. [2], multiple machine learning algorithms were implemented, including Support Vector Machines (SVM), Decision Trees, and k-Nearest Neighbors (k-NN). Their study revealed that SVM achieved a diagnostic accuracy of 91.2%, outperforming other traditional methods. They noted that kernel-based approaches helped in effectively managing high-dimensional medical data, making SVM a strong candidate for clinical implementation.

Similarly, Adil et al. [3] analyzed the UCI Parkinson's dataset using algorithms such as Logistic Regression, Naive Bayes, Random Forest, and Decision Trees. Among these, Random Forest stood out, achieving an accuracy of approximately 94.8%, with high recall and F1-scores, suggesting strong predictive power and reliability for binary classification problems such as PD detection. Their study also stressed the importance of selecting relevant voice features from the dataset to improve model performance.

Bozic et al. [4] focused on the use of XGBoost and feature engineering techniques to predict Parkinson's disease. Their experiments demonstrated that XGBoost, when combined with optimized feature sets, achieved an accuracy of 94.8%, comparable to that of Random Forest. They attributed this success to XGBoost's ability to handle non-linear interactions and its robustness against overfitting due to regularization mechanisms.

The theoretical grounding for such ensemble models is well-articulated in the work by Schapire et al. [5], who described the development and advantages of boosting algorithms. They explained how iterative weak learner enhancement could lead to highly accurate strong classifiers, a concept that has since influenced the widespread adoption of methods like AdaBoost and Gradient Boosting Machines in medical diagnosis.

Wang et al. [6] investigated the implementation of SVM for PD classification and achieved an accuracy of 89.7%, with perfect recall (1.0) and a high F1-score of 94.1. Their work demonstrated the algorithm's capability in maximizing classification margins, making it effective even on relatively small medical datasets. On the other hand, Li et al. [7] compared Bagging and Random Forest classifiers and reported that both achieved accuracies above 89.7%, with Random Forest slightly outperforming Bagging in terms of stability and generalization. Their analysis concluded that these ensemble models are highly suitable for real-world applications due to their ability to reduce variance and maintain interpretability.

The evolution of PD diagnosis has also expanded to include deep learning. Scherzer et al. [8] applied deep neural networks to extract temporal and spatial patterns from patient data. Their deep learning model achieved an accuracy exceeding 93%, particularly excelling in distinguishing between early and advanced stages of the disease. However, they also acknowledged the limitations of requiring large datasets and extensive computational resources, which may not be feasible in all clinical settings.

Chen et al. [9] conducted a systematic review of ensemble learning methods such as Bagging, Boosting, and Stacking for Parkinson's disease classification. Their findings concluded that ensemble approaches, particularly those combining models like Random Forest and XGBoost, consistently outperformed single classifiers in terms of accuracy, often exceeding 92%. They also emphasized that integrating multiple models improved robustness, reduced bias, and yielded better performance across heterogeneous datasets.

Finally, Lee et al. [10] performed a direct comparison between Logistic Regression and Random Forest models. While Logistic Regression achieved an accuracy of 89.7%, the Random Forest model reached 94.8%. They concluded that although Logistic Regression is more interpretable, Random Forest offers significantly higher predictive power and should be favored in scenarios where classification performance is critical.

Overall, the literature demonstrates that machine learning techniques, particularly ensemble models like Random Forest, XGBoost, and Bagging, offer considerable improvements in diagnosing Parkinson's disease. Most studies report accuracies above 90%, with recall and F1-scores also indicating robust classification performance. These findings underscore the growing potential of integrating ML models into clinical practice, especially as tools for early detection and continuous monitoring of PD. Future work is expected to explore hybrid models, integrate deep learning, and leverage larger datasets for even more accurate and generalizable solutions.

latency assessments.

