B.Tech. BCSE497J - Project-I

ANALYSIS OF SYMPTOM FOR PREDICTION OF PARKINSON'S DISEASE IN A MACHINE LEARNING FRAMEWORK

Submitted in partial fulfillment of the requirements for the degree of

Bachelor of Technology

in

Programme

by

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DECLARATION

We hereby declare that the project entitled Analysis of Symptom For Prediction of Parkinson’s in Machine Learning Framework submitted by us, for the award of the degree of *Bachelor of Technology in Computer Science and Engineering* to VIT is a record of bonafide work carried out by me under the supervision of Dr.Surendar M

We further declare that the work reported in this project has not been submitted and will not be submitted, either in part or in full, for the award of any other degree or diploma in this institute or any other institute or university.

Place : Vellore

Date :13/11/24

Signature of the Candidate

CERTIFICATE

This is to certify that the project entitled Analysis of Symptom For Prediction of Parkinson’s in Machine Learning Framework submitted by Kalwa Jayanth(21BCE3142), Aaryan Bansal(21BDS0011), Maheesh Dineshbhai Purohit(21BDS0027), **School of Computer Science and Engineering**, VIT, for the award of the degree of *Bachelor of Technology in Computer Science and Engineering*, is a record of bonafide work carried out by him / her under my supervision during Fall Semester 2024-2025, as per the VIT code of academic and research ethics.

The contents of this report have not been submitted and will not be submitted either in part or in full, for the award of any other degree or diploma in this institute or any other institute or university. The project fulfills the requirements and regulations of the University and in my opinion meets the necessary standards for submission.

Place : Vellore
Date :13/11/24

Signature of the Guide

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SCOPE

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Thank you all for your contributions and support.

Name of the Candidate

LIST OF ABBREVIATIONS

PD	Parkinson's Disease
PWP	People with Parkinson's
SVM	Support Vector Machine
ANN	Artificial Neural Network
RPDE	Recurrence Period Density Entropy
DFA	Detrended Fluctuation Analysis
HNR	Harmonics-to-Noise Ratio
SMOTE	Synthetic Minority Over-sampling Technique
XAI	Explainable Artificial Intelligence
SHAP	SHapley Additive exPlanations
LIME	Local Interpretable Model-agnostic Explanations
PPE	Pitch Period Entropy
EDA	Exploratory Data Analysis
RFE	Recursive Feature Elimination

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ABSTRACT

Parkinson’s disease (PD) is a progressive neurodegenerative disorder characterized by motor and speech impairments, affecting over 10 million individuals worldwide. Dysphonia, or vocal impairment, is one of the earliest and most prevalent symptoms of PD, making it a valuable biomarker for telemonitoring. However, class imbalance in voice-based PD datasets, with significantly fewer healthy samples, poses challenges for accurate detection. Machine learning models can improve PD classification, yet imbalanced datasets and feature redundancy often reduce model sensitivity toward the minority class, impacting diagnostic reliability.

This study develops a robust machine learning framework addressing these challenges by implementing the Synthetic Minority Over-sampling Technique (SMOTE) to balance the dataset, creating synthetic samples for the underrepresented class. Through feature analysis and outlier removal, redundant and noisy features were filtered, enhancing model accuracy and reducing bias. Support Vector Machine (SVM), Random Forest, Stacking Ensemble, and Artificial Neural Network (ANN) models were tested on SMOTE-enhanced data, with performance evaluated through accuracy, recall, and F1-scores.

Results demonstrated significant improvements in the sensitivity of SVM, Random Forest, and Stacking models, showing high accuracy and balanced predictions for both PD and healthy classes. ANN, while promising, exhibited limitations due to dataset size, indicating that traditional models may be more effective with small datasets. This framework provides a scalable approach for PD telemonitoring, supporting early diagnosis and continuous tracking with high interpretability and reliability for clinical application.

Keywords: Parkinson’s Disease, Telemedicine, Machine Learning, Support Vector Machine (SVM), Random Forest, Data Imbalance, Synthetic Minority Over-sampling Technique (SMOTE), Feature Selection, Outlier Removal, Model Sensitivity, Classification Accuracy, Telemonitoring, Clinical Applications.

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1. INTRODUCTION

1.1 Background

Parkinson's disease (PD) is a chronic, progressive neurodegenerative disorder that primarily impacts motor functions, manifesting symptoms such as tremors, rigidity, and bradykinesia, which collectively impair movement and reduce patient quality of life. Affecting more than 10 million people worldwide, PD prevalence continues to increase, particularly in aging populations, with approximately 1% of individuals over 60 and up to 5% of those over 85 affected by this condition. Early intervention and treatment are essential for improving patient outcomes; however, conventional diagnostic techniques often fail to detect PD in its earliest stages, as initial symptoms can be subtle and vary widely between individuals. This shortcoming underscores an urgent need for diagnostic tools that are both precise and capable of early detection.

Research has shown that vocal impairments are a prevalent and early symptom in up to 90% of people with Parkinson's Disease (PWP), offering a potential non-invasive biomarker for PD detection. Dysphonia, or voice disturbance, manifests as reduced loudness, vocal roughness, and breathiness, alongside other irregularities such as reduced harmonic spectrum energy and increased vocal tremor. These vocal impairments make dysphonia measurements an appealing metric for telemonitoring PD progression remotely, reducing the burden of frequent clinical visits and enabling consistent patient monitoring from home. Widening access to the Internet and improvements in telecommunication systems further support the feasibility of remote monitoring for PD patients, with significant potential for reducing the inconvenience and costs associated with in-person assessments.

Several methods have been developed to assess vocal symptoms in PWP. Traditional vocal analysis focuses on metrics like jitter (frequency variation) and shimmer (amplitude variation), as well as harmonics-to-noise ratios (HNR) that reflect the relative noisiness of voice. However, recent studies suggest that non-standard measures, particularly those derived from nonlinear dynamical systems and stochastic analysis, may provide more robust detection capabilities for PD-specific dysphonia. For instance, measures such as Recurrence Period Density Entropy (RPDE) and Detrended Fluctuation Analysis (DFA) quantify the complexity and self-similarity of voice signals, capturing irregularities in vocal fold vibration that are often associated with PD.

One of the primary challenges in developing telemonitoring tools for PD is achieving high reliability in diverse acoustic environments, as uncontrolled variables like background noise or patient condition can introduce significant variability into voice measurements. Traditional measures such as absolute sound pressure level are often impractical for telemonitoring, as they require calibrated equipment, which is not feasible in home settings. To address these issues, recent research has introduced new methods like Pitch Period Entropy (PPE), a robust measure that distinguishes PD-related dysphonia from healthy vocal variations by removing smooth, natural pitch modulations and focusing on irregular pitch fluctuations specific to PD.

PPE is highly robust to background noise and variations in patient voice characteristics, making it suitable for remote monitoring applications.

Given the diversity of available measures, one effective approach for discriminating PD from healthy controls is to combine several vocal features into a multidimensional feature vector and employ machine learning techniques such as Support Vector Machine (SVM) classification. Studies using SVM have demonstrated classification accuracies as high as 91.4% when combining features like HNR, RPDE, DFA, and PPE, suggesting that SVM is a powerful tool for PD detection in telemonitoring applications. Importantly, this approach also supports feature selection to ensure the model remains interpretable and clinically relevant, allowing healthcare providers to understand the most predictive features for PD, which is crucial for building trust in telemedicine applications.

In sum, the integration of advanced dysphonia measures and machine learning models offers a promising pathway toward more reliable, scalable telemonitoring solutions for PD. By leveraging techniques like SVM with robust feature sets that include both traditional and non-standard measures, researchers are developing tools that can track disease progression remotely, thereby enhancing patient care and reducing the logistical burden on both patients and healthcare systems.

1.2 Motivation

The motivation for this study stems from the need for accurate, scalable, and cost-effective diagnostic tools to monitor Parkinson’s Disease (PD), particularly in light of its increasing prevalence in aging populations. As a progressive neurodegenerative disorder, PD has no cure, and while treatments are available, their effectiveness largely depends on early intervention to manage symptoms and slow disease progression. Traditional PD diagnosis relies on clinical assessments of motor symptoms, which often develop gradually and can vary widely among individuals. This variability makes early diagnosis challenging, resulting in delayed interventions that can lead to worsened patient outcomes.

Voice analysis has emerged as a promising method for PD detection due to the high prevalence of vocal impairments in people with Parkinson’s Disease (PWP). Studies indicate that up to 90% of PWP experience dysphonia, often as one of the earliest indicators of the disease. Vocal biomarkers, such as jitter, shimmer, and harmonics-to-noise ratio (HNR), can be assessed remotely, making them ideal for telemonitoring applications. Telemedicine has grown rapidly with advancements in digital technology and Internet access, offering the potential to alleviate the burden of frequent clinic visits for PD patients by providing continuous monitoring in home environments. However, for telemonitoring to be viable, robust and reliable measurement tools are essential, as remote settings introduce variability in acoustic environments that can impact the accuracy of voice measurements.

Machine learning techniques, particularly classification models like Support Vector Machine (SVM), have shown promise in differentiating PD-related vocal symptoms from those of healthy individuals. However, challenges remain in adapting these tools for clinical use. One of the primary issues is data imbalance, as datasets typically contain far fewer healthy samples compared to PD samples, which can bias models toward the majority class, reducing their ability to accurately identify early cases of PD. Additionally, feature redundancy within vocal data, where certain measures may overlap in the information they provide, can lead to overfitting and reduce model generalization in real-world applications. Addressing these issues is critical for creating models that not only perform well in controlled environments but are also effective in diverse, real-world settings.

To enhance the accuracy and interpretability of PD telemonitoring systems, this study employs the Synthetic Minority Over-sampling Technique (SMOTE) to balance the dataset and mitigate class bias, improving the model's sensitivity to the underrepresented healthy samples. Feature selection methods are used to minimize redundancy, allowing the model to focus on the most relevant vocal biomarkers of PD. By incorporating these advanced techniques, the study seeks to develop a framework that is both accurate and interpretable, offering a tool that healthcare providers can trust for remote PD monitoring.

Furthermore, explainable AI (XAI) methods are integrated into the framework to enhance interpretability. In clinical settings, interpretability is essential, as healthcare providers must understand the model's decision-making process to ensure it aligns with clinical knowledge and builds confidence in AI-driven assessments. This interpretability also allows clinicians to identify the most influential features in the model's predictions, such as specific vocal markers, and apply these insights to inform diagnostic and treatment strategies for PD. Ultimately, this project is driven by the potential to bridge existing gaps in PD diagnostics by developing a reliable, interpretable, and scalable telemonitoring solution that can empower healthcare providers to deliver earlier, more effective care.

1.3 Scope of the Project

This project aims to develop a robust machine learning framework specifically designed to enhance the telemonitoring of Parkinson's Disease (PD) through early detection of vocal biomarkers, addressing critical challenges in data imbalance, feature redundancy, and model interpretability. Given the increasing prevalence of PD and the necessity for early intervention, this framework seeks to enable remote monitoring solutions that are both effective and scalable in real-world clinical settings.

