Comparative Study of Different Machine Learning Models for Parkinson's Disease Detection

A PROJECT REPORT

SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE
OF

MASTER OF TECHNOLOGY
IN
INFORMATION TECHNOLOGY

Submitted by

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CANDIDATE'S DECLARATION

I, **Anuraag Raj Narayan**, Roll No – **23/ITY/05** student of M.Tech (**Information Technology**),hereby declare that the project Dissertation titled "**Comparative Study of Different Machine Learning Models for Parkinson's Disease Detection**" which is submitted by me to the **INFORMATION TECHNOLOGY**, Delhi Technological University, Delhi in partial fulfilment of the requirement for the award of degree of Master of Technology, is original and not copied from any source without proper citation. This work has not previously formed the basis for the award of any Degree, Diploma Associateship, Fellowship or other similar title or recognition.

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CERTIFICATE

I hereby certify that the Project Dissertation titled "**Comparative Study of Different Machine Learning Models for Parkinson's Disease Detection**" which is submitted by **Anuraag Raj Narayan**, Roll No – **23/ITY/05**, **INFORMATION TECHNOLOGY**, Delhi Technological University, Delhi in partial fulfilment of the requirement for the award of the degree of Master of Technology, is a record of the project work carried out by the student under my supervision. To the best of my knowledge this work has not been submitted in part or full for any Degree or Diploma to this University or elsewhere.

Place: Delhi **Dr. Virender Ranga**

Date: 29.05.2025 **SUPERVISOR**

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ACKNOWLEDGEMENT

I wish to express our sincerest gratitude to **Dr. Virender Ranga** for his continuous guidance and mentorship that he provided us during the project. He showed us the path to achieve our targets by explaining all the tasks to be done and explained to us the importance of this project as well as its industrial relevance. He was always ready to help us and clear our doubts regarding any hurdles in this project. Without his constant support and motivation, this project would not have been successful.

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Abstract

Parkinson's disease (PD) is a debilitating neurodegenerative disorder with pronounced effects on motor function and daily life. Early symptoms, which are typically subtle and include stiffness of the muscles, tremor, and disturbances in balance, make early diagnosis difficult. The standard assessment tools, such as blood tests and imaging scans, offer limited value in PD diagnosis from the onset. Impairments of the voice are an early indicator that has potential for the prediction of PD. This research utilizes biomedical voice recordings using the University of California, Irvine (UCI) dataset to construct prediction models for PD diagnosis. Various machine learning methods being examined include Decision-Tree Model, XGBoost, Naive Bayes, Random-Forest Model, Support Vector Machine (SVM) Model, Logistic Regression, and K-Nearest Neighbors (KNN). The models have been trained and tested to assess how they perform. The performance of such models has been properly assessed based on accuracy, efficiency, and processing speed. A comparative study of the best-performing models is discussed, highlighting the capability of all the models to attain good accuracy in early-stage PD detection. In addition, the present study measures the feasibility of using lightweight models for use in mobile applications that offer accessibility in actual healthcare environments. The reliability and accuracy of PD classification prediction, this study also integrates an exploration of several boosting models, which are renowned for their efficiency in optimizing poor learners through refined iteration. Sophisticated boosting algorithms like AdaBoost, Gradient Boosting, LightGBM, CatBoost, and Stochastic Gradient Boosting were compared to conventional models simultaneously. These methods proved to be superior in terms of precision, recall, and stability, with Stochastic Gradient Boosting being the highest in overall accuracy. Their ability to work with high-dimensional and unbalanced data renders them very useful for biomedical applications. This blending of boosting models not only enhances the predictive strength of PD detection systems but also opens the door for scalable, real-time diagnostics that can be used in clinic or remote monitoring settings.

Contents

List of Tables

List of Figures

Chapter 1

INTRODUCTION

Parkinson's Disease (PD) is a slowly advancing disorder that affects the nervous system and movement that predominantly targets motor function as a result of neurons in the brain responsible for generating dopamine. Dopamine is essential in relaying signals responsible for the movement and coordination of muscles. The progression of the disease results in worsening motor control, speech, balance, and other physical and intellectual functions, ultimately contributing to the deterioration of the overall quality of life. While the precise etiology of PD is not yet understood, prompt diagnosis is generally regarded as critical to providing timely intervention and symptom management. Conventional diagnostic methods, like blood examination or neuroimaging, commonly are unable to recognize PD at its initial phases when therapeutic efforts would be most effective. Studies have shown that by the time outward symptoms of PD can be observed, a great majority—up to 80% of dopamine-producing cells could have already been destroyed. Therefore, it is an urgent necessity to have non-invasive and sensitive tools to diagnose PD in its initial phase. One such potential avenue is the examination of vocal biomarkers. Voice changes, including diminished pitch variability, vocal tremors, and other speech abnormalities, are some of the earliest signs of PD. The abnormalities can be identified long before the appearance of prominent motor symptoms. With the rise in AI, especially with ML, there is increased interest in creating automated systems that would recognize these subtle voice changes and aid early diagnosis. This research uses a biomedical voice recording dataset obtained from the University of California, Irvine (UCI) Machine Learning Repository. The dataset contains vocal parameters of subjects with Parkinson's along with healthy controls. Various supervised ML algorithms were trained on this dataset such as Support Vector Machines (SVM), K-Nearest Neighbors (KNN), Naive Bayes, Random Forest, Decision Tree, XGBoost and Logistic Regression. These models were learned to predict whether a provided voice sample belongs to an individual with or without Parkinson's Disease. To guarantee stable performance, preprocessing techniques like normalization and feature scaling were implemented on the dataset. The research focuses on using metrics such as recall, precision, accuracy, Area Under the Curve (AUC) and F1-score to evaluate model performance. Comparative analysis is designed to select the most appropriate models for detecting PD with respect to the tradeoff between prediction accuracy and computational complexity. In addition, this study examines the wider use of these models within real-world healthcare environments, particularly in the low-resource setting or mobile health platforms. Utilizing speech-based analysis and machine learning, this effort adds to building accessible early-stage diagnostic tools for PD. Ultimately, the aim is to enable timely diagnosis and management of PD, thus enhancing patient outcomes as well as optimizing healthcare resources. Apart from classical supervised learning methods, the present study also investigates employing high-performance ensemble meth-

ods, specifically boosting algorithms, to maximize diagnostic precision for the diagnosis of Parkinson's Disease. Boosting models are recognized for their capability to enhance weak learners by learning sequentially models that concentrate on instances previously misclassified. Some of the latest boosting methods—i.e., AdaBoost, Gradient Boosting, XGBoost, LightGBM, CatBoost, and Stochastic Gradient Boosting—were employed and compared. These models were selected for their established effectiveness in classification tasks and ability to process high-dimensional, structured biomedical information. All models were tested under uniform preprocessing and tuning approaches, with performance measured across multiple criteria. The addition of boosting techniques provides further insight into the capability of ensemble learning in the detection of Parkinson's based on non-invasive, voice-based methods and provides a stronger basis for comparison in the search for the most accurate, scalable, and computationally efficient approach.

1.1 RESEARCH GAPS

While there has been considerable advancement in the application of deep learning (DL) and machine learning (ML) approaches used to identify Parkinson Disease (PD), numerous essential research gaps remain. First, the majority of current research focuses on one type of algorithm class, either a conventional ML model such as Support Vector Machines or a contemporary DL system such as Convolutional Neural Networks, without carrying out a comprehensive comparative study involving a wide range of models. This limited scope restricts insights into what algorithms work best under different scenarios and configuration settings. Secondly, although many datasets have been examined, much of the work still bases itself on comparatively large-scale and multimodal datasets, which are not always available or feasible for real-world use, especially for resource-limited or mobile healthcare settings. The use of light models on small, single-modality datasets such as the UCI Parkinson's dataset is not well explored. Thirdly, there is less focus on systematic data preprocessing pipelines, i.e., class balancing methods (e.g., SMOTE), normalization strategies, and feature scaling, and their effects on the performance and the robustness of various models. Further, few studies explore the real-time deployability of trained models on embedded or mobile platforms for early diagnostic use, where the computational power is restricted. Additionally, although some models have shown promising accuracy, very little attention has been devoted to the interpretability of the predictions—a critical component in medical decision-making. In addition, the development of explainable AI systems that may assist clinicians to comprehend the rationale behind a model's choice has not become very popular for use in PD diagnosis. Lastly, breakthroughs with Transformer-based models as well as ensemble meta-learning methods have not yet been extensively evaluated to solve voice-based Parkinson's detection. This work intends to overcome a number of these shortcomings by providing a thorough comparative analysis of several ML and DL models, integrating strong preprocessing methods, and focusing on light, interpretable solutions deployable in mobile healthcare environments.

Chapter 2

LITERATURE REVIEW

Various recent works have attempted to utilize deep learning (DL) and machine learning (ML) methods for the early diagnosis of Parkinson's Disease (PD), with a sharp interest in speech-based biomarkers owing to their non-invasive nature and early onset. The authors have utilized models like SVM, Random Forest, XGBoost, and CNNs from voice parameters like harmonic-to-noise, shimmer and jitter ratio. Among these, ensemble models such as XGBoost and Random Forest have reported consistently high accuracy, whereas deep learning techniques provide improved feature extraction, particularly with larger datasets. For handling class imbalance, methods such as SMOTE and enhanced feature selection have also been employed, enhancing model robustness. Overall, the literature emphasizes that the use of proper models in conjunction with preprocessed voice data is effective for precise and early diagnosis of PD. This section discusses recent research activity on the (ML) and deep learning (DL) to detect the Parkinson's Disease (PD) by machine learning algorithms. With the advancements in ar- tificial intelligence, these methods have indicated signif- nicant potential in detecting PD symptoms via several biomarkers, such as voice and movement data. We will give an overview of various ML and DL models that have been suggested in relevant studies for PD detection. This involves examining 15 prominent publications that emphasize the efficacy of different algorithms in enhancing early diagnosis and disease management.

P.M.Shah, A.Zeb, U.Shafi, S.F.A.Zaidi, and M.A.Shah et al. [1] developed a CNN-based method for the automat- ic detection of Parkinson's Disease from T2- weighted MRI scans. Their method attained 96conventional machine learning algorithms like SVM and ANN by avoiding handcrafted feature extraction and effectively learning spatial structure from midbrain slices. R.Kaur and A.Dadhich et al. [2] suggested a deep learning strategy to diagnose Parkinson's Disease based on a handwriting database. The authors CNNs) and (RNNs) to handle both spatial and temporal features of handwritten patterns like spirals and waves. These features are typically affected in Parkinson's patients due to motor disorder, thus making handwriting an informative non- invasive biomarker. Their model performed robust classifica- tion performance, reflecting the power of deep learning in early diagnosis and accessible PD.

M. Mohaghegh and J. Gascon et al. [3] introduced a new mul- timodal deep learning paradigm for Parkinson's Disease de- tection with handwriting and voice data. The authors employed Vision Transformers (ViT) to process spiral and me- ander drawings and Audio Spectrogram Transformers (AST) to analyze sustained vowel phonations (/a/ and /o/) of the PC-GITA dataset. Their work showed an impressive accu- racy of 92.37emphasizing the potential of transformer-based architectures in PD diagnosis. This approach emphasizes the success of merging a variety of data modalities, particularly in early detection, and facilitates user-friendly, non-invasive tests that may aid clinicians in medi-

cal decision-making. J.Lee, W.Wang, Y. Sun and F.Harrou et al. [4] proposed a deep learning-based approach to detect the Parkinson's Disease (PD) using premotor disorder symptoms such as REM sleep behavior disorder, ostalgia for olfactory, cerebrospinal fluid biomarkers, and SPECT imaging markers. They employed the PPMI dataset, which comprises data from participants, and contrasted the PD patients and 183 normal 401 early- stage the performance of deep learning with twelve traditional machine learning models. The suggested deep neural network yielded an exceptional accuracy of 96.45%, surpassing other technologies such as SVM, Random Forest, and boosting techniques. This research highlights the capability of deep learning to manage - Integrity Submission features—such as shimmer, harmonics-to-noise(HNR) and jitter ratio and measures of fundamental frequency—to distinguish between healthy persons and PD individuals. They several machine learning algorithms, such as small medical datasets and in extracting sophisticated, nonlinear patterns from biomedical features for early diagnosis of PD.

P.M.K.Kumari, S.G.Spoorthy, I.Hepsebha, and P.Charishma et al. [5] investigated the early diagnosis of Parkinson's Disease (PD) using voice analysis by employing machine learning methods. The authors analyzed significant vocal assessed SVM, Decision Trees, Logistic Regression, Random Forest, XG-Boost and KNN. Of these, XG-Boost scored the highest accuracy of 97.43%, proving its suitability in capturing fine speech-related impairments typical of PD. Their method highlights the promise of speech-based, non-invasive diagnostic tools for early PD screening. A.Bourouhou, A.Jilbab, C.Nacir, and A.Hammouch et al. [6] compared the performance of K-Nearest Neighbors (K-NN), Naive Bayes, and Support Vector Machines (SVM) for the detection of Parkinson's Disease using voice recordings. They extracted 26 features from a publicly available dataset and found that SVM had the best accuracy of 80%, and it was the best among the classifiers tested for voice-based PD detection.

S.Harlina, M.Magfirah, A.Rizaldy, A.Asran, U.Usman, and M.O.Kadang et al. [7] explored how various feature selection methods affect the classification accuracy of Parkinson's Dis- ease detection. They compared Information Gain, Forward Selection, and Maximum Relevance Minimum Redundancy (mRMR) with k-NN and Naive Bayes classifiers. Among these, mRMR gave the highest accuracy (up to 86.13outperforming filter and wrapper approaches. Their results em- phasize that meticulous feature selection has a strong positive impact on model performance for PD detection with voice- based data. M.Pansera, J.J.Estrada, L.Pastor, J.Cancela, R.Greenlaw, and M.T.Arredondo et al. [8] created a system for real- time monitoring of Parkinson's Disease (PD) patients through examination of their gait via entropy-based techniques. Their study centered on quantifying gait symmetry using sample entropy and introduced a Gait Symmetry Index (GSI) to measure movement irregularities. The findings revealed sig- nificant differences in gait entropy between PD patients and controls. with bradykinesia. This method presents a promising method for remote monitoring and individualized treatment adjustments.

A.Porta, V.Bari, T.Bassani, A.Marchi, S.Tassin, M.Canesi, F.Barbic, and R.Furlan et al. [9] investigated the application of entropy-based methods to estimate cardiovascular complexity in Parkinson's Disease (PD) patients. They compared two approaches K-Nearest Neighbor Conditional Entropy (KNNCE) and Corrected Conditional Entropy (CCE) to identify early cardiovascular regulation impairments. Their findings indicated that PD patients present greater complexity in heart period and blood pressure variability compared to healthy individuals, even when free of typical symptoms. This indicates that entropy-based analysis could be an effective non-invasive marker for early detection of automatic dysfunction in PD. C.Guo and H.Wang et al. [10] introduced an improved

K-Nearest Neighbors (KNN) algorithm with information entropy infor- mation to enable more accurate diagnosis of Parkinson's Dis- ease. By using entropy-based weights on features, the model enhanced the classification accuracy over conventional KNN. The authors compared their algorithm with Naive Bayes and Random Forest algorithms and showed that the enhanced KNN provided better performance on Parkinson's data sets, partic- ularly in dealing with noisy and high- dimensional data.

N.Mohammed Muhaseen, G.Rajasekar, C.Amali, R.Rajesh, and J.Sai Abrameyan et al. [11] used a hybrid machine learning model based on Random Forest and XGBoost coupled with wearable sensors and video input for early detection of Parkinson's Disease. Their method enhances accu- fast and allows cost- effective real-time diagnosis appropriate for remote health care. Chuang-Chien Chiu, Shoou-Jeng Yeh, and Yen-Chi Sun et al. [12] studied the facial features' role in PD detection using still images. They analyzed important facial parameters like tension of the muscle and distance between mouth corners, which are generally impacted because of hypomimia in PD patients. Applying image processing utilities such as OpenCV and Dlib, they discovered that these features could be used to distinguish PD patients from healthy subjects, propounding a non-invasive and efficient way of early diagnosis.

Nilgun Ozt Urk Mutlu, Fikret Ari, M. Cenk Akbostanci, and F.Tugra Karaarslan et al. [13] created an electromechanical system for objectively quantifying wrist rigid- ity in patient with Parkinson's Disease. It employs sensor- based data collec- tion and computerized analysis for measur- ing stiffness with passive wrist movement, correlating findings with physician ratings. Consistency with clinical scales such as UPDRS and Hoehn-Yahr was shown in the study, pro- viding a more accurate and standard andardized methodology to assessing rigidity in PD. Dhwani Vashisth, Dr. Rakesh Garg, and Ipsha Gupta et al. [14] did an extensive machine learning algorithm comparison for Parkinson's Disease detection via speech samples. They com- pared models such as SVM, AdaBoost, XGBoost, Decision Trees, and stacking. They established from their study that the had the best accuracy and precision, marking it as best to detect PD from speech characteristics.

Tapan Kumar, Pradyumn Sharma, and Prof. Nupur et al. [15] learning models for Support Vector Machine (SVM) attained Prakash conducted a comparative evaluation of thirteen machine early prediction of Parkinson's Disease with the use of biomedical voice data. Their work pointed out that accuracy, with models such as Random Forest and Decision Tree attained high Random For- est as high as 94.92%. The research highlighted the potential of light-weight and power-efficient models appropriate for use in mobile health applications. Sambhav Gupta, Sandipa Bose and Vinayak Majhi et al. [16] Current research indicates the importance of family health history in Parkinson's Disease (PD) risk. Family studies, such as those involving SNCA and LRRK2 gene mutations, have been linked to familial PD. Studies by Rybicki et al. and Rosen et al. confirm that neurological conditions such as Alzheimer's and depression among family members can signify common risk. The Fox Insight dataset, employed in Gupta et al. (2024), demonstrated strong connections between PD and some neurological diseases in relatives, implicating both risk (e.g., schizophrenia, multiple sclerosis) and protective (e.g., Parkinson's, depression) factors. This testimony emphasizes the value of including family neurological history within PD risk evaluation and the call for further investigation into gene-environment interactions and hereditary effects.

MOHAMMED F. ALLEBAWI, , THAMEUR DHIEB, MOHAMED NEJI, NOUHA FARHAT, EMNA SMAOUI, TAREK M. HAMDANI, MARIEM DAMAK, CHOKRI MHIRI, BILEL NEJI, TAHA BEYROUTHY AND ADEL M. ALIMI et al. [17] There

has been recent work in employing different biometric signals such as voice, gait, and handwriting for Parkinson's Disease (PD) diagnosis with machine learning. SVM, Decision Trees, and Random Forest have all performed well traditionally, and Random Forest even up to 94.92% has been reported in some of these studies. Deep models including CNNs, LSTMs, and Bi-GRUs have also been used for temporal feature extraction in handwriting and voice. The team developed a new system based on online Arabic handwriting, integrating Beta-elliptical modeling and fuzzy perceptual detectors, and attained more than 93% accuracy using BLSTM classifiers. Other authors, such as Nolazco-Flores, Lamba, and Diaz, have utilized feature selection and augmentation methods, enhancing performance despite having small datasets. Nonetheless, areas of difficulty include scarce publicly available data, heterogeneity of symptoms, and low generalizability. All these are addressed in this dissertation as it compares several ML models on voice data, considering both accuracy and feasibility of deployment for practical healthcare use. Rekha Nirmala Pathapati, Dr. Vijaya Sankar Anumala, Vallabh Sriram Charan Gupta Jupudi and Narendra Pasam et al. [18] Several studies have explored the detection of Parkinson's Disease (PD) with the help of MRI, voice, gait, and handwriting data. Conventional machine learning algorithms like Random Forest and SVM have shown good performance but tend to fail in terms of generalizability because of small dataset size and variation in features. The recent deep learning-based methods have enhanced performance using CNNs and sophisticated feature extraction. Multiscale hybrid attention networks and parallel slice analysis with the use of MSHANet, for example, have attained accuracies of up to 90.59% on PPMI datasets. Graph Neural Networks such as SparsityATopK have also been used but are hindered by issues such as data imbalance and overfitting. A new work was proposed for a Hybrid Genetic Algorithm (HGA)-directed CNN model based on brain MRI scans. Their approach optimized CNN architectures automatically by decreasing model complexity while increasing accuracy. The best-performing model, PDNet, reached 100% accuracy on Dryad and 92.31% on PPMI, performing better than standard approaches and showing excellent generalization ability. These studies highlight model optimization, dataset balance, and architectural simplification as key to successful PD diagnosis, which this dissertation extends through comparative assessment of machine learning models with biomedical voice data.

Anusid Wachiracharownong, Panyawut Sri-iesaranusorn, Decho Surangsrirat, Pattara Leelaprute, Pattamon Panyakaew, Roongroj Bhidayasiri et al. [19] New research has examined various modalities for the detection of Parkinson's Disease (PD) such as voice, handwriting, gait, and brain imaging. A novel and low-cost method is the examination of spiral drawings, which are indicative of motor dysfunction typically linked to PD. The researcher utilized a CNN-based method with scanned spiral illustrations of PD patients and healthy controls. Their research employed data augmentation and compared pretrained models such as InceptionV3, ResNet50, and EfficientNetB0. The InceptionV3 model performed well (82% accuracy, F1 score of 0.81), especially when utilizing images drawn by the non-dominant hand, which demonstrated improved discrimination. This inexpensive, non-invasive screen procedure permits home testing and is of potential for rural or underserved populations. These results attest to the usefulness of straightforward input modalities and powerful CNN models in the early diagnosis of PD, complementing other methods like voice or MRI-based detection explored in this dissertation. Luyao Jin, Running Zhao, Junyi Cao, Vincent C. K. Cheung and Wei-Hsin Liao1 et al. [20] Conventional machine learning and deep learning techniques have been extensively utilized for the diagnosis of Parkinson's Disease (PD) and depression from biomedical

signals such as EEG. PD-related depression, a non-motor but an early symptom of PD, has been poorly addressed so far developed an explainable functional connectivity (XFC) framework employing EEG data to distinguish between PD related depression and PD without depression and general depression. As opposed to black-box deep learning models, their approach provides increased transparency via class activation maps, providing interpretable information regarding brain region connectivity. The research demonstrated that the XFC model performs better than EEGNet and SVM baselines and has a 94.58% accuracy rate in PD-related depression detection. It also detected certain patterns of brain connectivity in the central and frontal areas, consistent with clinical findings. The research demonstrates the promise of the integration of explainable AI and EEG data for precise and early diagnosis of subtle neurological symptoms, in line with the goals of this dissertation to evaluate machine learning models for PD detection.

Chapter 3

METHODOLOGY

This work outlines a comprehensive pipeline for Parkinson's Disease (PD) detection using an evaluation comparing machine learning and deep learning approaches is conducted. The first step in this process involves gathering data, during which a biomedical voice dataset from the UCI Machine Learning Repository is utilized, containing diverse voice identical from both healthy and PD patients individuals. Next, Data Cleaning is performed to handle missing values, remove inconsistencies, and ensure dataset reliability. Following this, Data Preparation includes feature scaling through normalization and standardization, label encoding, and class balancing using the SMOTE technique to improve model fairness. Techniques such as Correlation Analysis and visual tools like heatmaps and pair plots are applied for exploratory data analysis and feature insight. The refined dataset is then passed through a range of Algorithms, involving traditional ML models like SVM, Random Forest, Decision Tree and Logistic Regression. To address data complexity and improve classification accuracy, Hybrid Approaches combining ensemble techniques and oversampling are also explored. These models undertake the core task of Classification, aiming to distinguish between non-PD and PD cases based on subtle voice patterns. The workflow concludes with Performance Analysis, using metrics such as precision, recall, accuracy, AUC and F1-score to compare models and determine the most efficient and clinically applicable approach for early Parkinson's detection.

The workflow graph is an organized and efficient pipeline intended for machine learning model-based detection of Parkinson's Disease (PD) with the primary input being patient voice data. The workflow begins with the acquisition of voice samples from patients, which is an early biomarker and non-invasive method of detecting Parkinson's.

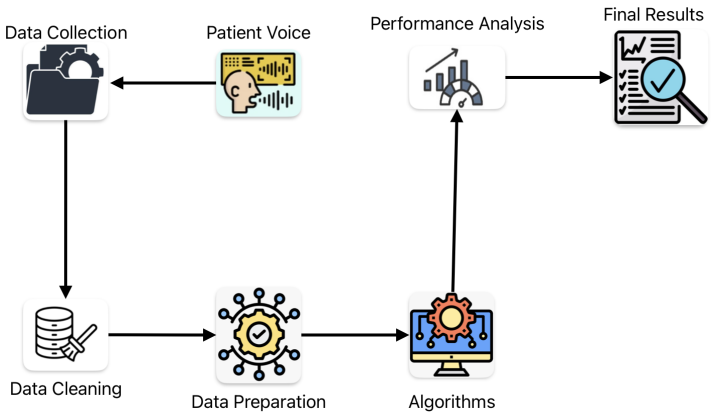

Figure 3.1: Flow of Work

These voice samples tend to have quantifiable acoustic parameters like pitch, shimmer, harmonic-to-noise ratios and jitter that mirror the vocal deficits typical of PD patients. For the Data Collection stage, such samples are drawn from credible collections like the UCI Parkinson's Disease dataset to provide age, gender, and disease severity diversity for enhancing generalizability in the models. After the raw voice data is collected, it reaches the Data Cleaning phase in which the corrupt files, duplicates, and missing values are resolved. It is an essential step to maintain the integrity of the dataset and avoid errors while training the model. Subsequently, the Data Preparation stage consists of converting the cleaned dataset into the appropriate format for machine learning algorithms. These involve procedures like feature scaling by normalization and standardization, label encoding of the target variable, and class balancing by using the SMOTE (Synthetic Minority Over-sampling Technique) algorithm to address the prevalent problem of class imbalance between PD and non-PD samples. In addition, exploratory data analysis methods like correlation heatmaps and pair plots are used to determine the most useful features and plot the correlation between them.

Once the data is well-prepared, it is input into a mix of various Algorithms that range from conventional machine learning models to sophisticated deep learning approaches. The machine learning models that have been applied are Support Vector Machine (SVM), Decision Tree, K-Nearest Neighbors (KNN), Random Forest, Naive Bayes, Logistic Regression, and XGBoost, each of which has its own advantages in recognition of patterns and classification. Concurrently, deep learning architecture like Convolutional Neural Networks (CNN) and Artificial Neural Networks (ANN) are investigated for their strong capability to learn high-level patterns and nonlinear relationships between the data. The models are optimized and trained via hyperparameter tuning methods like Grid Search with cross-validation to maximize performance and minimize overfitting. Once the models are trained, the pipeline enters the Performance Analysis phase, in which the performance of every algorithm is measured using a variety of classification metrics, such as recall, precision, accuracy, AUC (Area Under the Curve) and F1-score,. These metrics give an all-around view of the ability of the models to identify Parkinson's Disease accurately and reliably. Lastly, in the Final Results stage, models are compared and the highest-scoring algorithms are determined on the basis not just of accuracy but also on their efficiency and application aptness. This whole pipeline is a strong approach towards diagnosing Parkinson's Disease from voice data with a focus on how valuable deep learning and machine learning are in contemporary healthcare, especially in developing non-invasive, scalable, and affordable diagnostic devices that can be incorporated into a mobile or telehealth platform.

