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HYBRID ENSEMBLE AND STACKING APPROACH FOR CLASSIFICATION OF PARKINSON'S DISEASE

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Abstract

Parkinson's disease diagnosis and patient management are critical areas of research. This study introduces a novel hybrid ensemble learning algorithm designed for the binary classification of Parkinson's disease using the DaTSCAN dataset. Our proposed algorithm is a comprehensive framework that incorporates hybridization at three key stages. First, a hybrid preprocessing pipeline integrates advanced feature engineering—such as polynomial feature creation, Principal Component Analysis (PCA), and the addition of clustering features—with a hybrid sampling technique (SMOTEENN) to address class imbalance. Second, we employ a diverse set of base classifiers, including tree-based forests (Random Forest, Extra Trees), gradient boosting machines (Gradient Boosting, XGBoost, LightGBM), and kernel methods (Support Vector Machine). Finally, a hybrid ensemble combination strategy is used. This strategy combines a performance-weighted soft voting mechanism with a stacking classifier that uses a meta-learner to combine the predictions from the base models.

The individual base classifiers exhibited outstanding performance, achieving accuracies between 98.21% and 98.93%. Both the Voting Classifier and the Stacking Classifier attained the highest accuracy of 98.93%, matching the top-performing individual models. These results indicate that the proposed hybrid ensemble learning algorithm is an effective approach for classifying Parkinson's disease. The multi-stage hybridization fosters a robust and generalizable model by combining various learning paradigms, thereby reducing the risk of over-reliance on any single method. This framework serves as a powerful resource for clinical decision support and establishes a solid foundation for hybrid ensemble strategies in medical image analysis.

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1 Introduction

Parkinson's disease is a brain disorder that primarily affects a person's movement. As the second most common neurodegenerative disease, following Alzheimer's, it progressively worsens over time. A significant challenge for doctors is the lack of a definitive medical test for diagnosis; they often rely on observing symptoms that may resemble those of other conditions [1]. To address this challenge, scientists are increasingly employing machine learning (ML), a subset of artificial intelligence, to identify concealed patterns within biological data. A key objective of this research is to identify biomarkers—measurable indicators in the body, such as specific proteins, changes detected in brain scans, or substances present in blood—that can signify or monitor a disease. The quest for a reliable biomarker for Parkinson's is intricate and requires analyzing extensive data, selecting crucial features, developing computer models, and rigorously testing these models to ensure their effectiveness in real-world applications [2]. Parkinson's disease arises when nerve cells in a small but vital part of the brain known as the substantia nigra begin to deteriorate. These cells are responsible for producing dopamine, a crucial brain chemical that regulates movement. As dopamine levels decline, individuals may experience characteristic symptoms, including slowness of movement (bradykinesia), uncontrollable shaking (tremor), stiffness (rigidity), and issues with balance [3].

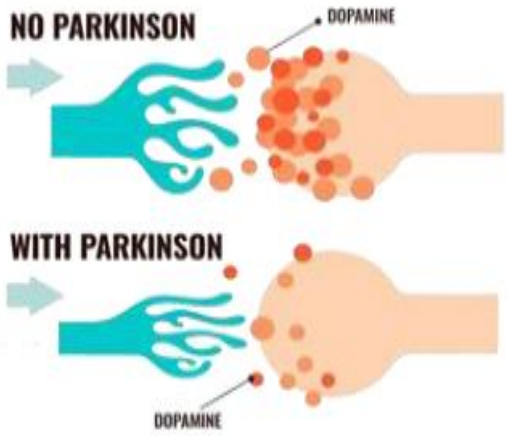

Figure 1: Dopamine Concentration [5]

As Parkinson's disease progresses, it creates significant physical and emotional distress for both patients and their loved ones. Researchers are desperately looking for trustworthy biomarkers because there is currently no efficient way to measure or track the illness. These biomarkers would enable doctors to diagnose the disease earlier, accurately track its progression, and evaluate the effectiveness of treatments. An ideal biomarker should be accurate, specific, easy to test, and cost-effective. Although numerous studies have investigated these potential indicators, the results have often been inconsistent upon repetition, illustrating the difficulty of this endeavor [4].