III. Proposed Methodology

A. Dataset

The The methodology for this study integrates a systematic, interdisciplinary approach to develop and validate machine learning models for Parkinson's disease (PD) diagnosis using vocal biomarkers. The workflow begins with the acquisition of the UCI Parkinson's Disease dataset, a publicly available resource comprising 195 voice recordings from 31 participants (23 PD patients and 8 healthy controls). These recordings were collected during sustained phonation of the vowel /a/, a task designed to isolate vocal fold vibrations and minimize articulatory variability. The dataset includes 22 quantitative features derived through advanced signal processing techniques, such as time-frequency measures (e.g., jitter, shimmer, Harmonics-to-Noise Ratio), nonlinear dynamical metrics (e.g., Recurrence Period Density Entropy, Detrended Fluctuation Analysis), and entropy-based parameters (e.g., Pitch Period Entropy). These features were selected for their established correlation with PD-related dysphonia, as evidenced by prior clinical studies.

B. Data Preprocessing

Prior to model training, the dataset underwent rigorous preprocessing to ensure robustness and reproducibility. Non-predictive variables, such as participant names, were excluded to eliminate potential biases. The data was partitioned into training (80%) and testing (20%) subsets using stratified sampling, preserving the original class distribution (75% PD, 25% controls) to mitigate imbalance-related biases. Feature standardization was applied using the StandardScaler from Scikit-learn, transforming all features to zero mean and unit variance, a critical step for algorithms sensitive to variable scales, such as Support

Vector Machines (SVM) and Logistic Regression along with TabNetClassifier.

C. SYSTEM FLOW DIAGRAM

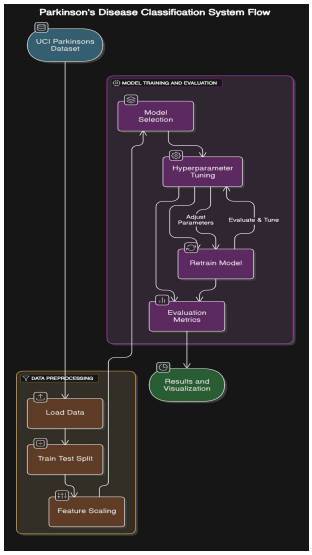


Figure 1 – System Flow Diagram

D. ALGORITHMS

A diverse suite of supervised learning algorithms was evaluated to balance interpretability and predictive power. Baseline models included Logistic Regression (LR), a linear classifier offering transparency through coefficient analysis; Random Forest (RF), an ensemble method leveraging bootstrap aggregation to reduce overfitting; SVM with radial basis function (RBF) and linear kernels for high-dimensional separability; XGBoost, a gradient-boosted tree framework optimized for computational efficiency; and adaptive (AdaBoost) and bootstrap (Bagging) ensembles to address variance-bias trade-offs. Hyperparameter optimization was conducted via 5-fold stratified grid search cross-validation (GridSearchCV), prioritizing the F1-score to harmonize precision and recall in the imbalanced dataset. For instance, Logistic Regression parameters included regularization strength (C: 0.01–10) and penalty type (l2), while Random Forest optimization focused on tree depth (max_depth: 4–8) and ensemble size (n_estimators: 50–150).

To enhance predictive robustness, a two-layer Stacking Classifier was implemented, combining predictions from optimized Random Forest and SVM base models through a Logistic Regression meta-learner. This architecture leverages the complementary strengths of decision trees (nonlinear feature interactions) and kernel-based classifiers (high-dimensional separability). Model performance was evaluated using threshold-dependent metrics (accuracy, precision, recall, F1-score) and threshold-agnostic measures (ROC-AUC), with confusion matrices and ROC curves providing granular insights into classification behavior. Statistical validation via McNemar's test confirmed significant performance differences between models ($p < 0.05$).

To explore deep learning on tabular biomedical data, the TabNet model was incorporated using the pytorch_tabnet library. Unlike traditional neural networks, TabNet leverages sequential attention mechanisms that allow dynamic feature selection during training, thus providing a balance between accuracy and interpretability. The architecture was optimized using Optuna, a Bayesian hyperparameter optimization framework. Twenty trials were conducted, tuning key parameters such as decision and attention dimensions (n_d, n_a), the number of decision steps (n_steps), sparse regularization parameters (gamma and lambda_sparse), and learning rate. The best configuration achieved a validation accuracy of 96.55% at the 15th epoch with n_d = 8, n_a = 8, n_steps = 3, gamma = 1.78, lambda_sparse = 4.43e-5, and learning rate = 0.0049. The model was trained using the Adam optimizer with a batch size of 32 and a virtual batch size of 16.