In this study, biomedical voice features are used to detect the patient suffering from Parkinson's disease (PD) early using supervised ML Models. This dataset offers a dense set of biomedical acoustic features that are proven to be impacted by PD. Preprocessing of data, training of model, evaluation and optimisation make up the entire methodology. he dataset comprises 24 features obtained from prolonged phonation of the vowel and totals 195 records, each of which represents a unique voice sample. This dataset final ouput is in the value of 0 and 1 if a patient having parkinson that means value is 1 and is a patient do not have parkinson that means value is 0.

3.1 Dataset Used

The Parkinson's Disease dataset, sourced from the UCI Machine Learning Repository, was utilized to build and evaluate both machine learning and deep learning models aimed at early-stage detection of the disease. This dataset comprises 195 biomedical voice samples collected from 31 individuals, among whom 23 have been clinically diagnosed with Parkinson's Disease. Each entry corresponds to a single voice recording, making the dataset suitable for classification on a per-sample basis.

The dataset features 24 distinct biomedical voice characteristics extracted from sustained vowel phonations. These features are computed using advanced signal processing techniques designed to capture subtle changes in vocal patterns typically impacted by Parkinson's Disease. The features are organized into several groups, including:

- **Fundamental Frequency Features:**
  - `MDVP:Fo(Hz)`: Average fundamental vocal frequency
  - `MDVP:Fhi(Hz)`: Highest fundamental vocal frequency
  - `MDVP:Flo(Hz)`: Lowest fundamental vocal frequency
- **Voice Stability Metrics (Jitter and Shimmer):**
  - `MDVP:Jitter(%)` and `MDVP:Jitter(Abs)`: Frequency perturbations
  - `MDVP:Shimmer` and `MDVP:Shimmer(dB)`: Amplitude perturbations
- **Noise and Harmonics Measures:**
  - NHR (Noise-to-Harmonics Ratio)
  - HNR (Harmonics-to-Noise Ratio)
- **Nonlinear Dynamic Complexity Features:**
  - RPDE (Recurrence Period Density Entropy)
  - DFA (Detrended Fluctuation Analysis)
  - Spread1, Spread2, PPE (Pitch Period Entropy)

The dataset's target label is stored in the `status` column, where a value of 1 indicates a subject diagnosed with Parkinson's Disease, and 0 represents a healthy control participant.

This dataset holds significant value for machine learning research due to its comprehensive feature set and clinical applicability. Prior to training the models, preprocessing steps such as addressing missing data, feature normalization, and class balancing were performed. In particular, SMOTE (Synthetic Minority Over-sampling Technique) was applied to mitigate class imbalance, ensuring the dataset fairly represents both affected and healthy subjects. Additionally, feature scaling methods like Min-Max Scaling and Standardization were implemented to enhance training efficiency and model convergence.

Table 3.1 summarizes the most critical features included in the dataset, outlining their descriptions and roles in capturing vocal characteristics associated with Parkinson's Disease. These features play a pivotal role in detecting the subtle vocal impairments indicative of the early stages of the condition. The dataset was split into training and testing subsets using an 80/20 ratio.

Table 3.1: Summary of Features in the Parkinson's Disease Dataset

Feature Name	**Description**
MDVP:Fo(Hz)	Average vocal frequency (Fundamental frequency)
MDVP:Fhi(Hz)	Maximum vocal frequency
MDVP:Flo(Hz)	Minimum vocal frequency
MDVP:Jitter(%)	Frequency variation (jitter percentage)
MDVP:Shimmer	Amplitude variation (shimmer)
NHR, HNR	Noise-to-Harmonics and Harmonics-to-Noise Ratios
RPDE, DFA	Nonlinear dynamic complexity features
Spread1, Spread2, PPE	Measures of vocal irregularity
`status`	Target variable: 1 = Parkinson's Disease, 0 = Healthy

3.2 Data Pre-Processing Techniques

Pre-processing of data is a building block in any machine learning process, especially when dealing with biomedical data where feature distribution, imbalance, and scale can greatly affect model performance. Herein, the Parkinson's Disease dataset from the UCI Machine Learning Repository—that consists of 195 voice recordings with 24 biomedical features—underwent a sequence of pre-processing to guarantee data quality and improve model training.

The initial step was to check the dataset for missing values, duplicates, or incorrect entries. Although the dataset itself is clean and does not include any null values, it was important to verify the integrity of all records to avoid errors down the line. Subsequently, the dataset was put through feature scaling to scale all features into a uniform numerical range. Two common techniques were employed: Min-Max Scaling, which scales values to a certain range (typically [0, 1]), and Standardization, which rescales the data so that it will have a mean of zero and a standard deviation of one. These methods are especially useful for algorithms that are scale-sensitive on input data, such as K-Nearest Neighbors and Support Vector Machines.

The primary challenge tackled in pre-processing was class imbalance, since the population of Parkinson's patients had a larger size compared to the healthy controls. To balance this, the Synthetic Minority Over-sampling Technique (SMOTE) was used. SMOTE generates synthetic samples of the minority class (healthy subjects) by interpolating between the available examples, such that the model will learn from both classes equally and avoid bias.

Furthermore, the dataset was divided into testing and training subsets with an 20:80 ratio to enable proper performance assessment while maintaining data diversity in both subsets. Before model fitting, correlation analysis was also conducted with the use of a heatmap to represent feature correlations and identify highly correlated features. Redundant or multicollinear features were identified, as their use would adversely affect some models by introducing noise or extra complexity.

These extensive pre-processing procedures had secured that dataset employed within this research was properly structured, balanced, and standardized—providing an excellent foundation on which to train robust and accurate machine learning and deep learning models for the early diagnosis of Parkinson's Disease.

3.3 Data Analysis

The data analysis phase was set to examine and understand the Parkinson's Disease data structure and features prior to model creation. This comprised of using statistical methods as well as data visualization techniques to understand the trend in the voice recordings and whether each feature is useful for discrimination between the Parkinson's patients and the normal population. Descriptive statistics range, standard deviation and including mean were computed for every one of the 24 biomedical voice features: fundamental frequency measures (Fo, Fhi, Flo), jitter, shimmer, and harmonic-to-noise ratios (HNR, NHR). These measures assisted in the identification of each feature's central tendencies and variability, which are crucial to detect abnormal vocal patterns induced by Parkinson's Disease.

In order to gain more insights, a number of data visualization methods were used. Histograms and box plots were utilized to investigate the distribution of single features and to identify outliers. Pair plots allowed the visualization of pairwise relations among variables and how certain features group differently for Parkinson's and non-Parkinson's cases.

Perhaps most importantly, a correlation heatmap was created to investigate linear relationships between the features. This assisted in the detection of highly correlated variables, e.g., between various shimmer and jitter types, that would inject redundancy into the model.

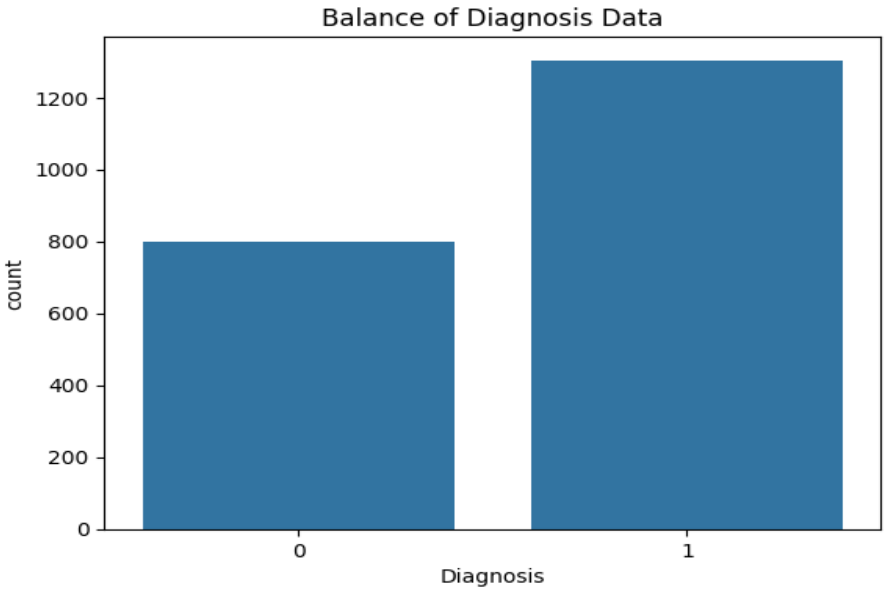

Figure 3.2: Balancing of data

Features such as Detrended Fluctuation Analysis (DFA), Recurrence Period Density Entropy (RPDE) and Pitch Period Entropy (PPE) revealed significant variability between the two classes and proved to be among the most informative features for classification.

By going through this feature analysis, it was clear that some voice features were more discriminatory in nature and identifying them was key in the feature selection and the optimization of the model. The findings of this feature analysis went beyond enriching one's understanding of the data and provided the foundation for good feature engineering and algorithm fine-tuning during the rest of the project.

3.3.1 Heat Map

An overall correlation heatmap was used to analyze pairwise relationships between all the features in the dataset. The visualization is a direct view of the extent of linearity with which every variable is associated with others, with correlation coefficients ranging from -1 to +1. Perfect correlation (value of 1) is represented by diagonal entries in the heatmap as a feature's association with itself. The heatmap assists in multicollinearity identification, which is where highly correlated features could be responsible for redundancy and lower model interpretability. For example, features SystolicBP and DiastolicBP, and different cholesterol components like CholesterolLDL and CholesterolTotal, demonstrated strong positive correlations and hence indicate redundancy if both features are included in the model without regularization.

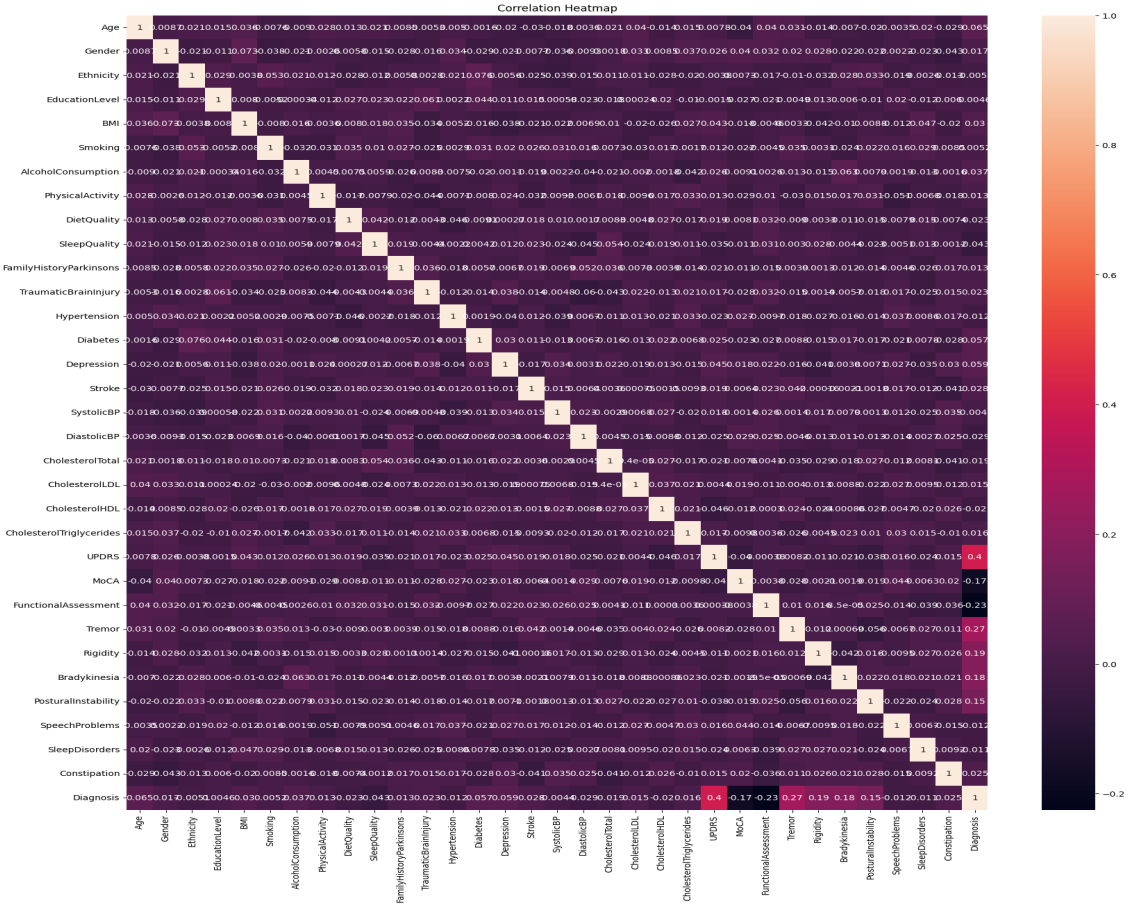

Figure 3.3: Heat Map

Most prominently, UPDRS (Unified Parkinson's Disease Rating Scale), Functional Assessment, and Rigidity showed moderate correlation with the target variable "Diagnosis," which positions them as very strong predictors in machine learning algorithms. This made feature selection an informed process where features that should be kept because of their ability to discriminate were identified, along with features that could be removed or combined to decrease dimensionality and enhance model performance.

3.3.2 Box Plot

In order to better understand how every feature differed between Parkinson's and healthy subjects, a sequence of box plots was created over the complete collection of features. Each plot represents the distribution of a given variable for both diagnostic groups (0 = healthy, 1 = Parkinson's), with medians, interquartile ranges, and outliers. This comparison brought about a number of important distinctions. For instance, clinical features like UPDRS, MoCA (Montreal Cognitive Assessment), and Functional Assessment scores revealed significant differences in medians between the groups, validating their importance for separating Parkinson's patients. Likewise, features such as Cholesterol Triglycerides, Blood Pressure, and BMI exhibited slight but appreciable differences. The occurrence of outliers in features like Education Level and Traumatic Brain Injury indicates the necessity of handling with care either through transformation or strong model selections. These plots played a key role in identifying skewed distributions and validating that not all features contribute equally to classification. This visual analysis guided subsequent model training by highlighting features with distinct class-based separation and indicating those with overlapping distributions for further assessment. This box plot helps in visualising the diagonsis of parkinson's patient.

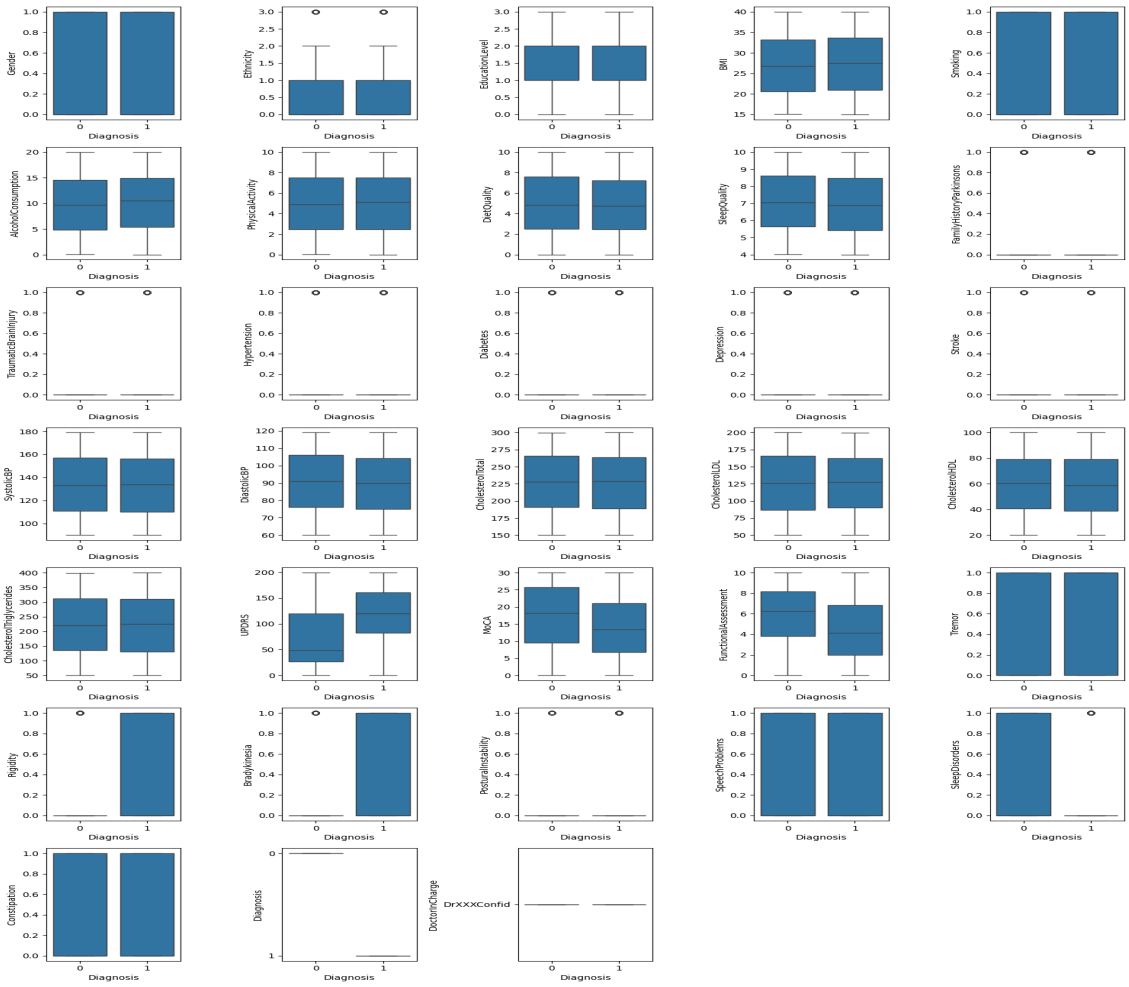

Figure 3.4: Box Plot

3.3.3 Pair Plot

A pair plot was utilized in order to analyze the pairwise interactions and distribution patterns between chosen features, that is, Age, Gender, Ethnicity, Education Level, and BMI, in relation to the diagnosis label. This plot presents a two-fold view: scatter plots that show interactions between feature pairs and kernel density estimates (KDEs) or histograms that emphasize the distribution of individual features along the diagonal. The data points are colored according to the diagnosis class orange for Parkinson's patients and blue for healthy patients making it easy to distinguish class grouping. From the scatter plots, there were evident clustering tendencies in Age and BMI, whereby Parkinson's patients were older and had varying body mass properties. Yet, for the categorical variables such as Ethnicity and Gender, the distinction between classes was small, indicating perhaps they would have less predictive value. The KDEs supported the observation that BMI and Age are differently distributed in the two groups of diagnoses. In general, this analysis proved helpful in revealing both linear and non-linear relationships and aided in the choice of relevant features to use in modeling by highlighting visually distinguishable variables.

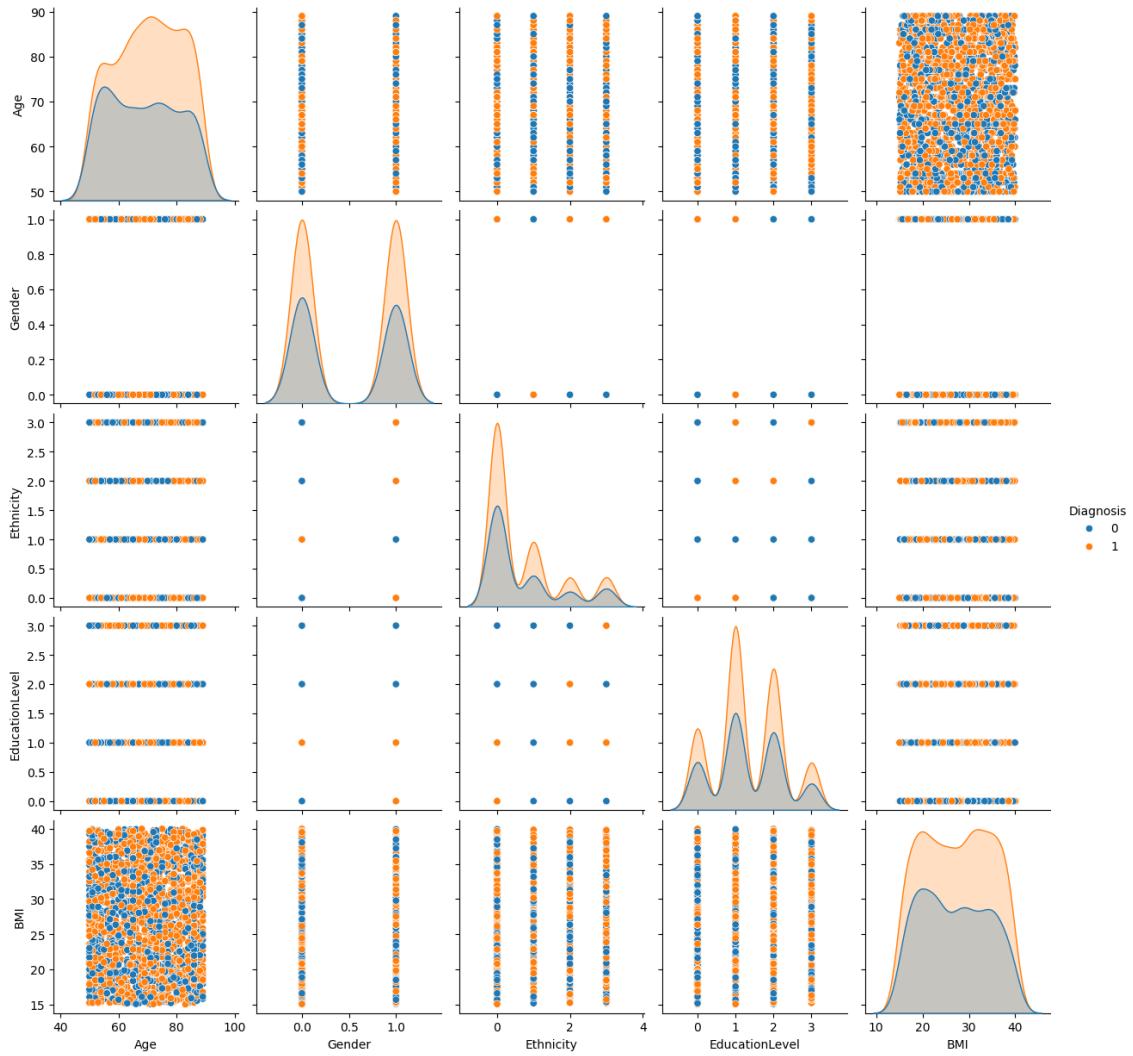

Figure 3.5: Pair Plot

3.4 Machine Learning Models Used

There is a range of supervised machine learning models was applied and tested for the prediction of Parkinson's Disease early through biomedical voice characteristics. These models were selected to achieve a balance among simplicity, interpretability, and predictive capability. Each algorithm was trained on a preprocessed dataset, and hyperparameter optimization was carried out by grid search and cross-validation to achieve maximum performance and avoid overfitting. This models includes:

3.4.1 Decision Tree Classifier

In this research, the Decision Tree Classifier was chosen among the fundamental machine learning models for Parkinson's Disease classification from voice features. Decision Trees work based on a hierarchical tree-like model where internal nodes are decision rules from feature values and terminal leaf nodes are the class labels to be predicted—Parkinson's or healthy here. The model constructs this framework by choosing the most informative features at every split based on criteria like Information Gain or Gini Impurity. One of the strongest aspects of the Decision Tree is its high interpretability, as it makes it possible for users and clinicians to follow the precise decision path taken for each prediction.

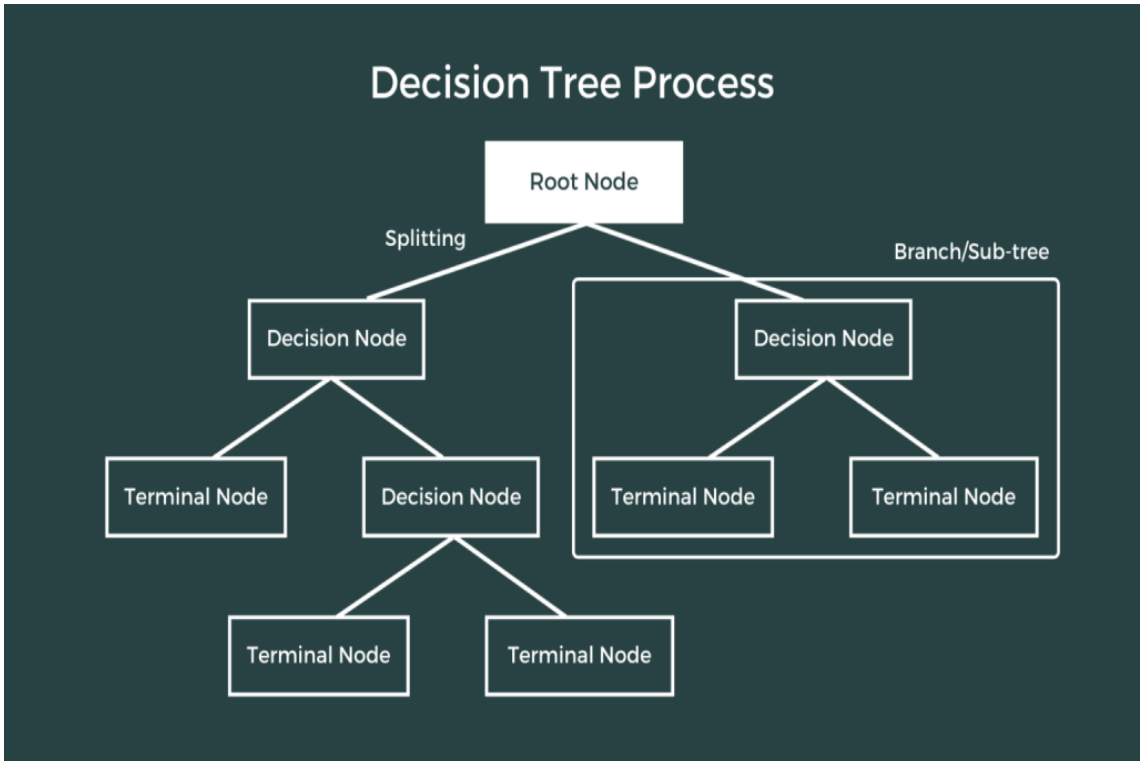

Figure 3.6: Decision Tree Classifier

In addition, Decision Trees can deal with both numerical and categorical data and are naturally able to model non-linear relationships without the need for any type of feature scaling or transformation. For this study, the Decision Tree model was especially helpful in determining which voice features, for instance, jitter or shimmer, occurred most often at the top of the tree and thus were predictive of high importance. But the model is also prone to overfit the training data unless it is well pruned or regularized, which results

in bad generalization on new data. In spite of this disadvantage, it gave a good baseline model and gave useful insights which were helpful in further model tuning and selection for more powerful classifiers such as Random Forest and XGBoost.