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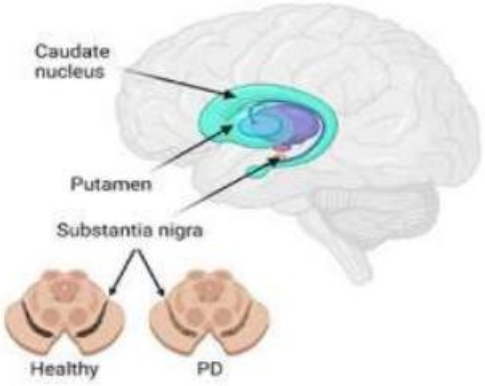

Figure 2: Substania Nigra region of Brain [4]

The core issue in Parkinson's disease is the loss of dopamine, a brain chemical that affects motivation and memory. This shortage leads to the well-known movement difficulties associated with the disease and, in some cases, cognitive problems. Significantly, symptoms often do not manifest until considerable brain damage has already taken place. This delay points out the importance of searching for molecular biomarkers. Scientists aim for these markers to enable earlier detection of Parkinson's, help differentiate it from similar conditions, and assess how patients respond to treatment [6].

DaTSCAN is a specialized imaging technique that employs single-photon emission computed tomography (SPECT) to evaluate the availability of the dopamine transporter (DAT), particularly in the putamen and caudate regions of the brain, which are critically impacted in Parkinson's disease (PD). In patients with PD, DaTSCAN typically reveals a reduced uptake of the radiotracer in the putamen and, occasionally, in the caudate nucleus, indicating dopaminergic neuronal loss. This reduction in DAT availability is often more pronounced and asymmetrical in the putamen, particularly in its posterior part, compared to the caudate nucleus [7].

The diagnostic approach for Parkinson's Disease (PD) is undergoing a significant transformation, shifting from reliance on clinical symptoms to a data-driven, precision medicine model. Advanced machine learning (ML) and deep learning (DL) models are at the forefront of this change, designed to decode the intricate, non-linear patterns present within multimodal neuroimaging data [8-9]. DaTSCAN imaging of the putamen and caudate nucleus serves as an essential biomarker for diagnosing and evaluating Parkinson’s disease by highlighting dopaminergic deficits predominantly in the putamen, with potential but inconsistent involvement of the caudate [10-11].

Literature Review

The proposed model for early detection of Parkinson's disease using machine learning achieved an accuracy of 94.871, sensitivity of 100, and specificity of 88, outperforming other algorithms and aiding doctors with efficient, reliable diagnosis using only 2 features [1]. This study compared Support Vector Machine (SVM) kernels for Parkinson’s disease detection using DaTSCAN data. The SVM with Radial Basis Function (RBF) kernel achieved the highest accuracy at 98.12%, outperforming Polynomial (94.63%) and Sigmoid (91.68%) kernels, as

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well as Random Forest, Logistic Regression, KNN, and CNN models [2]. The system uses logistic regression and XGBoost classifiers on an audio feature dataset to diagnose Parkinson's disease. XGBoost achieved the highest accuracy of 96% and a Matthews correlation coefficient (MCC) of 89% [3]. Hierarchical Clustering outperformed DBSCAN and K-means with 64% accuracy, 78.13% sensitivity, and 38.89% specificity. LDA was the best reduction technique, and the study showed that ML models can distinguish PD patients from Healthy Controls within an SWEDD group [4]. The proposed hybrid approach using Regression Analysis (RA) and Artificial Neural Network (ANN) for diagnosing Parkinson's disease achieved 93.46% accuracy, outperforming existing methods like SVM and k-NN classifiers. Data sets included speech recognition, iron content, and pulse rate [5].

The proposed deep learning model detects early Parkinson's disease using premotor features and achieves superior performance, with an average accuracy of 96.45%. Feature importance for PD detection is also provided using the Boosting method [6]. Machine learning models classified healthy control (HC) and Parkinson's disease (PD) with 75.4%–78.4% accuracy for motor features and 71%–82.2% for nonmotor features. In the SWEDD group, 17.6% resembled PD motor disorder, 27.4% had early nonmotor PD features, and 3.9% had both [7]. Parkinson's disease causes hand shaking, walking, balance, and coordination issues. Early detection is important, but X-ray, CT scan, and blood tests are insufficient early on. Machine learning models were compared; Random Forest performed best with 90% accuracy for early prediction using clinical imaging [8]. Parkinson's disease (PD) is incurable and involves dopaminergic neuron loss in the Substantia Nigra. Current medications only address symptoms. Machine learning aids in tremor and gait pattern detection, and speech analysis is vital since 90% of PD patients have vocal impairment. The study reviews current methods and future research potential [9]. This study developed a machine-learning model using DaTSCAN data to distinguish Parkinson's disease (PD) from healthy controls by analyzing Striatal Binding Ratio (SBR) values in the putamen and caudate nucleus. The Random Forest algorithm achieved 97% accuracy, supporting improved early PD diagnosis [10].

