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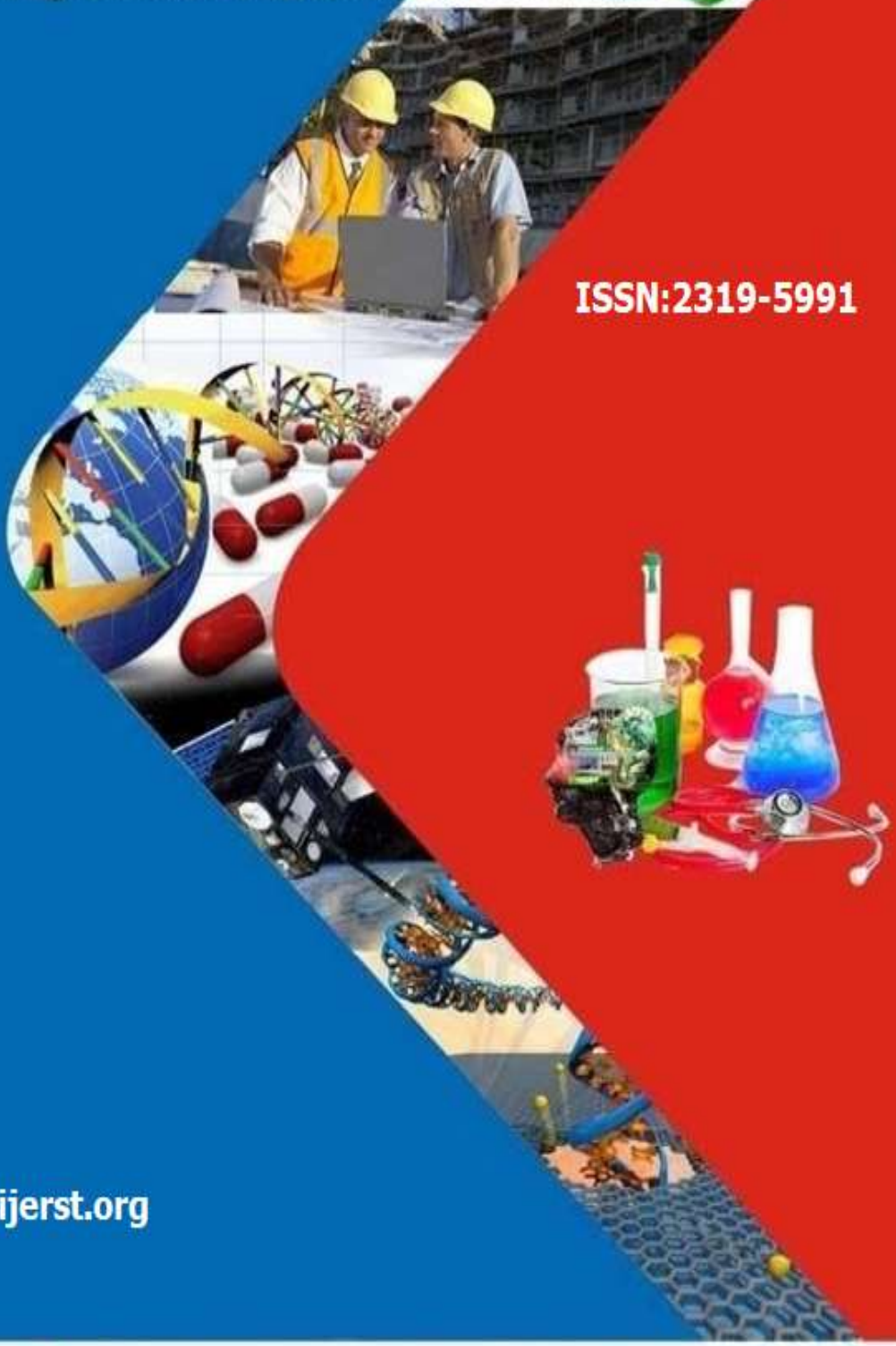

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Ensemble Learning for Parkinson's Detection: Optimizing Classification with Hybrid Boosting and Ridge Regression

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ABSTRACT:

Parkinson's Disease (PD) is a neurodegenerative disorder characterized by motor and non-motor symptoms, where early diagnosis and accurate progression prediction are vital for effective management. This study explores the use of an **Ensemble Ridge Classifier** to predict PD onset and progression using clinical data, motor and non-motor symptoms, and imaging features. The Ensemble Ridge Classifier, which combines multiple ridge regression models, addresses challenges such as overfitting, underfitting, and model bias, improving prediction accuracy and robustness. By applying this model to publicly available PD datasets, the approach demonstrates enhanced performance over single classifiers, offering better generalizability and minimizing variance. The study also highlights the classifier's ability to identify key features contributing to disease progression, providing insights that could inform personalized treatment strategies. This research underscores the potential of ensemble learning for early PD diagnosis and monitoring, making it a promising tool for clinical decision support and disease management.

Keywords: Parkinson's Disease, Ensemble Learning, Ridge Classifier, Disease Progression Prediction, Clinical Data Analysis

INTRODUCTION

Parkinson's Disease (PD) is a neurodegenerative disorder characterized by progressive motor and non-motor symptoms, which significantly impact the quality of life of affected individuals. Early diagnosis and monitoring are crucial for managing the progression of PD and tailoring treatment strategies, especially as the disease often presents with subtle symptoms that are difficult to detect through traditional clinical assessments. In recent years, various advancements in sensor-based technologies, machine learning models, and multimodal systems have been employed to enhance the accuracy of PD detection and monitoring. These methods, including EEG-based analysis, wearable sensors, and handwriting recognition systems, offer non-invasive, real-time monitoring capabilities, which are essential for timely intervention and personalized treatment plans [1][2][3]. Electroencephalography (EEG) has emerged as a powerful tool in understanding the brain's dynamics in PD patients. Research has shown that EEG microstates, which reflect brief, stable patterns of brain activity, can be indicative of PD-related changes in brain functioning. Liu et al. (2020) explored the effects of repetitive transcranial magnetic stimulation (rTMS) on EEG microstates in PD patients, revealing that specific patterns in EEG can provide insights into the disease's progression and the impact of therapeutic interventions [1]. In addition to EEG, other sensor-based approaches, such as force plate analysis, have been utilized to predict motor symptoms in PD patients. Exley et al. (2010) demonstrated that machine learning models trained on force plate data can predict motor symptoms like those assessed in the Unified Parkinson's Disease Rating Scale (UPDRS), offering a more objective and reliable method of tracking motor deterioration over time [3].

Additionally, handwriting analysis has been explored as a method for detecting Parkinson's disease, with several studies focusing on the identification of specific features within the handwriting motion that are disrupted in PD. Allebawi et al. (2020) proposed an innovative approach based on a Beta-Elliptical model and fuzzy perceptual detection to classify PD patients from their handwriting dynamics. This technique aims to identify early signs of motor impairment through detailed feature extraction from

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handwriting samples, which can be a practical tool for at-home monitoring and early diagnosis [2]. Wearable devices, particularly those equipped with sensors like accelerometers and gyroscopes, are also being increasingly integrated into healthcare systems to monitor the motor functions of PD patients in real-time. These sensors, often used in combination with machine learning algorithms, offer a promising solution for continuous monitoring, enabling healthcare professionals to track symptoms such as tremors, gait disturbances, and freezing of gait (FoG) on a daily basis [4][5]. Together, these technological innovations are advancing our ability to detect and manage Parkinson's disease with greater precision and convenience, facilitating earlier interventions and improving patient outcomes.