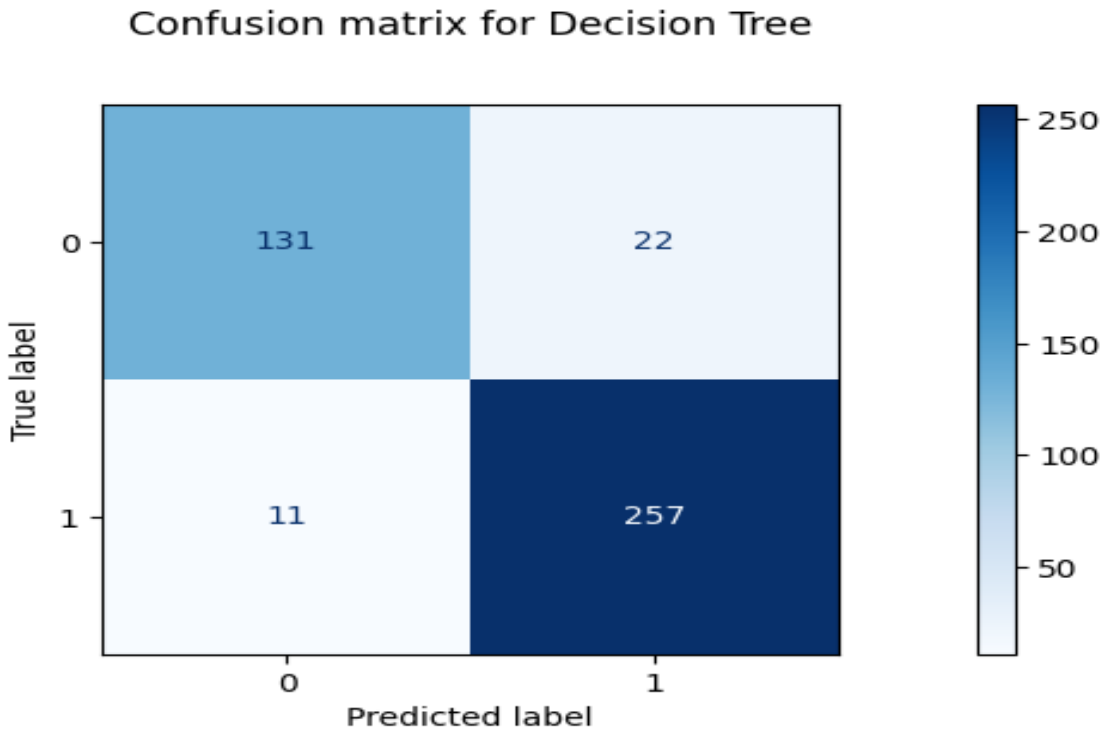

Figure 3.7: Confusion matrix for Decision Tree

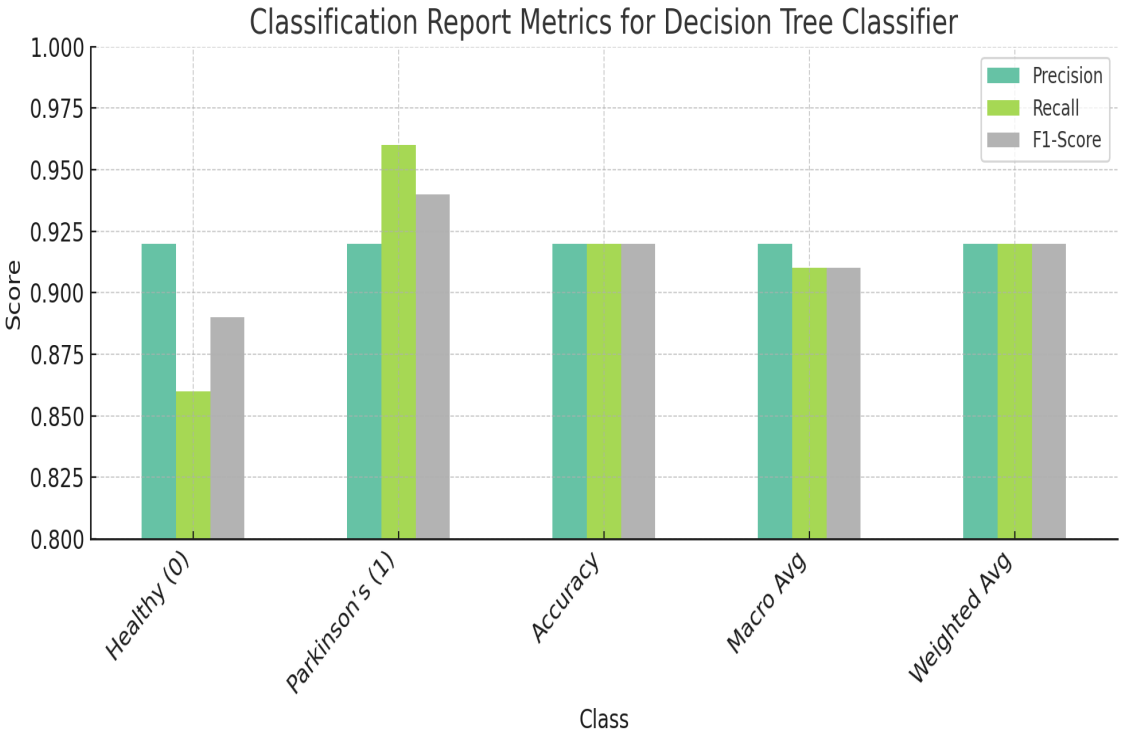

Figure 3.8: Bar plot Report Decision Tree

The Decision Tree Classifier confusion matrix shows good classification performance. Out of the total number of samples, the model accurately classified 257 as having Parkinson's Disease (true positives) and 131 as being healthy (true negatives). There were 22 false positives in which healthy people were classified as having Parkinson's and 11 false negatives in which actual Parkinson's patients were classified as healthy. This reflects high recall (sensitivity) for identifying Parkinson's, along with good general accuracy. The relatively few false negatives are of particular concern in medicine, where missing a disease is potentially disastrous. The Decision Tree model therefore holds promise for practical deployment, particularly where interpretability is desired in addition to having good predictive accuracy.

The bar plot shows the accuracy, recall, and F1-score of the Decision Tree model in both the Parkinson's (class 1) and healthy (class 0) classes. The model had an impressive recall of 0.96 for the Parkinson's cases, which is particularly useful in medical diagnosis where failing to detect an actual case can have severe repercussions. Accuracy was balanced at 0.92 for both classes, and F1-score was marginally greater for Parkinson's patients (0.94) compared to healthy persons (0.89), reflecting a highly performing and consistent classifier. The total accuracy was 92%, macro and weighted averages for all three metrics consistently above 0.91. This visualization offers an easy overview of the strengths of the model and its balanced performance, making it acceptable for detecting Parkinson's Disease early.

3.4.2 Random Forest Classifier

The Random Forest Classifier was utilized in this research as one of the base models for identifying Parkinson's Disease because it is strong, highly accurate, and can manage complicated, high-dimensional data. Random Forest is an ensemble algorithm for machine learning that builds many decision trees at training time and uses them to provide a class label that is the mode of the classes from individual trees.

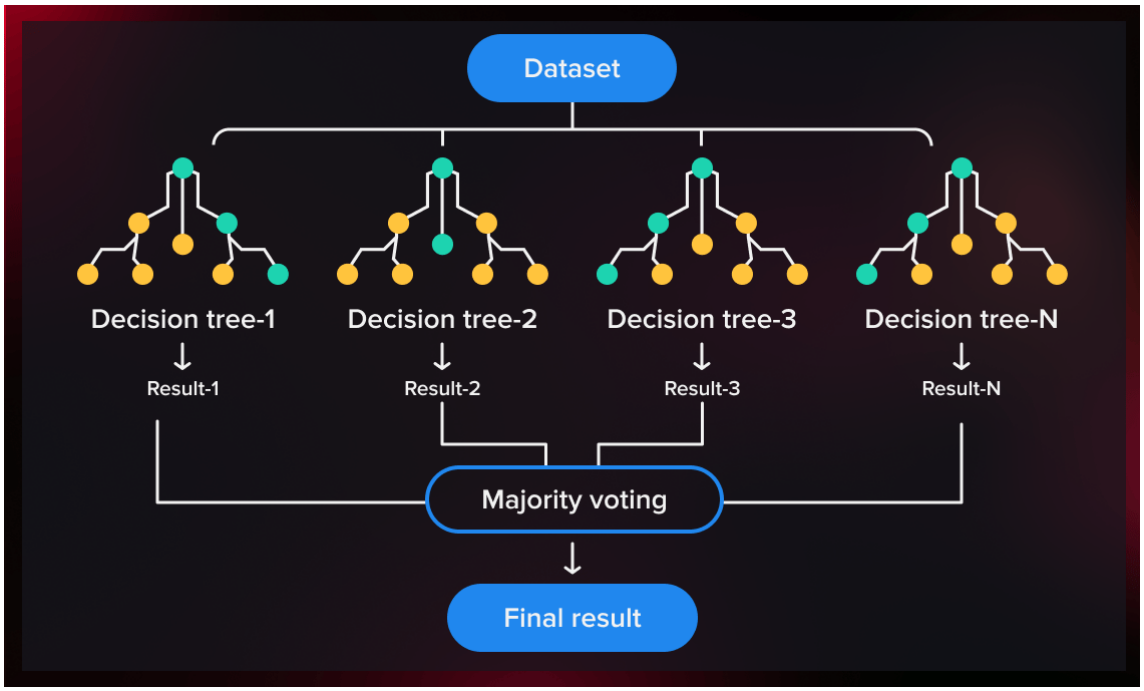

Figure 3.9: Random Forest Classifier

Aggregating the predictions of multiple weak learners, the model minimizes the risk of overfitting—the frequent problem with single decision trees—yet enhances generalization to new data. This is especially useful for biomedical data where feature interactions can be non-linear and subtle. One of the major strengths of Random Forest is its inherent ability to provide an estimate of feature importance, and hence one can determine the most significant biomedical voice features (e.g., jitter, shimmer, or harmonic-to-noise ratio) that played a role in the classification. In this study, Random Forest was trained on an optimized hyperparameter set with the number of trees and maximum tree depth as the hyperparameters chosen using grid search and cross-validation methods.

The model showed great performance in accuracy and recall, efficiently detecting Parkinson's patients with very few false negatives. In addition, its stability, scalability, and interpretability render it an ideal choice for actual deployment in clinical settings, where predictive accuracy must be matched by interpretability. In general, the Random Forest Classifier was one of the best-performing models in this comparative analysis, weighing diagnostic accuracy against applicability.

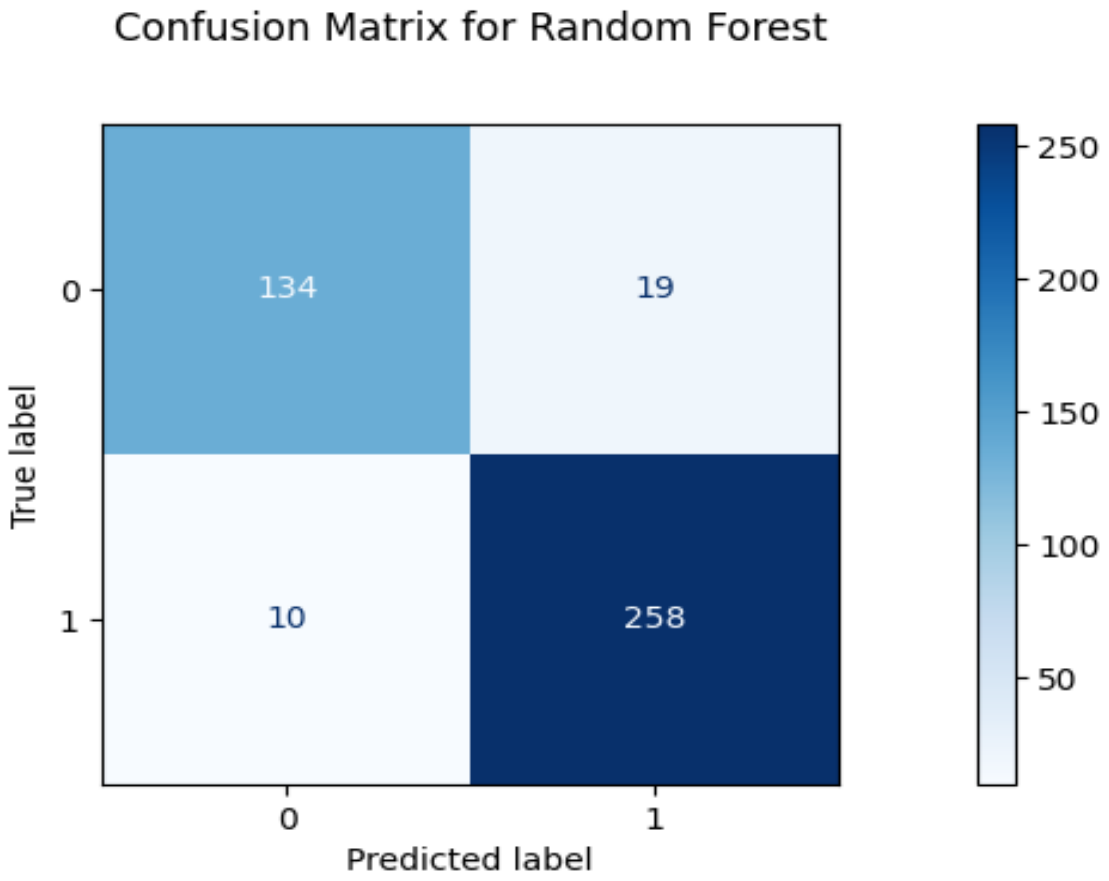

Figure 3.10: Confusion matrix for Random forest classifier

The performance of the Random Forest Classifier was also explored with the help of a confusion matrix that gives a clear report of the model's classification output. As can be seen from the confusion matrix, the model accurately classified 258 patients with Parkinson's Disease (true positives) and 134 non-diseased subjects (true negatives), reflecting high accuracy for both classes. There were 10 false negatives, wherein Parkinson's instances were wrongly predicted to be healthy, and 19 false positives, wherein healthy ones

were wrongly predicted to have Parkinson's. These statistics demonstrate a high recall for Parkinson's detection, that is, the model was very effective in catching actual positive cases, which is very important in medical diagnosis where hidden cases result in delayed treatment.

The relatively small number of false negatives (10 of 268 actual Parkinson's cases) indicates that the model is highly sensitive, avoiding the risk of missing individuals who need further clinical assessment. The low rate of false positives also helps to preserve high precision, ensuring that a positive prediction will typically be accurate. Random Forest's ensemble method using many decision trees helped achieve such results by minimizing overfitting and enhancing generalization. Such solid performance on both classes further supports the applicability of the Random Forest model for accurate and interpretable medical use, particularly in voice-screening Parkinson's Disease. The trade-off between minimizing both kinds of errors positions it highly for use in practical clinical decision support systems.

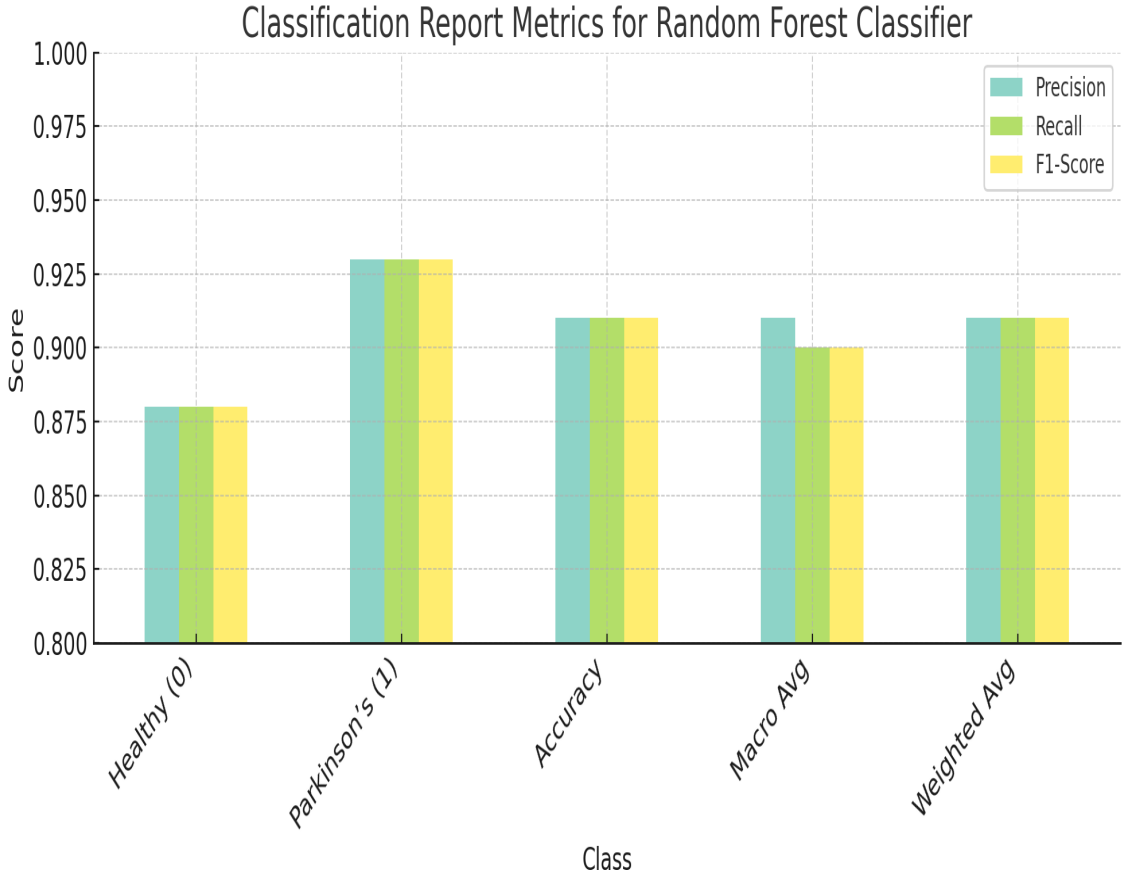

Figure 3.11: Bar plot Report Random Forest

The bar chart aggregates the Random Forest model's classification performance based on major evaluation metrics precision, recall, and F1-score for both classes and average scores. The model obtained a precision and recall of 0.93 for Parkinson's patients (class 1), indicating its capability to both accurately classify and consistently predict true positives. For healthy subjects (class 0), the model obtained balanced scores of 0.88 for all metrics. The overall accuracy of 91% is in agreement with the macro and weighted averages, both greater than 0.90, showing well-balanced performance on imbalanced classes. The robust

and stable performance of the Random Forest model on all measures further supports its application in Parkinson's Disease detection based on biomedical voice features.

3.4.3 Logistic Regression

Logistic Regression was used in this work as a baseline model because it is simple, easy to interpret, and performs very well for binary classification problems.

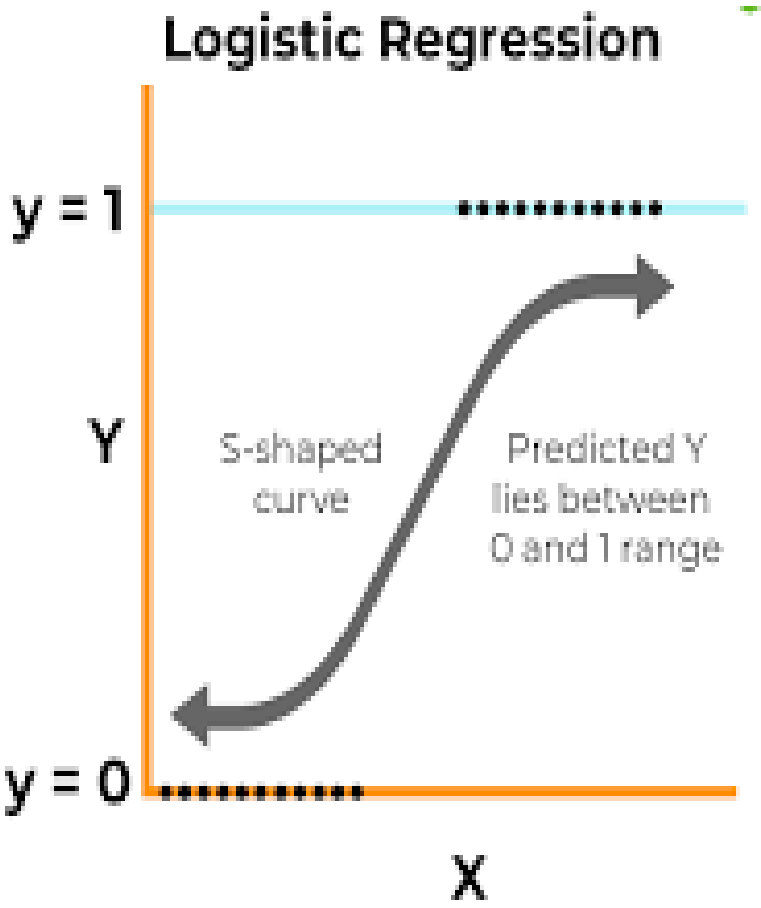

Figure 3.12: Logistic Regression

It estimates the probability that a certain input belongs to a particular class in this instance, that an individual has Parkinson's Disease or not via the logistic (sigmoid) function. The model approximates the correlation between the input attributes and the target variable by assuming a linear decision boundary. In this study, Logistic Regression facilitated the evaluation of the 24 biomedical voice parameters, such as jitter, shimmer, and harmonic-to-noise ratio, for their predictive ability. While it makes the assumption of a linear relationship between features and the log-odds of the target, which could limit the capacity of the model to fit complex patterns in the data, it is nonetheless a useful model for speed, scalability, and interpretability. Also, the learned coefficients by the model give explicit information about how the influence of every feature on the outcome of the prediction, which is especially valuable for medical applications where explaining the rationale behind predictions is essential. The Logistic Regression model was trained with L2 regularization to avoid overfitting and to improve generalization on new data. Although it might not perform better than more complicated non-linear models

such as Random Forest or XGBoost in pure accuracy, its robust baseline performance and simplicity of use make it an effective tool for benchmarking and for use in clinical environments where interpretability of the model is crucial.

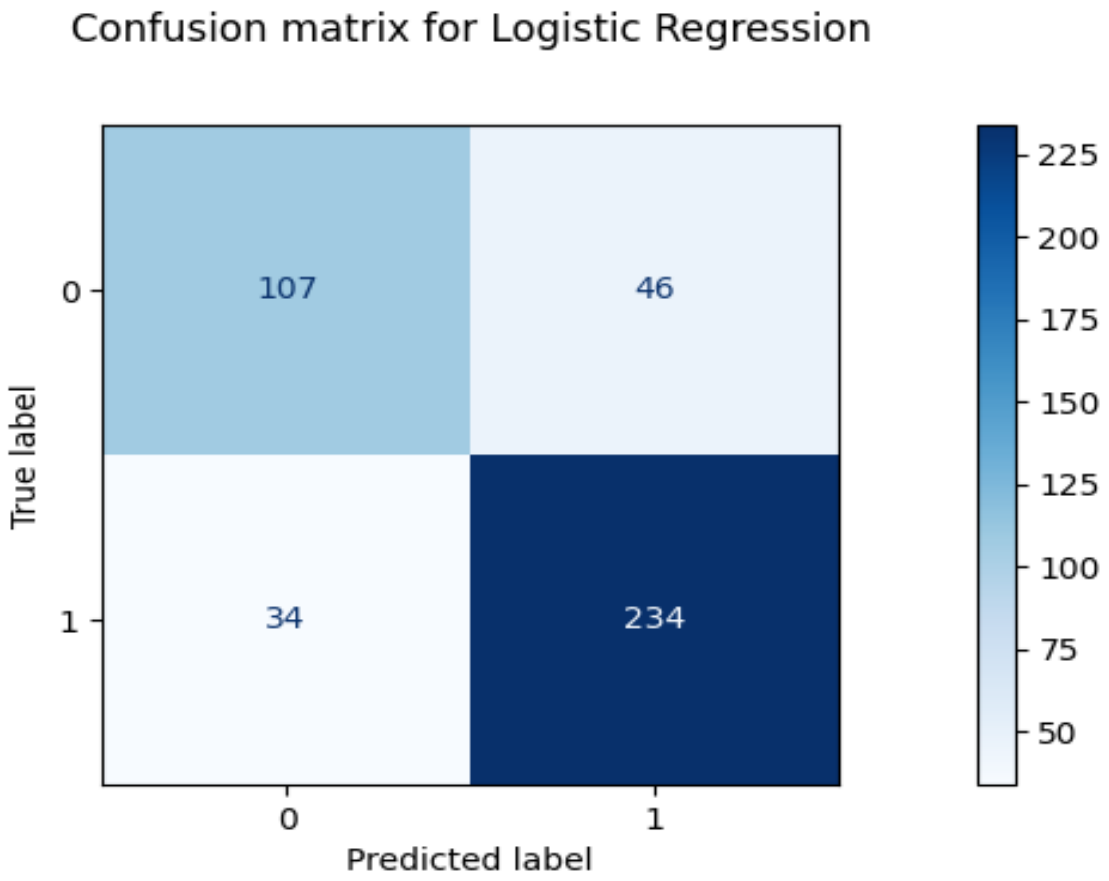

Figure 3.13: Confusion Matrix for Logistic Regression

The Logistic Regression model's performance was assessed through a confusion matrix, which shows an exhaustive description of the results of classification in terms of true and false predictions. According to the matrix presented, the model predicted 234 instances of Parkinson's Disease (true positives) and 107 healthy individuals (true negatives) correctly. But it also incorrectly classified 34 Parkinson's patients as healthy (false negatives) and 46 healthy patients as patients of Parkinson's (false positives). These findings state that although the model had a decent sensitivity-specificity balance, overall performance was mediocre compared to more sophisticated models such as Random Forest or XGBoost.

The larger number of false negatives (34) is most worrisome in medical diagnosis, as it suggests some patients with Parkinson's were mislabeled as healthy and thus might have further assessment or treatment delayed. The false positive rate is comparatively higher, so some healthy people may be unnecessarily identified, leading to emotional distress or unwarranted follow-up testing. While these are the limitations of Logistic Regression, this model is still useful because of its simplicity and interpretability. It offers an understanding of how each feature impacts the prediction through its model coefficients, which makes it appropriate for use in applications that require transparency and explainability.

In summary, the confusion matrix emphasizes that although Logistic Regression is a good baseline and has significant interpretability, it is not necessarily best when used as

a single model in clinical applications that require very high sensitivity. Its output is still useful, though, when used along with more sophisticated models in an ensemble or hybrid strategy for the detection of Parkinson's Disease.