The scope of this project encompasses several key stages:

1. **Data Collection and Preprocessing**: The project utilizes a dataset of vocal recordings from individuals with and without PD, focusing on acoustic features known to be sensitive to dysphonia—a common early symptom of PD. These features include traditional vocal metrics such as jitter and shimmer, alongside advanced nonlinear and stochastic measures like Recurrence Period Density Entropy (RPDE)

and Detrended Fluctuation Analysis (DFA), which have shown promise in previous studies for distinguishing PD-specific dysphonia. Initial preprocessing will involve outlier detection and removal to minimize the impact of noise and extreme values, followed by data normalization to ensure consistent input for the machine learning models.

2. **Data Balancing Using SMOTE**: A significant focus of this study is addressing the class imbalance typically found in PD datasets, where healthy samples are often underrepresented. To mitigate this, the Synthetic Minority Over-sampling Technique (SMOTE) will be applied, generating synthetic samples for the minority class to ensure balanced representation during training. This step is critical for improving the model's sensitivity to early-stage PD cases, as it mitigates the tendency of classifiers to favor the majority class.
3. **Feature Selection and Model Training**: The project employs feature selection techniques to identify and retain only the most relevant vocal features, reducing feature redundancy and preventing overfitting. Selected features will then be used to train multiple machine learning models, including Support Vector Machine (SVM), Random Forest, Stacking Ensemble, and Artificial Neural Network (ANN). Each model's performance will be evaluated to determine its suitability for PD classification, with a particular focus on how well it generalizes to unseen data. The SVM model, given its demonstrated success in prior research, will serve as a primary model, while ensemble methods and neural networks provide comparative insights into different modeling approaches.
4. **Integration of Explainable AI (XAI)**: To ensure that the framework's outputs are interpretable by healthcare providers, explainable AI techniques will be integrated. This aspect is crucial for building trust in the model's predictions and facilitating its adoption in clinical environments. XAI will allow the framework to highlight the most predictive vocal features for PD, enabling clinicians to better understand the rationale behind each classification and make informed decisions based on model insights.
5. **Evaluation and Validation**: The framework will be evaluated in both simulated and real-world clinical environments to assess its effectiveness and generalizability. Performance metrics such as accuracy, precision, recall, and F1-score will be used to quantify the model's accuracy and reliability in detecting PD. Additionally, bootstrapping techniques will validate the model's robustness across diverse subsets, ensuring consistency and resilience in real-world applications. Ethical considerations, including data privacy, transparency in AI-driven decisions, and patient consent, will also be addressed to meet standards for healthcare deployment.
6. **Potential for Real-World Application**: The ultimate goal of this project is to create a reliable, interpretable, and scalable machine learning tool for the telemonitoring of PD. By focusing on model interpretability and real-world testing, this project aims to bridge the gap between laboratory models and clinically viable tools, supporting healthcare providers in delivering early, personalized, and efficient care to PD patients through remote monitoring.

2. PROJECT DESCRIPTION AND GOALS

2.1 Literature Review

The application of machine learning in diagnosing and predicting Parkinson's Disease (PD) has gained momentum in recent years, offering the potential for earlier detection and improved monitoring through non-invasive methods. Traditional diagnostic methods for PD rely primarily on clinical observation of motor symptoms such as tremors, rigidity, and bradykinesia. However, these symptoms often emerge in the later stages of the disease, making early diagnosis challenging and limiting the potential for timely intervention. Machine learning presents a promising approach to detect PD at earlier stages by identifying subtle changes in non-motor symptoms, particularly vocal biomarkers, which can reflect early neurological changes that may go unnoticed in standard clinical assessments.

Use of Voice Data in PD Detection

Several studies have demonstrated the effectiveness of voice data as a biomarker for early PD detection. One foundational study by Little et al. (2008) utilized pitch period entropy alongside Support Vector Machines (SVM) to analyze vocal features and distinguish PD patients from healthy controls, achieving a classification accuracy of over 90%. This research underscored the potential of vocal biomarkers in accurately identifying early PD symptoms, paving the way for further research into machine learning-based PD diagnostics.

In parallel, Ho et al. (1998) explored the relationship between speech impairment and PD, confirming that vocal changes, such as alterations in pitch and amplitude, are significant indicators of early-stage PD. This study contributed to establishing a basis for using voice as a diagnostic tool, as it provided a strong correlation between PD and vocal impairments, suggesting that non-motor symptoms could play a critical role in early diagnosis.

Advancements in Machine Learning Techniques for PD

More recent studies have applied advanced machine learning techniques, such as deep learning and ensemble methods, to improve the accuracy of PD detection models. These techniques allow for more complex pattern recognition in vocal data, accommodating nonlinear relationships within the dataset. For instance, a study by Tsanas et al. (2014) incorporated nonlinear measures like Recurrence Period Density Entropy (RPDE) and Detrended Fluctuation Analysis (DFA) to capture complex vocal patterns associated with PD. These features have proven effective in enhancing model accuracy, with some studies reporting improvements in sensitivity to early-stage PD symptoms.

Ensemble models, combining multiple classifiers to achieve robust predictions, have also shown promise in PD detection. For example, Random Forest and Stacking methods have been evaluated for their ability to leverage diverse model strengths, leading to increased classification accuracy and stability in predictions. These models are particularly beneficial for their flexibility and robustness in handling variations in feature distribution, which is common in biomedical data.

Challenges in PD Machine Learning Models

Despite these advancements, significant challenges persist in the field. One major issue is data imbalance, where datasets contain more instances of PD patients than healthy controls. This imbalance can bias models, leading them to favor the majority class and reducing their effectiveness in detecting early PD cases. Techniques like the Synthetic Minority Over-sampling Technique (SMOTE) have been proposed to address this issue by generating synthetic samples for the minority class, thereby enhancing model sensitivity to underrepresented data.

Another key challenge is feature redundancy. Biomedical data often exhibit high correlations among features, which can lead to overfitting in machine learning models. High-dimensional feature spaces, while rich in information, can cause models to perform well on training data but poorly on new, unseen data. Feature selection and dimensionality reduction techniques, such as correlation analysis and exploratory data analysis (EDA), have been implemented in some studies to address this issue. By eliminating redundant features, these methods enhance model generalization and reduce overfitting, supporting more reliable predictions.

Gaps in Existing Literature

This literature review reveals ongoing gaps in the development of reliable and interpretable machine learning models for PD detection. The need for models that handle imbalanced datasets effectively, maintain transparency for clinical interpretability, and generalize well to new data remains evident. Moreover, while advanced machine learning techniques have shown promise, their complexity can often hinder interpretability, which is crucial in a healthcare setting where clinicians require clear, understandable outputs to inform patient care decisions. Future research should aim to refine models that balance accuracy with interpretability and adaptability to real-world clinical conditions, ultimately supporting the clinical utility of machine learning in early PD diagnosis.

2.2 Research Gap

Despite the advancements in using vocal biomarkers for Parkinson's Disease (PD) detection and telemonitoring, several research gaps remain that hinder the development of an accurate, scalable, and interpretable diagnostic tool. Addressing these gaps is crucial to enhance telemonitoring systems' reliability and applicability in real-world clinical settings. The specific gaps identified from recent literature are as follows:

1. **Limited Integration of Nonlinear and Traditional Features**: While studies have demonstrated the effectiveness of both traditional vocal features (e.g., jitter, shimmer, HNR) and nonlinear measures (e.g., RPDE, DFA) individually, there is limited

research on combining these features comprehensively to optimize accuracy and robustness in PD detection.

2. **Challenges in Real-World Acoustic Environments**: Existing models often rely on voice recordings collected in controlled environments, which reduces noise and variability. However, the real-world applicability of these models in diverse acoustic environments—such as patients' homes—remains largely unexplored, affecting the feasibility of telemonitoring in uncontrolled conditions.
3. **Overfitting Due to Feature Redundancy**: Many studies utilize a broad set of vocal biomarkers without adequately addressing feature redundancy. Excessive feature overlap can lead to overfitting, particularly when models are trained on smaller datasets, reducing generalization capacity in clinical applications.
4. **Limited Model Interpretability in Clinical Settings**: Although machine learning models like SVM and Random Forest show high accuracy for PD detection, the black-box nature of these models complicates their interpretability. Clinicians require insights into which features are most indicative of PD to trust and act upon model outputs effectively.
5. **Underutilization of Explainable AI (XAI)**: While some studies mention interpretability, few integrate explainable AI methods to provide transparent predictions, which is essential for clinical acceptance and integration of AI models into healthcare.
6. **Reliance on Imbalanced Datasets**: Many models are trained on imbalanced datasets, with a high prevalence of PD cases and fewer healthy samples, which leads to model bias toward the majority class. This imbalance reduces the accuracy of early-stage PD detection and affects the sensitivity of the model to detect healthy control samples.
7. **Lack of Longitudinal Validation**: Most studies provide cross-sectional analyses without evaluating model performance over time. The absence of longitudinal validation limits insights into the model's reliability for tracking PD progression, which is critical for effective telemonitoring.

These gaps underscore the need for an optimized, interpretable, and clinically viable framework that can address data imbalance, improve feature relevance, and ensure reliable performance in diverse real-world settings.

2.3 Objectives

The primary objective of this project is to develop a comprehensive machine learning-based framework for early PD detection through vocal biomarker analysis, addressing data imbalance, feature redundancy, and model interpretability. This framework will leverage SMOTE for data balancing, SVM and ensemble models for classification, and explainable AI for clinical interpretability, ultimately aiming to enhance the scalability and reliability of telemonitoring for PD.

SMART Goals:

1. **Comprehensive Vocal Data Collection and Preprocessing**
    a. **Specific**: The goal is to compile a high-quality, comprehensive dataset of vocal features that capture both traditional and nonlinear acoustic measures (e.g., pitch, jitter, MFCCs). This will involve data cleansing, normalization, and addressing any feature redundancy to optimize dataset utility.
    b. **Measurable**: The aim is to produce a final dataset with at least **200 samples** evenly divided between PD patients and healthy controls, achieved by using SMOTE to balance classes after collection.
    c. **Achievable**:
        i. **Data Sourcing**: Utilize public datasets (such as the Parkinson's Telemonitoring Voice Dataset) or institutional resources.
        ii. **Preprocessing Techniques**:
            1. **Outlier Removal**: Identify and remove outliers that may distort analysis.
            2. **Normalization**: Apply scaling techniques like min-max or z-score normalization to ensure consistency across features.
            3. **Feature Redundancy Reduction**: Conduct correlation analysis and Principal Component Analysis (PCA) to reduce any redundancy and focus on meaningful features.
    d. **Relevant**: High-quality data is critical for creating a model that can reliably distinguish between PD and non-PD samples, enhancing the model's accuracy and reliability.
    e. **Time-bound**: Complete data collection and preprocessing tasks within **3 weeks**.
2. **Implementation of SMOTE for Data Balancing**
    a. **Specific**: Implement the Synthetic Minority Over-sampling Technique (SMOTE) to create a balanced dataset with an equal number of samples for PD and healthy individuals. This will help reduce the risk of bias in model training.
    b. **Measurable**: Achieve a **50:50 balance** between PD and healthy samples, ensuring that the model isn't biased toward the majority class and can better identify PD in diverse cases.
    c. **Achievable**:
        i. **Tools**: Use the `imblearn` library in Python, which contains a robust SMOTE implementation compatible with most machine learning libraries.
        ii. **Verification**: After SMOTE application, verify class balance by analyzing distribution metrics and confirming an equal number of samples in each class.

   d. **Relevant**: Class balancing is essential to improve model performance, particularly for detecting PD cases at various stages and avoiding majority-class bias.
   e. **Time-bound**: Complete the SMOTE balancing process within **1 week**.