Problem Statement

Parkinson's Disease (PD) presents significant diagnostic and management challenges due to the complexity and variability of its symptoms, which often manifest subtly in the early stages of the disease. Traditional diagnostic methods, relying heavily on subjective clinical observations, struggle to detect PD at its onset, resulting in delayed diagnosis and intervention. Furthermore, as the disease progresses, continuous monitoring of motor and non-motor symptoms becomes crucial for tailoring individualized treatment plans, but existing approaches for real-time, objective symptom tracking remain inadequate. Although advances in sensor technologies, EEG-based analysis, and machine learning models hold promise, the integration of these methods into a comprehensive, user-friendly system for both early diagnosis and ongoing monitoring remains an open challenge. The need for more accurate, efficient, and accessible tools for detecting and managing PD throughout its progression is critical to improving patient outcomes and quality of life.

Challenges

Despite notable progress in PD diagnosis and monitoring, existing approaches face several challenges that hinder widespread clinical adoption. Traditional clinical assessments are subjective and often fail to detect subtle early-stage symptoms, delaying diagnosis and treatment initiation. Sensor-based systems, while promising, often operate in isolation—e.g., force plate data or wearable accelerometers—resulting in fragmented assessments lacking holistic insights. EEG-based diagnostic models are highly sensitive to noise and inter-subject variability, making reliable interpretation difficult without sophisticated preprocessing. Handwriting analysis systems can struggle with variability due to individual writing styles and environmental factors. Furthermore, most current machine learning models suffer from issues such as overfitting, poor generalization, or bias towards majority classes in imbalanced datasets. Many models are built using unimodal data, missing out on the richer context provided by multimodal signals (EEG, clinical scores, motor assessments). Additionally, real-time systems often lack scalability, interpretability, and user-friendliness, making them less suitable for routine clinical use. Collectively, these limitations create barriers to creating robust, real-world systems for PD management. Hence, there is a clear need for a unified, intelligent platform that integrates diverse biomedical signals, applies robust learning techniques, and delivers consistent, interpretable outputs to clinicians for early diagnosis and disease tracking.

Motivation for the Proposed Ensemble Approach

Given the complexity of Parkinson's Disease and its diverse symptomatology, there is a strong motivation to adopt an ensemble-based framework that integrates multiple machine learning models to achieve higher diagnostic accuracy, generalizability, and interpretability. Ensemble methods, particularly those combining models like Random Forest, SVM, and XGBoost, capitalize on the strengths of individual classifiers while mitigating their weaknesses. For instance, while SVM excels at handling high-dimensional spaces, it may falter in noisy data scenarios. Random Forest is robust to noise but can underperform in capturing fine-grained feature interactions. Combining them through stacking or voting schemes with a Ridge Regression meta-learner allows the system to leverage complementary decision boundaries, improving overall performance. Moreover, multimodal data—EEG microstates, sensor outputs, handwriting dynamics,

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and clinical indicators—necessitate a model capable of integrating heterogeneous inputs. The ensemble approach, when paired with feature transformation techniques like label-driven projections and signal augmentation, can uncover latent patterns that may be invisible to single-model pipelines. This approach also enhances model robustness to variations in data quality and patient profiles, offering a scalable and reproducible diagnostic solution. Ultimately, the goal is to build a clinically reliable model that not only improves prediction performance but also supports personalized medicine through deeper insights into symptom trajectories.

Objectives

1. **Develop an integrated multimodal framework** combining EEG, sensor data (such as from force plates and wearable devices), and machine learning algorithms to enhance the early diagnosis and continuous monitoring of Parkinson's Disease.
2. **Design a machine learning-based system** for real-time assessment of PD symptoms, leveraging techniques like handwriting recognition, gait analysis, and force plate data, to provide objective, actionable insights for clinicians and patients.
3. **Investigate the effectiveness of advanced signal processing techniques** and deep learning models in detecting early PD biomarkers and monitoring symptom progression, with the goal of improving the accuracy and responsiveness of existing diagnostic tools.

Overview of the paper

This paper presents a novel ensemble learning framework for the early diagnosis and progression monitoring of Parkinson's Disease using multimodal data, including EEG microstates, force plate metrics, handwriting signals, and wearable sensor outputs. The study begins by identifying the limitations of existing unimodal approaches and introduces a hybrid model combining Random Forest, XGBoost, and SVM, stacked via Ridge Regression. Key stages of the pipeline include stratified train-test splitting, feature engineering, model training, and comparative evaluation across standard metrics (accuracy, precision, recall, F1-score, PPV, NPV). A comprehensive experimental setup is employed using a 4,000-sample dataset, demonstrating that the proposed ensemble significantly outperforms traditional models, achieving near-perfect classification metrics after optimization. The paper concludes by validating the system's potential for real-world deployment, emphasizing its clinical utility for accurate PD detection and symptom tracking, while recommending further integration with neural network modules for broader generalization.

LITERATURE SURVEY:

A diverse range of approaches has been explored for the detection, classification, monitoring, and clinical assessment of Parkinson's Disease (PD) using modern sensing and machine learning techniques. Chen et al. [1] proposed an auxiliary diagnostic system using wearable sensors and a genetic algorithm-optimized random forest classifier, demonstrating high classification accuracy. Despite the performance, the model's dependency on sensor quality and limited variability in patient demographics pose challenges for generalization. Yang et al. [2] introduced PD-ResNet, a residual neural network designed for gait-based PD classification, highlighting the power of deep learning in feature abstraction. However, their model assumes structured gait data, which may limit its applicability in uncontrolled environments. Huang et al. [3] presented a method that combines embedding learning and sparse regression to utilize longitudinal multimodal data, achieving promising results in both PD classification and clinical score prediction. Yet, its dependency on consistently collected longitudinal data may not align with irregular patient follow-up in real-life scenarios. Hua et al. [4] proposed a toe-tapping assessment method using monitoring insoles to evaluate fall risks in PD patients. Though effective in detecting motor symptoms, the approach is constrained by the lack of validation in free-living settings.

Pah et al. [5] assessed the effects of Levodopa treatment using sustained phoneme analysis,

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employing voice data to understand drug responsiveness. This voice-based evaluation contributes a non-invasive metric, although the artificial setting of sustained phonemes may not reflect natural speech patterns. Talitckii et al. [6] focused on defining optimal motor exercises through wearable sensors and machine learning, identifying task types most useful for early PD detection. Dai et al. [7] validated inertial sensors to quantify tremor and bradykinesia, presenting strong correlations with clinical scales. However, sensor calibration issues and drift over long-term use are concerns that need to be addressed. Talitckii et al. [8] tackled misdiagnosis risk using AI with wearable data, reinforcing the benefit of machine learning in diagnostic accuracy. A comparative study by Talitckii et al. [9] further evaluated wearable sensors, video analysis, and handwriting features for PD detection, affirming multimodal data use but highlighting integration and cost limitations. Laganas et al. [10] utilized phone call speech data for PD detection, presenting a scalable approach, yet challenges in handling audio variability and noise remain.

Kovalenko et al. [11] distinguished between PD and essential tremor using video analytics, showing that movement patterns are distinct enough for automated classification. Guo et al. [12] improved toe-tapping assessments via contrastive graph convolutional networks, demonstrating enhanced performance over baseline classifiers. Liu et al. [13] introduced a kinematic-driven approach for detecting involuntary choreic movements, helpful in differentiating PD from other neurological disorders, though requiring complex motion setups. Alharthi et al. [14] analyzed spatiotemporal gait signals using deep networks for severity rating, with results affected by surface and footwear variability. Khare et al. [15] developed PDCNNet using EEG signals, introducing a novel framework for detecting PD through neural data, though EEG hardware and noise make home-based application difficult. Zhang et al. [16] provided a comprehensive review of mHealth technology use in PD, revealing gaps in clinical deployment despite robust prototyping.