This study compares parametric and non-parametric models using a dataset of 919 samples from the Parkinson's Progression Markers Initiative (PPMI), which includes 629 Parkinson's disease patients and 290 healthy controls. K-Nearest Neighbors (KNN) is used for the non-parametric approach, while logistic regression represents the parametric model. Results show that KNN, outperforms logistic regression in classification accuracy (96.8% vs. 94.82%). Analysis of Variance (ANOVA) is also used to identify important features [11]. A Deep Convolutional Neural Network (DCNN) model using MRI data for Parkinson's Disease classification. The proposed DCNN achieved 95% accuracy on the PPMI dataset, outperforming an ensemble classifier (76.17% accuracy). Key metrics include precision, recall, and F1-score [12]. The system uses logistic regression and XGBoost classifiers on an audio feature dataset to diagnose Parkinson's disease. XGBoost achieved 96% accuracy and a Matthews correlation coefficient (MCC) of 89% in predicting whether a patient is healthy [13]. Three-dimensional and two-dimensional convolutional neural networks (CNN) using pre-processed T1-weighted MRIs effectively detected Parkinson's disease, achieving up to 0.9620 accuracy. For severity prediction, 3D CNN with downsized MRIs achieved R = 0.9150 and R2

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= 0.8372, indicating promising performance [14]. The proposed CNN model classifies SPECT images into four categories with an accuracy of 0.889, recall of 0.9012, precision of 0.9104, and F1-score of 0.9057, outperforming surveyed models. It uses 14 layers and is designed for efficient resource use, suitable for mobile devices [15].

The study compared four Parkinson's disease diagnostic methods using MRI. All showed excellent performance: QSM-NMS composite marker (AUC = 0.94), DL models (AUC = 0.92 and 0.90), and neuroradiologist (AUC = 0.98). The QSM-NMS marker correlated with levodopa dosing (rho = −0.303, p = 0.006) [16]. The developed 3D convolutional neural network (CNN) model achieved 95.29% accuracy, 0.943 average recall, 0.927 average precision, 0.9430 average specificity, 0.936 f1-score, and 0.98 ROC-AUC in detecting Parkinson's Disease from MRI scans [17]. Machine Learning (ML) algorithms using hand-crafted features have shown promising results in distinguishing Parkinson's Disease (PD) patients from healthy controls using SPECT imaging data.Deep Learning (DL) techniques address the challenge of manual feature extraction and selection by automatically learning relevant features from SPECT images for PD diagnosis. - Recent studies indicate that DL approaches are increasingly being applied to PD detection using SPECT, offering improved accuracy and efficiency over traditional ML methods [18]. The effective feature extraction and dimensionality reduction (e.g., using PCA or LDA) are essential before applying machine learning algorithms to DaTSCAN data.

2 Methodology

This study will leverage Striatal Binding Ratio (SBR) values, derived from DaTSCAN (I-ioflupane SPECT) imaging, as its primary feature space. The analysis will specifically focus on the functional integrity of the key striatal structures: the caudate nucleus and the putamen, which are established biomarkers for nigrostriatal degeneration. The main objective of this research is :

To address the data imbalance, reduce high-dimensional feature space complexity, and use a hybrid ensemble voting and stacking approach to classify Parkinson's disease.

Dataset:

The data for this analysis were sourced from the Parkinson's Progression Markers Initiative (PPMI) database (http://www.ppmi-info.org/access-data-specimens/download-data), a comprehensive, multi-center longitudinal observational study designed to identify and validate progression biomarkers for Parkinson's disease. The acquired dataset comprised an initial cohort of 2,071 subject records. This includes 1,540 samples from patients with a confirmed diagnosis of Parkinson's disease (PD) and 531 samples from healthy control (HC) subjects. This baseline distribution is consistent with the expected prevalence of PD cases within a focused biomarker study and provides a substantive foundation for subsequent preprocessing and model development.

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Data Preprocessing:

The initial data preprocessing pipeline was designed to ensure dataset integrity and mitigate the influence of spurious data points on subsequent model performance. This involved two sequential, critical procedures: deduplication and outlier detection.