3. **Model Development Using SVM and Ensemble Techniques**
   a. **Specific**: Develop predictive models using **Support Vector Machine (SVM)** and **Ensemble techniques** (e.g., Random Forest, Stacking Ensemble) to maximize accuracy and generalizability in PD classification.
   b. **Measurable**: Target **90% accuracy** and sensitivity/specificity of at least **85%** to ensure the model meets clinical relevance standards.
   c. **Achievable**:
      i. **Model Development**: Use libraries like `scikit-learn` and `XGBoost` for training, and leverage cross-validation and hyperparameter tuning for optimization.
      ii. **Hyperparameter Tuning**: Conduct a grid search or random search on model parameters to find the best-performing configurations for each algorithm.
      iii. **Ensemble Approach**: Consider stacking multiple models (e.g., SVM with Random Forest) to enhance predictive strength by combining their unique capabilities.
   d. **Relevant**: High-performing models lay the groundwork for creating a tool that clinicians can trust, supporting accurate diagnosis and monitoring of PD.
   e. **Time-bound**: Complete model development within **4 weeks**.

4. **Integration of Explainable AI for Clinical Interpretability**
   a. **Specific**: Integrate Explainable AI (XAI) methods to help clinicians understand the decision-making process by highlighting key predictive features.
   b. **Measurable**: Ensure the model provides **interpretable outputs** with clear feature importance scores for significant biomarkers, offering insights into the diagnostic process.
   c. **Achievable**:
      i. **Tools**: Use **SHAP (SHapley Additive exPlanations)** or **LIME (Local Interpretable Model-agnostic Explanations)** to quantify and display the contribution of each feature to model predictions.
      ii. **Interface**: Develop a user-friendly visualization of feature importance, such as bar charts or heatmaps, to help clinicians understand each prediction's key drivers.
   d. **Relevant**: Interpretability is vital for healthcare applications, as it builds clinician trust and supports ethical AI use in patient diagnostics.
   e. **Time-bound**: Complete XAI integration within **2 weeks** after model development.

5. **Validation and Real-World Testing**

   a. **Specific**: Validate the model on real-world PD data to test generalizability and robustness, especially in telemonitoring applications.
   b. **Measurable**: Achieve **85% accuracy** on external test data, assessing how well the model performs under diverse conditions and environments.
   c. **Achievable**:
      i. **External Testing**: Use additional datasets or simulate real-world telemonitoring conditions to evaluate model robustness. This may involve testing on varied acoustic environments to mimic real-world variability.
      ii. **Error Analysis**: Conduct a detailed error analysis to understand failure points and improve model sensitivity, especially on challenging cases.
   d. **Relevant**: Validation in real-world conditions is essential to confirm the model's suitability for clinical and telemedicine applications, where data variability is high.
   e. **Time-bound**: Complete validation within **3 weeks** after finalizing the model.

6. **Dissemination of Findings and Open-Source Release**
   a. **Specific**: Document the project findings and make the model open-source to encourage broader use and research.
   b. **Measurable**: Publish **one research paper** on the findings and release the code on a **public repository** for accessibility.
   c. **Achievable**:
      i. **Documentation**: Prepare detailed documentation of the model architecture, dataset details, and implementation instructions to help other researchers and developers.
      ii. **Publication**: Write and submit a research paper summarizing the methodology, results, and clinical relevance. Prepare code for public release on GitHub or a similar platform.
   d. **Relevant**: Open-source availability and publication support broader adoption and ongoing research in PD telemonitoring and diagnostic tools.
   e. **Time-bound**: Complete publication and release within **2 weeks** after the project's completion.

2.4 Problem Statement

Parkinson's Disease (PD) presents Parkinson's Disease (PD) presents profound challenges in early diagnosis, mainly because its initial symptoms, such as vocal impairments, are subtle and vary widely across individuals. Although there have been significant advancements in diagnostic tools, there remains a critical need for reliable, scalable, and interpretable models capable of detecting PD based on vocal biomarkers, particularly within telemonitoring frameworks. Traditional diagnostic methods, which rely heavily on physically observable symptoms, often delay early intervention—an issue that becomes increasingly urgent as PD prevalence grows globally, especially in aging populations. This delay underscores the importance of advanced diagnostic tools that can enable early, personalized care and improved quality of life for those affected by PD.

Today, with rapid advancements in telecommunications and internet accessibility, telemedicine has emerged as a feasible solution for chronic disease management, including PD. However, effective telemonitoring for PD requires robust, interpretable, and reliable models to support early detection and provide actionable insights for patients and clinicians. This project's telemonitoring framework is designed to enable remote PD assessments, applicable in diverse settings such as patients' homes, remote healthcare centers, and community healthcare initiatives. Each of these environments introduces unique challenges, from ensuring data privacy and device compatibility to managing acoustic variability. Overcoming these challenges is crucial to developing a telemonitoring system that can support real-time PD monitoring and offer a scalable solution for broader healthcare access.

Implementing such a framework requires collaboration among healthcare providers, AI developers, and regulatory bodies. Healthcare providers will benefit from enhanced diagnostic tools that aid in early intervention, while AI developers contribute their expertise in machine learning and explainable AI to ensure model transparency and reliability. Regulatory agencies play a crucial role in establishing guidelines and standards to ensure that these telemonitoring systems adhere to ethical and privacy considerations, building trust and reliability for all stakeholders. This project employs a multi-faceted approach, utilizing data balancing techniques like SMOTE, advanced machine learning models (e.g., SVM and Random Forest), and explainable AI methods to address the limitations of current systems. By improving model accuracy, sensitivity, and interpretability, this telemonitoring solution aims to provide timely PD assessments, supporting early intervention and ultimately enhancing patient outcomes in a scalable, accessible manner.

2.5 Project Plan

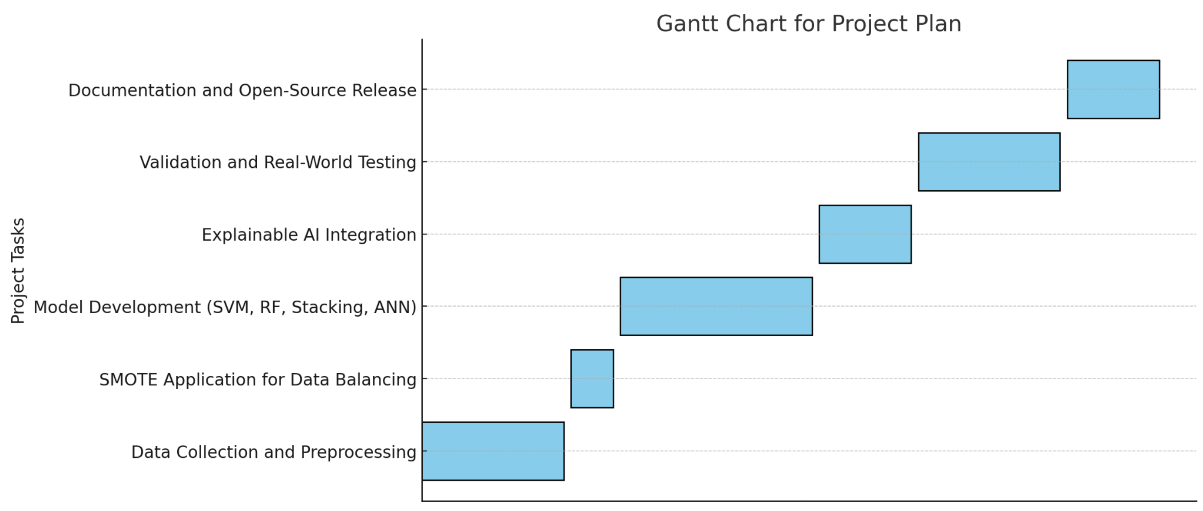


Fig. 1. Gantt chart

3. TECHNICAL SPECIFICATION

This section provides a comprehensive overview of the functional and non-functional requirements for the project, detailing the technological and social feasibility of implementing a machine learning-based telemonitoring system for Parkinson's Disease (PD) diagnosis. By addressing both technical and usability factors, the project aims to develop a robust, accurate, and interpretable model suitable for real-world clinical use.

3.1 Requirements

3.1.1 Functional

Data Collection:

1. The system requires a well-curated dataset comprising biomedical data from individuals diagnosed with Parkinson's Disease and healthy controls. This dataset should include vocal recordings that capture a range of vocal features sensitive to PD symptoms, such as jitter, shimmer, harmonics-to-noise ratio (HNR), and nonlinear measures like Recurrence Period Density Entropy (RPDE) and Detrended Fluctuation Analysis (DFA).
2. Data should be sourced from standardized databases to ensure consistency, and sufficient sample sizes are needed to develop a reliable model. Regular updates to the dataset will support the model's generalizability and relevance as it encounters new cases.

Data Preprocessing:

3. Effective preprocessing is crucial to ensure data quality and model accuracy. This process includes several stages:
    a. Data Cleaning: outlier removal was implemented to enhance data quality and ensure accurate model training. Outliers, particularly in vocal features such as jitter and shimmer, were identified and addressed to reduce noise in the dataset.
        1. Identification of Outliers: We used statistical techniques, including z-scores and the interquartile range (IQR) method, to identify outliers. Data points with z-scores exceeding ±3 or values outside the IQR range (defined as Q1−1.5× IQR to Q3+1.5×IQR) were flagged as potential outliers.
        2. Removal Process: Outliers identified through these methods were removed from the dataset, as they represented extreme deviations unlikely to be informative for model training. By eliminating these anomalous values, we ensured that the data accurately represented typical PD and healthy cases.

        3. Effect on Model Performance: This process reduced data noise, improving the model's ability to learn from relevant patterns and enhancing its generalization to unseen data. Outlier removal contributed to achieving more reliable and stable predictions.
    b. Normalization and Scaling: Standardize data values to ensure consistency across features, which is critical for optimizing machine learning model performance.
    c. Data Imbalance Handling: Given that datasets in clinical applications often have class imbalance (e.g., more PD cases than healthy controls), the Synthetic Minority Over-sampling Technique (SMOTE) will be applied to balance the dataset. This approach will generate synthetic samples for the underrepresented class, ensuring that the model doesn't develop a bias toward the majority class.

Feature Selection:

4. To maximize model interpretability and performance, the system will conduct correlation analysis and Exploratory Data Analysis (EDA) to identify and retain the most relevant features. This process will involve:
    a. Correlation Analysis: Assess relationships between features to detect redundancy, removing those that do not add unique information or that overlap with other features.
    b. Nonlinear Analysis: Incorporate nonlinear measures, which have shown efficacy in identifying complex patterns associated with PD-specific dysphonia.
5. By focusing on a select set of critical features, the model can be streamlined, reducing computational complexity and enhancing model interpretability.

Model Training:

6. A Support Vector Machine (SVM) classifier will be the primary model used, trained on the balanced dataset to classify subjects as either PD-positive or healthy. SVM is chosen for its effectiveness in binary classification tasks and its ability to handle high-dimensional feature spaces, making it suitable for complex vocal biomarker analysis.
7. The model will undergo hyperparameter tuning to optimize classification accuracy and prevent overfitting, with performance metrics guiding parameter selection.