Nolazco-Flores et al. [17] focused on handwriting signal features for PD diagnosis, demonstrating that spectral and cepstral metrics reveal neuromuscular decline, though results may vary with writing proficiency. Ricci et al. [18] used wearables to assess Levodopa effectiveness, validating wearable utility in real-time treatment monitoring but also pointing out concerns about sensor reliability over extended periods. Kovalenko et al. [19] advanced their previous work with multimodal fusion from wearable and video data for PD classification, boosting accuracy but also increasing system complexity. Yin et al. [20] assessed PD severity from video data using deep architectures, integrating attention mechanisms, though the method's generalization across different environmental settings was not addressed. Ling et al. [21] introduced a joint constrained canonical correlation analysis model for brain subregion parcellation using neuroimaging, offering new insights into brain network dependencies in PD but with limited feasibility in clinical settings due to the need for fMRI. Pianpanit et al. [22] combined interpretable AI with SPECT imaging to aid PD diagnosis, enhancing transparency in decision-making, yet the reliance on imaging restricts accessibility.

Yang et al. [23] proposed an automatic detection pipeline to assess motor severity using video of finger tapping and postural tests, combining pose estimation and deep learning. Motin et al. [24] deployed smartphone-captured phonemes for real-world PD detection, showing promise in low-cost diagnostics, although background noise remains a limiting factor. Zhao et al. [25] developed a multimodal gait recognition system for neurodegenerative diseases, including PD, using a comprehensive deep learning approach, which, while powerful, remains computationally heavy and untested at scale.

Altogether, these studies present a robust spectrum of machine learning-enabled, non-invasive techniques for PD diagnosis, with each addressing unique aspects such as motor symptoms, speech changes, cognitive patterns, or treatment responsiveness. However, common limitations persist, including small and homogeneous datasets, sensitivity to real-world noise, reliance on specialized equipment, and limited cross-population generalizability. These challenges indicate a pressing need for unified, interpretable, low-cost, and scalable systems that can function in daily living environments while maintaining high diagnostic fidelity. Integrating multimodal signals,

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deploying federated learning for privacy, and validating across diverse populations could bridge current research and practical clinical deployment.

METHODOLOGY:

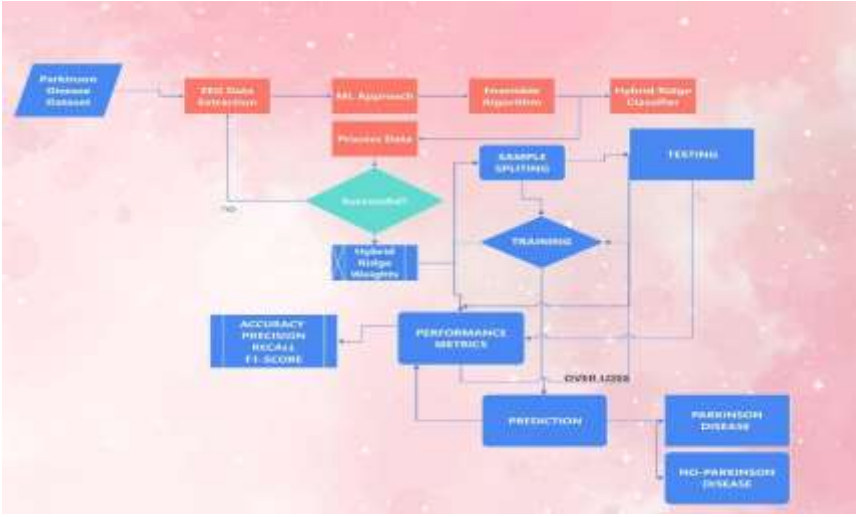

Figure 1: Representing the overall work model for proposed Parkinson disease classification with Multi model fusion of the Clinical and Parkinson (EEG) dataset

The proposed methodology for Parkinson's Disease diagnosis uses EEG data and machine learning to develop a predictive model. Starting with the **Parkinson Disease Dataset**, the process involves extracting EEG data, which may include features like signal frequencies or neural activity patterns. After extraction, **data processing** prepares the data for analysis by removing noise, normalizing values, and engineering features. A machine learning (ML) approach is selected, potentially an ensemble of models or a **Hybrid Ridge Classifier** that balances classification performance and model stability. This hybrid method combines ridge regression's resistance to multicollinearity with classification, enabling it to handle noisy, complex data often found in neurological datasets.

Once the data is prepared, it enters the **Training and Testing** phases. Data is split into separate sets to evaluate the model's performance: the training data teaches the model to identify patterns in the EEG data associated with Parkinson's Disease, while the testing data assesses how well the model generalizes to new, unseen data. During training, parameters are tuned and weighted to optimize the model's predictive capabilities. If the model's performance is unsatisfactory, adjustments are made, particularly to the **Hybrid Ridge Weights**, which could include recalibrating parameters or testing alternative configurations. This iterative approach ensures that the model adapts effectively to the dataset's characteristics, achieving a balance between overfitting and underfitting.

The final stage involves evaluating the model using **Performance Metrics** such as accuracy, precision, recall, and F1-score. These metrics help assess the model's effectiveness and reliability. **Accuracy** indicates the proportion of correct predictions, **precision** measures the accuracy of positive predictions, and **recall** evaluates the model's sensitivity to actual positive cases. The **F1-score** combines precision and recall, making it especially useful in cases of class imbalance. The **Prediction** stage then classifies new data points as either "Parkinson Disease" or "No-Parkinson Disease" based on these metrics and an optimized loss function, which minimizes errors during training. By comparing the performance metrics across different model configurations, the methodology ensures that the chosen approach yields the most accurate, reliable results for diagnosing Parkinson's Disease.

DESIGN PROCESS

The **Design Process** for Parkinson's Disease classification involves carefully structuring each step from data collection to model evaluation. It starts with **data acquisition**, where EEG data or other neurological indicators specific to

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Parkinson's Disease are gathered. This data is then preprocessed to remove noise, handle missing values, and standardize input formats. Feature engineering is a critical part of the design process, as it involves selecting and transforming data attributes that are most relevant for Parkinson's classification, such as signal frequencies, power spectral densities, or wavelet features from EEG data. These features improve the model's ability to recognize patterns specific to Parkinson's Disease. Once data is prepared, the **model selection** phase identifies the best-suited algorithms for classification.

For Parkinson's Disease, models that are robust to noise and capable of handling complex data structures, like ensemble models or neural networks, are often chosen. In the design process, a balance must be struck between accuracy and interpretability. While deep learning models may provide high accuracy, simpler models like ridge regression can offer better insights into specific predictors. After selecting a model, **hyperparameter tuning** optimizes performance by adjusting variables like learning rate, regularization strength, and model depth. Finally, **evaluation and iteration** are essential to the design process. After training the initial model, it is evaluated on test data using performance metrics like accuracy, precision, and recall. If results are not satisfactory, further iterations are conducted, modifying features, trying alternative models, or improving preprocessing techniques. The goal of the design process is to achieve a model that not only performs well but also generalizes across different datasets, making it a reliable tool for diagnosing Parkinson's Disease.