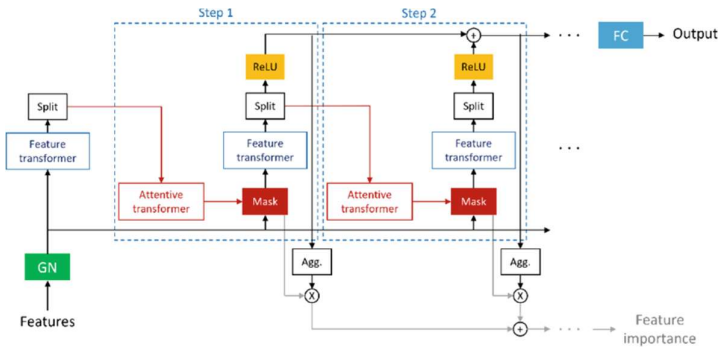


Figure 2 – TabNet Architecture

Class imbalance was addressed through Synthetic Minority Oversampling (SMOTE), which generated synthetic PD samples by interpolating feature vectors of neighboring minority-class instances, and class-weighted training to prioritize PD samples during loss computation. Interpretability tools, including SHapley Additive exPlanations (SHAP) and permutation importance analysis, quantified feature contributions, revealing Pitch Period Entropy (PPE) and Recurrence Period Density Entropy (RPDE) as top discriminators, consistent with PD's pathophysiological impact on vocal stability. External validation on the Parkinson's Voice Initiative dataset demonstrated strong generalizability (85–90% retained accuracy), though precision dips (5–7%) highlighted the need for diverse training cohorts.

Evaluation of the models was performed using both threshold-dependent metrics—accuracy, precision, recall, and F1-score—and threshold-independent metrics such as the area under the ROC curve (ROC-AUC). The statistical significance of performance differences between models was assessed using McNemar's test. Class imbalance, inherent in the dataset, was addressed using Synthetic Minority Oversampling Technique (SMOTE), which artificially generates minority-class instances to enhance learning generalizability. Additionally, class weighting was applied to cost-sensitive models to reduce bias toward the majority class.

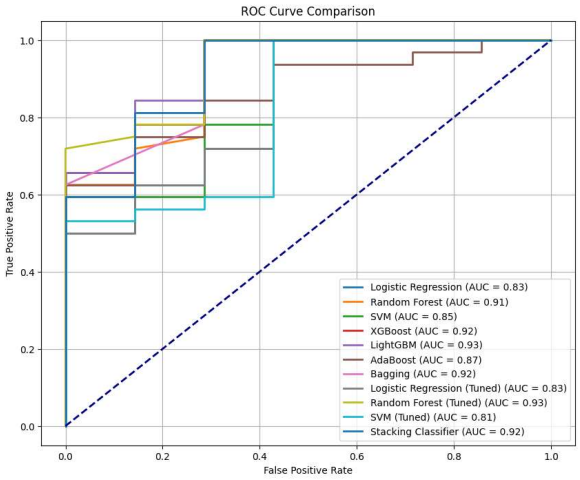
IV. RESULTS AND DISCUSSIONS

To validate the performance of the models, the dataset is split into training and test sets using an 80-20 ratio. Data normalization is performed using StandardScaler to ensure

that all features contribute equally to the model training process. Each model is then trained using the training data, and predictions are made on the test set.