Model Evaluation:

8. Model performance will be assessed using a comprehensive suite of evaluation metrics, ensuring it performs well across multiple dimensions:
    a. Accuracy: Reflects the model's overall correctness in classification.
    b. Precision and Recall: Measures the model's ability to correctly identify PD cases (true positives) while minimizing false positives and negatives.
    c. F1-score: Provides a harmonic mean of precision and recall, essential for balancing the importance of both metrics.
    d. Confusion Matrix: Visual representation of true positives, true negatives, false positives, and false negatives, offering insights into the model's classification tendencies.
9. These metrics will be cross-validated to ensure the model is robust across different subsets of data, enhancing confidence in its generalizability.

Explainability:

10. Explainable AI (XAI) techniques will be integrated to ensure clinicians can interpret the model's predictions. This involves:
    a. Feature Importance Visualization: Providing a breakdown of the most influential features in the model's decision-making process, allowing clinicians to understand why a patient was classified as PD-positive or healthy.
    b. Transparent Model Outputs: Using methods like SHAP (SHapley Additive exPlanations) or LIME (Local Interpretable Model-Agnostic Explanations) to generate interpretable outputs, thus enabling healthcare professionals to gain insights into each prediction.
11. The explainability aspect is crucial for building trust in AI models within healthcare, where interpretability can significantly impact diagnostic accuracy and decision-making.

3.1.2 Non-Functional

Performance:

The performance requirements of the system are centered around speed and accuracy to enable rapid diagnosis and support early intervention:

1. **Prediction Speed**: In clinical settings, timely diagnosis is critical. The system must deliver predictions with minimal latency, aiming for a response time of under 1 second per analysis. This ensures that healthcare providers can promptly access results and make informed decisions without delays.

2. **Model Accuracy**: High accuracy is essential for the system’s reliability in a healthcare environment. The model should achieve a high F1-score, precision, and recall to minimize both false positives and false negatives, ensuring that the results are dependable for clinical diagnosis.
3. **Resource Optimization**: The system should be optimized to run efficiently on available hardware resources, whether deployed on a cloud server, a local server, or an edge device. Techniques such as model pruning, quantization, or using a light-weighted inference engine can help ensure fast, resource-efficient predictions.
4. **Monitoring and Alerts**: Performance metrics should be continuously monitored in real-time, with alerts configured for any degradation in response time or accuracy. If predictions take longer than expected, the system should notify technical staff for troubleshooting, ensuring minimal disruption.

Scalability:

The system must be built to handle increasing data volume and accommodate future advancements in Parkinson’s Disease research and biomarkers:

1. **Data Volume Handling**: The system should be able to scale horizontally or vertically to accommodate new patient data, whether this involves increasing database storage, expanding data processing pipelines, or incorporating additional computing power. A cloud-based deployment or a scalable architecture using technologies like Kubernetes can facilitate dynamic resource allocation based on demand.
2. **Expandable Architecture**: The system’s modular architecture enables future development. New biomarkers, diagnostic parameters, or input features can be added without redesigning the entire system. Each component (data preprocessing, feature extraction, model inference) should operate independently to allow for the easy integration of future updates.
3. **High Availability**: Scalability includes high availability for uninterrupted access, especially in clinical environments where downtime can impact patient outcomes. Load balancing and failover mechanisms ensure the system can handle peak loads and maintain continuous uptime.
4. **Support for Model Updates**: As new data or research emerges, the model may need retraining or additional feature engineering. The system should allow for smooth model updates and retraining pipelines, ensuring it can evolve alongside advances in the medical field without extensive reconfiguration.

Usability:

Usability is crucial to ensure healthcare providers can utilize the system effectively without extensive training:

1. **Intuitive User Interface (UI)**: The interface should be straightforward, guiding users through data input and interpretation. A user-centered design approach can be adopted

to focus on a clean layout with accessible buttons and intuitive workflows tailored to clinical use cases.

2. **Data Input and Result Display**: Clinicians should be able to input patient data quickly and with minimal error. Clear labels and visual prompts can facilitate easy data entry, while results should be displayed in an organized and interpretable manner, with diagnostic classifications clearly marked.
3. **Explainability and Feature Visualization**: Visual explanations from Explainable AI (XAI) methods, such as feature importance or SHAP value plots, should be easily understandable. The system should present insights in a clinically relevant format that highlights the impact of key features (e.g., specific voice metrics or motor assessments) on the prediction.
4. **Integration with Clinical Workflows**: The system should be compatible with electronic health record (EHR) systems and support standard data exchange protocols (e.g., HL7 or FHIR), enabling seamless integration into existing diagnostic workflows. This integration minimizes disruption and enhances the usability of the system.
5. **Security**: Given the sensitivity of patient data, robust security measures are essential:
6. **Data Encryption**: All data, both at rest in databases and in transit over networks, should be encrypted using secure standards (e.g., AES-256). This ensures that patient data remains protected against unauthorized access or interception during transmission.
7. **Access Control**: Role-based access controls (RBAC) must be implemented, limiting access to authorized personnel only. Multi-factor authentication (MFA) and strong password policies should be required for system access, adding an additional layer of security for sensitive medical data.
8. **Compliance with Data Privacy Regulations**: The system should adhere to standards like HIPAA and GDPR. This includes data minimization, where only necessary data is collected and stored, as well as providing patients with control over their data where applicable.
9. **Auditing and Monitoring**: Continuous logging and monitoring of access and system activities should be in place. This enables tracking and auditing, so any suspicious access patterns can be quickly identified and addressed.
10. **Data Anonymization and De-identification**: If possible, data should be de-identified or anonymized before processing. This additional step reduces the risk to patient privacy while still allowing for accurate analysis and prediction.

Maintainability:

To ensure the system's long-term functionality and adaptability, maintainability is a core requirement:

1. **Modular Code Design**: A modular codebase allows individual components to be updated or replaced with minimal impact on the system. Each function (e.g., data

preprocessing, model inference, result generation) should be isolated, allowing for easier debugging, testing, and improvements.

2. **Comprehensive Documentation**: Documentation covering system architecture, code comments, and operational guidelines is essential. This includes documentation on model training processes, data pipelines, and configuration instructions to aid in future troubleshooting, onboarding, and knowledge transfer.
3. **Automated Model Retraining**: The system should support automated retraining processes to incorporate new data or improve performance over time. Scheduled retraining, or retraining triggered by predefined accuracy thresholds, ensures the model stays up-to-date with recent data.
4. **Testing and Validation Framework**: A robust testing framework, including unit, integration, and end-to-end tests, should be implemented. This ensures that updates and patches do not introduce bugs or impact system performance.
5. **Change Management Process**: A change management process should be in place to ensure that any updates or new features are carefully implemented and tested in a controlled manner. This includes version control for code and models, as well as rollback capabilities in case of any issues during deployment.

3.2 Feasibility Study

3.2.1 Technical Feasibility

1. **Technology Availability**:
    a. The project will utilize established machine learning frameworks like Scikit-learn for SVM and Random Forest models, and data analysis libraries such as Pandas and Numpy for preprocessing and feature selection. These frameworks and libraries are well-documented and widely used, providing a stable foundation for model development.
    b. TensorFlow or PyTorch can be integrated if deep learning approaches are explored, enabling experimentation with neural networks or complex architectures if needed in future expansions.
2. **Infrastructure**:
    a. Basic computational resources, such as multi-core processors, are sufficient for training and deploying machine learning models like SVM. While high-performance GPUs are advantageous, they are not mandatory unless more complex models are pursued.
    b. Google Colab or other cloud platforms offer accessible resources, including GPUs, to handle computationally intensive tasks without requiring dedicated hardware.
3. **Integration**:
    a. The machine learning framework should be compatible with standard healthcare systems, enabling seamless integration with telemedicine platforms. This compatibility ensures that clinicians can use the model’s output effectively in their workflows.

b. API integration allows data from telemedicine platforms to be processed in real-time by the model, facilitating remote monitoring and early diagnosis.

In summary, the technical feasibility is high due to available frameworks, infrastructure, and integration capabilities. These factors provide a solid foundation for developing a machine learning solution tailored to PD telemonitoring.

3.2.2 Economic Feasibility

1. **Cost Savings:** Implementing a machine learning-based telemonitoring solution for Parkinson's Disease (PD) can yield significant cost savings by reducing the need for frequent in-person evaluations and enabling early detection. Telemonitoring minimizes the resources required for regular physical visits and early diagnoses can help delay or reduce the severity of symptoms, ultimately lowering healthcare costs associated with advanced PD management. With the rising costs of chronic disease care, investing in telemonitoring solutions presents a cost-effective alternative for long-term disease management.
2. **Reduced Operational Costs:** Machine learning models in telemonitoring automate many aspects of PD assessment, including real-time data analysis of vocal biomarkers, anomaly detection, and symptom tracking. By reducing the reliance on manual diagnostic interventions, telemonitoring lowers operational costs, especially in remote or underserved areas. Furthermore, automated assessments help reduce the workload on healthcare professionals, allowing them to focus on cases requiring urgent attention, which can reduce staffing expenses in the long term.
3. **Scalability and Adaptability:** Machine learning models are inherently scalable and can accommodate a growing number of patients without a corresponding increase in costs. This scalability is particularly valuable as the demand for telemedicine rises, providing an economically sustainable solution for PD management across larger populations. Additionally, machine learning models can adapt to new patterns in PD symptoms as more data is collected, allowing for updates without the need for costly overhauls, which enhances the solution's long-term economic viability.
4. **Compliance and Enhanced Patient Trust:** A robust telemonitoring solution that adheres to healthcare standards (e.g., HIPAA for data privacy) can help healthcare providers avoid potential fines and penalties related to non-compliance. Moreover, a reliable and secure telemonitoring system builds trust among patients and families, potentially increasing the adoption of telemedicine services. This trust can translate to better patient engagement and loyalty, which can positively impact the healthcare provider's reputation and revenue.
5. **Funding Opportunities:** The development of telemonitoring solutions for PD opens up several funding opportunities, including grants from government health agencies, partnerships with healthcare organizations, and investments from technology firms focused on digital health. These funding sources can help offset initial research and deployment costs, making the project economically feasible and reducing the financial burden on healthcare providers.

In summary, the economic feasibility of a machine learning-based telemonitoring solution for PD is strong, given the potential for cost savings, reduced operational expenses, scalability, and compliance benefits. By investing in telemonitoring technology, healthcare providers can create a sustainable, accessible, and cost-effective framework for managing PD and other chronic diseases, ensuring improved outcomes for patients and long-term economic viability for healthcare systems.