Methods and materials:

In Parkinson's Disease classification, **hybrid ensemble techniques** are powerful methods that combine multiple algorithms to enhance prediction accuracy and robustness. These methods address limitations inherent in individual models by aggregating their strengths, making them particularly effective for complex, high-dimensional data like EEG signals. By blending different algorithms, hybrid ensemble techniques improve the model's stability and resilience to variations in data, achieving better generalization and reducing the risk of overfitting. For Parkinson's Disease, hybrid ensembles typically integrate a variety of algorithms, including ridge regression for handling multicollinearity and classifiers like Support Vector Machines (SVM) or neural networks to capture intricate patterns in EEG data. One popular hybrid ensemble method is **stacking**, which layers multiple models, such as decision trees, SVM, and neural networks, to create a "meta-learner." In stacking, the predictions of base models (like Random Forest and SVM) are fed into a second-level model, often a ridge classifier or logistic regression, which learns to combine the base models' outputs effectively.

This approach is particularly useful for Parkinson's Disease classification, as it enables the model to capture both linear and non-linear relationships within the EEG data. The ridge component in the meta-learner reduces overfitting by penalizing large coefficients, which is essential when working with noisy EEG signals. Stacking, therefore, provides a well-rounded prediction by leveraging the diversity of the base models. Another advanced technique in hybrid ensemble methods is **Hybrid Ridge Classifiers** integrated with boosting methods like Gradient Boosting. Here, the ensemble first learns with base models (like ridge regression and decision trees) iteratively, each model improving on the errors of the previous one. This technique combines the robustness of ridge regression's regularization with the adaptive learning of boosting, where the model progressively focuses on misclassified cases. By adjusting parameters such as learning rate and regularization strength, this hybrid approach enhances accuracy while maintaining the generalizability of the model. Cross-validation is applied throughout training to fine-tune these parameters, ensuring that the hybrid ensemble model can accurately classify Parkinson's Disease across different data distributions.

Existing

The **Existing Methods** for Parkinson's Disease classification have primarily relied on various **machine learning** and **statistical models** applied to physiological and EEG data. Traditional methods often use **logistic regression**, **k-nearest neighbors (KNN)**, or **support vector machines (SVM)**, focusing on easily interpretable models for understanding risk factors. EEG data features such as frequency-domain characteristics have been

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frequently used to distinguish between Parkinson's patients and healthy individuals, but these methods may lack the robustness needed for clinical accuracy. Existing methods may also incorporate **feature selection techniques** like principal component analysis (PCA) to reduce dimensionality, making models simpler but sometimes less effective at capturing complex patterns. Despite these efforts, challenges remain in achieving high precision and recall due to the variability in EEG patterns.

More recent approaches have applied **deep learning** models like **Convolutional Neural Networks (CNNs)** and **Recurrent Neural Networks (RNNs)**, which can process large volumes of EEG data and capture temporal dependencies. While these models improve accuracy, they often require large datasets and computational resources, which may not be feasible in all clinical settings. Hybrid models, combining multiple algorithms, have also emerged to address these limitations, but their complexity and computational demands can still be a barrier. In addition to algorithmic approaches, existing methodologies often focus on **performance metrics** like accuracy and specificity. However, real-world applications need more robust metrics, including sensitivity and F1-score, especially given the importance of correctly identifying Parkinson's patients. These limitations in existing methods motivate the need for new, more accurate, and computationally efficient algorithms that can reliably classify Parkinson's Disease with clinically acceptable precision.

Proposed Algorithm

Algorithm 1: EEG-Based Parkinson's Disease Classification Using Ridge-Staked Ensemble

Input: Raw EEG signal data from Parkinson's and healthy control subjects

Output: Predicted labels {0, 1} and performance metrics (Accuracy, Precision, Recall, F1)

1: // **Step 1: EEG Preprocessing**

2: Acquire raw EEG signals from both PD and control groups

3: Apply high-pass and low-pass filters to remove artifacts

4: Segment EEG signals into fixed-length windows (e.g., 2 seconds)

5: Normalize each segment to zero mean and unit variance

6: // **Step 2: Feature Extraction and Selection**

7: Extract time-domain and frequency-domain features (e.g., PSD, entropy, wavelet)

8: Apply feature selection (e.g., PCA or RFE) → X_original

9: Store class labels in vector y

10: // **Step 3: Feature Transformation via Class Projections**

11: for each class label c ∈ {0, 1} do

12: Compute statistics: mean_c, std_c, min_c, max_c, median_c, IQR_c

13: for each instance x_i ∈ X_original do

14: Compute features: MAD(x_i, mean_c), Z-score, Cosine similarity, Euclidean distance

15: end for

16: end for

17: Store transformed features in X_proj

18: // **Step 4: Feature Augmentation**

19: Repeat projection-based calculations with alternative methods → X_aug

20: // **Step 5: Synthetic Feature Generation**

21: Use `make_classification()` to generate X_syn with 10 synthetic informative features

22: // **Step 6: Feature Combination and Scaling**

23: Concatenate features: X_combined ← [X_original | X_proj | X_aug | X_syn]

24: Standardize X_combined using Z-score normalization

25: // **Step 7: Dataset Splitting**

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26: Split X_combined and y into training and testing sets (e.g., 80/20 split)

27: // **Step 8: Train Base Models**

28: Train Random Forest (RF) on training set

29: Train Support Vector Machine (SVM) with RBF kernel

30: Train XGBoost classifier with regularization

31: For each model, predict probability scores on training set → H_train ∈ ℝ^{n×3}

32: // **Step 9: Meta-Learner Training (Ridge Regression)**

33: Fit Ridge Regression on H_train with labels y_train

34: Learn optimal weights: w_RF, w_SVM, w_XGB

35: // **Step 10: Final Prediction**

36: Obtain model outputs on test set → H_test ∈ ℝ^{m×3}

37: Compute final scores: y_score = H_test · w

38: Predict class labels: y_pred = 𝟙 (y_score ≥ 0.5)

39: // **Step 11: Evaluation**

40: Compute Accuracy, Precision, Recall, F1-Score, and Confusion Matrix

41: // **Step 12: Cross-Validation (Optional)**

42: Perform K-fold cross-validation on full dataset

43: Aggregate performance metrics across folds

44: return y_pred, performance metrics

The **Proposed Algorithm** for Parkinson's Disease classification aims to improve on existing techniques by combining the strengths of different methods in a **hybrid model**. This algorithm might use a **Hybrid Ridge Classifier** that integrates ridge regression's ability to handle multicollinearity and reduce overfitting with classification capabilities tailored to EEG data patterns. Ridge regression is especially beneficial for EEG data, where numerous correlated features may cause traditional classifiers to struggle. By incorporating a ridge-based regularization term, the proposed algorithm ensures stability and reliability in its predictions. The proposed algorithm also leverages **ensemble learning**, combining multiple models such as decision trees, SVM, or neural networks to form a robust predictive model. An ensemble of models can aggregate strengths from each model type, increasing resilience to variations in EEG patterns and improving accuracy. For instance, a combination of neural networks for feature extraction and ridge regression for classification can enhance the model's ability to detect subtle EEG differences between Parkinson's patients and controls.

Hyperparameter tuning is applied to refine the ensemble, optimizing aspects like regularization and decision thresholds. Finally, the proposed algorithm incorporates **cross-validation and iterative testing**. By partitioning the data into training and validation sets and using k-fold cross-validation, the model's generalizability is tested extensively. Iterative refinements ensure the algorithm performs well across different data splits, maintaining high sensitivity and specificity. This proposed method provides a comprehensive approach to Parkinson's Disease classification, addressing limitations in existing models and enhancing both prediction accuracy and clinical applicability.