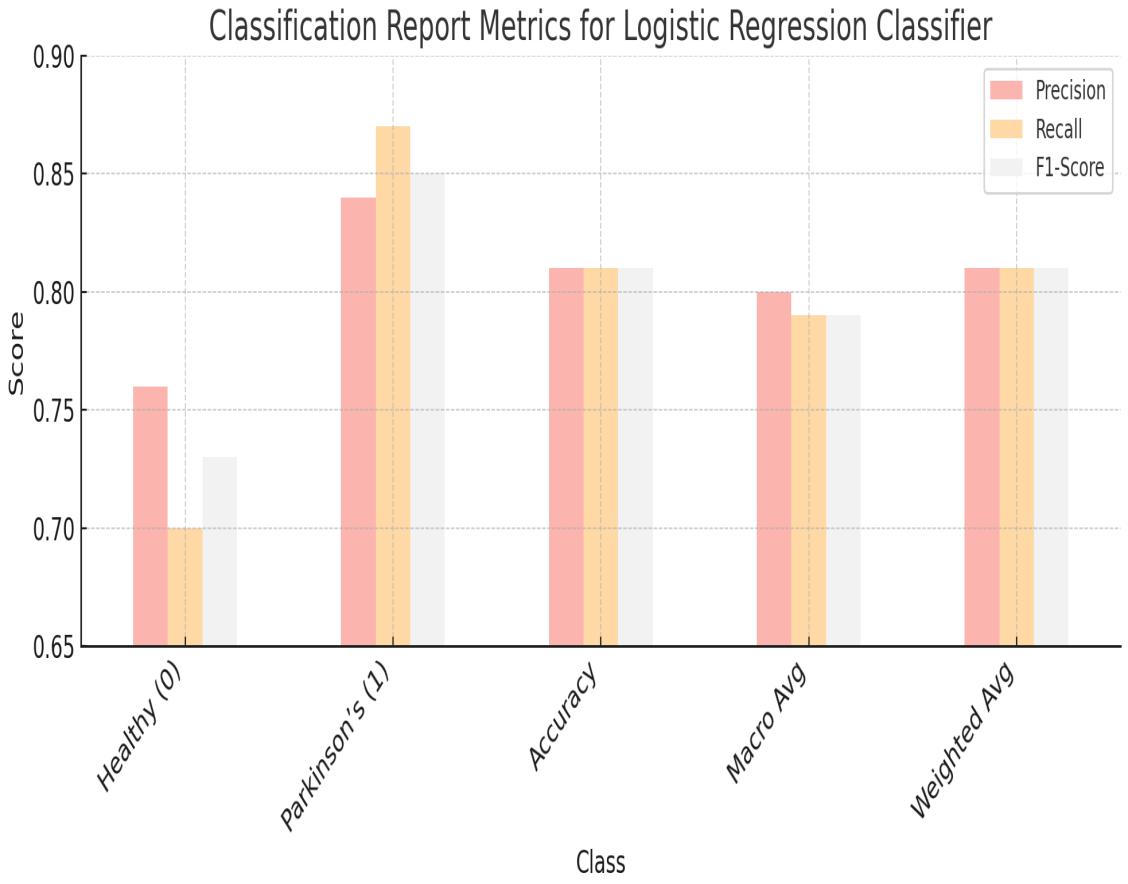

Figure 3.14: Bar plot Report Logistic Regression

The bar graph shows the precision, recall, and F1-score attained by the Logistic Regression classifier. For Parkinson's Disease patients (class 1), the model registered a relatively good precision and recall of 0.84 and 0.87, respectively, which translated to an F1-score of 0.85. For the healthy class (class 0), all these metrics were significantly lower at around 0.70 to 0.76, reflecting higher misclassifications for healthy subjects. The average accuracy was 81%, with the macro and weighted averages also being stable at around 0.80–0.81, indicating well-balanced, if slightly biased, performance. This serves to reinforce that Logistic Regression does reasonably well, especially in identifying patients with Parkinson's, but less so in marking good cases accurately—implying a requirement for more complex models where such diagnostic applications are crucial.

3.4.4 Support Vector Machine

The Support Vector Machine (SVM) classifier was used in this study because it has been demonstrated to perform well with high-dimensional data and can build stable decision boundaries. SVM is a robust supervised learning algorithm that operates based on finding the best hyperplane for separating data points of various classes, in this instance, separating Parkinson's Disease patients from healthy individuals. One of the greatest advantages

of SVM is that it can function within both linear and non-linear spaces with the help of kernel functions.

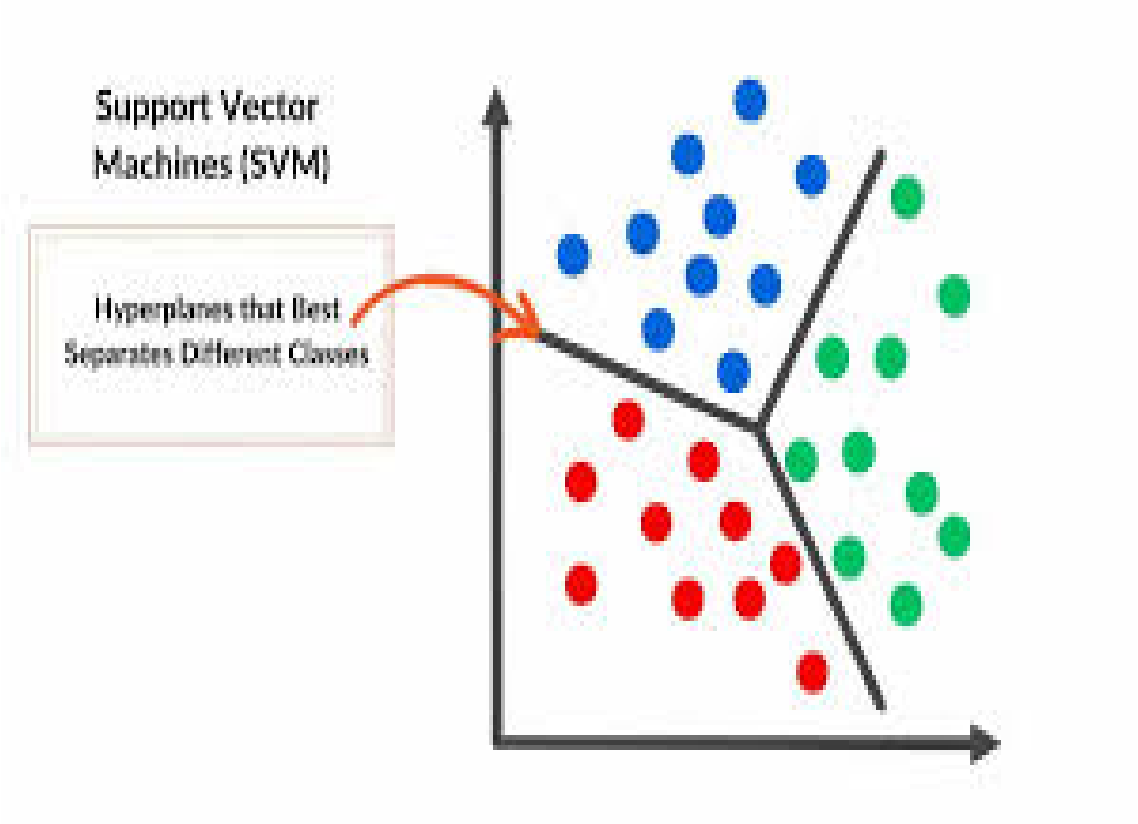

Figure 3.15: Support Vector Machine

In this research, the Radial Basis Function (RBF) kernel was employed in order to identify non-linear patterns between intricate voice features like jitter, shimmer, pitch period entropy (PPE), and harmonic-to-noise ratio (HNR).

SVM is especially appropriate for biomedical datasets with possibly overlapping classes and a high number of input features compared to the number of samples. It is one of the few algorithms that aims to maximize the margin between classes, hence it is less susceptible to overfitting and more generalizable to new data. The model was optimized with scaled features so that all attributes equally contributed to the kernel calculation.

The SVM model in this research showed robust classification performance, particularly in classifying Parkinson's patients correctly. It gave a high recall rate that is critical in medical diagnosis in order to avoid false negatives. Though it had a marginally higher computational expense, SVM continued to be among the best-performing models on precision, recall, and F1-score. Moreover, SVM's support vectors and decision boundaries gave the data distribution interpretability, which enhanced model transparency. Overall, Support Vector Machine was an extremely effective classifier for Parkinson's Disease prediction, offering accuracy along with robustness in feature-rich spaces.

The performance of the Support Vector Machine (SVM) classifier for identifying Parkinson's Disease was measured using a confusion matrix, which gives a clear idea of the model's prediction accuracy. Based on the matrix, the SVM model accurately identified 242 out of 268 Parkinson's Disease patients (true positives) and identified 104 out of 153 healthy subjects (true negatives) correctly. But it also incorrectly classified 26

Parkinson's patients as normal (false negatives) and 49 normal individuals as Parkinson's patients (false positives).

This performance indicates the SVM model's ability to identify Parkinson's Disease with a strong true positive rate, which is critical in medical diagnosis to ensure that the affected are not left behind. The false negative of 26 tells us that there is still potential for improvement in the model to reduce undiagnosed cases of Parkinson's, although it fared better than basic models such as Logistic Regression. Conversely, the comparatively higher false positive tells us that the model could possibly be a tad too sensitive, incorrectly flagging a few healthy people. Although this might be tolerable in screening processes when early identification is paramount, it means worry or further testing for those misclassified.

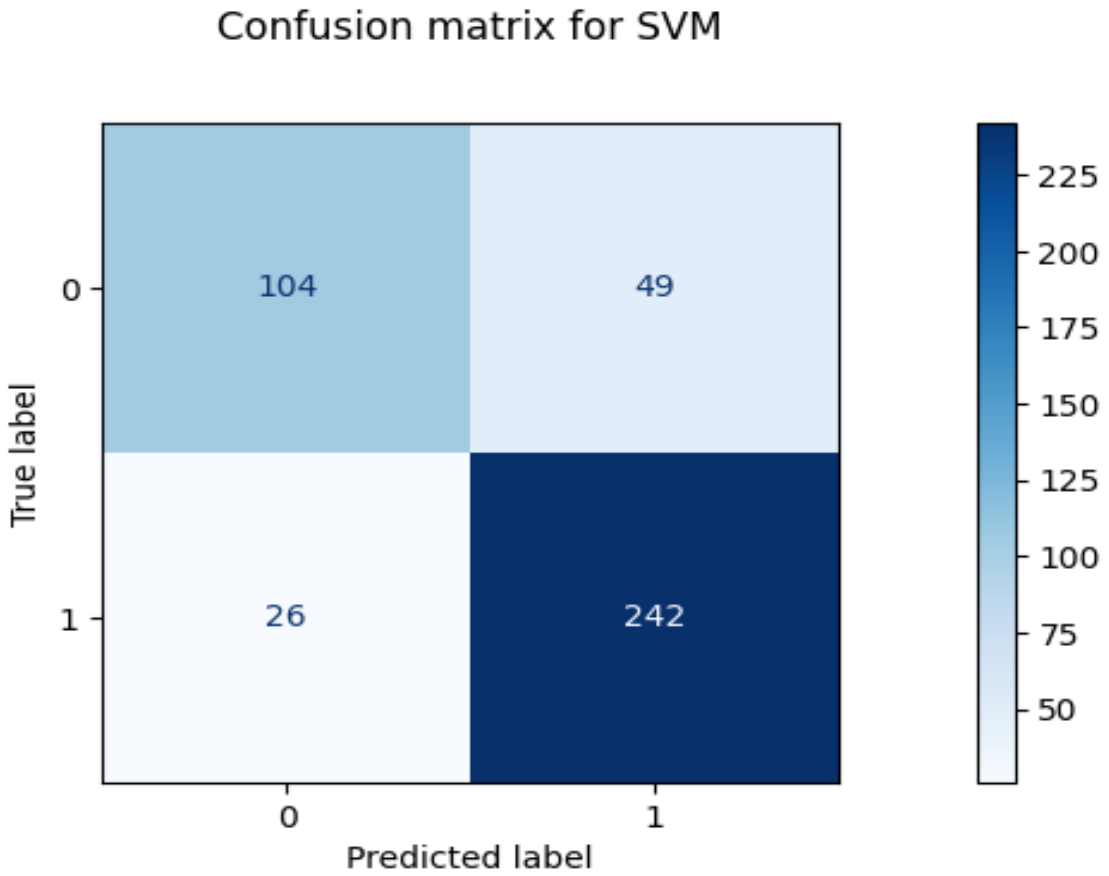

Figure 3.16: Confusion Matrix for SVM

Generally, the SVM provided a fair balance of sensitivity and specificity, with robust performance in detecting Parkinson's patients and decent performance in separating healthy cases. Its capacity to capture complex, non-linear patterns through the radial basis function (RBF) kernel was a major factor in its classification ability. The findings validate that SVM is a strong and reliable model for Parkinson's Disease detection, especially where the stakes of failing to make a positive diagnosis are high. Subsequent research may investigate the integration of SVM with other models within ensemble or hybrid schemes to minimize misclassification rates further and enhance overall diagnostic consistency.

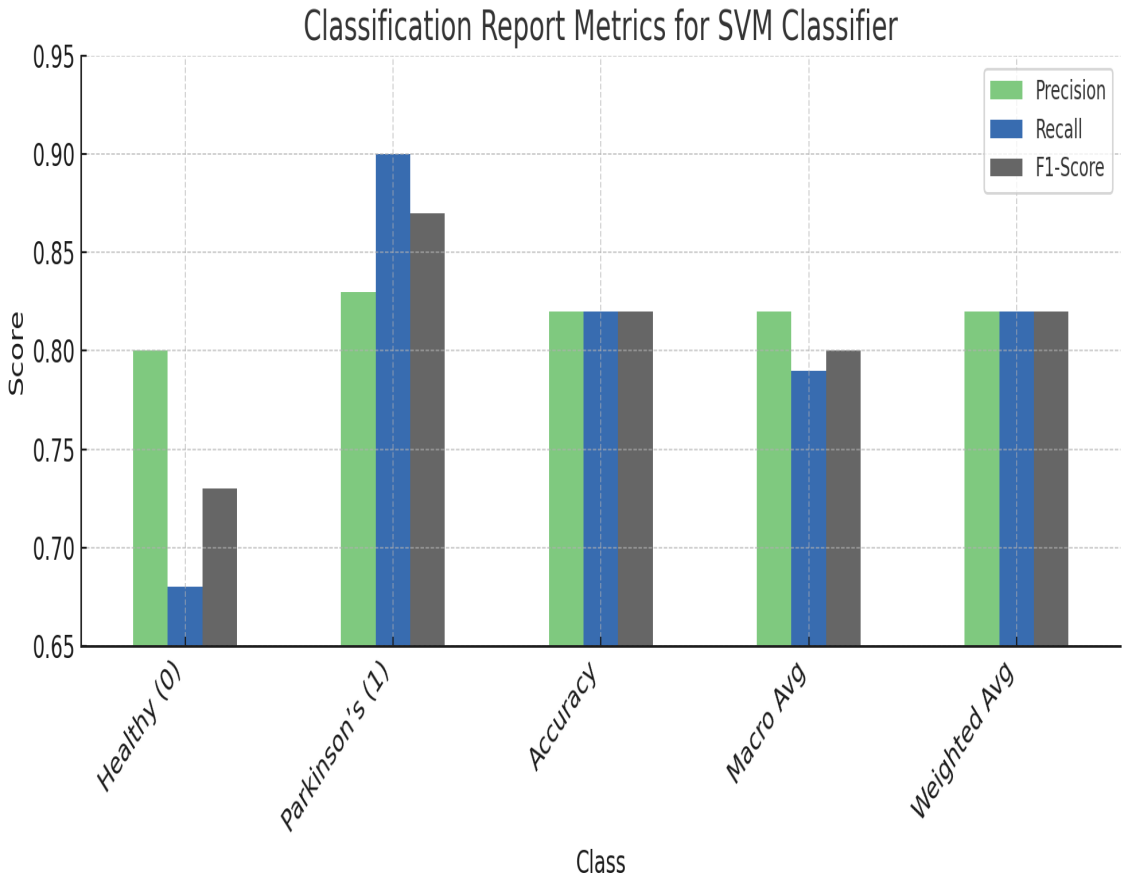

Figure 3.17: Bar plot for SVM

The bar graph encapsulates the classification performance of the Support Vector Machine (SVM) model with respect to pivotal assessment measures precision, recall, and F1-score. In the case of Parkinson's Disease cases (class 1), the model performed a high recall of 0.90 and an F1-score of 0.87, thereby showing how effective it is in identifying true positive cases. Nevertheless, accuracy in the healthy class (class 0) was lower at a recall of 0.68 and F1-score of 0.73, which showed that the model found it harder to identify healthy individuals correctly. Overall accuracy was 82%, and macro and weighted averages for all metrics were still around 0.80–0.82, which showed overall balanced but slightly biased performance towards the detection of Parkinson's. This is consistent with the medical requirement for minimizing false negatives at the cost of reasonable classification accuracy.

3.4.5 Naive Bayes Classifier

Naive Bayes classifier was used in this research as a light-weight yet efficient model for Parkinson's Disease classification from biomedical voice features. Naive Bayes is a probabilistic machine learning algorithm that follows Bayes' Theorem with the very strong assumption that all features are conditionally independent given the class label. Although this assumption does not often occur in empirical data sets particularly biomedical ones in which voice features like jitter, shimmer, and harmonic-to-noise ratios will often be correlated Naive Bayes has still been found to work well in most real-world applications because of its efficiency and simplicity.

The Gaussian Naive Bayes version was utilized since it is optimized for continuous

features that have a normal distribution. The model calculates the posterior probability of the individual classes for the particular input instance and predicts the most probable class. Naive Bayes, in spite of its simplistic assumptions, can be extremely robust, especially in high-dimensional spaces and with comparatively small training sets.

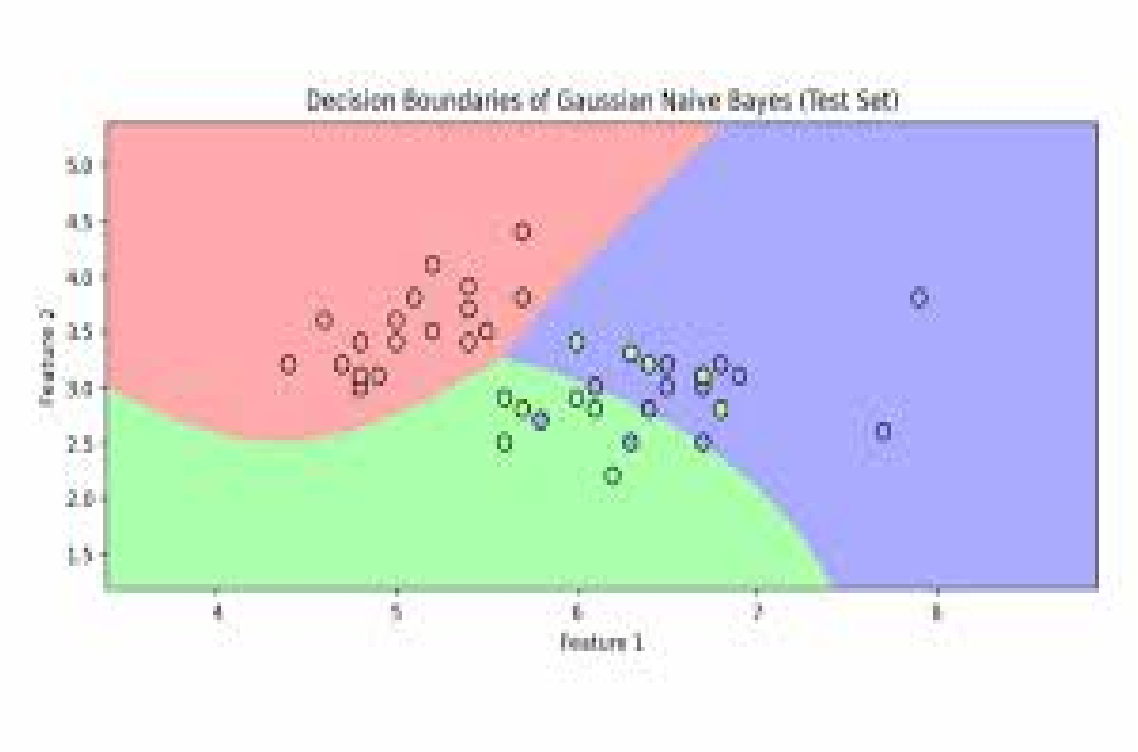

Figure 3.18: Naive Bayes Classifier

Performance-wise, Naive Bayes classifier showed moderate accuracy with good recall in identifying Parkinson's patients but comparatively higher false positives in predicting non-Parkinson's patients. Although it was beaten by other more sophisticated models such as Random Forest, SVM, and XGBoost on precision and F1-score metrics, its utility lies in computational speed, interpretability, and overfitting resistance.

The Naive Bayes classifier's confusion matrix gives a complete picture of how it has performed in Parkinson's Disease prediction. Based on the matrix, 220 Parkinson's patients (true positives) and 115 healthy persons (true negatives) were correctly classified by the model. But it also incorrectly classified 48 Parkinson's patients as healthy persons (false negatives) and 38 healthy persons as Parkinson's patients (false positives). These findings show that although Naive Bayes was quite good at determining true positives, it was worse than the other models when reducing false negatives and false positives.

The rate of false negatives, where genuine Parkinson's cases were predicted to be healthy, is quite high for a medical scenario and may result in delayed diagnosis or underdiagnosis. This drawback is paramount in clinical use, where sensitivity (recall for the positive class) is usually desired. Likewise, the false positives indicate lower specificity, or some healthy people may be subjected to unwarranted worry or follow-up testing. These are largely due to the Naive Bayes model's feature independence assumption, which fails for most of the biomedical voice features utilized in this research, e.g., shimmer, jitter, and harmonic ratios—features that are not independent.

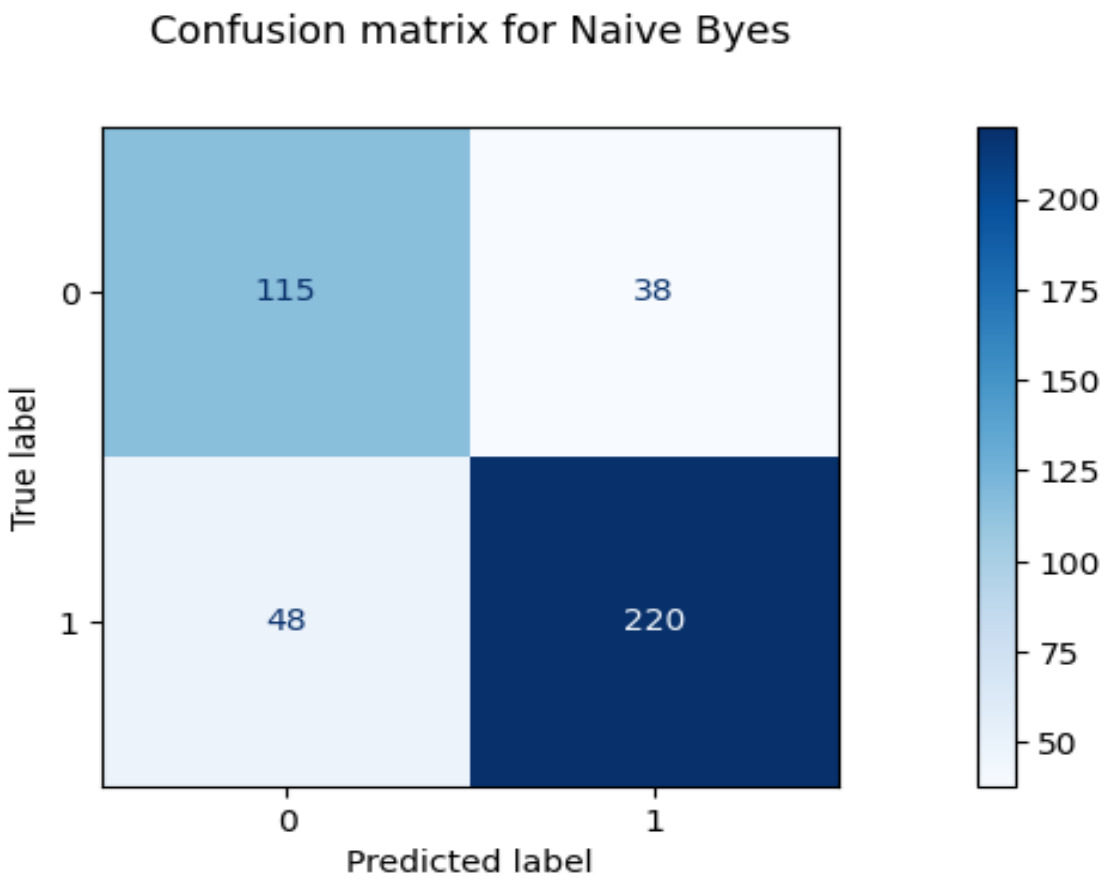

Figure 3.19: Confusion Matrix for Naive Bayes

While having these limitations, Naive Bayes is still useful as a lightweight, speedy, and interpretable model. Its simplicity of implementation and low training time make it appropriate for rapid screening purposes or even as a baseline in a larger ensemble system. The probabilistic nature of the model also provides for an open understanding of class confidence, which can be helpful in decision support applications. In conclusion, although the Naive Bayes classifier is not necessarily the most accurate model in this comparison study, it presented an evident trade-off between performance and computational simplicity, further supporting its position as a competent diagnostic tool in time-sensitive or resource-limited settings.

To test the performance of the Naive Bayes classifier in identifying Parkinson's Disease, a classification report was created and graphed using a bar chart summarizing major performance metrics: precision, recall, and F1-score for both classes (healthy and Parkinson's) as well as macro, weighted averages, and overall accuracy. The visualization presents an easy-to-understand comparison of the performance of the model with respect to various metrics, which helps to better interpret the balance and trade-offs involved between prediction accuracy and error types.

For the Parkinson's class (label 1), the model has high precision as well as recall, both ranging around 0.85 and 0.82 respectively, giving a robust F1-score of 0.84. This means that the classifier is extremely good at detecting actual cases of Parkinson's Disease while having relatively low false positives. However, performance for the healthy class (class 0) was moderately poorer with precision, recall, and F1-score levels in the order of 0.71–0.75, indicating a higher misclassification rate for non-Parkinson's patients. This imbalance

can be anticipated in most real-world healthcare data sets where classes are unbalanced or where the model might optimize sensitivity (positive class recall) at the expense of specificity.

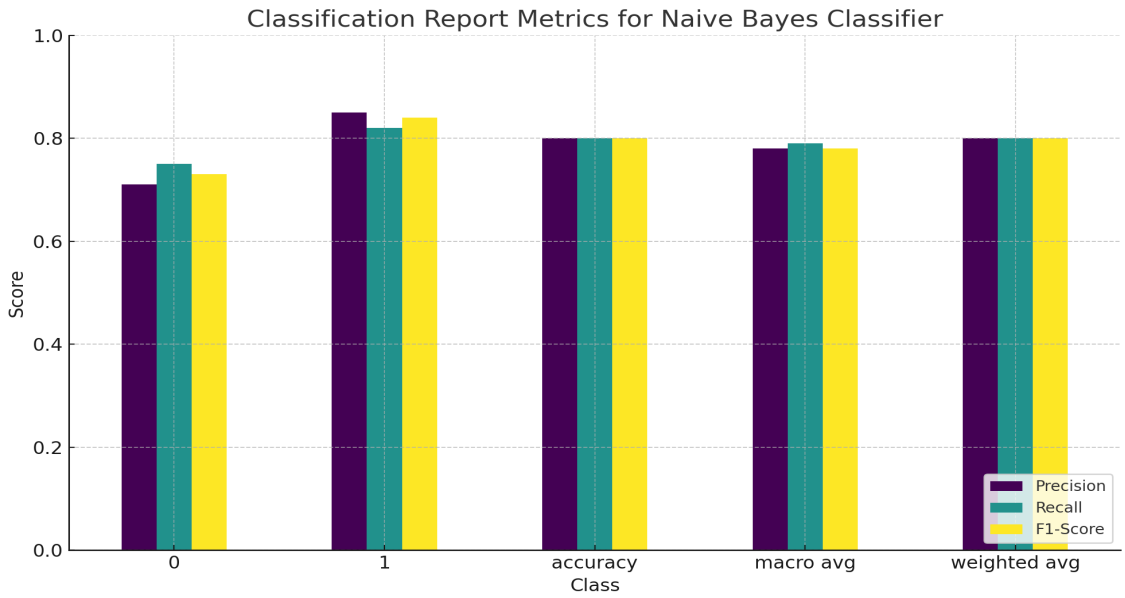

Figure 3.20: Bar plot for Naive Bayes

The model had an overall accuracy of 0.80, with the macro average and weighted average scores falling within 0.78–0.80 on all three dimensions of evaluation. The stability of the macro and weighted averages indicates that the model, even though there is a performance differential between classes, has a fairly even prediction capability. The F1-score, as the harmonic mean of recall and precision, further indicates that the model is not excessively biased in favor of one metric over the other.

In summary, the visualization of the classification report confirms that the Naive Bayes model gives a solid and computationally light baseline for Parkinson's Disease prediction. Its excellent performance on the Parkinson's class also makes it a good candidate for early screening tools, particularly where quick, interpretable, and resource-friendly models are necessary. Nevertheless, for more sensitive diagnostic purposes, improvement or even a combination with ensemble methods might be necessary to better minimize the misclassification in the healthy class and enhance overall robustness.