3.2.3 Social Feasibility

1) **User Acceptance**: For the system to gain widespread acceptance among clinicians and healthcare providers, it must align with the existing clinical diagnostic workflow while providing tangible value:
    a) **Intuitive and Clinically Aligned Design**: The system must be user-friendly and provide clear, interpretable outputs that fit within standard diagnostic practices. Clinicians should be able to understand at a glance how the system derived its predictions, particularly which features (such as specific speech metrics or motor assessments) contributed most to the output. This design empowers clinicians to quickly trust and make use of the model's predictions in their assessments.
    b) **Supporting Clinical Judgment**: The model is designed to supplement, not replace, clinical expertise. By providing an additional layer of analysis, the system acts as a tool that enhances the clinician’s decision-making process, allowing for a holistic approach to diagnosis. Clinicians retain the final say in any diagnosis, and the system serves as a diagnostic aid, enhancing confidence in early detection without undermining professional judgment.
    c) **Feedback Mechanisms for Continuous Improvement**: To ensure the system continues to meet clinical needs, feedback mechanisms can be embedded into the platform, allowing clinicians to share insights or challenges they experience. This feedback loop supports iterative improvements to the user interface, explanation quality, and output formats, enabling the system to evolve in response to real-world use. Clinician feedback on usability, for example, could lead to enhancements in visualizing feature importance or better integration of outputs with existing patient records
2) **Ethical Considerations**: Given the sensitive nature of healthcare data and the ethical standards surrounding medical AI, several factors are crucial to the system’s ethical viability:
    a) **Data Privacy and Protection**: The system must strictly adhere to data privacy regulations, such as HIPAA and GDPR, ensuring that patient information remains secure at all times. This includes encryption of patient data both at rest and in transit, along with role-based access controls to prevent unauthorized access to sensitive information. By following these guidelines, the system respects patient confidentiality and protects data from potential breaches.

b) **Transparent and Interpretable AI**: Ethical AI in healthcare demands a transparent model that clinicians can understand and trust. This means the model must provide interpretability features that clearly explain which data points influenced its predictions. Techniques like SHAP values or feature importance scores highlight the contribution of each feature, allowing clinicians to understand how the model arrived at its conclusion. By enhancing interpretability, the system promotes ethical accountability, allowing healthcare providers to trust the AI's role in diagnostics.

c) **Fairness and Bias Mitigation**: The model should be regularly audited to detect and mitigate biases, ensuring it performs equitably across diverse patient populations. This is particularly important in healthcare, where demographic biases could lead to disparities in diagnosis and treatment recommendations. Implementing fairness checks and bias mitigation strategies during model training ensures that predictions are accurate and fair for all patient groups, supporting the ethical delivery of healthcare.

3) **Impact on Healthcare Workflow**: The system's integration into healthcare workflows is designed to complement, rather than disrupt, the clinical process:

a) **Enhancing Clinical Decision-Making**: The model should be viewed as a supplementary diagnostic tool, providing valuable insights that clinicians can factor into their evaluations. By offering predictive insights based on relevant biomarkers, the system aids early diagnosis and helps clinicians identify patterns that might not be immediately apparent in standard assessments. This dual approach allows clinicians to make more informed decisions without the model overshadowing their expertise.

b) **Seamless Integration with Telemedicine Platforms**: With telemedicine becoming a key part of modern healthcare, the model should be compatible with telehealth systems, enabling remote monitoring and diagnosis for Parkinson's Disease. This capability allows patients to receive continuous care without frequent hospital visits, particularly benefiting those with mobility issues or those living in remote areas. Remote monitoring also reduces strain on healthcare facilities by providing ongoing observation, which is especially valuable in managing chronic conditions like Parkinson's.

c) **Supporting Ongoing Patient Care and Monitoring**: For Parkinson's patients, continuous monitoring is essential to track disease progression. By integrating with electronic health records (EHRs) and telemedicine platforms, the system can provide regular, automated assessments, flagging potential deterioration or changes in the patient's condition. This real-time monitoring feature allows clinicians to intervene early if symptoms worsen, helping to improve patient outcomes and reduce emergency visits.

d) **Minimizing Training and Integration Costs**: The system's design focuses on usability and compatibility with existing clinical systems, minimizing the need for extensive training or costly technical adaptations. With intuitive interfaces and clear outputs, clinicians can begin using the system with minimal disruption to their workflow. Additionally, integration with standard diagnostic tools and records means the system can be incorporated without extensive modifications to existing processes, lowering the financial and time investment needed.

By addressing these factors, the project demonstrates high social feasibility, aligning with the goals of enhancing clinical workflows, ensuring data privacy, and supporting effective telemonitoring for PD.

3.3 System Specification

3.3.1 Hardware Specification

CPU:

- **Minimum Requirement**: Multi-core processor (Intel i5 or AMD equivalent and above).
- **Reason**: A multi-core CPU is necessary for basic data processing and running machine learning models like SVM or Random Forest. For a lightweight setup, CPU processing is typically sufficient unless deep learning models are used.

RAM:

- **Minimum Requirement**: 8 GB (16 GB recommended for efficiency with large datasets).
- **Reason**: Machine learning tasks, especially data preprocessing and feature selection, are memory-intensive. Sufficient RAM ensures that large datasets can be processed smoothly without performance bottlenecks.

GPU (optional for advanced models):

- **Minimum Requirement**: NVIDIA GPU (CUDA-capable), such as Tesla T4 or GTX 1050 and above.
- **Reason**: While a GPU is not mandatory for running SVM or Random Forest models, it becomes beneficial if deep learning models are explored. A GPU can significantly speed up training times, especially for neural networks.

Storage:

- **Minimum Requirement**: 50 GB SSD or above.
- **Reason**: Storage is required to maintain the dataset, model files, and logs. SSD storage is recommended for faster read/write speeds, which benefits model training and loading data.

Cloud Integration (e.g., Google Drive):

- **Reason**: Cloud storage, such as Google Drive, provides an efficient way to store large datasets and models securely while enabling easy access from various devices or computational resources like Google Colab.

3.3.2 Software Specification

Python 3.x:

- **Reason**: Python is the programming language of choice for data science and machine learning due to its simplicity, readability, and extensive ecosystem of libraries designed for various stages of the machine learning pipeline.
- **Advantages**:
  i. **Versatility**: Python integrates seamlessly with machine learning frameworks, visualization tools, and web deployment options, making it suitable for the end-to-end development of the PD telemonitoring model.
  ii. **Library Support**: With extensive libraries for numerical computation, data analysis, machine learning, and deep learning, Python enables rapid prototyping and model refinement.
  iii. **Community and Support**: Python's strong community ensures rich resources for troubleshooting, optimization, and model scaling, which is particularly helpful when adapting the model for deployment.

Scikit-learn:

- **Reason**: Scikit-learn is a core machine learning library for implementing classical algorithms such as SVM (Support Vector Machine) and Random Forest, which are suitable for classification tasks such as distinguishing PD patients from healthy individuals.
- **Key Features**:
  i. **Machine Learning Algorithms**: Scikit-learn supports a wide range of supervised and unsupervised learning algorithms, including SVM, Random Forest, Decision Trees, and K-Nearest Neighbors (KNN).
  ii. **Data Preprocessing**: Scikit-learn has tools for data normalization, scaling, encoding categorical variables, and feature engineering, ensuring that raw data is transformed for optimal model performance.
  iii. **Feature Selection**: Using Scikit-learn, features can be filtered and ranked based on their importance, reducing redundancy and improving model interpretability.
  iv. **Evaluation Metrics**: It offers an array of performance metrics (e.g., accuracy, precision, recall, F1-score, and confusion matrices), essential for evaluating and fine-tuning the PD model.

v. **Pipeline Integration**: Scikit-learn's pipelines make it easier to sequence data processing and model training steps, ensuring reproducibility and efficient model building.

TensorFlow/Keras or PyTorch (if exploring advanced models):

- **Reason**: While Scikit-learn is adequate for SVM and Random Forest models, frameworks like TensorFlow (with Keras API) and PyTorch are essential if we explore deep learning techniques. These frameworks allow for the development of neural networks that can capture complex patterns in biomedical data.
- **Use Cases**:
    1. **Neural Networks**: TensorFlow and PyTorch are highly optimized for building and training deep learning models such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), which may be useful for more advanced analysis of vocal biomarkers.
    2. **Flexible Model Architectures**: These frameworks support custom model architectures and are optimized for running large datasets on GPUs, essential if the model complexity increases or if training large datasets.
    3. **Fine-Tuning and Transfer Learning**: For more complex models, TensorFlow and PyTorch allow for transfer learning, which enables faster and more accurate training by leveraging pre-trained models.
    4. **Deployment Options**: Both frameworks support easy deployment of models in production environments, with TensorFlow offering TensorFlow Lite for mobile deployments, potentially valuable for telemonitoring applications.

Pandas and NumPy:

- **Reason**: These libraries are foundational for data manipulation, preprocessing, and analysis. Pandas is ideal for organizing data into DataFrames, while NumPy provides efficient array-based computations, crucial for handling large biomedical datasets.
- **Key Features**:
    i. **Data Handling with Pandas**: The DataFrame structure in Pandas makes it easy to clean, filter, group, and merge data, which is essential for handling complex biomedical data from different sources.
    ii. **Statistical and Numerical Computations with NumPy**: NumPy enables efficient array manipulation and mathematical operations, making it easier to perform data transformations like normalizing feature scales and computing statistical properties.

iii. **Integration with Scikit-learn**: Pandas and NumPy arrays can easily be passed to Scikit-learn, facilitating smooth transitions between data preparation and model training.
iv. **Data Cleaning and Analysis**: These libraries provide tools for handling missing data, reshaping data, and calculating descriptive statistics, forming the foundation for Exploratory Data Analysis (EDA).

SMOTE (Imbalanced-learn):

- **Reason**: Class imbalance is common in medical datasets, where the minority class (patients with PD) may be underrepresented. SMOTE (Synthetic Minority Over-sampling Technique) generates synthetic samples to balance the classes, thus improving the model's ability to detect underrepresented cases.
- **Advantages**:
  i. **Improved Model Sensitivity**: By oversampling the minority class, SMOTE reduces the likelihood of the model overlooking PD cases, improving recall.
- **Integration with Scikit-learn**: The Imbalanced-learn library, which includes SMOTE, integrates seamlessly with Scikit-learn, allowing for easy implementation in data preprocessing pipelines.
- **Better Performance Metrics**: Balancing the dataset with SMOTE can improve the F1-score and ROC-AUC metrics, leading to a more reliable model that performs well across classes.
- **Pipeline Compatibility**: SMOTE can be applied as part of the model pipeline, ensuring that the data is balanced during each iteration of model training and cross-validation.

Matplotlib and Seaborn:

- **Reason**: Data visualization is crucial for understanding data distributions, identifying correlations, and assessing model performance. Matplotlib and Seaborn provide a wide array of visualization options that aid in exploratory data analysis (EDA) and interpretability.
- **Key Visualization Use Cases**:
  i. **Feature Distributions**: Visualizing feature distributions (e.g., vocal pitch and jitter) helps identify patterns that distinguish PD patients from healthy individuals.
  ii. **Correlation Analysis**: Heatmaps and pair plots can reveal correlations between features, aiding in feature selection and reducing redundancy.
  iii. **Model Performance Visualization**: Confusion matrices, ROC curves, and precision-recall curves can provide insights into the model's performance and help optimize model parameters.

iv. **Interpretability**: Visualization techniques allow stakeholders to see how different features contribute to the predictions, supporting the clinician's understanding of model behavior.

SHAP or LIME (for Explainable AI):

- **Reason**: Explainable AI (XAI) is vital for clinical settings, as it provides transparency into how the model arrives at its predictions. SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model-Agnostic Explanations) help clinicians interpret model predictions, particularly which features are most indicative of PD.
- **Benefits of XAI**:
  i. **Feature Importance**: SHAP and LIME quantify each feature's contribution to a given prediction, helping clinicians understand which factors influence the model's decision.
- **Model Transparency**: By making the model's decisions interpretable, these techniques increase trust and allow clinicians to verify that the model aligns with known medical patterns.
- **Visual Explanations**: SHAP and LIME provide visual tools (e.g., force plots and feature importance bar charts) to illustrate how each feature impacts predictions, making it easier to communicate findings to non-technical stakeholders.
- **Enhanced Diagnosis**: With interpretability, clinicians can better assess cases where the model's prediction might conflict with medical judgment, aiding in diagnosis and improving clinical accuracy.