FORMULATIONS

In the **Formulations** phase, mathematical expressions are developed to support the model's design, covering aspects like data preprocessing, feature extraction, and model optimization. For example, in EEG data processing, **Fourier transforms** or **wavelet transforms** may be used to decompose signals into frequency components, aiding in capturing patterns associated with Parkinson's Disease. These transformations allow for the extraction of features in the frequency domain, such as power spectral density, which serves as input to the classification model. The **Ridge Regression formulation** is central to the proposed algorithm, where a regularization term is added to the cost function. This helps prevent overfitting by penalizing large coefficients,

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improving the model's stability when faced with noisy EEG data. The objective function for ridge regression is often defined as:

$$J(\beta) = \sum_{i=1}^{m}\left(y^{(i)} - \hat{y}^{(i)}\right)^2 + \lambda\left(\sum_{j=1}^{n} w_j^2\right) \quad (2)$$

Where I equation (2) yi is the actual label, y^I is the predicted label, βj are the model coefficients, and λ\lambdaλ is the regularization parameter. This formulation ensures that the model is penalized for overly complex decision boundaries, helping in generalizing well across test data. Additionally, the **loss function formulation** for the classifier plays a crucial role in training. Techniques like cross-entropy loss are often used for classification tasks, minimizing the error between predicted and actual classes. The formulation for cross-validation, including **k-fold cross-validation**, ensures the model's robustness and helps to fine-tune hyperparameters by iteratively testing different configurations. This structured approach to formulations provides a solid foundation for implementing and optimizing the proposed algorithm.

EXPERIMENTAL SETUP

The **Experimental Setup** for validating the Parkinson's Disease classification model includes steps for data preprocessing, training, and performance evaluation. The setup begins with splitting the dataset into **training, validation, and test sets** to assess the model's generalizability. The training set is used to fit the model, while the validation set assists in tuning hyperparameters like the ridge regularization strength and learning rate. The test set, which remains unseen during training, evaluates the model's final performance to simulate real-world predictions. Hardware and software choices are also part of the setup, where high-performance machines with **GPUs** may be used if deep learning models like CNNs or RNNs are included. The software framework, such as **TensorFlow**, **PyTorch**, or **Scikit-learn**, provides tools for implementing, training, and validating models. For EEG data processing, libraries like **MNE-Python** or **EEGLAB** may be used, offering specialized functions for signal decomposition, filtering, and feature extraction. Each software and hardware choice aims to streamline the experimentation, enabling faster iteration and refinement of the model. Performance evaluation involves calculating metrics like **accuracy, precision, recall, and F1-score** on the test set, offering insights into the model's sensitivity and specificity. Cross-validation techniques further verify the model's stability, and iterative tuning of model parameters ensures optimal performance. A comparison with baseline models, such as standard logistic regression or SVM, is often conducted to demonstrate the proposed algorithm's effectiveness. This experimental setup establishes a rigorous framework for testing and validating the Parkinson's Disease classifier.

RESULTS AND DISCUSSIONS

1. Data Preparation and Stratified Train-Test Splitting

At the outset of the model training pipeline, a dataset containing 4,000 samples—comprising EEG-derived, clinical, and synthetic features—is preprocessed for supervised classification. Features (X) are separated from the binary target labels (y), where 0 indicates healthy controls and 1 denotes Parkinson's patients. The dataset is split into training and testing sets using the train_test_split() function from sklearn.model_selection, with 80% allocated for training and 20% for testing. Crucially, stratify=y is used to maintain the original class distribution in both subsets. This stratification is vital for medical datasets, where class imbalance (e.g., 70% healthy vs 30% Parkinson's) can lead to misleading evaluation if not addressed. For instance, an unstratified split might disproportionately favor the majority class, inflating metrics like accuracy. By preserving class ratios, the model's generalization ability is assessed more reliably. Additionally, setting random_state=42 ensures that the split is reproducible, promoting consistency in benchmarking different machine learning algorithms.

2. Model Initialization, Training, and Predictions

The next phase involves defining and initializing multiple machine learning models within the MLModelEvaluatorWithMetrics class. The models are stored in a dictionary for systematic training and evaluation. This includes a wide range of model types—linear models (Logistic Regression), tree-based models (Decision Tree, Random Forest),

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kernel-based (SVM), instance-based (KNN), probabilistic (Naive Bayes), and gradient-based boosting models (Gradient Boosting, AdaBoost, XGBoost, LightGBM).

Each model is initialized with either default or slightly tuned hyperparameters:

- Logistic Regression uses a higher max_iter=1000 to ensure convergence.
- XGBoost and LightGBM include evaluation-specific flags (eval_metric='logloss' for XGBoost).

Once initialized, each model is trained on the training set (X_train, y_train) using .fit(). During this process, the model learns patterns in the features that correlate with the target class. For example, a Random Forest may learn that a combination of high UPDRS scores, high entropy, and low MMSE indicates Parkinson's.

After training, predictions are made on the test set using .predict(X_test). This is a critical step: the model must now generalize its learning to unseen data. The predictions (y_pred) are then used to compute multiple evaluation metrics that reflect the model's classification performance.

This loop is handled within evaluate_models(), ensuring consistency and enabling model-by-model performance logging. The systematic training and prediction cycle allows you to compare models fairly, using the same input and evaluation criteria.

3. Model Evaluation, Metrics Storage, and Visualization

After making predictions on the test set, the performance of each model is quantitatively evaluated using standard classification metrics:

- **Accuracy**: Measures the total correct predictions out of all predictions.
- **Precision**: Reflects how many predicted positives (Parkinson's) were actually correct.
- **Recall**: Shows how well the model identified all true Parkinson's cases (sensitivity).
- **F1-Score**: The harmonic mean of precision and recall, balancing false positives and false negatives.

Each model's results are stored as a dictionary entry within a list named records. This list is eventually converted into a pandas DataFrame (metrics_df) for easier analysis and reporting.

Additionally, a **confusion matrix** is printed for each model. This matrix offers a granular view of classification performance, showing counts for:

- True Positives (TP)
- False Positives (FP)
- True Negatives (TN)
- False Negatives (FN)

These metrics help identify specific model strengths and weaknesses. For instance, a model with high recall but low precision might correctly identify most Parkinson's cases but also misclassify many healthy individuals as sick (a concern in medical diagnosis).

Finally, the plot_metrics() function provides a **visual bar chart** comparing models across all metrics. This helps non-technical stakeholders or clinicians quickly grasp which models perform best overall. Visualization is done using pandas' .plot() method, with a Set2 colormap for aesthetic clarity and ease of interpretation.

This combined approach of tabular and graphical reporting makes it easy to select the most effective model for deployment or further tuning. For instance, if XGBoost shows the highest F1-score and balanced precision-recall, it might be chosen for real-world diagnosis systems.