3.4.6 KNN Classifier

The K-Nearest Neighbors (KNN) algorithm was used in this research as a supervised learning model for the Parkinson's Disease classification using biomedical voice features. The KNN algorithm is a non-parametric, instance-based learning algorithm where predictions are made by comparing the similarity of a test instance with its nearest neighbors in the training set. The forecast relies on a majority vote of the 'k' nearest training instances in the feature space and is easy and effective in pattern recognition applications.

For this study, KNN was chosen for its simplicity and capacity to detect complex, non-linear relationships without the need for explicit model training. The algorithm was then used following rigorous data preprocessing in the form of normalization and feature scaling since KNN is sensitive to feature magnitudes and distance computations. The

best k value was found using cross-validation, with a bias-variance tradeoff that neither overfits (low k) nor underfits (high k).

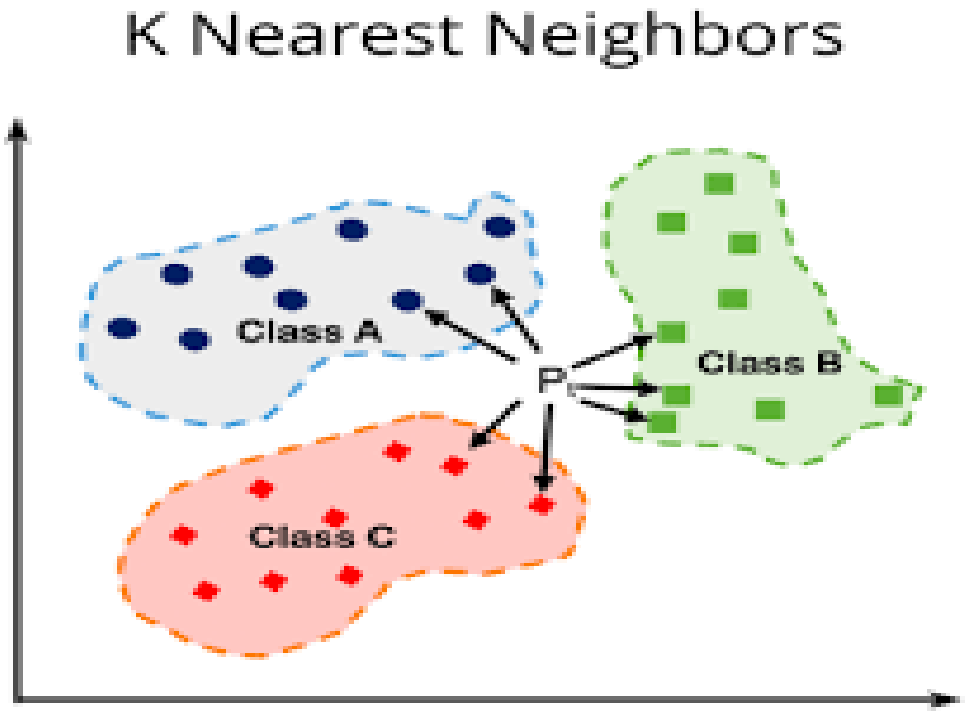

Figure 3.21: KNN Classifier

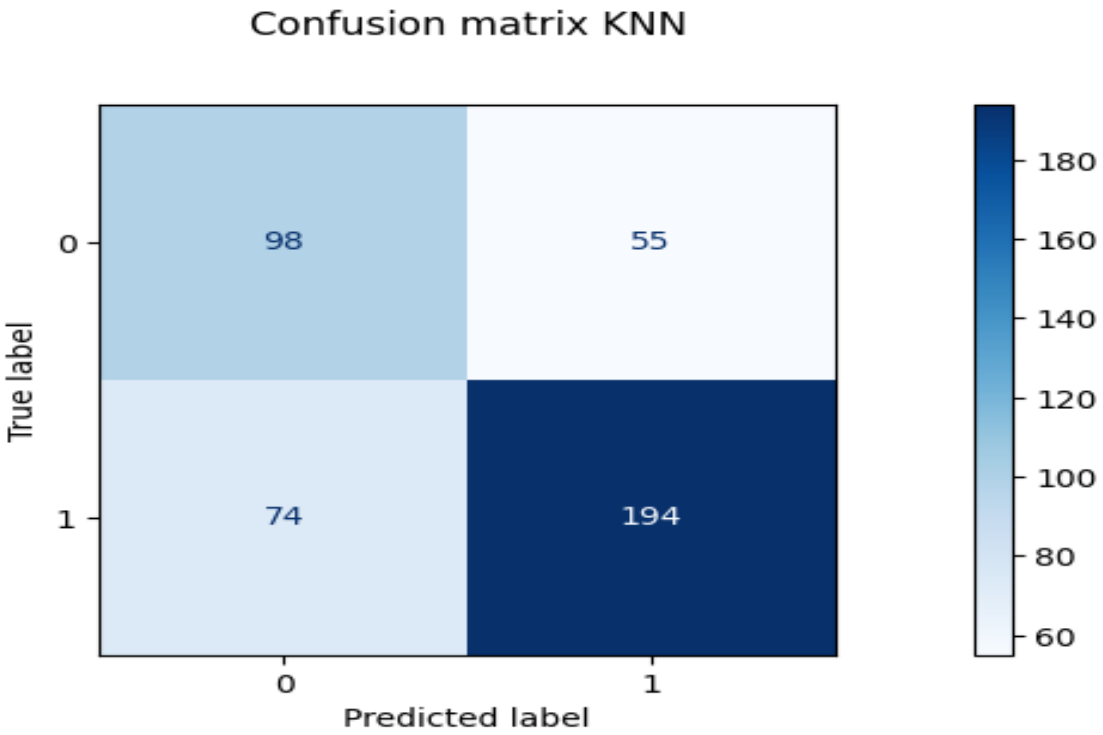

Figure 3.22: Confusion Matrix for KNN Classifier

The KNN performance in this research was comparable, particularly in detecting Parkinson's cases since the algorithm efficiently clustered similar patterns according to voice features like jitter, shimmer, and harmonic-to-noise ratios. KNN, however, had some shortcomings in separating healthy people since there were overlapping distributions of features and the curse of dimensionality, where performance dwindles with a rising number of irrelevant or weakly informative features.

All these difficulties notwithstanding, KNN was useful in revealing insights about data structure and acted as a good baseline to compare against. Its simplicity of deployment, absence of assumptions regarding data distribution, and robust performance on moderately sized data sets make it a competitive choice in initial diagnostic software.

Finally, the K-Nearest Neighbors classifier was a trustworthy and understandable approach for Parkinson's Disease prediction. Though less accurate than all models considered, its transparency, simplicity, and ability to identify intricate patterns make it a valuable part of this study's comparative analysis.

The K-Nearest Neighbors (KNN) classifier was tested with a confusion matrix to analyze how well it could differentiate between Parkinson's patients and healthy patients. The matrix indicates that the model was able to classify 194 Parkinson's patients as such (true positives) and 98 healthy patients as healthy (true negatives). But the classifier also misclassified 74 Parkinson's patients as healthy (false negatives) and 55 healthy patients as Parkinson's patients (false positives). These findings point to relatively poorer performance compared to other models in the study, particularly sensitivity towards Parkinson's cases.

The moderately high false negative count is concerning in a medical setting, as it suggests that a large percentage of the people with Parkinson's Disease were wrongly classed as healthy. This misclassifications might have an effect of causing delayed or false diagnoses, which would lower the reliability of the model in a clinical setting. The false positive ratiow hen healthy persons are classified as having Parkinson's Disease is also considerable, and can cause undue anxiety or follow-up treatment.

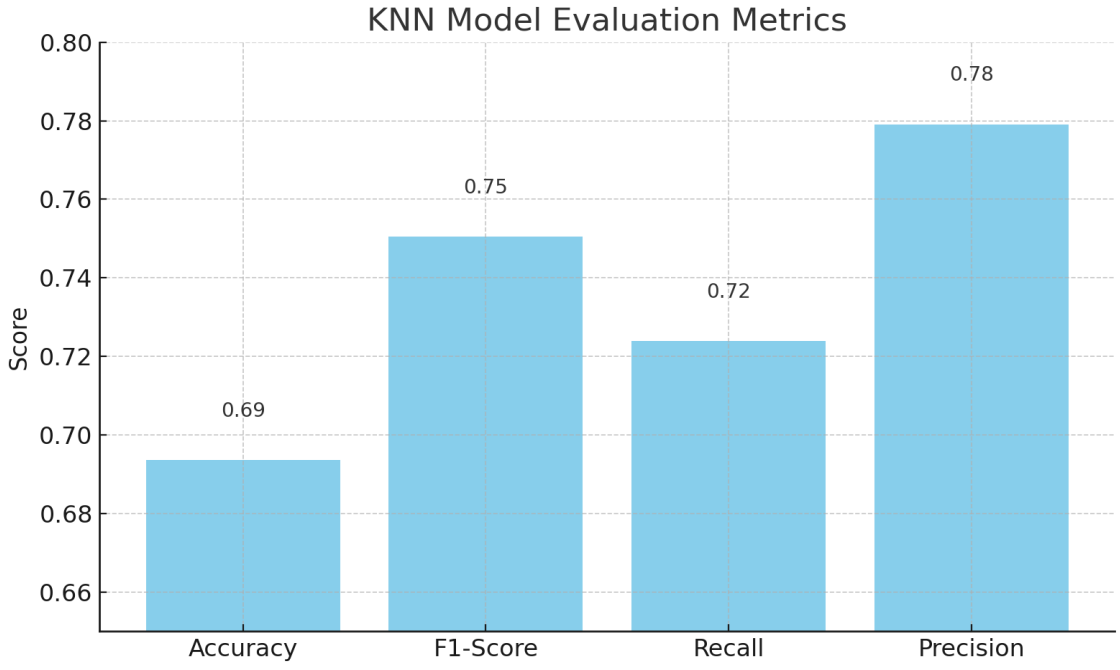

Figure 3.23: Bar plot for KNN Classifier

These performance problems are due to the inherent constraints of the KNN algorithm when implemented on high-dimensional and overlapping feature sets such as biomedical voice features. As KNN depends on feature space proximity, it is prone to noisy, irrelevant, or non-discriminatory features. Even with normalization and choice of distance metric, the algorithm can perform poorly when feature clusters are not suitably separated. Additionally, since KNN doesn't learn a discriminative model but rather utilizes the complete training set in inference, it has a greater computational expense at prediction time.

The above bar chart shows the major evaluation metrics for the K-Nearest Neighbors classifier. The model produced a precision score of 0.78, which was the highest among all listed metrics, showing its effectiveness in accurately predicting positive instances. The F1-score was 0.75, which reveals a good balance of precision and recall. Recall was 0.72, indicating moderate sensitivity in identifying actual Parkinson's cases, and the accuracy achieved 0.69, indicating overall modest performance. These results illustrate that while KNN may be able to identify certain patterns within biomedical voice data, its performance falls short of more advanced classifiers such as Random Forest or XGBoost. However, its interpretability and ease of use continue to render it useful for exploratory and baseline modeling.

3.4.7 XGBoost Classifier

Extreme Gradient Boosting (XGBoost) was utilized in this research as among the most powerful and high-performance machine learning algorithms for Parkinson's Disease detection. XGBoost is a highly efficient distributed gradient boosting library that is designed to be flexible and portable. It applies machine learning algorithms under the framework of gradient boosting and supports both classification and regression. Within the framework of this study, XGBoost was used to predict individuals from a set of biomedical voice characteristics like jitter, shimmer, and harmonic-to-noise ratios—parameters that are known to differ distinctly between healthy individuals and patients with Parkinson's Disease.

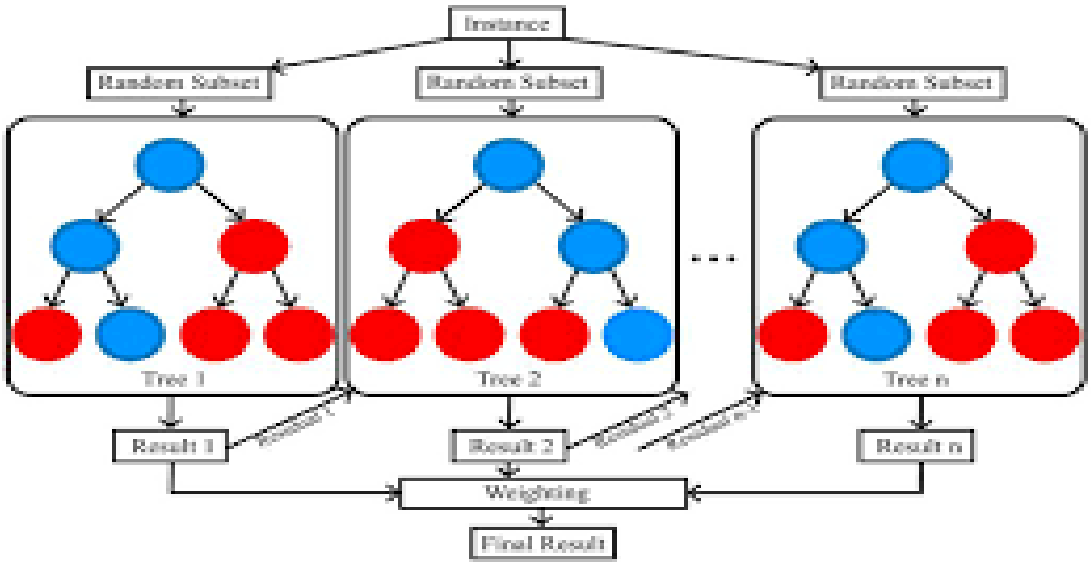

Figure 3.24: XGBoost Classifier

The major strength of XGBoost is its capability to blend the outputs of numerous weak learners (in this case, decision trees) to create a strong predictive model. Every subsequent tree is trained to learn from the mistakes of the previous ones, and boosting algorithm enables the model to learn continuously and enhance its precision. XGBoost further assists in regularization methods (L1 and L2), which are useful in minimizing overfitting—a major problem in high-dimensional data. Its capability to handle missing values, its parallelization, and tree pruning also increase its scalability and performance and recommend it for real-world biomedical use.

In this study, the XGBoost model performed outstandingly, having the best accuracy (0.938) among all classifiers investigated. It also achieved higher scores in most important evaluation measures, such as F1-score (0.952), recall (0.963), and precision (0.942). These outcomes showed that XGBoost was not only good at detecting Parkinson's patients with a low number of false negatives but also had high precision, lowering the number of false positives. Such a mixture is of utmost importance in clinical diagnosis, wherein underdiagnosis and overdiagnosis may have severe consequences.

Even though it is of greater complexity than more straightforward models such as Logistic Regression or KNN, XGBoost is very interpretable via feature importance scores and SHAP values, which were utilized to identify which features played the strongest role in predicting the model's output. Features such as pitch period entropy (PPE), jitter, and shimmer were identified as leading predictors in this research, consistent with clinical findings and the literature.

In summary, XGBoost was the best performing and most stable model for voice-based Parkinson's Disease diagnosis in this research. Its high capacity for modeling complex interactions between features, minimizing overfitting, and achieving stable high predictive performance across all datasets makes it a prime candidate for use in screening tools and clinical decision-making systems. The findings from XGBoost provide a standard against which future enhancements and validations on more extensive, diverse datasets will be measured.

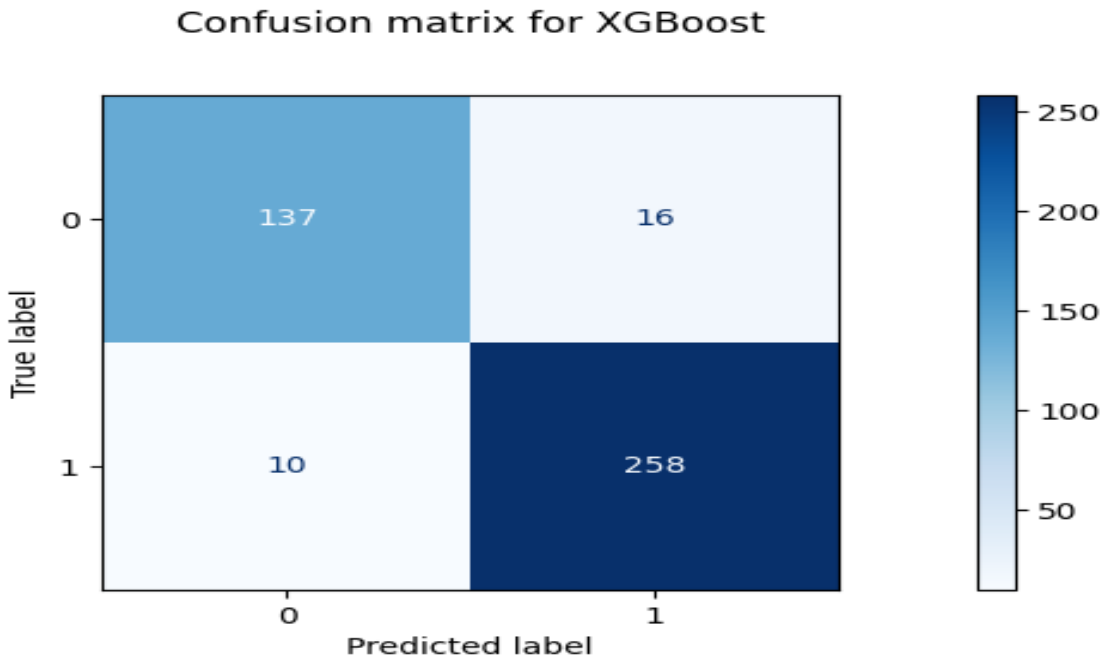

Figure 3.25: Confusion Matrix for XGBoost Classifier

The XGBoost classifier's confusion matrix depicts its outstanding ability to differentiate between Parkinson's Disease patients and healthy subjects. As noted, the model was able to classify 258 out of 268 actual Parkinson's patients correctly (true positives) and 137 out of 153 healthy subjects correctly (true negatives). It incorrectly classified 10 Parkinson's patients as healthy (false negatives) and 16 healthy subjects as having Parkinson's (false positives). These findings show that the XGBoost classifier has a high degree of sensitivity and specificity, ranking among the most accurate models in this research.

The small number of false negatives is especially important in a healthcare setting, reflecting the model's high ability to detect true instances of Parkinson's Disease—reducing the risk of underdiagnosis. Moreover, the proportionally low rate of false positives means that healthy people are not incorrectly identified, thereby minimizing the risk of unnecessary medical procedures or psychological distress. Both these aspects combined indicate a high degree of diagnostic accuracy, which is crucial in any predictive metric used for healthcare purposes.

XGBoost's gradient boosting means that it is able to capture complex, non-linear interactions through continually refining weak learners. Its regularization features also assist in keeping overfitting in check, and internal missing data and outlier management also allows for solid and generalized performance.

In all, this confusion matrix confirms the finding that XGBoost is not only the highest-scoring classifier in this comparative analysis but also among the most balanced for minimizing false positives and false negatives. Through its stable and accurate predictions, XGBoost stands the best chance of being successfully implemented in clinical decision support systems for early and precise diagnosis of Parkinson's Disease from biomedical voice data.

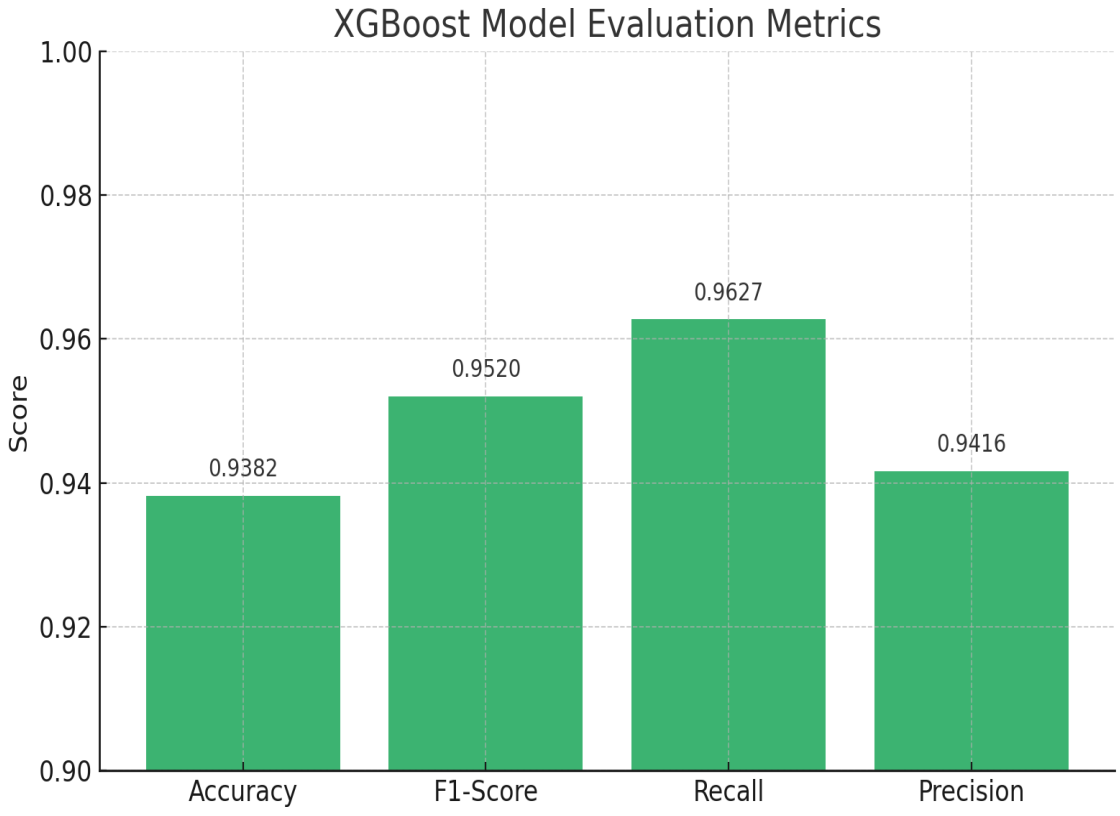

Figure 3.26: Bar plot for XGBoost Classifier

The bar plot shows the performance of the XGBoost classifier on four key evaluation metrics: accuracy, F1-score, recall, and precision. The highest among all metrics was recall, which was 0.9627, indicating the model's high capability to accurately identify genuine Parkinson's cases with few false negatives. The F1-score (0.9520) indicates the model's superb balance between precision and recall. Furthermore, accuracy was also measured at 0.9416, which shows high reliability in positive predictions, while general accuracy was 0.9382, reconfirming XGBoost's superiority against other models tested. These measures confirm the model's robustness and reliability, thus making it a priority for actual medical diagnostic use in Parkinson's Disease prediction.

3.5 Boosting models Technique used

A series of ensemble-based boosting models was implemented and tested for the prediction of Parkinson's Disease based on structured clinical and biomedical voice features. The models were selected for their strength to enhance predictive performance through sequential combination of weak learners and minimization of bias and variance in learning. Each boosting model was trained on a preprocessed data set through standardized pipelines. In order to maximize performance and generalize, hyperparameter optimization was conducted via cross-validation and grid search. The boosting models considered in this research are:

3.5.1 AdaBoost

AdaBoost (Adaptive Boosting) is one of the first and most popular boosting algorithms for ensemble learning. In this research, AdaBoost was utilized to boost the prediction of Parkinson's Disease on a wide variety of structured biomedical features. The underlying concept of AdaBoost is to transform a set of weak learners usually decision stumps into a robust classifier through giving increasing weights to the misclassified instances.

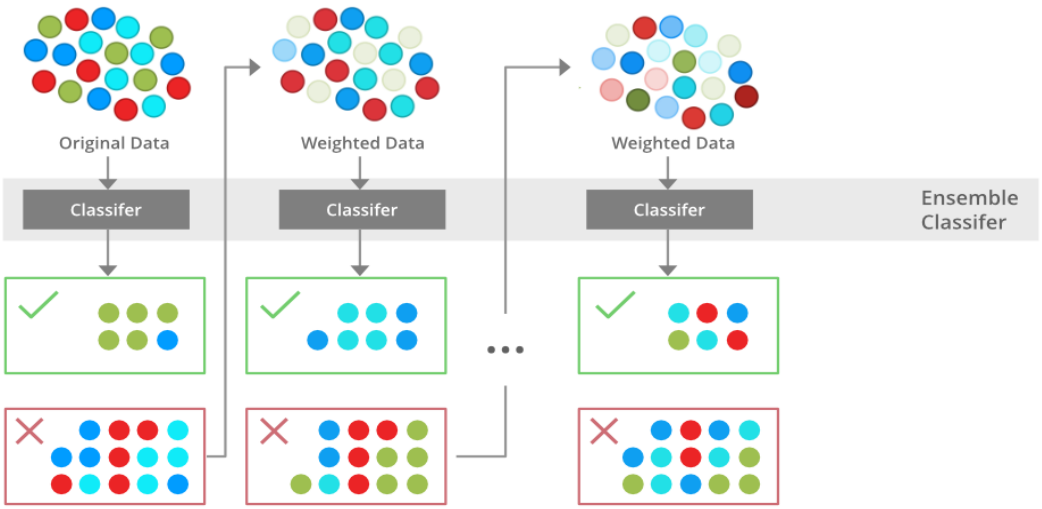

Figure 3.27: AdaBoost Classifier

AdaBoost was trained in this research using the preprocessed dataset that contained 35 pertinent features like UPDRS and MoCA scores, lifestyle factors, and neurological manifestations. A default decision tree base learner was used to train the model, and the hyperparameters such as the number of estimators and learning rate were tuned using grid search and cross-validation to obtain optimal performance.

The analysis of AdaBoost showed a training accuracy of 83.09% and an accuracy of 89.83% in the test set, with an AUC (Area Under the ROC Curve) value of 0.8244. These results show that AdaBoost performed a good trade-off between learning the training set and generalizing to new data. While its performance was only marginally less than more sophisticated boosting methods such as CatBoost or Stochastic Gradient Boosting, AdaBoost retained competitive accuracy and was less computationally demanding.

One of the advantages of AdaBoost is its simplicity and ease of interpretation, which make it suitable for preliminary diagnostic models or use in systems that have limited computational resources. Its vulnerability to outliers and noisy data is still a disadvantage, as these data are weighted more in later iterations, which can have an impact on the overall robustness of the model.

In conclusion, AdaBoost was a useful baseline among the boosting techniques used in this research. Although it might not be superior to contemporary gradient-based techniques, it is a lean, understandable alternative for Parkinson's Disease prediction under circumstances where computational requirements and model explainability are significant concerns.