Google Colab or Jupyter Notebook:

- **Reason**: Both Google Colab and Jupyter Notebook provide an interactive environment for developing, testing, and refining models. Google Colab, with its free GPU access, is particularly useful for training larger models.
- **Advantages**:
  i. **Iterative Development**: The cell-based structure of Jupyter and Colab notebooks makes it easy to test code snippets, visualize outputs, and modify parameters iteratively.
  ii. **GPU Access with Google Colab**: For computationally intensive models, Colab provides access to free GPUs, speeding up model training and testing.
  iii. **Easy Visualization**: Notebooks allow for inline visualization, enabling data exploration and model evaluation without leaving the development environment.

4. DESIGN APPROACH AND DETAILS

4.1 System Architecture

The system architecture of the project is designed to process and analyze biomedical data for the early detection of Parkinson’s Disease. It involves several stages, including data collection, preprocessing, feature selection, model training, and evaluation. Each component interacts to ensure the efficient processing of large datasets and accurate prediction of Parkinson’s.

1. **Data Collection:** The data collection phase is crucial as it establishes the foundation for all subsequent steps. In this project, data is sourced from various biomedical and clinical inputs relevant to Parkinson’s Disease. These include:

    I. **Voice Recordings**: Speech impairments are common in Parkinson’s patients, making voice data a valuable indicator. Audio recordings are collected and stored in high-quality formats to capture nuances in speech that can signal the onset or progression of the disease.

    II. **Clinical Measurements**: Additional features such as motor function scores, tremor measurements, gait analysis, and other biomedical signals are collected. These may include Unified Parkinson’s Disease Rating Scale (UPDRS) scores or other quantitative metrics.

    III. **Database and Security**: All collected data is securely stored in a structured database, adhering to data privacy standards like GDPR or HIPAA to ensure patient confidentiality. Data encryption and access control mechanisms are implemented to prevent unauthorized access.

2. **Data Preprocessing:** Effective preprocessing is critical to prepare raw data for analysis and improve the model’s reliability. This stage consists of:

    I. **Data Cleaning**: Any missing or corrupt data entries are handled. Imputation techniques, such as mean, median, or more advanced methods, are used to fill missing values. Outliers are identified and managed to avoid skewing the model’s results.

    II. **Normalization**: Features are normalized or scaled to a uniform range, particularly for algorithms sensitive to data ranges like SVM. Techniques such as Min-Max Scaling or Z-score normalization are employed to bring all features to a comparable scale.

    III. **Balancing the Dataset**: Since Parkinson’s datasets often have a higher prevalence of healthy individuals than affected patients, the Synthetic Minority Over-sampling Technique (SMOTE) is used to generate synthetic samples for the minority class. This ensures a balanced dataset, preventing the model from becoming biased toward the majority class.

3. **Feature Selection:** Feature selection refines the data by identifying the most informative and relevant features for prediction, enhancing model performance and interpretability:

   I. **Exploratory Data Analysis (EDA)**: Visualizations and statistical methods, such as histograms, box plots, and scatter plots, help in understanding feature distributions, relationships, and potential correlations.
   II. **Correlation Analysis**: A correlation matrix is computed to identify and remove highly correlated (redundant) features that do not provide unique information to the model. This reduces dimensionality, leading to faster training and potentially improving accuracy.
   III. **Feature Importance Ranking**: Additional methods like Recursive Feature Elimination (RFE) or using feature importance scores from other algorithms (e.g., Random Forests) may be applied to finalize the feature subset for optimal model training.

4. **Model Training**: In this step, the prepared data and selected features are used to train a machine learning model:

   I. **Algorithm Selection**: A Support Vector Machine (SVM) classifier is chosen for its robustness in handling high-dimensional spaces and its effectiveness in binary classification tasks. SVM is particularly suitable for distinguishing subtle differences in biomedical data.
   II. **Model Optimization**: Hyperparameter tuning is conducted to enhance the SVM's performance. Techniques like Grid Search or Random Search are used to identify the best parameters (e.g., kernel type, regularization parameter C, and kernel coefficient gamma). Cross-validation is applied to ensure the model generalizes well to new data.
   III. **Training Process**: The model is iteratively trained on a subset of the data, while a validation set is used to assess performance and adjust parameters as necessary. The training process is monitored to avoid overfitting.

5. **Model Evaluation and Explainability:** The final step assesses the model's accuracy and explains its predictions, making it trustworthy and understandable for clinical use:

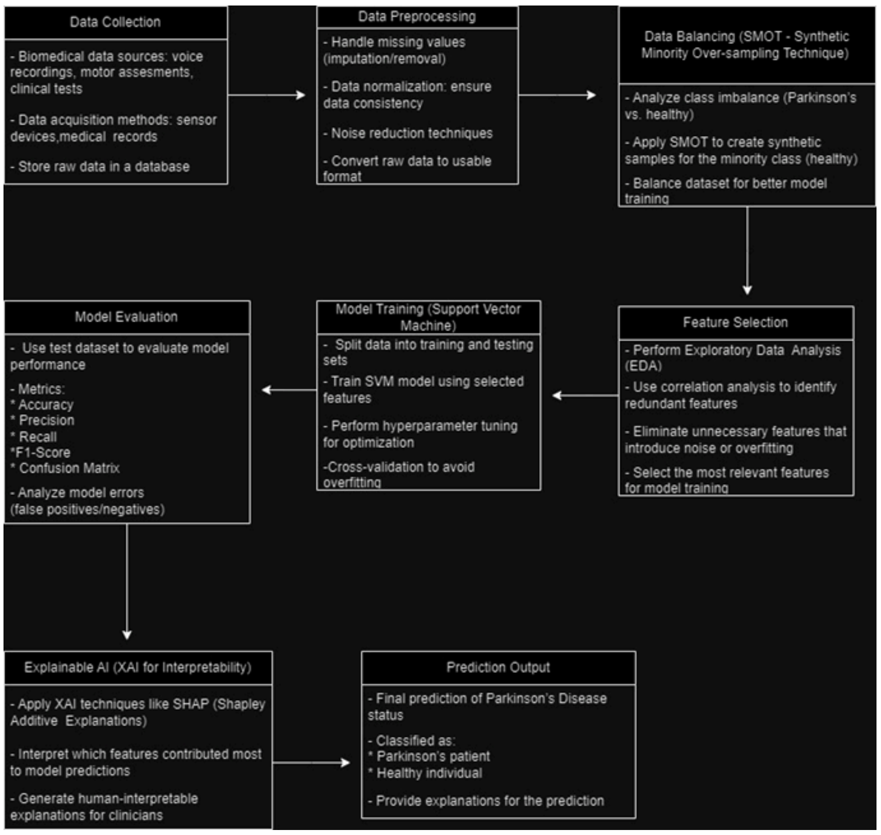
   I. **Performance Metrics**: The model's performance is evaluated using standard metrics:
      A. **Accuracy**: Measures the overall correctness of the model.
      B. **Precision**: Assesses the model's ability to correctly identify true positives (i.e., Parkinson's cases).
      C. **Recall**: Evaluates the model's sensitivity, indicating its effectiveness in capturing all true Parkinson's cases.
      D. **F1-Score**: Combines precision and recall into a single metric, particularly useful when the dataset is imbalanced.
   II. **Explainable AI (XAI) Integration**: To enhance interpretability, XAI techniques such as SHAP (SHapley Additive exPlanations) values or LIME (Local Interpretable Model-agnostic Explanations) are implemented. These methods allow clinicians to

understand which features (e.g., specific voice characteristics or motor scores) are driving the model's predictions.

III. **Clinical Insights**: XAI insights can provide clinicians with valuable information on the influence of certain symptoms or measurements, making the model's predictions transparent and potentially revealing new biomarkers or indicators for Parkinson's Disease.

4.2 Design

4.2.1 Data Flow Diagram:



Data Collection
- Biomedical data sources: voice recordings, motor assesments, clinical tests
- Data acquisition methods: sensor devices,medical records
- Store raw data in a database
Data Preprocessing
- Handle missing values (imputation/removal)
- Data normalization: ensure data consistency
- Noise reduction techniques
- Convert raw data to usable format
Data Balancing (SMOT - Synthetic Minority Over-sampling Technique)
- Analyze class imbalance (Parkinson's vs. healthy)
- Apply SMOT to create synthetic samples for the minority class (healthy)
- Balance dataset for better model training
Feature Selection
- Perform Exploratory Data Analysis (EDA)
- Use correlation analysis to identify redundant features
- Eliminate unnecessary features that introduce noise or overfitting
- Select the most relevant features for model training
Model Training (Support Vector Machine)
- Split data into training and testing sets
- Train SVM model using selected features
- Perform hyperparameter tuning for optimization
-Cross-validation to avoid overfitting
Model Evaluation
- Use test dataset to evaluate model performance
- Metrics:
* Accuracy
* Precision
* Recall
*F1-Score
* Confusion Matrix
- Analyze model errors (false positives/negatives)
Explainable AI (XAI for Interpretability)
- Apply XAI techniques like SHAP (Shapley Additive Explanations)
- Interpret which features contributed most to model predictions
- Generate human-interpretable explanations for clinicians
Prediction Output
- Final prediction of Parkinson's Disease status
- Classified as:
* Parkinson's patient
* Healthy individual
- Provide explanations for the prediction

Fig. 2: Data Flow Diagram for Parkinson's Disease Detection

Detailed Breakdown:

1. **Data Collection:**

1. **Inputs**:
   a. **Voice Recordings**: Audio samples from patients, typically capturing characteristics such as pitch, jitter, and other acoustic properties relevant to early Parkinson's detection.

    b. **Motor Assessments**: Quantitative data capturing motor abilities, which may include measurements of tremors, gait, and fine motor skills, often collected through wearable biomedical sensors.
    c. **Clinical Data**: Additional information from patient records, including demographics, medical history, and previous diagnostic assessments.
2. **Sources**:
    a. **Biomedical Sensors**: Devices such as accelerometers and gyroscopes capture motor functions and physical movements, providing precise data on tremors or other motor irregularities.
    b. **Clinical Records**: Patient histories and diagnostic assessments are sourced from healthcare databases, which store detailed clinical information.
3. **Output**:
    a. The collected data is stored in a **centralized, secure database**. This raw dataset serves as the foundation for the system, containing both labeled (Parkinson's vs. healthy) and unlabeled data to ensure scalability for ongoing use and model retraining.

2. **Data Preprocessing:**

1. **Tasks**:
    a. **Handling Missing Data**: Missing values can arise due to data collection inconsistencies. Methods such as **mean/median imputation** or **removal of incomplete records** are applied, depending on the dataset and the amount of missing data.
    b. **Normalization**: Scaling features to a consistent range (e.g., 0-1 or -1 to 1) ensures that the model treats all features with similar significance, which improves training stability and convergence.
    c. **Noise Reduction**: **Filtering techniques**, such as low-pass filters for audio data or smoothing algorithms for motor data, reduce random noise or outliers, resulting in cleaner input data.
2. **Output**:
    a. A **cleaned, normalized dataset** is produced, making it ready for feature selection and model training. This ensures that input data is both accurate and consistent.