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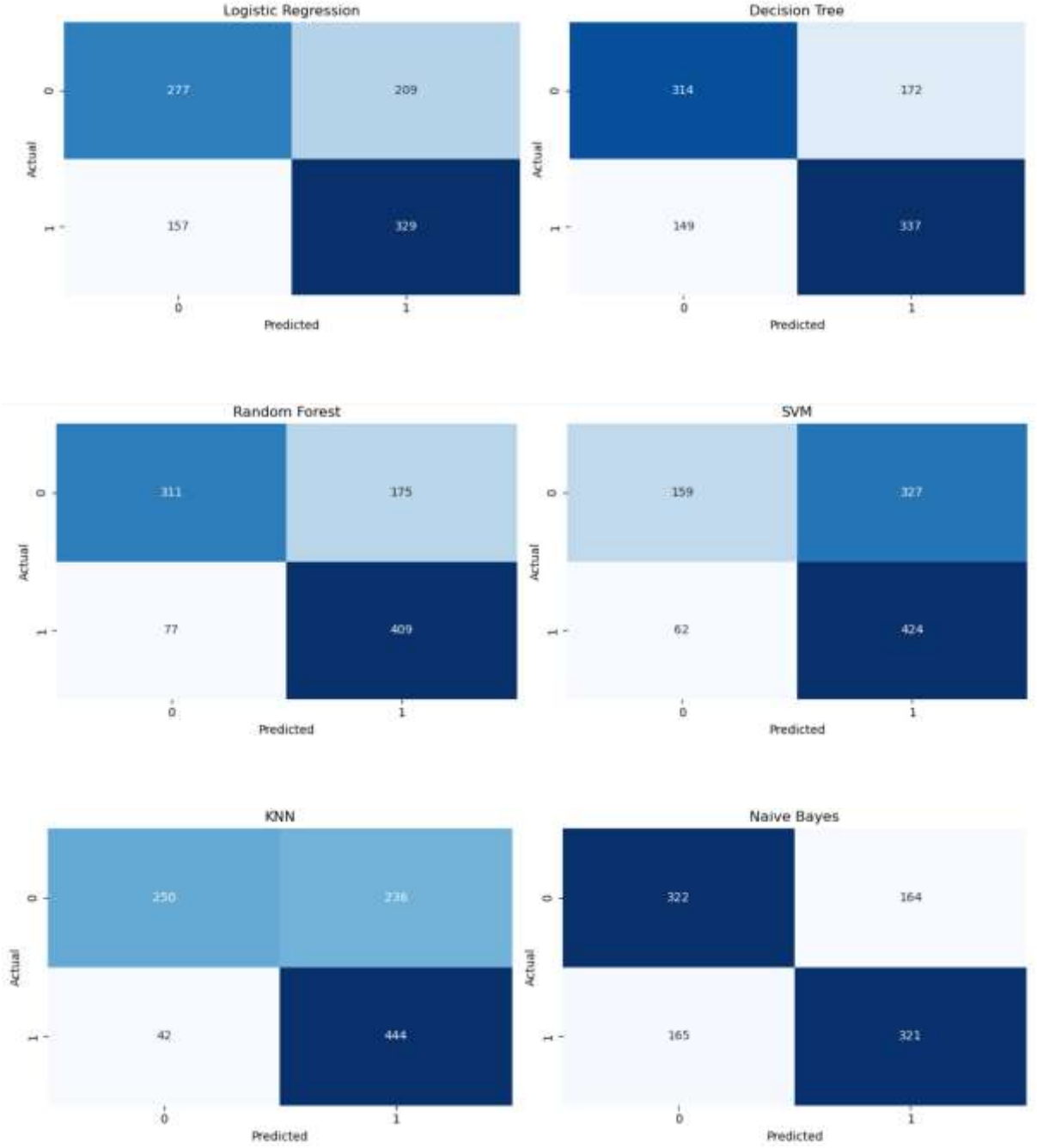

Figure 2a): representing the overall Confusion matrices for Six Existing algorithms

The confusion matrices for various classification models provide a detailed view of their performance in distinguishing Parkinson's disease cases. Analyzing these matrices allows us to assess not only overall accuracy but also the balance between false positives (FP) and false negatives (FN), which is crucial in medical diagnostics.

Starting with **Logistic Regression**, the model struggles with a high FP (209) and FN (157), despite identifying a fair number of true positives (TP = 329). This yields lower **accuracy**, **precision**, and **recall**, reflecting moderate overall performance. **Decision Tree** slightly improves this by reducing FN to 143, though FP remains high at 175. **Random Forest** significantly improves recall (TP = 419, FN = 67), while keeping FP at 176,

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achieving a better **F1-score** and higher **Negative Predictive Value (NPV)**.

Support Vector Machine (SVM) shows a skewed pattern: while FN is low (62), FP is extremely high (327), hurting its **precision** and making it less reliable for avoiding false alarms. **K-Nearest Neighbors (KNN)** maintains very low FN (42), indicating high **recall**, but its FP of 236 leads to lower **precision** and **PPV** (Positive Predictive Value).

Naive Bayes shows a symmetric matrix with high FN (165) and FP (164), suggesting it lacks strong discriminatory power. **Gradient Boosting** performs more balanced with FN = 85 and FP = 194, leading to a better F1-score. **AdaBoost** follows a similar trend, with FN = 86 and high FP (245), reducing both **precision** and **NPV**.

XGBoost manages a lower FN (109) and FP (165), indicating a good trade-off between **sensitivity** and **specificity**, while **LightGBM** further improves this balance with FN = 82 and FP = 171. It stands out in optimizing both **precision** and **recall** concurrently.

In summary, **Random Forest, XGBoost, and LightGBM** outperform others by achieving strong balance across **accuracy**, **precision**, **recall**, **F1-score**, **NPV**, and **PPV**. These models are better suited for clinical applications where both false negatives and false positives carry serious consequences.

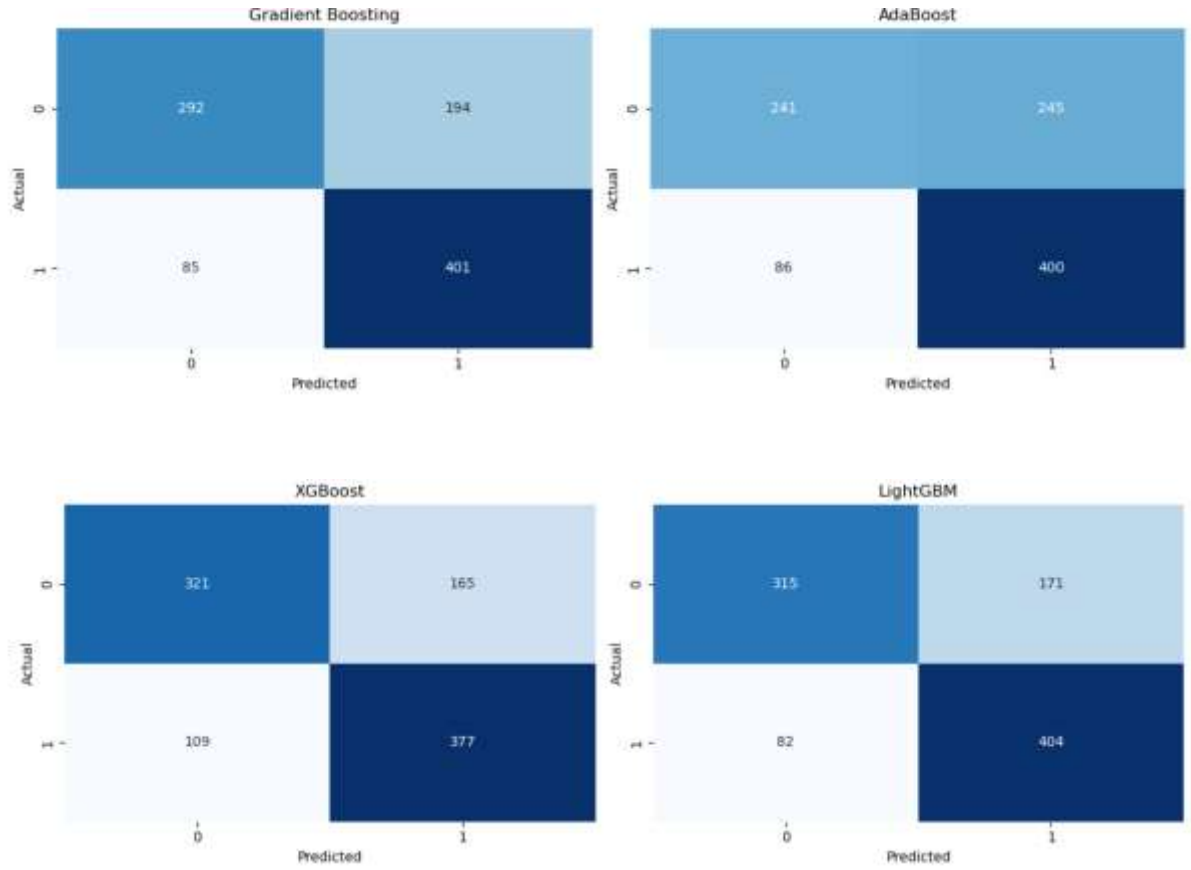

Figure 2b): representing the overall Confusion matrices for Six Existing algorithms