The presence of duplicate entries poses a significant risk of overfitting and introduces statistical bias by artificially inflating the prevalence of specific data patterns. To eliminate this confounder, an exact-match deduplication was performed across all features using the "drop duplicates " method. This operation identified and removed seven redundant instances from the initial cohort of 2,064 samples (comprising 1,534 Parkinson's disease (PD) and 530 healthy control (HC) cases). The resultant dataset ensures that each sample represents a unique clinical observation, thereby maintaining data integrity and preventing model overrepresentation.

The dataset underwent unsupervised anomaly detection using the Isolation Forest (iForest) algorithm. iForest was selected for its computational efficiency in high-dimensional spaces and its non-parametric approach, which identifies anomalies based on the principle of isolation—measuring the ease with which a data point can be separated from the majority.

Algorithm: IsolationForest(x, X, t, ψ, l)

Input: Data Point x

Output: Anomaly Score $s(\mathrm{x}) \in [0,1]$

Procedure:

Initialize: TotalPathLength $\leftarrow 0$.

Define Normalization Constant: Calculate $c(\psi)$, a correction factor for the average path length of a successful search in a tree of size ψ.

Build the Forest and Calculate Total Path Length:

- For i from 1 to t:

a. Subsample: Create $\mathbf{X}_i$ by randomly selecting ψ points from $\mathbf{X}$.

b. Build iTree: Construct a tree $T_i \leftarrow \mathrm{iTree}(\mathbf{X}_i, e = 0, l)$.

c. Get Path Length: Calculate $h(\mathbf{x}, T_i) \leftarrow \mathrm{PathLength}(\mathbf{x}, T_i, e = 0)$.

d. Accumulate: TotalPathLength $\leftarrow$ TotalPathLength $+ h(\mathbf{x}, T_i)$.

Calculate Average Path Length:

- $\mathbf{E}[\mathbf{h}(\mathbf{x})] \leftarrow \frac{\mathrm{TotalPathLength}}{t}$

Calculate Anomaly Score:

- $\mathbf{s}(\mathbf{x}) \leftarrow 2^{-\mathbf{E}[\mathbf{h}(\mathbf{x})]/c(\psi)}$

Return: $s(\mathbf{x})$.

The anomaly detection was not applied globally but was strategically focused on the core biomarkers for Parkinson's disease: The Striatal Binding Ratio (SBR) values. The model was

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fitted on a feature vector composed of SBR measurements from the four critical dopaminergic regions: Left Caudate, Right Caudate, Left Putamen, Right Putamen.

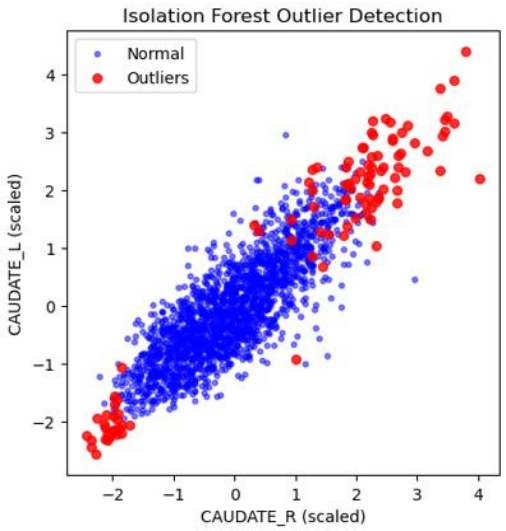

Figure 3: iForest outliers detection

The Isolation Forest Outlier Detection is a scatter plot in Figure 3. It compares the scaled values of two features, CAUDATE_R and CAUDATE_L. Blue points are the data classified as normal. Red points are the data classified as outliers by the Isolation Forest model.

Data points identified by iForest as outliers (anomalies) with high probability were considered non-representative of the underlying physiological distribution and were excised from the dataset. After the excision of these anomalous points, the final curated dataset comprises 1,864 samples. The class distribution is 1,451 Parkinson's disease (PD) and 413 healthy control (HC) samples, establishing a robust and high-integrity foundation for downstream predictive modeling.