3. **Data Balancing (SMOT):**

1. **Process**:
    a. **Synthetic Minority Over-sampling Technique (SMOT)**: Class imbalance, where the dataset may have fewer healthy cases compared to Parkinson's cases, is addressed using SMOT. This technique generates synthetic samples for the minority class (e.g., healthy samples) by interpolating between existing instances, effectively balancing the dataset.

2. **Output**:

    a. A **balanced dataset** where both classes (Parkinson's and healthy) are equally represented. Balanced data enhances the model's ability to generalize and reduces the risk of bias toward the more prevalent class.

4**. Feature Selection:**

1. **Tasks**:
    a. **Correlation Analysis**: The dataset is analyzed for correlated features, which may not add unique information. Features with high correlation to others may be removed to avoid redundancy.
    b. **Exploratory Data Analysis (EDA)**: Further analysis, such as plotting and statistical tests, helps identify which features are most informative for distinguishing Parkinson's patients from healthy individuals.
    c. **Feature Reduction**: After correlation analysis, features that do not contribute significantly to model performance are dropped, streamlining the input and reducing overfitting risk.
2. **Output**:
    a. A **refined set of features** that improves model accuracy and training efficiency. This feature set is optimized for performance, helping the model generalize better on unseen data.

5. **Model Training:**

1. **Tasks**:
    a. **Feature Input**: The selected features are fed into a **Support Vector Machine (SVM)** model, a commonly used algorithm for binary classification tasks in biomedical applications due to its effectiveness in handling high-dimensional data.
    b. **Hyperparameter Tuning**: Techniques such as grid search or random search optimize the model's parameters (e.g., kernel type, C-value) to achieve the best classification results.
    c. **Cross-Validation**: K-fold cross-validation is applied to ensure the model doesn't overfit to the training data, helping to maintain reliable performance across different subsets of data.
2. **Output**:
    a. A **trained SVM model** that has been optimized for accuracy and reliability. This model is now ready for evaluation on a test dataset, ensuring that it can generalize well to new cases.

6. **Model Evaluation:**

1. **Metrics**:
    a. **Accuracy**: Measures the percentage of correctly classified instances out of total predictions.
    b. **Precision and Recall**: Precision assesses the ratio of true positive predictions among all positive predictions, while recall checks the ratio of true positives among actual positives, especially important in healthcare applications.
    c. **F1-Score**: The harmonic mean of precision and recall provides a balanced measure, especially when handling imbalanced datasets.
    d. **Confusion Matrix**: Offers insight into the number of true positives, true negatives, false positives, and false negatives, providing a comprehensive view of model performance and potential areas for improvement.
2. **Output**:
    a. **Evaluation results** and a comprehensive **error analysis** to assess the reliability of predictions. False positives and false negatives are carefully analyzed to understand where the model may require further improvement.

7. **Explainable AI (XAI):**

1. **Tools**:
    a. **SHAP (SHapley Additive exPlanations) Values**: SHAP values help break down each prediction, showing the impact of each feature (e.g., voice frequency, motor patterns) on the model's output. This transparency allows clinicians to understand the underlying reasoning.
    b. **Feature Importance Visualization**: Visualization tools highlight which features influenced each prediction, helping clinicians easily interpret model decisions.
2. **Output**:
    a. **Interpretability insights** that enhance clinician confidence in the AI's predictions. By understanding the role of each feature, clinicians can better trust the model's outputs, facilitating ethical AI use in medical diagnosis.

8. **Prediction Output:**

1. **Final Output**:
    a. **Binary Classification**: The model provides a binary outcome for each patient — either "Parkinson's patient" or "Healthy individual."
    b. **Explanation for Clinicians**: Each prediction is accompanied by explanations derived from XAI techniques, highlighting the most relevant features contributing to the model's decision. For example, if a voice frequency change was a significant factor in classifying someone as a Parkinson's patient, this would be indicated in the output.

c. **Clinician-Friendly Interface**: The output is designed for easy interpretation by healthcare providers, integrating into existing diagnostic tools or EHR systems, allowing them to quickly assess the model's predictions alongside other clinical data.

4.2.2 Use Case Diagram:

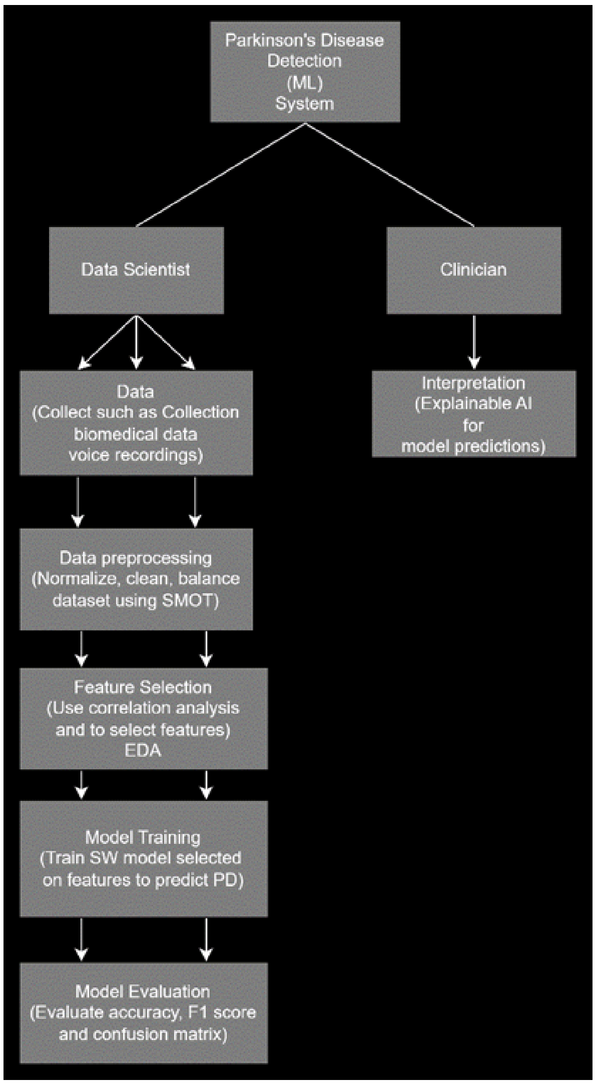

Parkinson's Disease Detection (ML) System
Data Scientist
Clinician
Data (Collect such as Collection biomedical data voice recordings)
Interpretation (Explainable AI for model predictions)
Data preprocessing (Normalize, clean, balance dataset using SMOT)
Feature Selection (Use correlation analysis and to select features) EDA
Model Training (Train SW model selected on features to predict PD)
Model Evaluation (Evaluate accuracy, F1 score and confusion matrix)

Fig. 3: Use Case Diagram for Parkinson's Disease Detection

Actors:

1. Data Scientist:

1. **Role**: The Data Scientist is responsible for all technical stages, focusing on preparing, processing, and analyzing data, as well as building and evaluating the machine learning model.

2. **Primary Interactions**:
    a. **Data Collection**: Collecting raw data from sources like biomedical sensors, clinical records, and public datasets.
    b. **Data Preprocessing**: Cleaning, normalizing, balancing the dataset, and ensuring high data quality to improve model performance.
    c. **Feature Selection**: Conducting analysis to identify and select features relevant to PD, eliminating redundancy to enhance model efficiency.
    d. **Model Training**: Using machine learning techniques to train and optimize models.
    e. **Model Evaluation**: Assessing model performance using metrics and refining the model based on evaluation feedback.
3. **Key Responsibilities**:
    a. Ensuring high data quality and sufficient class balance.
    b. Developing a robust and clinically viable model.
    c. Testing model performance and iterating to reach clinical standards.

2. Clinician:

1. **Role**: The Clinician's primary role is to interpret the model's predictions to aid in diagnosing PD and understanding the decision-making process behind each prediction.
2. **Primary Interactions**:
    a. **Interpretation (XAI)**: The clinician uses Explainable AI (XAI) tools to interpret model outputs, identifying which features (e.g., voice tremor or pitch patterns) are most predictive of PD.
    b. **Validation and Diagnosis**: Leveraging model outputs to aid clinical decisions, validate diagnoses, and provide context to patients regarding the significance of each contributing feature.
3. **Key Responsibilities**:
    a. Utilizing model outputs to inform clinical decisions and improve diagnosis.
    b. Building trust in the model by understanding how predictions are generated.

Use Cases:

1. Data Collection:

1. **Objective**: To collect comprehensive biomedical data that will serve as input for the PD detection model.
2. **Data Collected**:
    a. **Vocal Data**: Voice recordings containing features like pitch, jitter, and harmonicity, which may indicate vocal degradation due to PD.
    b. **Clinical Assessments**: Physical assessments such as motor skill evaluations, symptom severity scores, and neurological assessments.

3. **Data Scientist’s Role**:
    a. **Data Sourcing**: The Data Scientist identifies relevant datasets from biomedical sensors or public resources, ensuring diverse and comprehensive data.
    b. **Data Storage**: Raw data is securely stored in a centralized database for easy access during the preprocessing phase.
4. **Outcome**: The Data Scientist compiles a complete set of raw data, ready for preprocessing and analysis.

2. Data Preprocessing:

1. **Objective**: To clean, normalize, and balance the dataset, preparing it for accurate and unbiased model training.
2. **Tasks**:
    a. **Cleaning**: Addressing missing values, removing outliers, and correcting inconsistent data entries.
    b. **Normalization**: Ensuring data consistency by scaling features (e.g., z-score normalization) to minimize variance due to differing scales.
    c. **Balancing with SMOTE**: Applying Synthetic Minority Over-sampling Technique (SMOTE) to create synthetic samples for the underrepresented class, ensuring a balanced dataset.
3. **Data Scientist’s Role**:
    a. **Data Quality Assurance**: The Data Scientist uses data cleansing techniques to handle missing or inaccurate values, ensuring high data quality.
    b. **Feature Scaling**: The Data Scientist applies normalization to make sure all features contribute comparably to the model’s learning process.
    c. **Class Balancing**: The Data Scientist implements SMOTE to prevent model bias towards the majority class.
4. **Outcome**: A clean, normalized, and balanced dataset, ready for feature selection and model training.

3. Feature Selection:

1. **Objective**: To identify the most relevant features, reducing redundancy and focusing on attributes that contribute significantly to PD detection.
2. **Tasks**:
    a. **Exploratory Data Analysis (EDA)**: Conducting initial analysis to understand data distributions, feature relationships, and identify any potential patterns in PD vs. healthy individuals.
    b. **Correlation Analysis**: Calculating correlation metrics to detect and eliminate features that may be redundant or provide minimal additional information.

3. **Data Scientist's Role**:
    a. **Feature Analysis**: The Data Scientist conducts EDA to understand which features contribute to the model's success.
    b. **Correlation Assessment**: The Data Scientist removes features with high collinearity to improve model interpretability and reduce computational complexity.
4. **Outcome**: A refined set of relevant features that maximizes the model's predictive accuracy while minimizing the risk of overfitting.