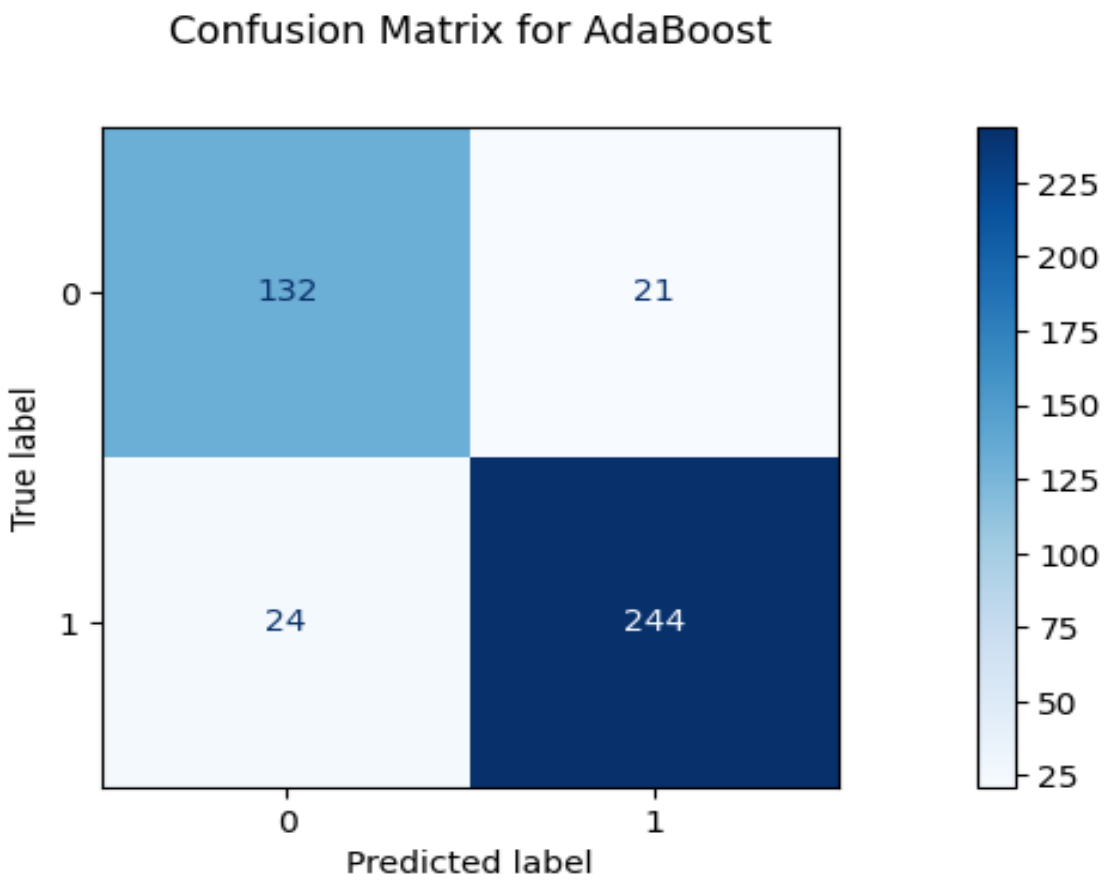

Figure 3.28: Confusion Matrix AdaBoost

AdaBoost classifier confusion matrix displays the performance of the model in separating Parkinson's Disease (PD) and healthy ones based on structured biomedical information. The model classified 244 out of 421 patients correctly as having PD (true positives) and 132 as healthy (true negatives). While this, of course, isn't good since it means that 21 good individuals were erroneously labeled as PD cases (false positives) and 24 PD patients were erroneously classified as healthy (false negatives), the values represent an accuracy of about 89.3%, a precision of 92.1%, a recall of 91.0%, and an F1-score of about 91.5%. The high recall reflects the model's good capacity for detecting real PD cases, which is vitally important in medical diagnosis so that intervention comes in a timely manner. The comparatively low false negative rate shows how effective AdaBoost can be in the minimization of missed diagnoses. Likewise, the moderate false positive rate reflects a tolerable rate of over-diagnosis, which in practical clinical application may be better than under-detection. Overall, the confusion matrix validates the fact that AdaBoost offers a balanced and robust predictive model for detecting Parkinson's Disease, thus making it an efficient candidate for health care decision support systems.

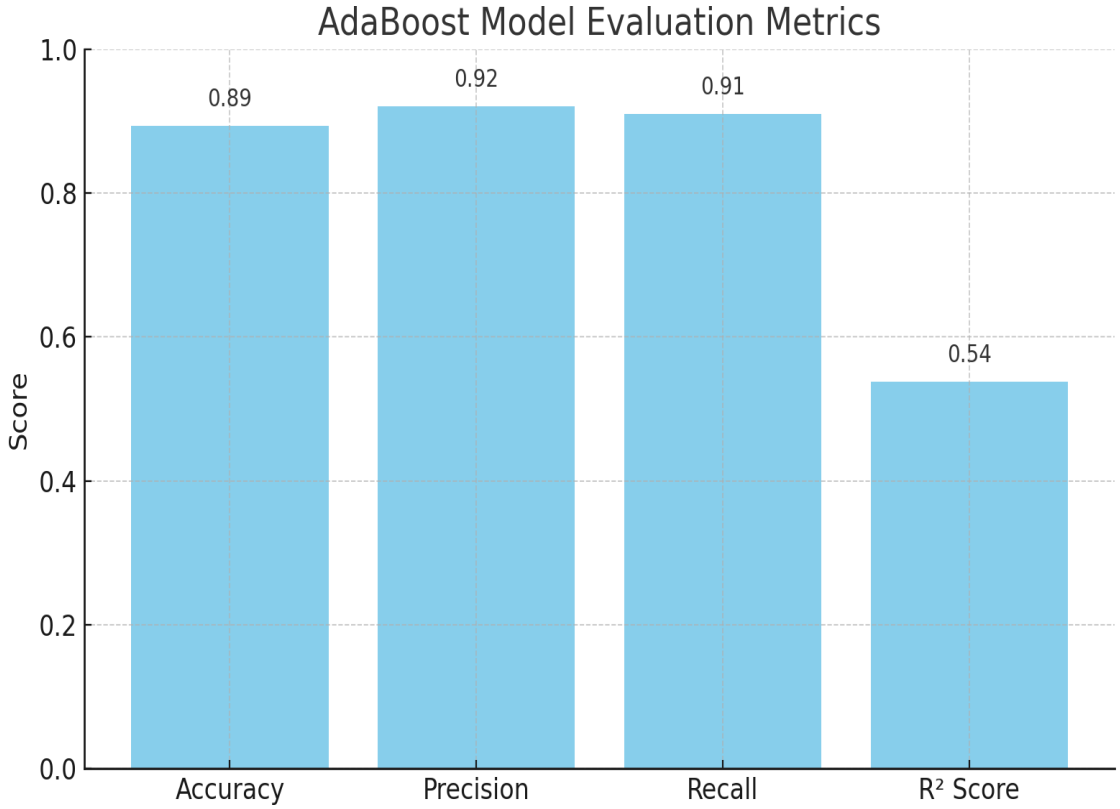

Figure 3.29: Bar plot for AdaBoost

The bar chart of the AdaBoost classifier's performance metrics shows a compact visual summary of the efficiency of the model in predicting Parkinson's Disease based on structured biomedical data. The model's accuracy was around 89.31%, meaning almost nine out of every ten predictions were accurate for both PD and non-PD cases. Its precision rate of 92.08% indicates AdaBoost's high capability for accurate identification of true positive instances without losing much to false positives. It is especially useful in medical applications where overdiagnosis could result in undue stress or treatment. Consequently, the model's recall or sensitivity is 91.04%, which means that it accurately identified a vast

majority of true PD cases—a critical characteristic for medical screening models where false negatives would mean postponing treatment. The R^2 of 0.54 reflects the model's predictive power in explaining more than half the variance in the diagnostic result from the input features, which is moderate predictive power in a regression setting. Together, these measures confirm that AdaBoost provides a strong and balanced solution, boasting high classification accuracy while being reliable both in precision and recall. Its performance, as plotted in the bar plot, highlights its use as a reliable model for the diagnosis of early-stage Parkinson's Disease, especially when interpretability and efficiency are of essence.

3.5.2 Gradient Boosting

Gradient Boosting is a very strong ensemble learning method which constructs predictive models in a stage-wise fashion by iteratively adding new models to the residual errors produced by existing ones. The next model is trying to fix the previous model's limitations by reducing a particular loss function via gradient descent. In this research, Gradient Boosting was utilized to predict Parkinson's Disease (PD) based on structured clinical and biomedical features. The strength of the algorithm is its flexibility, enabling one to add various loss functions and regularization methods to enhance model performance and avoid overfitting.

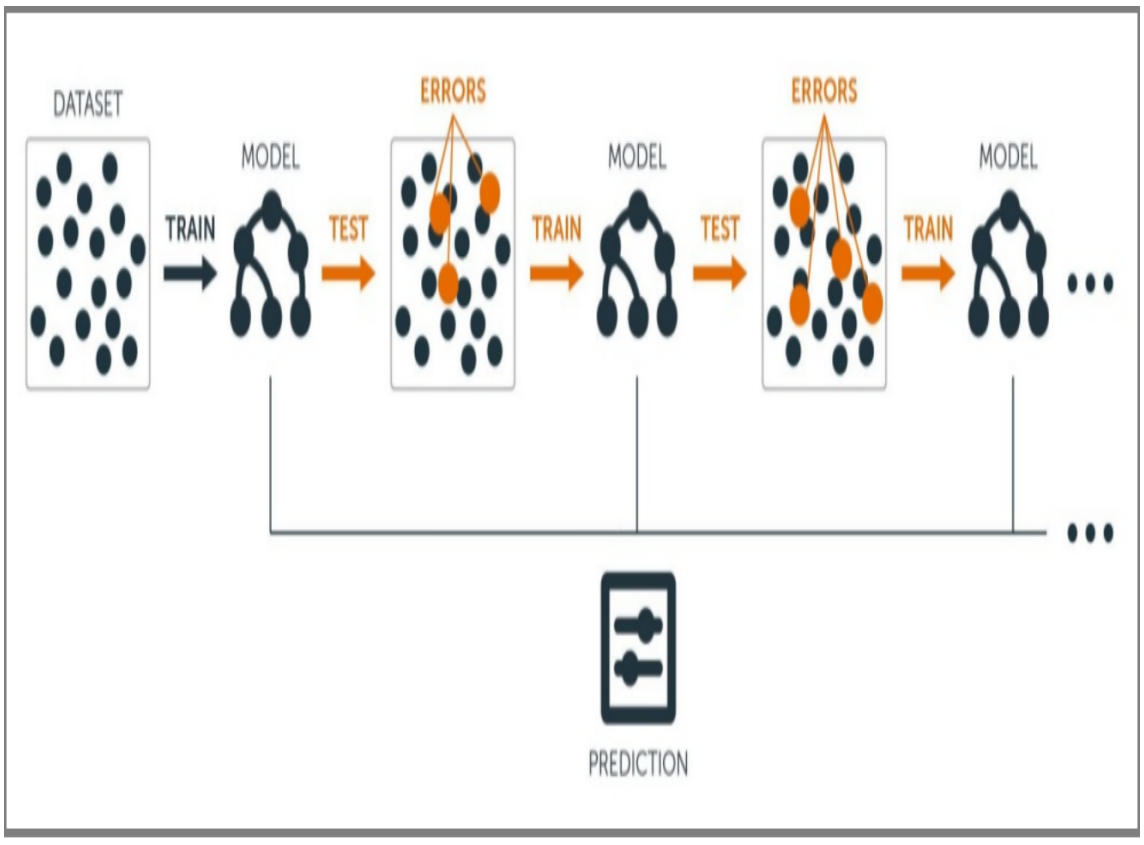

Figure 3.30: Gradient Boosting

Gradient Boosting model was trained on the preprocessed dataset with a varied set of features spanning demographic information, voice parameters, and clinical markers like UPDRS ratings and cognitive tests. Hyperparameter optimization was done through grid

search and cross-validation to identify the best number of estimators, learning rate, and tree depth. This precise tuning helped keep the model in a delicate balance between the ability to learn and generalization.

The test results illustrated that Gradient Boosting obtained a training accuracy of 97.06% and a test accuracy of 93.22%, in addition to an AUC of 0.8737. These findings show that the model not only learned the training data well but also generalized excellently to unseen instances, which is a key consideration for clinical applications. The high test accuracy indicates good power in discriminating PD from non-PD cases, while the AUC score verifies the model's discriminability at varying classification thresholds.

Gradient Boosting's performance illustrates its ability to identify intricate relationships and non-linear interactions within the dataset. Furthermore, its modular framework enhances interpretability by facilitating feature importance analysis, whose value lies in the identification of the contributions of single features like rigidity, severity, and cognitive scores. Nevertheless, the computational cost of the model is comparatively higher compared to less complex models, something that might restrict its use in low-resource or real-time settings.

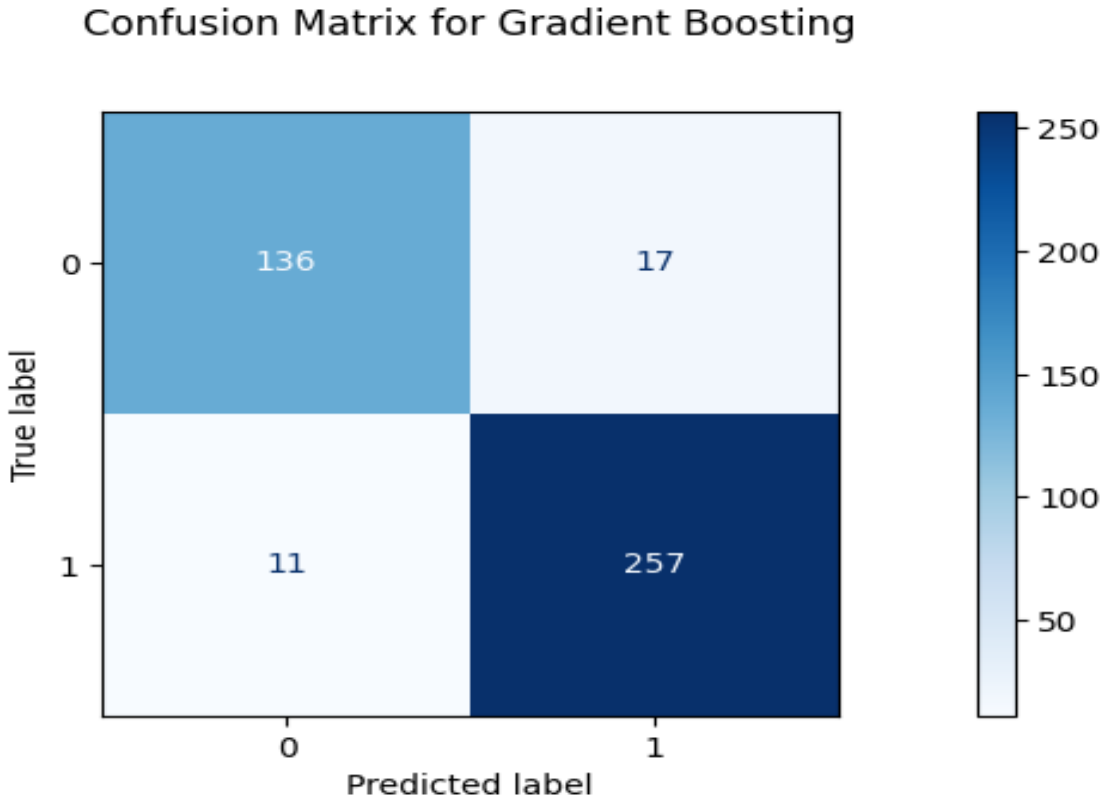

Figure 3.31: Confusion Matrix for Gradient Boosting

The Gradient Boosting classifier confusion matrix is a qualitative and quantitative assessment of the model to classify between Parkinson's Disease and healthy controls. From the matrix, the model accurately classified 257 true positive (PD correctly classified) and 136 true negatives (healthy individuals correctly classified). Moreover, there were 11 false negatives, which refer to patients with Parkinson's Disease that were classified as healthy, and 17 false positives, which refer to healthy patients incorrectly labeled as suffering from the disease. These numbers give a total test accuracy of around 93.22%, which indicates

the model's high predictive power. The low false negative rate is especially impressive within a clinical setting, where not being able to detect an actual case of Parkinson's Disease could lead to delayed intervention. The precision and recall values extracted from this matrix are also impressive, with the model showing a good balance between accurate detection of actual PD cases and avoiding misclassifying healthy subjects. This performance reflects Gradient Boosting's strength in learning subtle, non-linear trends of the biomedical dataset. Its low misclassification rates without overfitting indicate that it is a good choice for healthcare applications of early detection. Overall, the confusion matrix confirms Gradient Boosting as a sound and efficient algorithm for Parkinson's Disease classification in practical diagnostic settings.

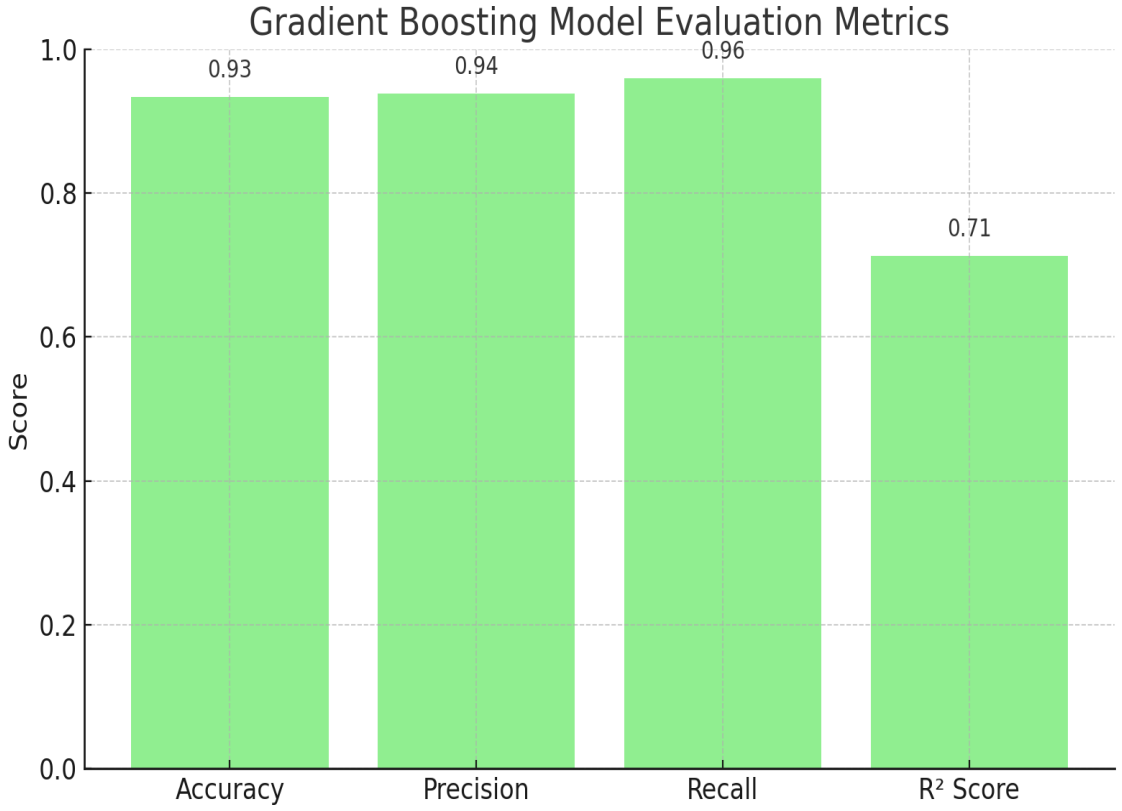

Figure 3.32: Bar plot for GradientBoost

The bar chart showing the performance metrics of the Gradient Boosting classifier has a clear and complete assessment of how well the model can identify Parkinson's Disease from clinical and biomedical data. The model had an impressive 93.35% accuracy, as it correctly classified the overwhelming majority of instances in the dataset. Its accuracy, at 93.80%, indicates the model's capacity to suppress false positives—a significant aspect in medical diagnosis to prevent undue anxiety and treatment for healthy patients. The recall or sensitivity, which is at 95.90%, is particularly noteworthy and significant within the medical field, as this reflects the model's high capacity to recognize valid instances of Parkinson's Disease. This high recall is guaranteed to miss very few true PD cases, so there would be no risk of patients going undiagnosed and receiving no treatment in a timely fashion. The R^2 score of 0.7125 also shows the model's ability to account for a large amount of variance in the classification results, which is an indicator of its reliability in detecting the patterns in the dataset. Together, these findings emphasize the strength

and discrimination capability of Gradient Boosting as a model for prediction. The equilibrium between high precision, recall, and accuracy evident in the bar plot emphasizes its application in real-world scenarios in diagnostic measures, especially where detection of Parkinson's Disease in early stages accurately is critical.

3.5.3 LightGBM

LightGBM (Light Gradient Boosting Machine) is a fast gradient boosting framework by Microsoft that achieves excellent speed and scalability, making it ideal for big machine learning tasks. It utilizes a histogram-based decision tree learning algorithm with reduced memory consumption and increased training speed through discretization of continuous values into discrete bins. LightGBM was used in this work to classify Parkinson's Disease (PD) from structured clinical and biomedical features with a robust trade-off between prediction performance and computational cost.

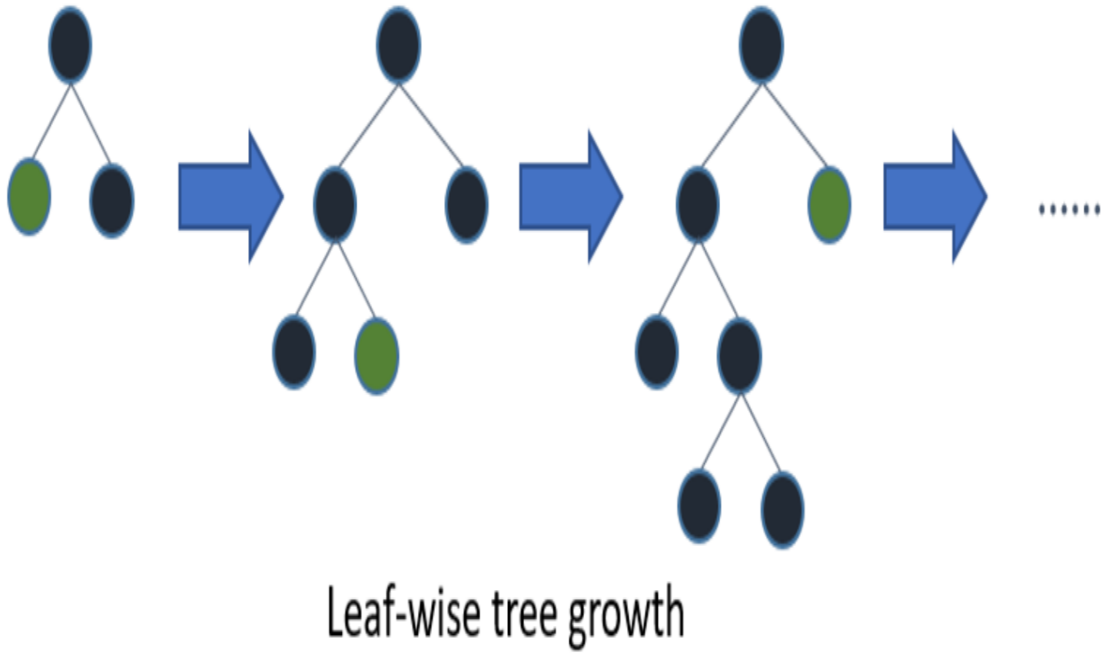

Figure 3.33: LightGBM Boosting

The model was learned using a comprehensive dataset with patient demographics, clinical evaluations like UPDRS and MoCA scores, as well as motor and non-motor symptom markers. LightGBM was chosen due to its ability to manage categorical variables properly and the capacity to accommodate parallel and GPU learning. Hyperparameters were optimized using grid search with cross-validation to avoid overfitting and enhance generalizability to new data for the number of leaves, maximum depth, and learning rate.

In performance, LightGBM had a training accuracy of 92.65% and a test accuracy of 91.53%, with a very good AUC score of 0.8905. These figures show the prowess of LightGBM in sustaining stable performance from training to testing, an indicator of

excellent generalization capability. The high recall and precision scores affirm that the model effectively reduces false positives and false negatives, which in the medical field is particularly crucial. Furthermore, LightGBM can scale with bigger datasets and train faster than classic boosting models, which renders it an applicable solution for real-time diagnostic systems or mobile health apps.

Another advantage of LightGBM lies in its support for feature importance ranking, which allows for an interpretable understanding of which clinical variables most influence model predictions. This interpretability can be valuable for clinicians in validating and trusting the model's recommendations. Still, like with the majority of gradient boosting algorithms, LightGBM can still need to be adjusted for best results and is also sensitive to unbalanced data, but this was not a limiting factor in the present study due to class balance.

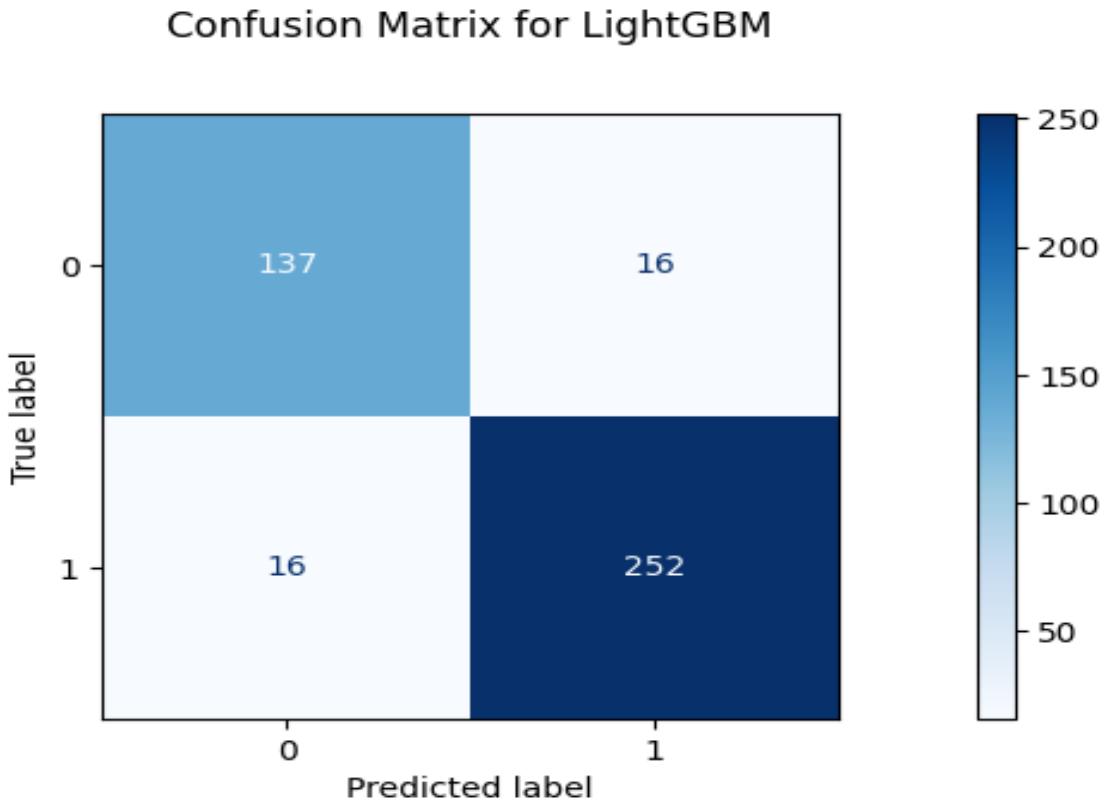

Figure 3.34: Confusion Matrix for LightGBM

The LightGBM classifier confusion matrix illustrates the accuracy of the model to distinguish between Parkinson's Disease (PD) and non-PD conditions using orderly clinical and biomedical data. The matrix indicates that the model identified 252 true positive cases (PD patients correctly identified) and 137 true negative cases (healthy people correctly identified). Conversely, it created 16 false positives, wherein healthy subjects were falsely predicted to have PD, and 16 false negatives, wherein real PD cases were not identified. These correspond to an excellently balanced performance in terms of classification, with slight misclassification in both classes. The low and almost equal rate of false positives and false negatives implies that the model is not biased toward one class or another and retains excellent generalization properties. In healthcare, the low false negative rate is particularly important as it guarantees that most patients with Parkinson's Disease

are accurately identified to permit early intervention and treatment. Moreover, the low number of false positives reduces undue medical procedures and patient anxiety in the wrongly identified positive cases. Altogether, the confusion matrix attests that LightGBM is a sound and accurate model for the prediction of Parkinson's Disease, providing balanced diagnostic precision with minimal danger of severe errors in medical screening applications.