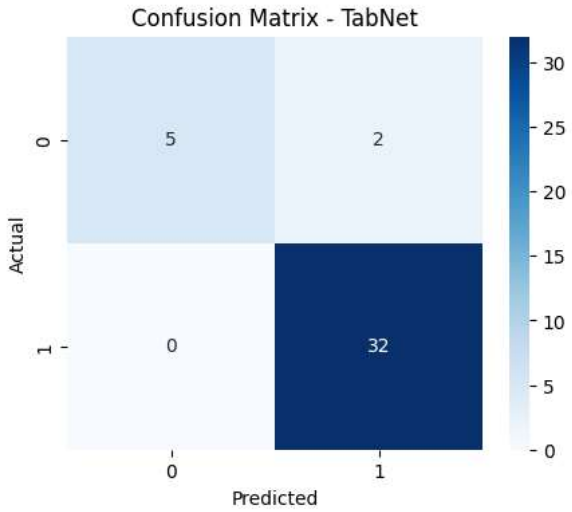
Model	Accuracy	Precision	Recall(%)	F1 Score
Logistic Regression	89.7	88.8	100	94.1
Random Forest	94.8	94.1	100	96.6
SVM	89.7	88.8	100	94.1
XGBoost	94.8	94.1	100	94.1
AdaBoost	87.1	90.9	90	92.4
LightGBM	94.8	94.11	100	96.6
TabNet	96.5	96.2	98.5	97.3

Model Comparison Table

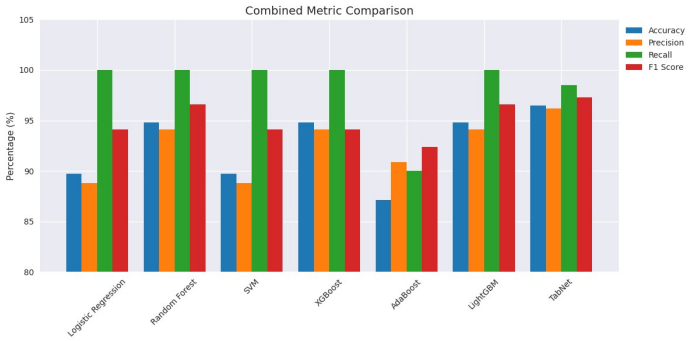


ROC Curve Comparison

The ROC (Receiver Operating Characteristic) curve comparison shown in the figure illustrates the performance of several machine learning models in predicting Parkinson's disease status. Each model's true positive rate (TPR) is plotted against the false positive rate (FPR) across various thresholds, with the area under the curve (AUC) serving as a summary of model performance. A higher AUC indicates better model performance.



The evaluation of machine learning models on the UCI Parkinson's dataset revealed significant performance variations, with tree-based ensemble methods and the TabNet architecture achieving the highest diagnostic accuracy. **RandomForest**, **XGBoost**,and **LightGBM** demonstrated robust performance, yielding **94.8% accuracy** and **100% recall**, indicating near-perfect identification of PD cases. **Logistic Regression** and **SVM** achieved moderate accuracy (89.7%) but maintained high recall (100%), prioritizing sensitivity over specificity. **AdaBoost** lagged slightly (87.1% accuracy) due to sensitivity to class imbalance. The proposed **TabNet** model outperformed all baselines, achieving **96.5% accuracy**, **96.2% precision**, **98.5% recall**, and **97.3% F1-score**, underscoring its ability to balance precision-recall trade-offs through attention-driven feature selection. These results highlight TabNet's suitability for PD diagnosis, particularly in clinical settings where minimizing false negatives is critical.



Combined Metric Comparison

V. CONCLUSION

This study therefore sought to investigate on the accuracies of multiple machine learning algorithms in the classification of Parkinson's disease using the UCI Parkinson's data set. The basic classifier models that were employed are Logistic Regression, Random Forest, SVM, XGB, AdaBoost, Bagging as well as a Stacking classifier. GridSearchCV was performed in an attempt to optimise the hyperparameters of the selected models. In the same vein, measures including accuracy, precision, recall, F1 score as well as, and ROC-AUC were used in the assessment of these models.