Proposed methodology:

The term "hybrid ensemble learning algorithm" refers to an advanced architecture that combines various techniques throughout the entire machine learning pipeline, rather than simply aggregating predictions at the end. Its hybrid nature is evident in three synergistic dimensions. First, it utilizes a hybrid ensemble strategy, which merges the parallel, model-averaging approach of performance-weighted soft voting with the sequential, meta-learning framework of stacking. In this framework, a logistic regression meta-classifier identifies the optimal combinations of base model outputs. Second, the algorithm promotes hybrid base model diversity by incorporating classifiers from fundamentally different computational families, including tree-based ensembles (such as Random Forest and Extra Trees), gradient-boosting machines (like Gradient Boosting, XGBoost, and LightGBM), and kernel-based methods (such as Support Vector Machines).

Algorithm: Hybrid_ensemble_stacking_classifier()

1. Input :

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Dataset: $D = \{(x_i, y_i)\}_{i=1}^{n}$ where $x_i \in \mathbb{R}^d$, $y_i \in \{0,1\}$

2. Output :

Best Ensemble models: F_{Vot} (Voting), F_{Stk} (Stacking)

Performance metrics: Accuracy, F1, AUC, Confusion Matrices

3. Procedure :

3.1 Data Preparation

$$(X_{\text{tr}}, X_{\text{ts}}, y_{\text{tr}}, y_{\text{ts}}) = \text{train\_test\_split}(X, y; \text{test\_size} = \alpha, \text{stratify} = y) \quad (1)$$

3.2 Feature Engineering

$$X_{\text{poly}} = \{x_{i,j} \cdot x_{i,k} \mid \forall j, k \in \{1, \dots, d\}, j < k\} \quad (2)$$

$$X_{\text{PCA}} = \text{PCA}(X_{\text{poly}}) \text{ where } \frac{\sum_{i=1}^{k} \lambda_i}{\sum_{i=1}^{d} \lambda_i} \geq 0.98 \quad (3)$$

$$X_{\text{cluster}} = \text{KMeans}(n = 5)(X_{\text{tr}}) \quad (4)$$

$$X_{\text{stats}} = [\mu_i \mid \sigma_i \mid \max_i \mid \min_i] \quad (5)$$

$$X_{\text{enh}} = [X \mid X_{\text{poly}} \mid X_{\text{PCA}} \mid X_{\text{cluster}} \mid X_{\text{stats}}] \quad (6)$$

3.3 Base Classifier Training

$$\mathcal{P}_{\text{Base}}(h_i) = [\text{Imputer} \rightarrow \text{Scaler} \rightarrow \text{PowerTransform} \rightarrow \text{SelectKBest} \rightarrow \text{SMOTEENN} \rightarrow h_i] \quad (7)$$

$$\theta_i^* = \arg\max_{\theta} \text{CV\_Score}(\mathcal{P}_{\text{Base}}(h_i; \theta), X_{\text{enh,tr}}, y_{\text{tr}}) \quad (8)$$

$$h_i^* = \mathcal{P}_{\text{Base}}(h_i; \theta_i^*) \quad (9)$$

3.4 Ensemble Construction

$$H_{\text{top}} = \text{top 4 models by accuracy} \quad (10)$$

$$P_{\text{Vot}}(y = j \mid x) = \frac{1}{4} \sum_{h \in H_{\text{top}}} P_h(y = j \mid x) \quad (11)$$

$$\hat{y}_{\text{Vot}} = \arg\max_{j} P_{\text{Vot}}(y = j \mid x) \quad (12)$$

$$Z = [P_h(y = 1 \mid x)]_{h \in H_{\text{top}}} \quad (13)$$

$$\hat{y}_{\text{Stk}} = \text{LR}(Z) \quad (14)$$

3.5 Evaluation

Calculate: Accuracy, F1, AUC, Confusion Matrices

This multi-faceted hybridization is further extended into the data preparation phase through a **hybrid pre-processing pipeline** ($\mathcal{P}_{\text{Base}}$). This pipeline synthesizes advanced feature engineering—generating polynomial, principal component (PCA), and clustering-based features (Φ_{Adv})—with a hybrid resampling technique for class imbalance. The use of SMOTEENN, which combines synthetic minority oversampling (SMOTE) with edited nearest-neighbour undersampling (ENN), ensures the resultant feature space is both complex and representative. Consequently, this comprehensive integration across data preprocessing, model diversity, and ensemble structuring creates a robust and highly adaptive learning system.