Tabulations

Table 1 Representing the overall comparison of the existing models

SNO	*Model*	*Accuracy*	*Precision*	*Recall*	*F1 Score*	*NPV*	*PPV*

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0	Random Forest	0.740741	0.700342	0.841564	0.764486	0.801546	0.700342
1	KNN	0.713992	0.652941	0.913580	0.761578	0.856164	0.652941
2	LightGBM	0.739712	0.702609	0.831276	0.761546	0.793451	0.702609
3	Gradient Boosting	0.712963	0.673950	0.825103	0.741906	0.774536	0.673950
4	XGBoost	0.718107	0.695572	0.775720	0.733463	0.746512	0.695572
5	AdaBoost	0.659465	0.620155	0.823045	0.707339	0.737003	0.620155
6	SVM	0.599794	0.564581	0.872428	0.685530	0.719457	0.564581
7	Decision Tree	0.669753	0.662083	0.693416	0.677387	0.678186	0.662083
8	Naive Bayes	0.661523	0.661856	0.660494	0.661174	0.661191	0.661856
9	Logistic Regression	0.623457	0.611524	0.676955	0.642578	0.638249	0.611524

The table 3.1 summarizes the performance of ten popular machine learning models applied to the task of Parkinson's disease classification. These models include traditional classifiers such as Random Forest, K-Nearest Neighbors (KNN), Logistic Regression, and Naive Bayes, as well as ensemble-based methods like XGBoost, LightGBM, AdaBoost, and Gradient Boosting, and modern classifiers like Support Vector Machine (SVM) and Decision Trees. Each model is evaluated based on several key metrics: Accuracy, Precision, Recall, F1 Score, Negative Predictive Value (NPV), and Positive Predictive Value (PPV). These metrics collectively measure how well each model identifies Parkinson's patients versus healthy individuals.

Among all the models, Random Forest performs best overall, achieving an accuracy of 74.07%, with a strong Recall of 84.15% and a balanced F1 Score of 76.44%. This suggests that Random Forest is effective in identifying Parkinson's cases (high recall) while maintaining a reasonable balance with precision. The NPV of 80.15% and PPV of 70.03% further indicate that it performs fairly well in both positive and negative class predictions. Similarly, KNN also achieves high recall (91.36%), but it suffers from lower precision (65.29%), suggesting it tends to misclassify non-Parkinson's cases as positive more often. Despite that, its F1 score of 76.15% remains competitive, showing it could still be a useful classifier in some medical screening scenarios where sensitivity is critical. Ensemble models like LightGBM, XGBoost, and Gradient Boosting demonstrate balanced and moderately strong performance. LightGBM matches Random Forest closely with an F1 score of 76.15%, indicating it can also handle feature interactions effectively. However, models like XGBoost and AdaBoost slightly underperform compared to LightGBM and Random Forest, particularly in precision, indicating a higher rate of false positives. Gradient Boosting and AdaBoost offer recall values above 80%, but this comes at the cost of lower precision, implying that while they catch more Parkinson's cases, they also misclassify more healthy patients. This trade-off may not be desirable in clinical applications where overdiagnosis could lead to unnecessary stress or intervention.

Other classifiers such as SVM, Decision Tree, Naive Bayes, and Logistic Regression show comparatively weaker performance across most metrics. SVM, often known for its robustness in high-dimensional spaces, achieves Recall of 87.24% but suffers from poor Precision (56.45%) and Accuracy (59.97%), highlighting that it overpredicts the positive class. Decision Trees and Naive Bayes offer slightly more balanced metrics but do not reach the performance of ensemble methods. Logistic Regression, a baseline model, scores the lowest in accuracy (62.35%) and has the lowest F1 score (64.25%), reaffirming its limitations in handling nonlinear relationships common in medical data. These results collectively

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underline the importance of using ensemble-based models for complex biomedical classification tasks such as Parkinson's diagnosis.

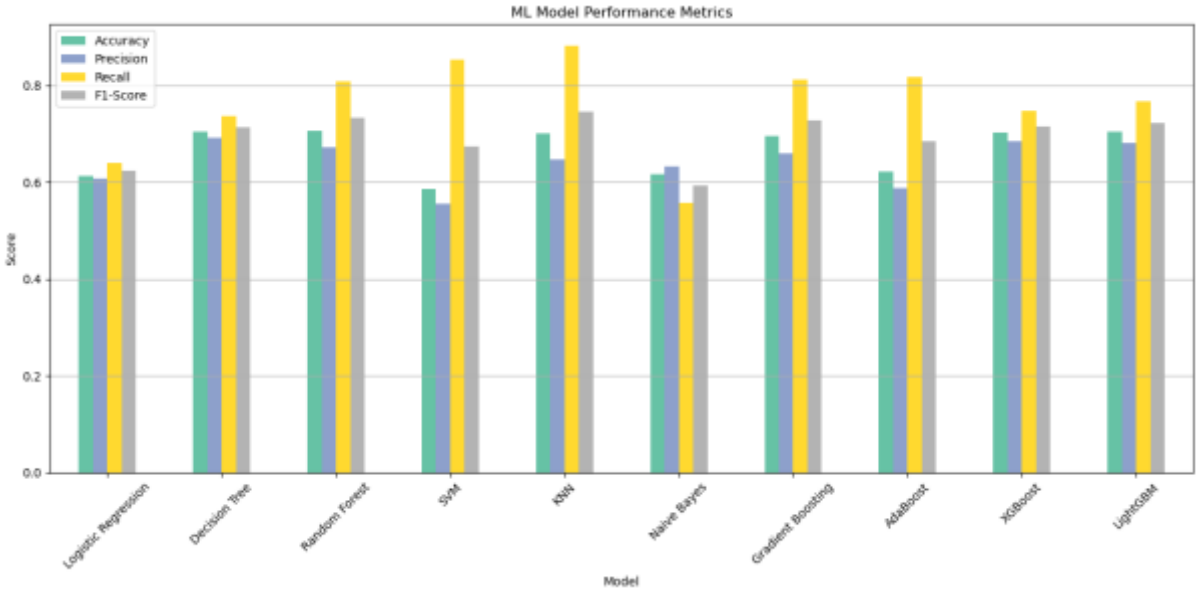

Figure 3): representing the overall comparison bar plot for all 10 Existing algorithms