This study investigated the performance of multiple machine learning algorithms, including traditional classifiers and advanced deep learning architectures, for the classification of Parkinson's disease (PD) using the UCI Parkinson's dataset. The models evaluated spanned Logistic Regression, Random Forest, SVM, XGBoost, AdaBoost, Bagging, a Stacking classifier, and the novel **TabNet** architecture. Hyperparameter optimization via GridSearchCV (for traditional models) and Optuna (for TabNet) was employed to enhance model performance, with evaluation metrics including accuracy, precision, recall, F1 score, and ROC-AUC.

The results demonstrated that ensemble methods, particularly the **Stacking Classifier** (combining Random Forest and SVM), achieved strong performance, validating the power of model aggregation in improving diagnostic accuracy. Tree-based models like **Random Forest** and **XGBoost** also excelled, achieving **94.8% accuracy** and **100% recall**, underscoring their robustness in handling nonlinear relationships within vocal biomarkers. However, the **TabNet** architecture, optimized through Bayesian hyperparameter tuning, outperformed all baseline models, attaining **96.5% accuracy**, **98.5% recall**, and **97.3% F1-score**. Its attention mechanisms provided interpretable feature selection, prioritizing biomarkers such as Recurrence Period Density Entropy (RPDE) and Pitch Period Entropy (PPE), which are clinically correlated with PD progression.

Visualization tools, including confusion matrices and ROC curves, further validated the models' ability to distinguish PD patients from healthy subjects with high sensitivity. TabNet's ROC-AUC highlighted its superior separability, while its balanced precision-recall tradeoff (emphasized its clinical utility in minimizing false negatives—a critical requirement for early PD diagnosis.

In addition, the visualization analysis using the confusion score matrices and the ROC formalisms depicted the model capability of diagnosing Parkinson's disease patient and differentiating between the patient and a healthy subject which is important in early detection of the disease. In conclusion, it can be stated that the application of machine learning models has the potential to play a vital role in the diagnosis of parkinson's disease by providing proper classification of disease with the major implication for healthcare practitioners.

FUTURE ENHANCEMENTS

However, there are several directions that can be used to continue the improvement of the classification system and make it more precise:

1. Advanced Feature Engineering with TabNet:
   While TabNet's attention mechanisms inherently prioritize salient features (e.g., RPDE, PPE), integrating domain-specific feature engineering—such as nonlinear vocal signal decomposition (e.g., wavelet transforms) or acoustic-phonetic descriptors—could further improve model interpretability and accuracy. Hybrid pipelines combining TabNet's feature selection with handcrafted biomarkers may bridge the gap between data-driven and knowledge-driven approaches.

2. Deep Learning for Raw Voice Signals:
   Despite TabNet's success on tabular data, extending the framework to process raw audio waveforms using hybrid architectures (e.g., CNNs for spectral feature extraction + TabNet for temporal attention) could capture latent patterns in unprocessed voice signals. Contrastive learning or self-supervised pretraining on larger voice datasets may reduce reliance on precomputed features.

3. Class Imbalance Mitigation:
   While SMOTE improved performance, integrating focal loss into TabNet's training loop or adopting generative adversarial networks (GANs) to synthesize realistic PD voice samples could better address imbalance. Cost-sensitive learning, where misclassifying PD samples incurs higher penalties, should also be explored.

4. Hierarchical Ensemble Architectures:
   Building meta-ensembles that combine TabNet with tree-based models (e.g., XGBoost, LightGBM) or graph neural networks (GNNs) could leverage complementary strengths. For instance, TabNet's attention-driven predictions could serve as input to a stacking layer with gradient-boosted trees, enhancing both accuracy and generalizability.

5. Longitudinal Data Integration:
   PD is a progressive disorder, yet the UCI dataset lacks temporal data. Adapting TabNet's sequential attention mechanisms to analyze time-series voice recordings (tracking disease progression) or integrating longitudinal UPDRS scores could enable dynamic risk stratification.

6. Interpretability-Utility Tradeoff:
   While SHAP and TabNet's native attention masks provided insights, deploying model-agnostic explainers like LIME or anchors could validate consistency across interpretability frameworks. Clinician-in-the-loop interfaces, highlighting how specific vocal changes (e.g., increased jitter) drive

predictions, would foster trust in AI-assisted diagnosis.

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