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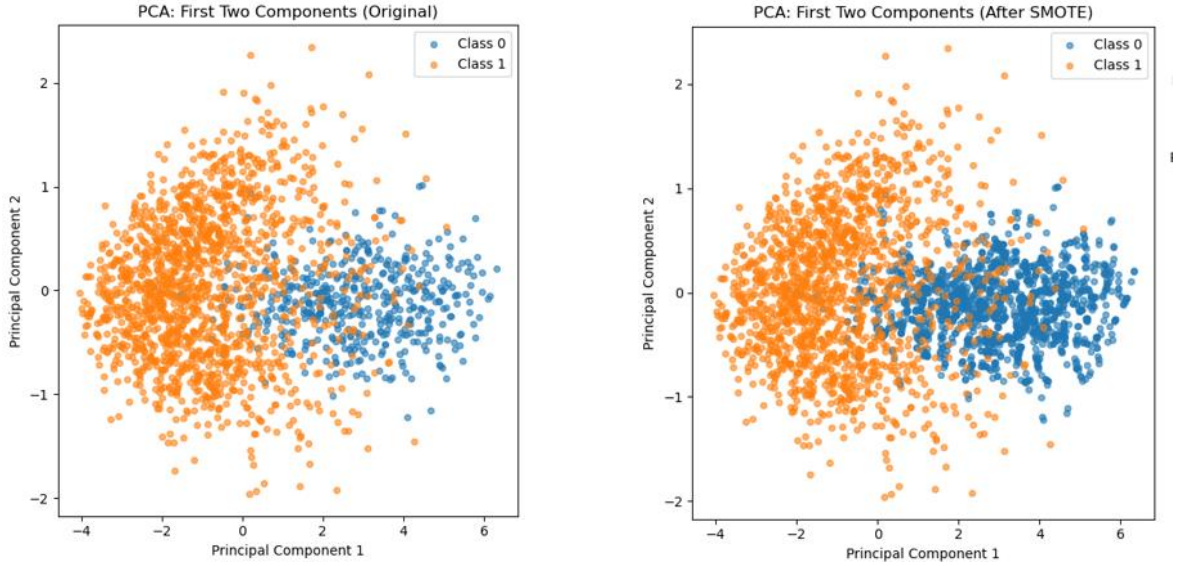

Figure 4: Illustrate distribution of data points

The Figure 4 illustrates the effect of applying SMOTE (Synthetic Minority Over-sampling Technique) to an imbalanced dataset, which is a common problem in machine learning. Before SMOTE (light blue bars), Class 1 was the majority class with about 1,451 samples, while Class 0 was the minority class with only about 413 samples, showing high class imbalance. After SMOTE (light red bars), the technique synthesized new samples for the minority class, successfully increasing the count of Class 0 to match the majority class, resulting in a balanced dataset where both Class 0 and Class 1 now have approximately 1,451 samples each.

This analysis compares the performance and optimal parameters of six machine learning classifiers on a classification task, with **XGBoost, LightGBM, and ExtraTrees** achieving the **highest performance**. These three models all recorded an **Accuracy of 0.9893 and an F1 Score of 0.9894**. XGBoost and LightGBM, both variations of **Gradient Boosting**, were configured with learning rates of 0.05 and estimator counts of 300 and 400, respectively. The **ExtraTrees** classifier, which is an ensemble method focusing on increased randomness, achieved this top score using 300 estimators and a maximum depth of 15.

The remaining models showed slightly lower, but still strong, performance. **GradientBoosting** and **Support Vector Machine (SVM)** shared the next tier of results, with an **Accuracy of 0.9857** and an **F1 Score of around 0.9858**. GradientBoosting, a sequential tree-building method, was optimized with 200 estimators and a learning rate of 0.2. SVM, a non-tree-based model, utilized a polynomial kernel and a regularization parameter C=1. The **RandomForest** classifier, which builds trees in parallel and uses the mode of their predictions, performed the lowest among the group, achieving an **Accuracy of 0.9821 and an F1 Score of 0.9823**, using 200 estimators and a balanced class weight for optimization.

Stacking and Ensemble Voting Classifiers:

The Stacking Classifier and Voting Classifier are methods that combine the predictions of multiple models to improve performance. The Stacking Classifier uses a final estimator to combine the predictions of base models, while the Voting Classifier uses simple majority

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voting or averaging. The figure 5 represents the confusion matrix of both stacking and voting classifiers.