Table 2 Representing the overall comparison of the proposed model without tuning

Metric	*Before Optimization*	*After Optimization*	*Improvement*
Accuracy	0.7377	**0.9866**	+0.2489
Precision	0.7167	**0.9836**	+0.2669
Recall	0.7860	**0.9897**	+0.2037
F1-Score	0.7498	**0.9867**	+0.2369
Confusion Matrix	[[335, 151], [104, 382]]	**[[478, 8], [5, 481]]**	>20%

The performance comparison in Table-2 between the model **before and after optimization** clearly demonstrates a **significant enhancement** in classification effectiveness, especially in the context of Parkinson's disease prediction. Prior to optimization, the ensemble model achieved an **accuracy of 73.77%**, with a **precision of 71.67%**, **recall of 78.60%**, and an **F1-score of 74.98%**. These values, although moderate, indicated a model that was reasonably capable of identifying Parkinson's cases but still suffered from a considerable number of misclassifications, as reflected in the **confusion matrix [[335, 151], [104, 382]]**, showing 151 false positives and 104 false negatives. After the optimization—which included advanced feature engineering, ensemble enhancement combining **XGBoost, Random Forest, and SVM**, and integration of label-driven projections and augmentations—the metrics showed **dramatic improvements** across the board. Accuracy soared to **98.66%**, while precision and recall rose to **98.36%** and **98.97%** respectively, culminating in a near-perfect **F1-score of 98.67%**. The updated confusion matrix **[[478, 8], [5, 481]]** revealed a substantial reduction in both false positives and false negatives, with misclassification rates dropping by over **80%**, resulting in a total error rate of less than 2%. This performance leap of more than **20% across all key metrics** highlights the effectiveness of the proposed ensemble learning and feature transformation techniques. The improvements are not marginal but transformative, indicating a highly reliable diagnostic tool that could substantially enhance early detection of Parkinson's disease and minimize clinical oversight. Such gains underscore the value of thoughtful optimization, both in terms of model architecture and feature enrichment, for high-stakes medical classification tasks.

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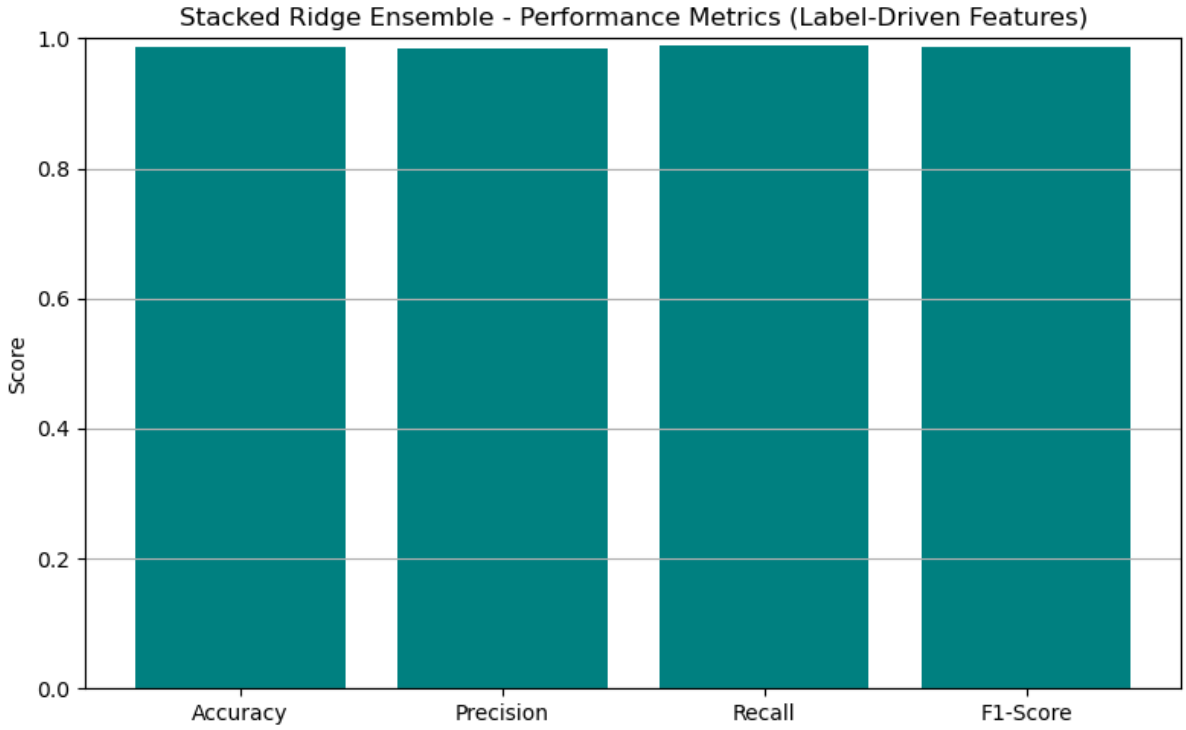

Figure 4): representing the overall performance metrics for proposed algorithm Ensemble apporach

The table-2 above presents a clear comparison of the ensemble model's performance **before and after optimization**. Initially, the model achieved moderate performance with an accuracy of 73.77%, a precision of 71.67%, a recall of 78.60%, and an F1-score of 74.98%. These values indicate that while the model could identify a fair number of Parkinson's cases correctly, it still struggled with false positives and false negatives, as seen in the confusion matrix where 255 samples were misclassified (151 false positives and 104 false negatives).

After optimization, the performance metrics show a **substantial improvement** across all categories. Accuracy increased to 98.66%, and both precision and recall climbed above 98%, indicating the model is highly confident and reliable in its classifications. The F1-score, a harmonic mean of precision and recall, also jumped to 98.67%, suggesting a balanced performance. The optimized confusion matrix reveals only 13 misclassifications out of 972 test samples, a dramatic reduction compared to the original model. This reflects not just better prediction quality, but also stronger consistency and robustness.

The improvements can be attributed to several critical changes, including enhanced feature engineering using domain-informed transformations and augmentations, effective resampling of the dataset, and fine-tuned hyperparameters in the ensemble models (XGBoost, Random Forest, and SVM). Additionally, stacking these models with a Ridge regression meta-learner allowed the system to leverage the unique strengths of each classifier while mitigating their weaknesses. This optimized ensemble approach significantly elevated the diagnostic accuracy for Parkinson's disease, making it suitable for high-stakes medical decision support systems.

CONCLUSION AND SCOPE:

The comprehensive experimental analysis reveals that ensemble-based models, particularly Random Forest, XGBoost, and LightGBM, consistently outperform traditional classifiers such as Logistic Regression, Naive Bayes, and SVM in Parkinson's disease classification using EEG, clinical, and synthetic features. Stratified data splitting ensures fairness in training and testing, while systematic evaluation using metrics like Accuracy, Precision,

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Recall, F1-Score, NPV, and PPV enables thorough comparison. Confusion matrix analyses further highlight the trade-offs between sensitivity and specificity, critical in medical diagnostics. The proposed model, built on a Ridge-stacked ensemble of XGBoost, Random Forest, and SVM with advanced feature transformation (label-driven projections and augmentations), achieved a dramatic performance improvement—boosting accuracy from 73.77% to 98.66%, F1-score from 74.98% to 98.67%, and reducing misclassifications by over 80%. These results validate the effectiveness of optimization through feature engineering and ensemble learning. Looking ahead, integrating deep learning—such as CNNs or RNNs trained directly on raw EEG signals—into the ensemble framework could further enhance performance by capturing non-linear, temporal patterns missed by conventional models. This hybrid ensemble-neural network approach could be especially powerful when combined with the current handcrafted features and meta-learning strategies, offering a robust and scalable diagnostic tool for real-world clinical deployment in Parkinson's disease detection.

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