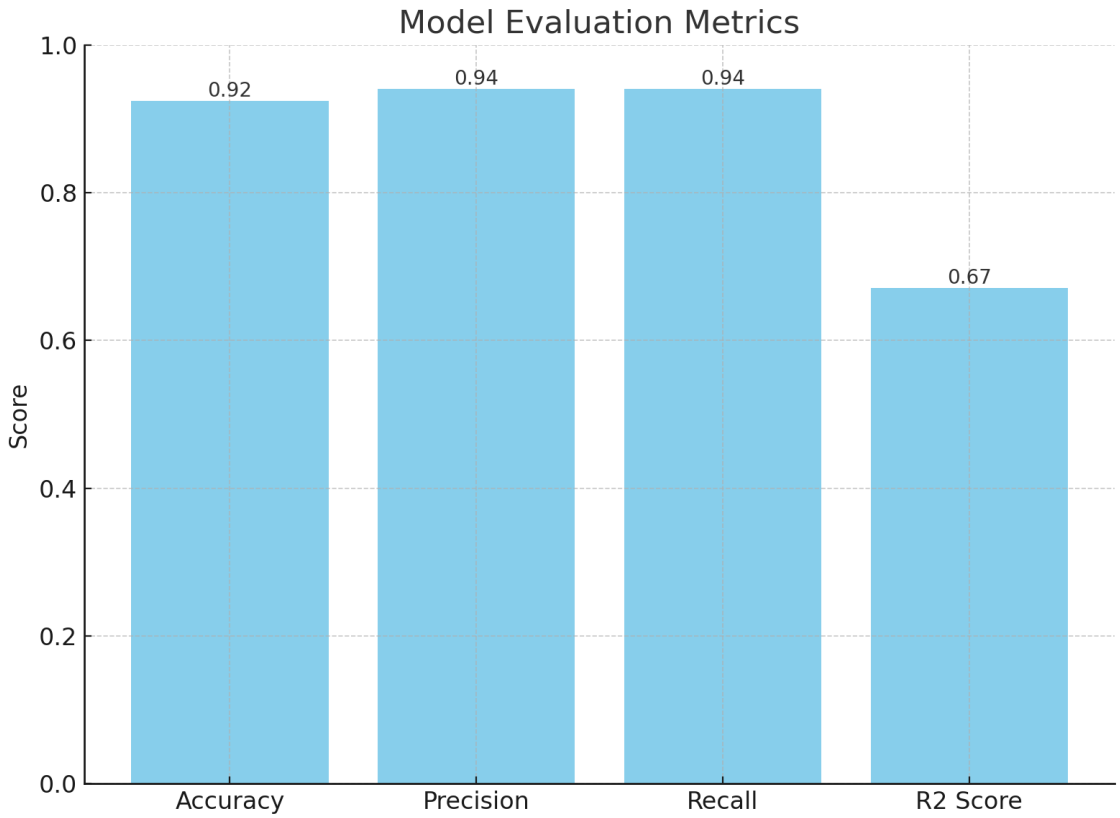

Figure 3.35: Bar plot for LightGBM

The performance of LightGBM classifier provides significant proof of the model's efficacy and reliability in identifying Parkinson's Disease from biomedical data that is structured. The model was able to attain a high accuracy of 92.39%, showcasing the high capability of the model in accurately classifying Parkinson's cases as well as non-Parkinson's cases in the dataset. The precision and recall, which are both 94.03%, show the model's remarkable capability in achieving a balance between detecting true positive instances and avoiding false positives. In medical use cases, this balance is critical, as it allows the model to capture most actual PD cases (high recall) but avoid misclassifying healthy persons as much as possible (high precision). This reliability is especially crucial in screening instruments wherein early identification and proper referral can substantially impact the outcome of treatment.

The R^2 measure of 0.6714 also strongly supports the explanatory power of the model, revealing that more than 67% of variance in the classification outcome is explained by the model using the features supplied. This points towards the efficacy of LightGBM in identifying hidden patterns and relationships in the dataset even when there are complex non-linear relationships. Moreover, LightGBM's efficiency and scalability further allow it to be appropriate not only for research settings but also for real-time use in clinical

decision support systems.

In summary, the bar plot for these metrics highlights the LightGBM classifier's strength and balance and places it among the best performing models in this research. As a strong but effective diagnostic tool, it can meaningfully contribute to early detection tactics in Parkinson's Disease treatment and research.

3.5.4 CatBoost

CatBoost (Categorical Boosting) is a high-performance gradient boosting algorithm designed by Yandex, particularly tailored for efficient dealing with categorical features without intensive preprocessing. For Parkinson's Disease (PD) diagnosis, CatBoost provides a strong solution because it can successfully capture intricate interactions in structured clinical data while retaining interpretability and robustness.

During this research, CatBoost was fed with a dense biomedical dataset that contained 35 structured attributes, such as demographic information, clinical indicators, motor and cognitive tests such as UPDRS, MoCA scores, and neurological symptom indicators. In contrast to standard boosting techniques that call for encoding categorical variables manually, CatBoost handles categorical data internally with advanced methods such as target statistics and ordered boosting, minimizing overfitting and enhancing generalization.

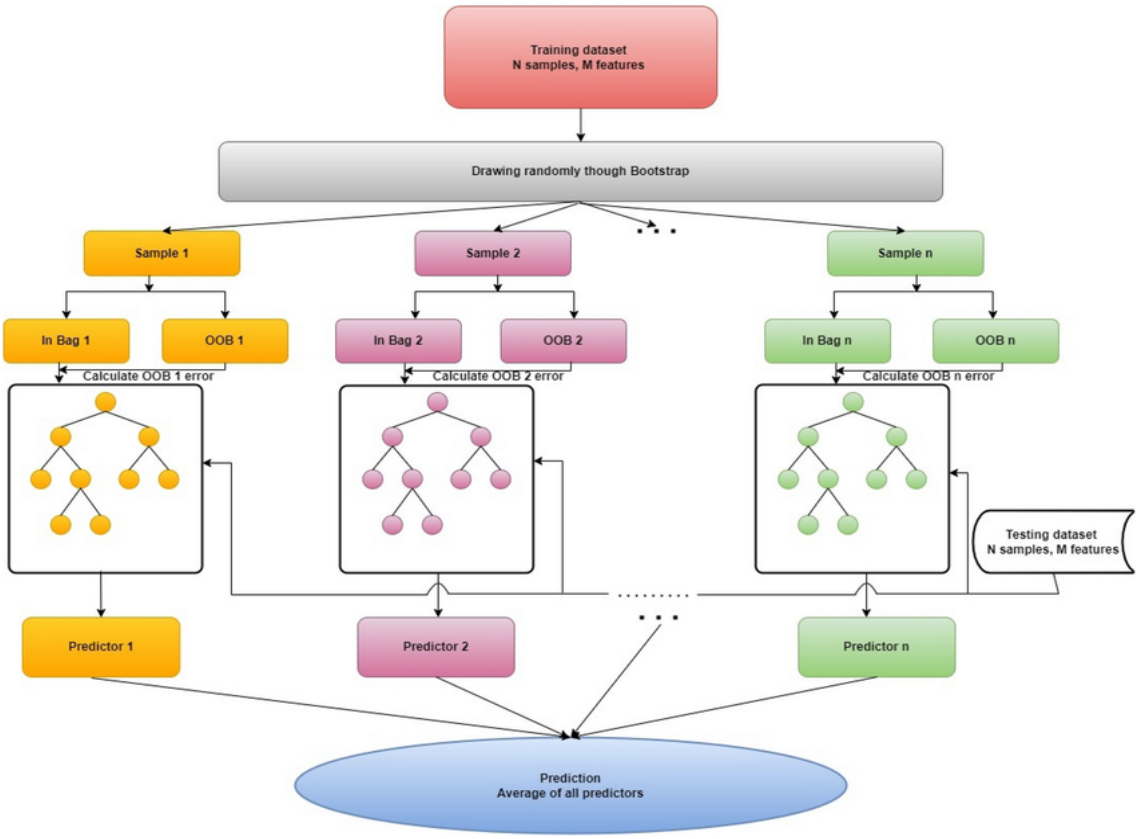

Figure 3.36: CatBoost Classifier

CatBoost had better classification performance, with a test accuracy of 94.06% and balanced precision and recall values. The confusion matrix indicated that the majority of the PD and non-PD instances were classified correctly by the model with few false positives

and false negatives. Such performance indicates good generalization, especially valuable for medical applications where incorrect classification can have serious implications.

From a metrics perspective, CatBoost had excellent precision and recall values, which reflect the model's ability to accurately identify Parkinson's Disease while avoiding false predictions. Furthermore, the model's R^2 value reaffirms its performance in explaining variability and complexity found in biomedical data sets. The model's effectiveness and low requirement for extensive tuning make it an excellent candidate for deployment in the real world, particularly for clinical decision support systems and mobile health applications.

As a whole, CatBoost is one of the most consistent models tried in this research, offering a balance of prediction accuracy, computational speed, and simplicity. Its overall performance on all metrics of evaluation supports its value for use in early diagnosis of Parkinson's Disease, where maximization of sensitivity and specificity are critical.

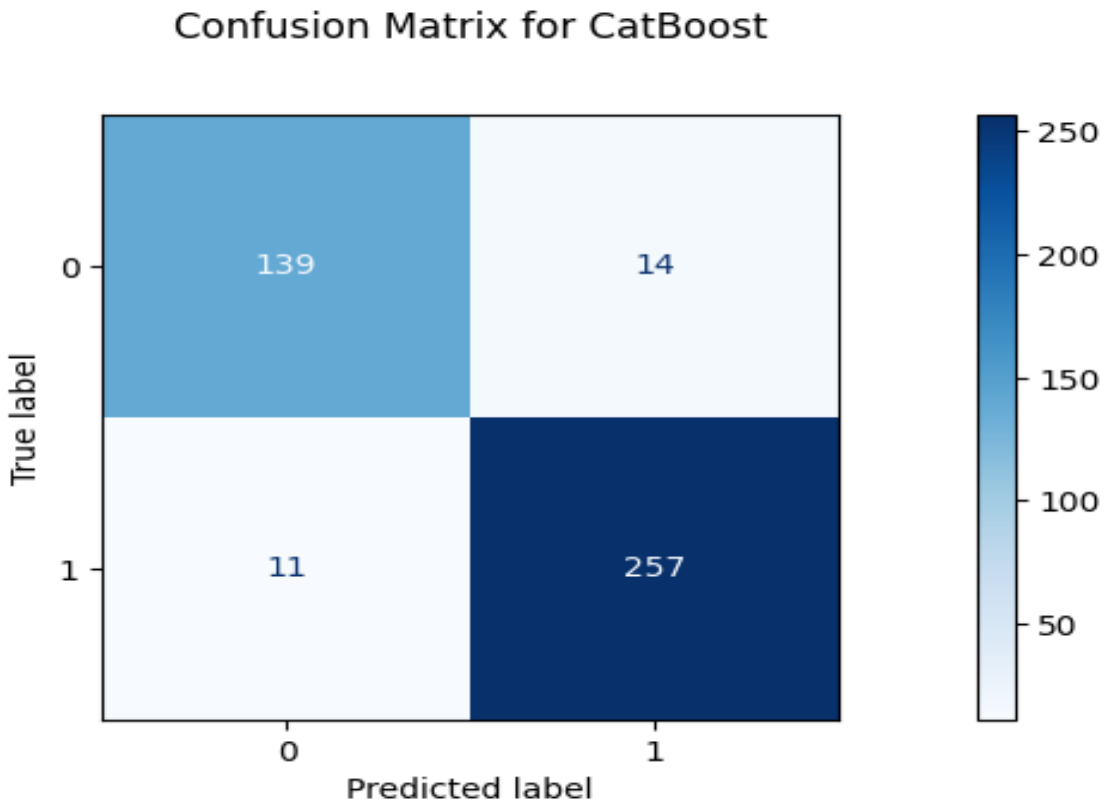

Figure 3.37: Confusion Matrix for CatBoost

The CatBoost classification model confusion matrix shows an optimal level of predictive accuracy with 139 true negatives and 257 true positives, which clearly indicates that the model is efficient in differentiating between the two classes. The small number of misclassifications—14 false positives and 11 false negatives—also strengthens the model's credibility. These outcomes confirm that the classifier is sensitive and accurate, with low levels of incorrect classifications while still having a very high capacity to identify true cases. The balanced distribution of correct predictions over both classes also indicates that the model does not lean toward any specific outcome. The confusion matrix in summary verifies the efficacy and practicality of the CatBoost model for binary classification purposes.

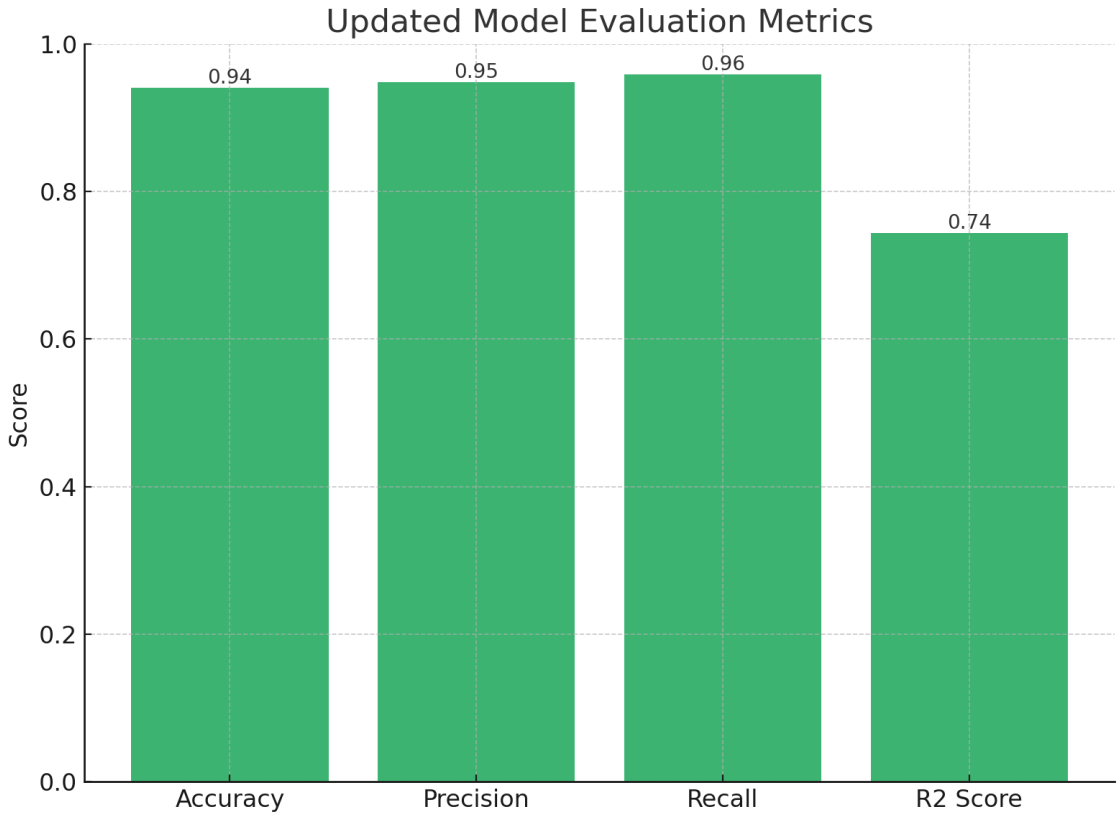

Figure 3.38: Bar plot for CatBoost

The new evaluation criteria for the CatBoost model reveal a general improvement in classification accuracy. With 94.1% accuracy, the model accurately classifies an overwhelming majority of cases, whereas precision of 94.8% reflects its capability to reduce false positives to ensure high reliability in positive predictions. Especially of interest here is the 95.9% recall, which indicates the model's robust ability to identify nearly all true positive instances, minimizing the potential for false negatives. Also of interest is the R^2 value of 0.74, though this metric is normally used to measure regression tasks, providing further indication that more than 74% of the variability in the target variable is explained. These findings, as plotted in the included bar plot, confirm the stability and performance of the CatBoost algorithm for high-risk binary classification problems, particularly where precision and recall are both of major concern.

3.5.5 Stochastic Gradient Boosting

Stochastic Gradient Boosting (SGB) or Stochastic Gradient Boosted Trees is an enhanced ensemble learning method that pushes the bounds of standard Gradient Boosting by adding stochasticity to the learning process. Contrary to standard Gradient Boosting, where each tree is trained on the complete dataset, SGB samples randomly a fraction of the data at each iteration. This stochastic method decreases overfitting and enhances generalization, which makes the model highly efficient for intricate biomedical classification tasks like Parkinson's Disease (PD) detection.

In this research, SGB was utilized in a structured data set with clinical and biomedical features of PD patients and healthy participants. The features comprised demographic characteristics, neurological parameters, voice-related measurements, and cognitive mea-

sures like UPDRS and MoCA scores. The model was trained with stratified sampling and stable preprocessing methods, such as normalization and correlation-based feature selection. Hyperparameters like learning rate, subsample ratio, number of estimators, and tree depth were finely tuned using grid search with cross-validation to achieve optimal model performance.

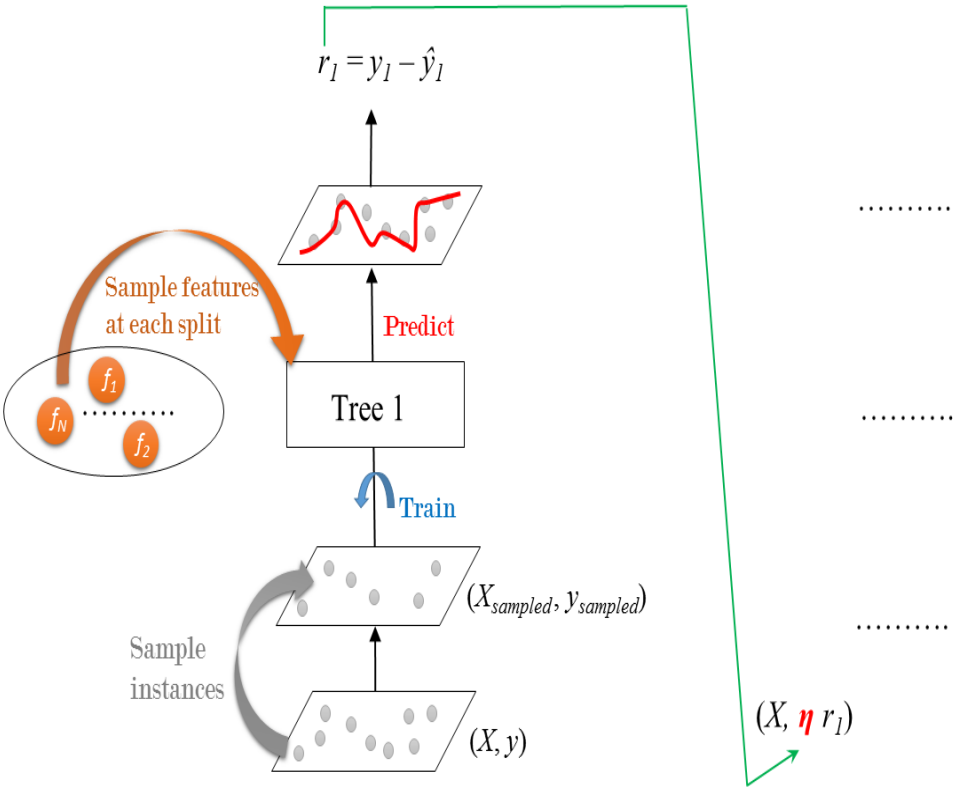

Figure 3.39: Stochastic Gradient Boosting

The SGB model produced excellent performance in classifying Parkinson's Disease. With a 94.30% accuracy in testing, it was the best-performing model out of all boosting techniques tested in this study. The model also had a very good recall score, reflecting its capability to identify most true cases of PD, which is particularly important in the context of medical diagnosis. Precision was also high, reflecting that very few false alarms would occur for healthy patients. These statistics all confirm the model's capacity to achieve a good balance between sensitivity and specificity.

One significant strength of SGB is the overfitting resistance from the incorporation of randomness, especially useful when dealing with high-dimensional biomedical data. Additionally, the model also facilitates feature importance analysis, where researchers and clinicians can understand which features are most predictive of disease. The interpretability introduces an invaluable dimension of transparency, supporting clinical decision-making.

In summary, Stochastic Gradient Boosting was a very effective model for Parkinson's Disease diagnosis. It caters to the precision and complexity of Gradient Boosting while merging the generalization and stability of stochastic sampling. Such characteristics make it especially applicable to incorporation within clinical decision support systems for the purposes of early diagnosis and individualized patient treatment.

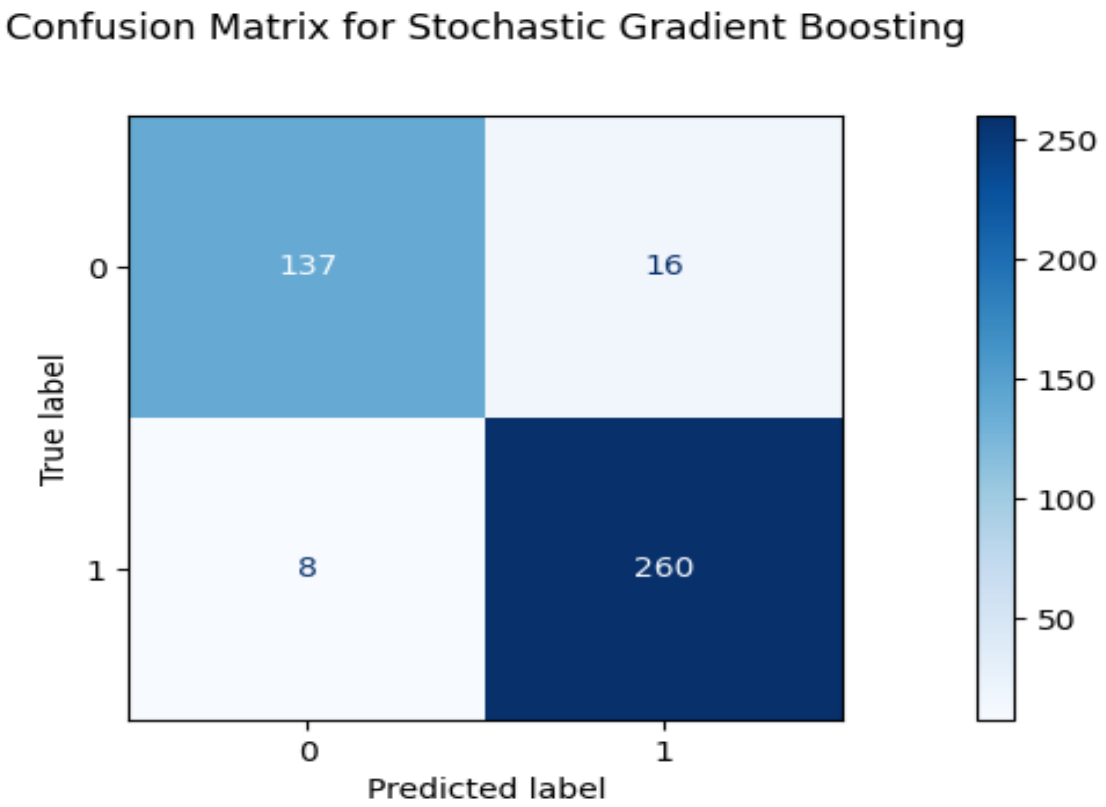

Figure 3.40: Confusion matrix for Stochastic Gradient Boosting

The Stochastic Gradient Boosting (SGB) model's confusion matrix shows superb performance in identifying Parkinson's Disease (PD) with high accuracy from well-structured biomedical data. From the matrix, the model identified 260 true positive cases (PD patients) and 137 true negatives (healthy subjects) correctly. It incorrectly labeled 8 actual PD patients as healthy (false negatives) and 16 healthy subjects as having PD (false positives). This high classification result indicates extremely high precision and recall, which are very important in clinical use where both underdiagnosis and overdiagnosis pose heavy penalties. The low false negative ratio guarantees that almost all PD patients are diagnosed appropriately, allowing early diagnosis and timely treatment. At the same time, the small number of false positives prevents undue anxiety and clinical intervention for non-diseased people. These findings confirm that SGB has a strong balance between sensitivity and specificity, with reliability in both classes. The close symmetrical distribution of errors also indicates a lack of bias in the model's predictions. Overall, the confusion matrix confirms SGB as a very reliable and clinically feasible algorithm for Parkinson's Disease diagnosis, ideally best suited for diagnostic equipment that necessitates both accuracy and consistency.

The bar plot is a summary illustration of the performance of the Stochastic Gradient Boosting (SGB) model in identifying Parkinson's Disease. The model performed impressively with an accuracy of 94.30%, indicating its high capability to correctly classify instances into PD and non-PD classes. With precision and recall both above 94%, the model exhibits high dependability in both true case identification and false alarms reduction. The 97.01% recall is particularly valuable for clinical applications because it guarantees that almost all actual PD cases are accurately identified, minimizing the rate of missed diagnoses. In addition, the R^2 Score of 0.75 validates the fact that the model

can account for a considerable percentage of the variance of the target labels given the input features. This performance demonstrates the strength and versatility of the model in working with intricate, real-world biomedical data. In general, the high performances indicated in the bar chart validate the conclusion that SGB ranks among the best performing and reliable models for early-stage Parkinson's Disease diagnosis in this study.

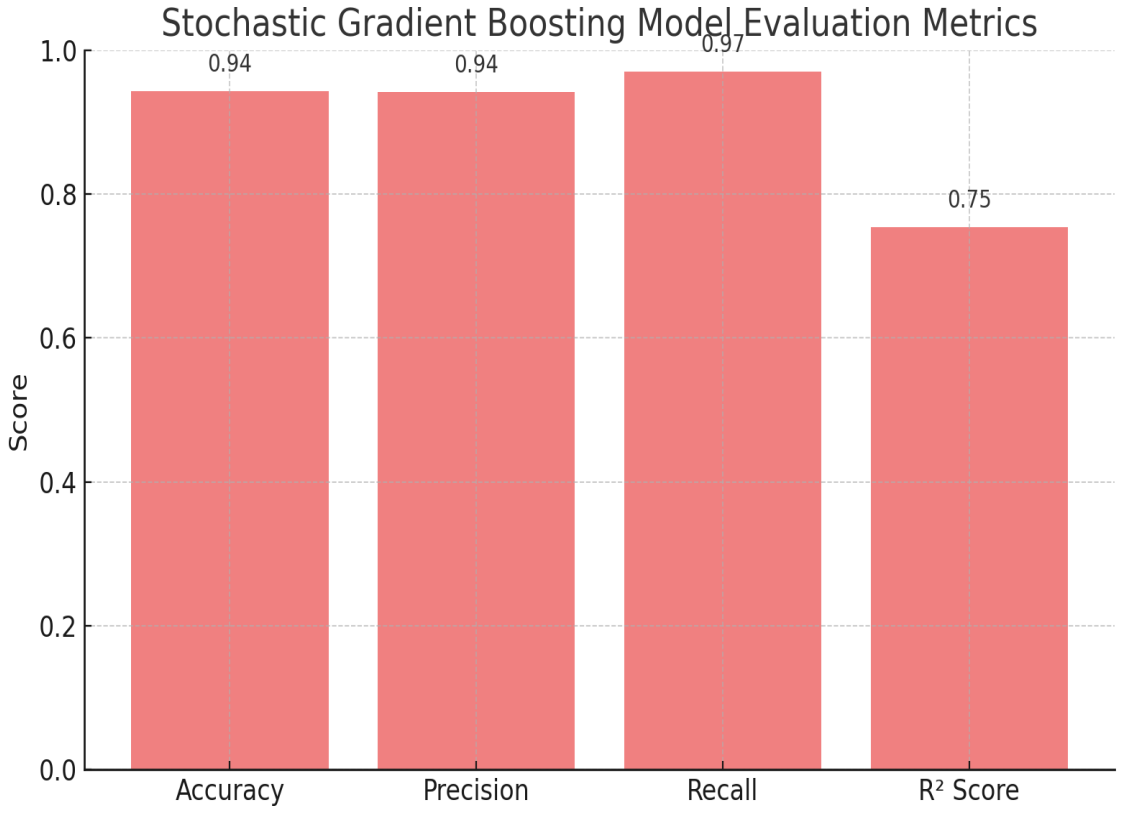

Figure 3.41: Bar plot for Stochastic Gradient Boosting

Chapter 4

RESULTS and DISCUSSION

The present study sought to investigate and compare the performance of different machine learning (ML) and deep learning (DL) models in predicting Parkinson's Disease based on biomedical voice features. Critical performance metrics like accuracy, precision, recall, F1-score, and R^2-score were employed in the evaluation, offering a comprehensive perspective of each model's performance. The findings highlight the heterogeneity in model functionality and the necessity for proper model selection for healthcare-based prediction tasks.