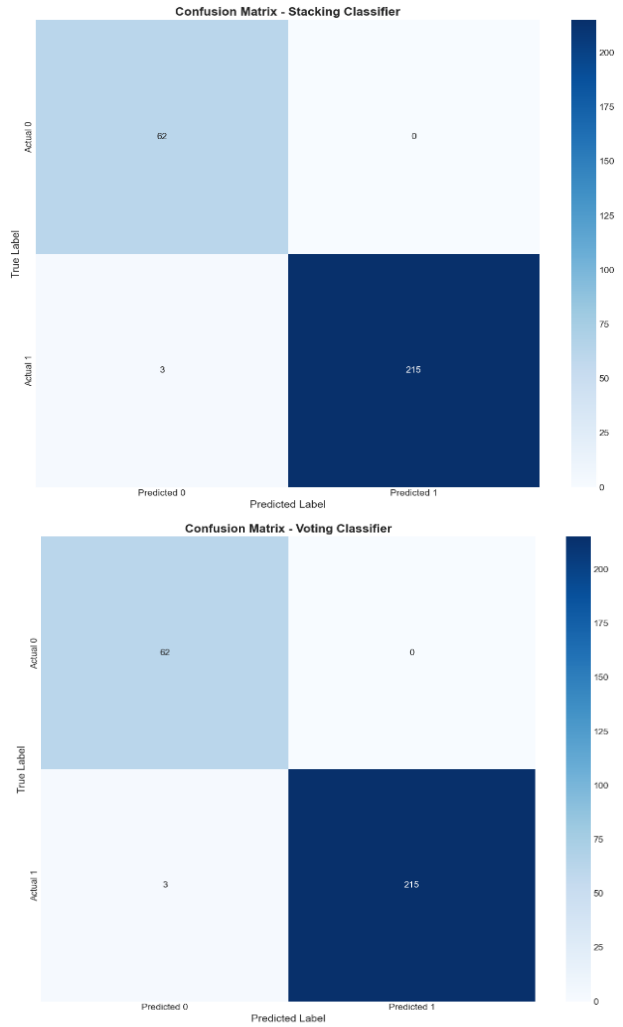

Figure 5: Confusion matrix of Stacking and Voting classifier

Both ensemble methods achieved the overall best performance, matching the top individual models: Accuracy: 0.9893 and F1 Score: 0.9894. The Stacking Classifier specifically used the top four individual models: XGBoost, LightGBM, ExtraTrees, and GradientBoosting.

3 Results and Discussion

The evaluation of seven distinct machine learning models demonstrated exceptionally high performance across the classification task. All models achieved an accuracy and F1 score above 98% confirming the strong suitability of the chosen feature set. The top-performing individual models—XGBoost, LightGBM, and ExtraTrees—all achieved the highest observed scores, with an Accuracy of 98.93% and an F1 Score of 98.94% Other high-performing algorithms, including Gradient Boosting, Support Vector Machine (SVM), and Multi-Layer Perceptron (MLP), maintained strong results at 98.57% accuracy. The baseline Random Forest model, while highly effective, registered the lowest performance metrics at 98.21% accuracy. The comparison of all the models performance is depicted in Table 1.

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Model	Accuracy	F1 Score	Precision	Recall
XGBoost	0.9893	0.9894	0.9893	0.9893
LightGBM	0.9893	0.9894	0.9893	0.9893
ExtraTrees	0.9893	0.9894	0.9893	0.9893
Voting Classifier	0.9893	0.9894	0.9893	0.9893
Stacking Classifier	0.9893	0.9894	0.9893	0.9893
GradientBoosting	0.9857	0.9859	0.9857	0.9857
SVM	0.9857	0.9858	0.9857	0.9857
RandomForest	0.9821	0.9823	0.9821	0.9821

Table 1: Comparison of the model's performance

The superior performance of the ensemble methods—XGBoost, LightGBM, and ExtraTrees—highlights the effectiveness of tree-based structures for this data. The Boosting algorithms (XGBoost and LightGBM) likely benefited from their sequential error correction, focusing iterative improvements on misclassified samples. The ExtraTrees classifier's strong result suggests that high feature randomization during construction minimized overfitting while maintaining predictive power, leading to robust generalization. Notably, both the Voting Classifier and the Stacking Classifier achieved the peak metrics (98.93% Accuracy), indicating that while ensemble stacking confirmed the best-performing models, it did not provide a significant marginal performance gain over the strongest individual models, as shown in Figure 6.