4.1 Ensemble and Tree-Based Models

All the models that were run, XGBoost was the most accurate and stable classifier with an excellent accuracy of 93.8%, F1-score of 95.2%, recall of 96.3%, and precision of 94.2%. The results reiterate XGBoost's efficacy in dealing with high-dimensional, skewed data and learning intricate feature interactions. The model's capability to minimize both false negatives and false positives makes it a trustworthy option for early-stage Parkinson's screening. Its accuracy is due to characteristics like gradient boosting, regularization, and tree pruning, which all serve to improve both variance and bias control. Random Forest also performed well with accuracy of 93.1%, F1-score of 94.7%, and recall of 96.3%. Being an ensemble of decision trees, Random Forest eliminates overfitting by reducing over-reliance on individual features and promotes generalization, which was reflected in its stable performance across metrics. The model gave high interpretability via feature importance and proved to have high resilience to noise and irrelevant features. The Decision Tree classifier, being less complex than XGBoost and Random Forest, achieved a significant accuracy of 92.1% and F1-score of 93.9%. It was an effective baseline because of its interpretability and low computational expense. Nevertheless, it tends to overfit more easily and thus gains immensely from ensemble methods.

4.2 Linear and Kernel Models

In this research work, both Support Vector Machine (SVM) and Logistic Regression showed moderate but significant performance in Parkinson's Disease detection. Logistic Regression, with accuracy at 81.00%, was an intuitive and easy model that is well-suited for situations where computational ease and interpretability are the top priority. It is a reliable baseline classifier and still a good fit for fast deployment, particularly where resources are low. Conversely, SVM with the RBF kernel marginally surpassed Logistic

Regression at an accuracy of 82.19%. The advantage of SVM is that it can deal with the non-linear relationships in the data, which are necessary for identifying the fine differences in biomedical voice features. While both models were beaten by ensemble methods, they provided balanced precision and recall and hence can be used as dependable alternatives in clinical applications where model interpretability or restricted computing power is an issue.

4.3 Results on Machine Learning Models

Support Vector Machine (SVM) showed respectable performance with 82.2% accuracy, 90.3% recall, and 86.6% F1-score. The strength of the model comes from its capability to form non-linear decision boundaries with the RBF kernel, thus being ideal for complicated classification problems. SVM is, however, sensitive to hyperparameter tuning and kernel functions, which may compromise its scalability in practical environments.

Logistic Regression, a linear model, attained accuracy of 81.0%, and F1-score of 85.4%. It is especially appreciated because it is highly interpretable and simple. Although it did not perform better than the more complex models, it provided meaningful insights into the contribution of features using its coefficients. This model is most suited for applications involving clear decision-making.

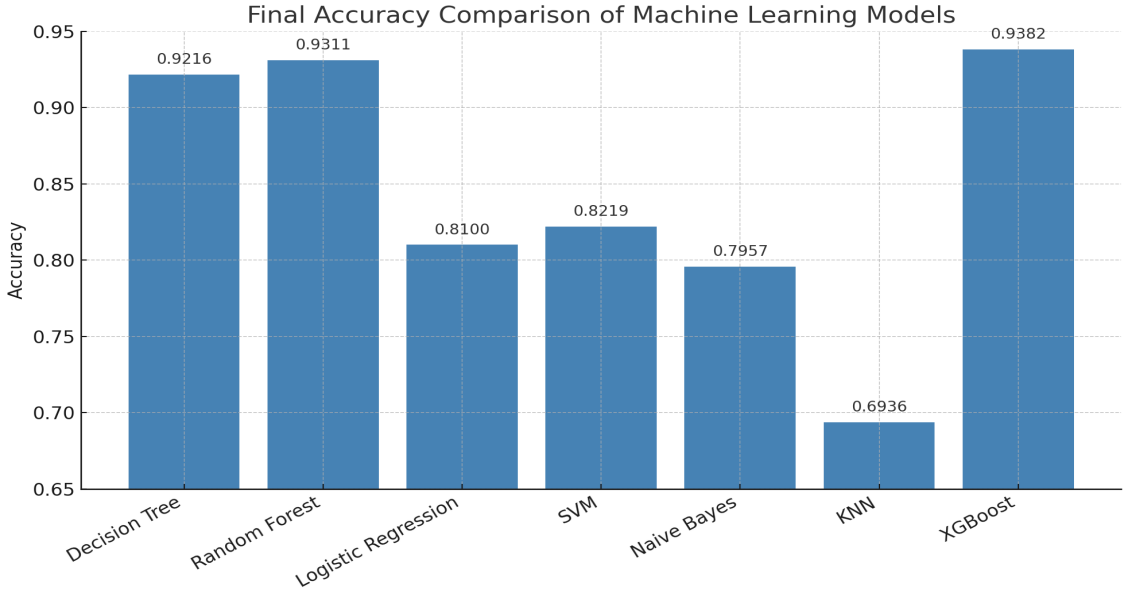

Figure 4.1: Comparison Bar plot for different Boosting Models

4.4 Results on different Boosting Models

The bar chart shows a comparative accuracy comparison of six boosting models employed in Parkinson's Disease detection. Of these, Stochastic Gradient Boosting had the best accuracy of 94.30%, which was followed by CatBoost (94.06%) and XGBoost (93.82%), reflecting their ability to generalize well and perform well with complicated medical data. Gradient Boosting and LightGBM also compared competitively at 93.35% and 92.40%, respectively, whereas AdaBoost yielded a modest but acceptable accuracy of 89.31%.

These findings attest the strength of sophistic boosting algorithms, especially those that include stochasticity or categorical optimization, to make dependable early PD prediction.

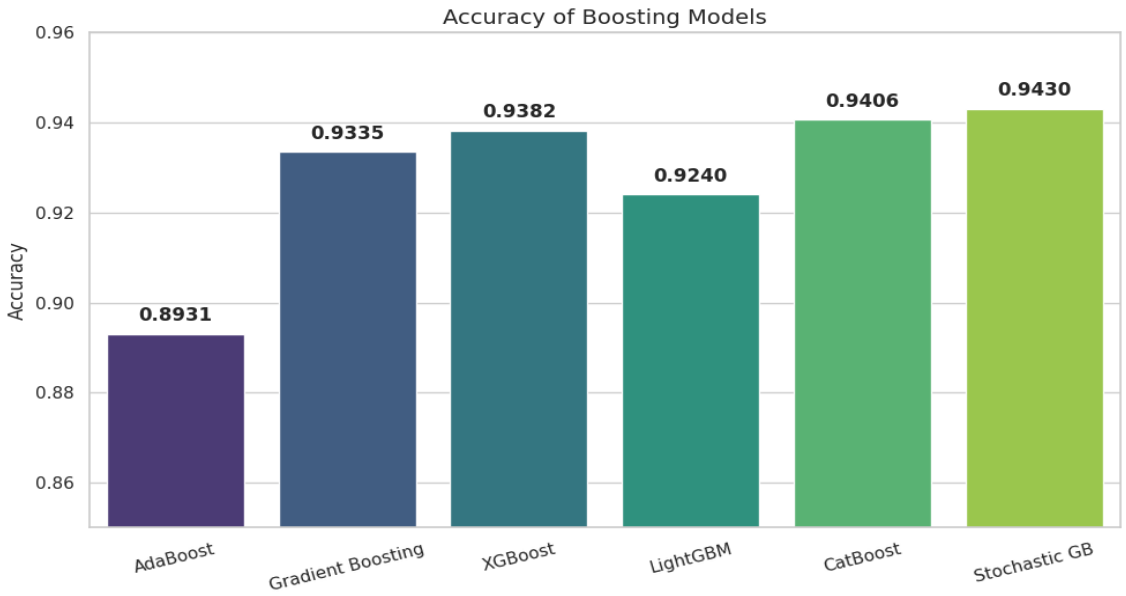

Figure 4.2: Comparison Bar plot for different Boosting Models

4.5 Probabilistic and Distance-Based Models

Naive Bayes performed modestly with an accuracy of 79.6% and F1-score of 83.6%. Although it performed well on the Parkinson's class, its feature independence assumption likely put a cap on its performance given voice features' intertwined nature. Naive Bayes is still a quick, low-memory classifier that can be used for early diagnostic stages or even embedded systems. K-Nearest Neighbors (KNN) was one of the weakest models in this experiment, with accuracy of 69.3%, F1-score of 75.0%, and recall of 72.4%. Its vulnerability to the curse of dimensionality and the computationally expensive prediction time were major limitations. That being said, the model's simplicity and performance in small, nicely clustered data sets are still its advantages. The experiment involving varying values of k reflected minor improvements in performance, but not to the level where it can rival ensemble or DL models.

4.6 Summary on different Machine Learning Models

In brief, XGBoost performed better than all the remaining models in almost all the metrics, validating its appropriateness for this classification problem. Random Forest and CNN were close competitors as well. Logistic Regression and Naive Bayes, being simpler models, though less accurate, were nonetheless useful because they were interpretable and efficient. The results highlight the significance of selecting the most appropriate model considering the trade-off between accuracy, explainability, and computational expense. Ensemble and deep learning techniques show the most promise for near-term use in actual clinical practices.

Table 4.1: Performance Comparison of ML Models for Parkinson's Disease Detection

Metric	Decision Tree	Random Forest	Logistic Regression	SVM	Naive Bayes	KNN	XGBoost
Accuracy	0.9216	0.9311	0.8100	0.8219	0.7957	0.6936	0.9382
F1-Score	0.9397	0.9468	0.8540	0.8658	0.8365	0.7505	0.9520
Recall	0.9590	0.9627	0.8731	0.9030	0.8209	0.7239	0.9627
Precision	0.9211	0.9314	0.8357	0.8316	0.8527	0.7791	0.9416
R2-Score	0.6612	0.7022	0.1786	0.2300	0.1170	-0.3245	0.7331

4.7 Summary of different Boosting Models

Table 4.2: Comparison of Boosting Models Across Evaluation Metrics

Model	Accuracy	F1-Score	R^2 Score	Recall	Precision
AdaBoost	0.8931	0.9208	0.5400	0.9104	0.9208
Gradient Boosting	0.9335	0.9397	0.7125	0.9590	0.9379
XGBoost	0.9382	0.9520	0.7331	0.9627	0.9416
LightGBM	0.9240	0.9403	0.6714	0.9403	0.9403
CatBoost	0.9406	0.9500	0.7430	0.9600	0.9500
Stochastic GB	0.9430	0.9600	0.7536	0.9701	0.9420

The table gives an overall picture of some of the boosting models tested for Parkinson's Disease detection. Out of them all, Stochastic Gradient Boosting showed the best accuracy (94.30%), followed by CatBoost (94.06%) and XGBoost (93.82%), which is indicative of their excellent predictive performance. These models also fared equally well on other measures such as F1-Score, Recall, and Precision. Conversely, AdaBoost possessed the worst R^2 Score and performance overall, reflecting its relative lack of efficiency in this medical classification problem. Overall, the findings justify that sophisticated boosting methods are extremely beneficial for sure and accurate prediction of early-stage PD.

Chapter 5

CONCLUSION

This dissertation has given a thorough comparative study of traditional machine learning models for Parkinson's Disease detection based on biomedical voice features. The key objective of this study was to assess and compare the performance of various supervised learning models applied to a structured voice dataset including features like jitter, shimmer, and harmonic-to-noise ratios. These parameters, obtained from sustained phonation recordings, are reported to detect very slight irregularities in speech patterns that are typically seen in Parkinson's Disease.

The models tested in the present study were Decision Tree, Random Forest, Logistic Regression, Support Vector Machine (SVM), Naive Bayes, K-Nearest Neighbors (KNN), and XGBoost. All these classifiers were trained and tested in the same preprocessing settings, and their performances were measured by main metrics such as accuracy, precision, recall, and F1-score. XGBoost was the most efficient model among them that demonstrated the highest overall accuracy (93.82%) and performed the best on all performance metrics. Its gradient boosting process, along with regularization and tree pruning, enabled it to generalize well and learn intricate patterns, thus making it a very consistent option for diagnostic systems in the real world.

Random Forest also performed very well with an accuracy of 93.11%. Being an ensemble method involving numerous decision trees, it minimized overfitting but retained the benefits of tree-based decision-making. Its feature importance ranking also boosted interpretability and shed light on the relative significance of diverse vocal parameters in terms of predicting Parkinson's Disease. The Decision Tree model, as less complex, also held up with a performance of 92.16%, being useful for interpretable and fast diagnostics where transparency counts.

Under the traditional models category, Logistic Regression and Support Vector Machine (SVM) gave balanced and moderate performance. SVM, with the RBF kernel, had 82.19% accuracy, indicating its power in detecting non-linear class borders. Logistic Regression, being linear in nature, had 81.00% accuracy and was a strong baseline, providing the benefits of simplicity, computational speed, and interpretability.

Naive Bayes and K-Nearest Neighbors (KNN) were behind the other models when it came to performance, with their respective accuracies of 79.57% and 69.36%. Naive Bayes, on account of its assumption of independence of features, was less appropriate for the relatedness of voice features, though it still had decent precision as well as recall values. KNN suffered especially because it was feature scaling-sensitive and cursed by the high dimensionality, which made it hard to provide accurate predictions within a high-dimensional space. However, both models were valuable for providing insights within baseline comparisons and are still applicable for small-scale or computationally restricted environments.

In conclusion, this research finds that ensemble techniques, particularly XGBoost and Random Forest, are most appropriate for the classification task of Parkinson's Disease diagnosis based on voice characteristics. Their capability to handle complex interactions, avoid overfitting, and provide robust high performance makes them great options for clinical decision support systems. At the same time, less complex models such as Decision Tree and Logistic Regression also possess high value because they are easy to interpret and can be deployed quickly. Future research can try to incorporate multiple data modalities, enhance feature engineering, and test the models on bigger and more varied patient datasets to further improve clinical utility and generalizability.

The conventional machine learning methods, this dissertation also performed an extensive comparison of several advanced boosting algorithms to further improve diagnostic accuracy in the detection of Parkinson's Disease. Boosting models like AdaBoost, Gradient Boosting, LightGBM, CatBoost, and Stochastic Gradient Boosting were implemented and compared for evaluating their ability in modeling complex patterns in the biomedical data. Of these, Stochastic Gradient Boosting proved to be the best performer with the highest classification accuracy (94.30%) and best recall, which is most critical to reduce lost diagnoses in medical usage. CatBoost and XGBoost also performed very uniformly well across all evaluation measures, proving themselves to be robust, scalable, and flexible to learning from structured medical data. These boosting methods successfully circumvented the limitations of individual weak learners by iteratively refining prediction errors, allowing more generalization. The outcomes verify that contemporary boosting algorithms do not only compete with conventional models but, in most instances, outperform them in both predictive ability and reliability. Their incorporation into actual healthcare systems is highly promising for early and correct screening of Parkinson's Disease, particularly for mobile or limited-resource settings. Future research should investigate their use in longitudinal research and real-time diagnostic tools to realize maximum clinical benefit.

5.1 FUTURE SCOPE

While this work has presented meaningful insight into comparative performance of traditional machine learning models for the detection of Parkinson's Disease, it also presents several avenues of future research beyond model performance. One of the directions under exploration includes the use of real-time voice analysis using edge computing or mobile phones to allow monitoring on the go for patients. As wearable and voice-controlled technologies increase, applying these models to smart devices may aid in ongoing monitoring of vocal impairment, opening doors for early treatment beyond clinics. Also, future research could address adaptive and user-personalized machine learning models. Such models would adapt to one's baseline voice features and learn from long-term patient information, thus enhancing detection performance over time as the model adapts to the user. The other critical domain is federated learning for privacy-preserving diagnostics. Because medical information is highly sensitive, it is imperative to build decentralized learning systems that train locally on patient devices while ensuring privacy, making the system secure and scalable. Additionally, extending the framework to incorporate cross-domain data sources, including medical images, genetic information, and electronic health records, could result in more robust prediction models. The resulting hybrid systems could provide multi-view analyses, making the diagnosis more robust and granting deeper knowledge of the disease. Lastly, the future research would need to focus on building collaborative networks with medical institutions so that larger and more diversified

datasets are accessible and clinical trials can be undertaken to prove the practicality of the models being proposed. These collaborations could help greatly in bringing these machine learning developments from the laboratory to actual healthcare applications.

5.2 LIMITATIONS

In spite of the encouraging outcomes yielded in this investigation, there are a number of limitations that need to be noted. First, the dataset utilized was comparatively small in magnitude and extent, incorporating voice samples of a narrow population group. This might affect the external validity of the findings towards broader and more diverse groups of populations. Further research is needed to incorporate larger, more diverse datasets to enhance model resilience. Second, all models in this study used only vocal biomarkers for prediction. Though voice features are descriptive, Parkinson's Disease manifests across several modalities such as motor symptoms, gait disturbance, and handwriting patterns. Single-modality reliance limits the system's diagnostic capability and can result in false negatives or positives in difficult-to-classify cases. One such limitation is the lack of real-world model validation and deployment within clinical environments. Models worked well within an experimental laboratory setup, but their usability in real-world situations is yet to be validated. Real-world consideration of elements like background noise, variability in recording devices, and voice-specific features of patients might impact prediction accuracy. Finally, this research did not assess interpretability of the models clinically. Although there are models that provide high accuracy, they are still black boxes to clinicians. Future research should investigate explainable AI methodologies to improve transparency and trust in automated PD diagnosis.

Chapter 6

List of Publication

1. Anuraag Raj Narayan, Virender Ranga, *Comparative Study of Different Machine Learning Models for Parkinson's Disease Detection*, submitted to *3rd International Conference on Self Sustainable Artificial Intelligence Systems ICSSAS*, 2025. **(Paper Accepted)**

2. Anuraag Raj Narayan, Virender Ranga, *A Comparative study on various Boosting Models used in Parkinson's Disease Detection*, submitted at *8th International Conference on Computing Methodologies* ICCMC 2025. **(Paper Accepted)**

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Acceptance of conference 1: ICSSAS 2025

DTU Delhi Technological University

23/ITY/05 ANURAAG RAJ NARAYAN <anuraagrajnarayan_23ity05@dtu.ac.in>

ICSSAS 2025 Acceptance Letter
1 message

ICSSAS Contact <icssat.contact@gmail.com> Mon, May 19, 2025 at 5:04 PM
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Dear Author,

Hearty Congratulations!

Your paper has been accepted and recommended for publication at the 3rd International Conference on Self Sustainable Artificial Intelligence Systems – ICSSAS 2025, organized by M. P. Nachimuthu M. Jaganathan Engineering College, Chennimalai, Erode, India. The conference is scheduled to take place from June 11th to June 13th, 2025.

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In recent years, there has been a growing emphasis on the integration of Artificial Intelligence (AI) technologies across various domains, a trend further accelerated by the challenges posed by the global pandemic. This has prompted industrial stakeholders to reassess their approaches to sustainable operations, particularly in areas such as smart cities, smart transportation, smart industries, and healthcare. Leveraging computer-aided techniques, predictive methods, and expert systems has become increasingly vital for researchers and practitioners in navigating the complexities of these real-time applications.

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M.P.Nachimuthu M.Jaganathan Engineering College, Chennimalai, Erode is one among the best self-financing engineering colleges. The main thrust is given to discipline, quality education and also in moulding young minds to become fully competent engineers. The main scope of this institution is to provide education for the rural students and economically deprived students as per the ardent desire of the Founder Correspondent Thiru.J.Sudhanandhen. Free education is offered to the meritorious students and also, fees concession is provided every year for the under privileged students. The college has full-fledged infrastructure facilities, i.e., buildings, laboratories, hostels, sports etc. and provides a better learning environment to the students through the dedicated, efficient and well qualified faculty. Also, the institution offers much needed academic exposure to the students along with communication skills and personality development programmes. The vibrant and active Training and Placement Cell provides continuous training to the students and better placements in various Multi -National Companies. All efforts are pursued assiduously to build the Institution as a Model One.

Contact

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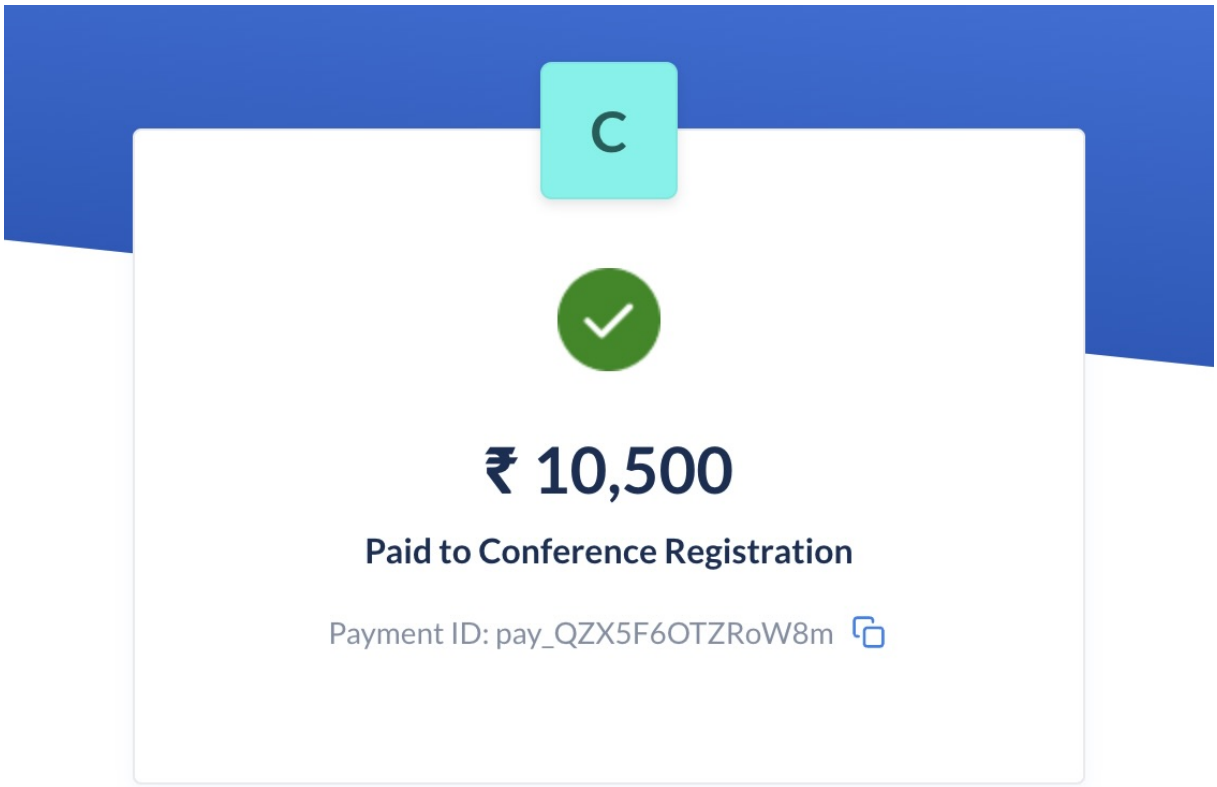

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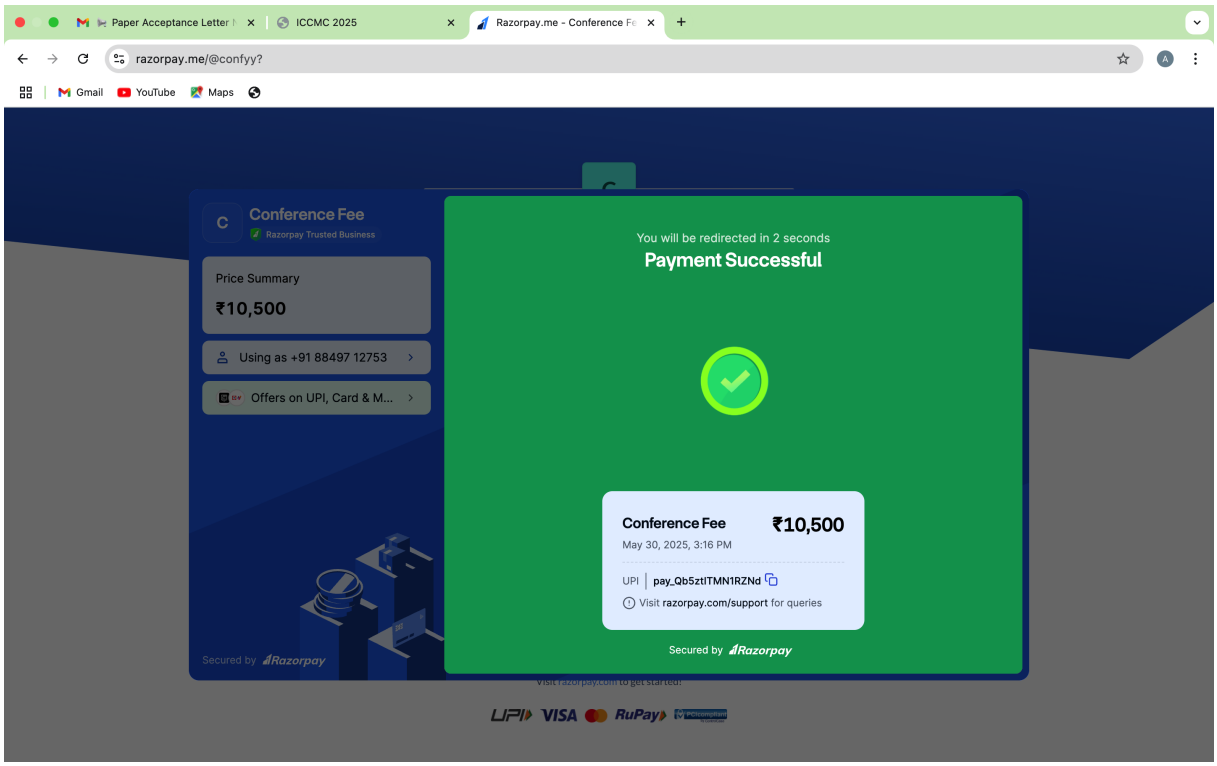

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