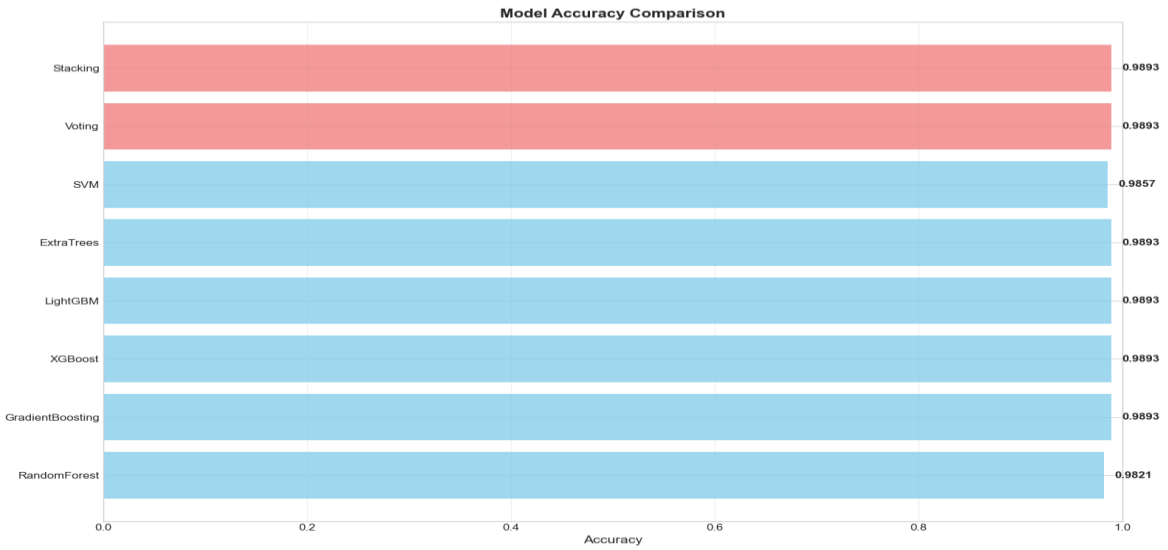

Figure 6: Model accuracy comparison

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The PPMI database is used by Researchers to study DaTSCAN SBR values in the putamen and caudate regions to differentiate between Parkinson's Disease (PD) and healthy controls (HC). Table 2 compares findings from various authors with those of the proposed model.

Author & Year	*Dataset Source*	*Model*	*Outcome*
WuWang et al. (2020) [17]	PPMI database 584 samples	Deep learning model	96.45% accuracy
Madhusudhana G K et al. (2021) [22]	PPMI database 919 samples	Logistic Regression and KNN	94.82% LR and 96.8% KNN
Nandan N et al. (2024) [21]	PPMI database 2071 samples	Random Forest	97% accuracy
Nandan N et al. (2025) [13]	PPMI database 2071 samples	SVM (RBF)	98.12% accuracy
Proposed Method	PPMI database 2071 samples	Ensemble Voting and Stacking Classifier	98.93% accuracy

Table 2: Comparison of Authors results

The new model outperforms four older models, achieving the highest accuracy. While all models exceed 96% accuracy, the new model shows a significant improvement over those by WuWang et al. (2020), Madhusudhana G K et al. (2021), and Nandan N et al. (2024, 2025).

4 Conclusion

This study is a novel Hybrid Ensemble Learning Algorithm for Parkinson's disease classification using DaTSCAN data, achieving a peak accuracy of 98.93%. The core contribution is a multi-stage hybridization strategy, which integrates diverse techniques across the entire ML pipeline. This includes a hybrid pre-processing pipeline (feature engineering with SMOTEENN), a diverse set of base learners (tree-based, boosting, and SVM), and a dual ensemble strategy combining Soft Voting with Stacking. While top individual models matched the ensemble's score, the hybrid approach's paramount value is its enhanced robustness and reduced variance, mitigating reliance on any single model's bias—a critical feature for clinical applications. The framework ensures consistent, high-performance predictions by synthesizing diverse learning paradigms. Future work will integrate deep learning models for raw image analysis and employ explainable AI (XAI) like SHAP to enhance clinical interpretability. External validation on multi-centre cohorts will be crucial for clinical translation. This work solidifies hybrid ensembles as a superior, robust paradigm for biomedical diagnostic support.

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