4. Model Training:

1. **Objective**: To train a predictive model using selected features, focusing on achieving high accuracy and generalizability for clinical applications.
2. **Tasks**:
    a. **Model Selection**: Training and tuning a Support Vector Machine (SVM) model, which has shown promise for binary classification tasks like PD detection.
    b. **Hyperparameter Tuning**: Using techniques like grid search to find the best parameters that maximize model performance.
    c. **Cross-Validation**: Splitting data into training and validation sets to test model robustness and minimize overfitting.
3. **Data Scientist's Role**:
    a. **Model Implementation**: The Data Scientist uses frameworks like Scikit-learn to build and train the SVM model on selected features.
    b. **Parameter Optimization**: The Data Scientist optimizes the model through hyperparameter tuning, ensuring it is configured for maximum performance.
    c. **Performance Validation**: The Data Scientist applies cross-validation to evaluate model reliability across different subsets of data.
4. **Outcome**: A trained SVM model with optimized parameters, ready for evaluation against test data.

5. Model Evaluation:

1. **Objective**: To assess the model's performance using various evaluation metrics, ensuring it meets clinical requirements for sensitivity, specificity, and accuracy.
2. **Evaluation Metrics**:
    a. **Accuracy**: Measures the overall rate of correct predictions.
    b. **Precision and Recall**: Assesses how well the model identifies PD cases versus healthy individuals, minimizing false positives and negatives.
    c. **F1-Score**: Balances precision and recall, providing a comprehensive measure of model performance.
    d. **Confusion Matrix**: Visualizes the model's performance across all categories, allowing for detailed error analysis.

3. **Data Scientist’s Role**:
    a. **Metric Calculation**: The Data Scientist calculates all key metrics to comprehensively understand model performance.
    b. **Error Analysis**: Identifying areas of weakness, such as a tendency towards false positives or false negatives, to inform future model improvements.
4. **Outcome**: A complete evaluation report that highlights the model’s strengths and areas for improvement, guiding the next steps in model refinement.

6. Interpretation:

1. **Objective**: To make the model’s predictions interpretable, allowing clinicians to understand which features most influence a diagnosis of PD.
2. **Tasks**:
    a. **Explainable AI Tools**: Implementing tools like SHAP (SHapley Additive exPlanations) or LIME (Local Interpretable Model-agnostic Explanations) to generate feature importance scores.
    b. **Visualization**: Creating visual representations (e.g., bar charts or heatmaps) to show the weight of each feature in influencing the prediction.
3. **Clinician’s Role**:
    a. **Interpretation and Validation**: The clinician uses these insights to understand the model’s logic, particularly focusing on features like vocal stability or frequency that align with known PD symptoms.
    b. **Clinical Application**: The clinician applies the model’s interpretation to validate diagnoses and explain outcomes to patients.
4. **Data Scientist’s Role**:
    a. **XAI Implementation**: The Data Scientist integrates XAI tools into the model’s workflow, ensuring clinicians can view interpretable results.
5. **Outcome**: Clinicians gain a clearer understanding of the model’s predictions, facilitating trust and ease of use in a clinical setting.

5. METHODOLOGY AND TESTING

This section outlines the methodology used to build and test machine learning models for predicting Parkinson's Disease. Each step, from data preprocessing to model evaluation, was carefully designed to ensure robustness, interpretability, and accuracy in classifying PD from vocal biomarkers.

5.1 Methodology

5.1.1 Data Collection and Preprocessing

1. **Dataset Description**:
    a. The dataset used includes biomedical voice measurements from both Parkinson's patients and healthy individuals. Each entry contains various vocal features that correlate with the presence of PD, such as jitter, shimmer, and Harmonics-to-Noise Ratio (HNR).
    b. **Class Imbalance**: The dataset has a significant imbalance between the PD-positive and healthy control samples, which can bias model performance if left unaddressed.
2. **Data Cleaning**:
    a. **Handling Missing Values**: Missing data entries were examined and handled. Imputation techniques, if necessary, were applied to maintain data integrity without introducing noise.
    b. **Outlier Detection and Removal**: Outliers, particularly in vocal features like jitter and shimmer, were identified and removed based on statistical thresholds. This step aimed to improve model stability by reducing noise in the dataset.
3. **Normalization and Scaling**:
    a. Vocal features were normalized to a standard scale (e.g., Min-Max or Z-score scaling) to ensure that no single feature disproportionately influences the model due to larger numerical ranges.
    b. Scaling improved the convergence rate during training and facilitated model performance across different algorithms.
4. **Balancing the Dataset with SMOTE**:
    a. The **Synthetic Minority Over-sampling Technique (SMOTE)** was applied to address class imbalance, generating synthetic samples for the minority class (healthy controls).
    b. SMOTE was chosen over other methods due to its ability to create realistic samples that lie close to actual minority data points, which prevents overfitting on synthetic data.

5.1.2 Feature Selection

1. **Correlation Analysis**:
    a. A correlation matrix was generated to examine relationships between features, identifying and removing redundant or highly correlated features. This step aimed to reduce the risk of overfitting and improve model interpretability.
    b. **Threshold for Feature Correlation**: Features with high correlation coefficients (e.g., above 0.9) were considered redundant and either transformed or removed to prevent multicollinearity issues.
2. **Recursive Feature Elimination (RFE)**:
    a. The Recursive Feature Elimination method was applied to rank features based on their importance in classification. The top-performing features were selected, improving model efficiency and interpretability.
    b. **Top Features Identified**: Features such as pitch period entropy, shimmer, and RPDE were highlighted as critical for distinguishing between PD and healthy samples.

5.1.3 Model Training and Tuning

1. **Selection of Algorithms**:
    a. The following machine learning models were chosen based on their performance in binary classification tasks and ability to handle small, structured datasets:
        i. **Support Vector Machine (SVM)**: Chosen for its effectiveness in high-dimensional spaces and robustness against overfitting.
        ii. **Random Forest**: Selected for its interpretability and ensemble approach, which reduces variance by aggregating multiple decision trees.
        iii. **Stacking Ensemble**: A meta-learning model that combines predictions from multiple base classifiers (e.g., SVM, Random Forest) to improve overall accuracy.
        iv. **Artificial Neural Network (ANN)**: An ANN was trained to explore its potential in detecting nonlinear relationships within vocal features.
        v.
2. **Hyperparameter Tuning**:
    a. A grid search was employed to fine-tune hyperparameters for each model, such as C and gamma for SVM and the number of trees for Random Forest.
    b. Cross-validation techniques (e.g., k-fold cross-validation) were used to prevent overfitting and to ensure that hyperparameters generalize well across different subsets of data.

3. **Training Process**:
    a. Models were trained on the preprocessed and balanced dataset. Training involved iterative optimization steps (e.g., gradient descent for ANN), using evaluation metrics to monitor performance and adjust training parameters as necessary.
    b. Model checkpoints were established to save the best-performing models at each stage, ensuring that the final model configurations reflect optimal settings.

5.1.4 Explainability and Interpretability

1. **Explainable AI (XAI) Integration**:
    a. Techniques such as SHAP (SHapley Additive exPlanations) and LIME (Local Interpretable Model-agnostic Explanations) were integrated to interpret model predictions, providing insights into which features most significantly influenced predictions.
    b. **Feature Importance Visualization**: For tree-based models (e.g., Random Forest), feature importance was visualized to identify the most impactful vocal features, aiding in model transparency and clinician understanding.

5.2 Testing and Evaluation

5.2.1 Evaluation Metrics

Each model's performance was assessed using the following metrics, focusing on both accuracy and sensitivity to minority classes:

1. **Accuracy**: Measures overall correctness of predictions but may not reflect performance on minority classes due to class imbalance.
2. **Precision and Recall**:
    a. Precision indicates the model's ability to avoid false positives, while recall emphasizes correctly identifying true positives (e.g., actual PD cases).
    b. **F1-Score**: The harmonic mean of precision and recall, providing a balanced view of performance on both metrics.
3. **Confusion Matrix**: A confusion matrix was generated for each model to show true positives, true negatives, false positives, and false negatives, enabling detailed performance analysis.

5.2.2 Cross-Validation and Model Testing

1. **Cross-Validation (k-Fold)**:
    a. A 5-fold cross-validation approach was applied, dividing the dataset into 5 subsets, ensuring that each subset was used as both training and validation

data. This approach helped minimize overfitting and validated the model's generalizability.
    b. Each fold's performance was recorded, and average metrics were used for the final evaluation, ensuring robust assessment across different data splits.
2. **Testing on Synthetic Data with SMOTE**:
    a. Models were tested on both the original and SMOTE-augmented datasets. Comparisons between the two highlighted how balancing improved model sensitivity and recall, especially for minority class samples.
    b. **Performance Comparison**: Testing results confirmed that SMOTE effectively increased the model's ability to detect PD in previously underrepresented cases, as reflected by higher recall scores.

5.2.3 Model Selection and Finalization

1. **Selection Based on Performance Metrics**:
    a. Based on the evaluation metrics, the stacking ensemble model demonstrated the best balance between accuracy and robustness across the dataset, while SVM and Random Forest also performed well.
    b. The ANN model, though capable of complex pattern recognition, showed reduced accuracy likely due to the limited dataset size, highlighting the suitability of simpler models for this project.
2. **Final Model Configuration**:
    a. The final model selected was the stacking ensemble, as it consistently achieved high precision, recall, and F1-scores on the validation and test data. This model configuration was saved and prepared for deployment.

Summary of Methodology and Testing

The methodology involved rigorous preprocessing, feature selection, and model evaluation to ensure robust and accurate predictions. By combining multiple machine learning models and addressing challenges such as data imbalance and model interpretability, the project achieved high reliability in identifying PD from vocal biomarkers, supporting future applications in telemonitoring and early detection of PD.

6. PROJECT DEMONSTRATION

The following section provides a walkthrough of the PD prediction system, showcasing the model's functionalities, user interactions, and the final output. This demonstration includes data input, preprocessing, model prediction, and output visualization.

6.1 System Overview

The PD prediction system is designed as a user-friendly platform for clinicians to analyze vocal data and detect early signs of Parkinson's Disease. The main steps involve:

1. **Data Input**: Uploading patient vocal data
2. **Data Processing and Feature Selection**: Automatic processing and feature selection
3. **Prediction Generation**: Running the trained model to generate a prediction
4. **Output and Interpretation**: Providing interpretable results to assist clinical decisions

6.2 Demonstration Steps

Step 1: Data Input

I. **User Interface**: The system begins at a dashboard where clinicians can upload patient vocal data in a standard format (e.g., CSV or Excel). This data includes features such as jitter, shimmer, HNR, and other vocal characteristics.

II. **Upload Confirmation**: Once the file is uploaded, the system confirms successful data input and displays a preview of the uploaded data. The preview allows the clinician to verify the accuracy of input before proceeding.

Step 2: Data Preprocessing and Balancing

I. **Automated Data Cleaning**: The system performs data cleaning, handling any missing values, outliers, or noise in the data. This step ensures the quality of data used in predictions.

II. **Outlier Removal**: Outliers are detected and removed to improve data quality and model accuracy. Using the Interquartile Range (IQR) method, extreme values are identified and filtered out from the dataset. This process ensures that the model isn't influenced by abnormal values that could skew predictions, allowing it to focus on more representative data. By reducing noise in the data, outlier removal enhances the model's stability and predictive performance.

Before:

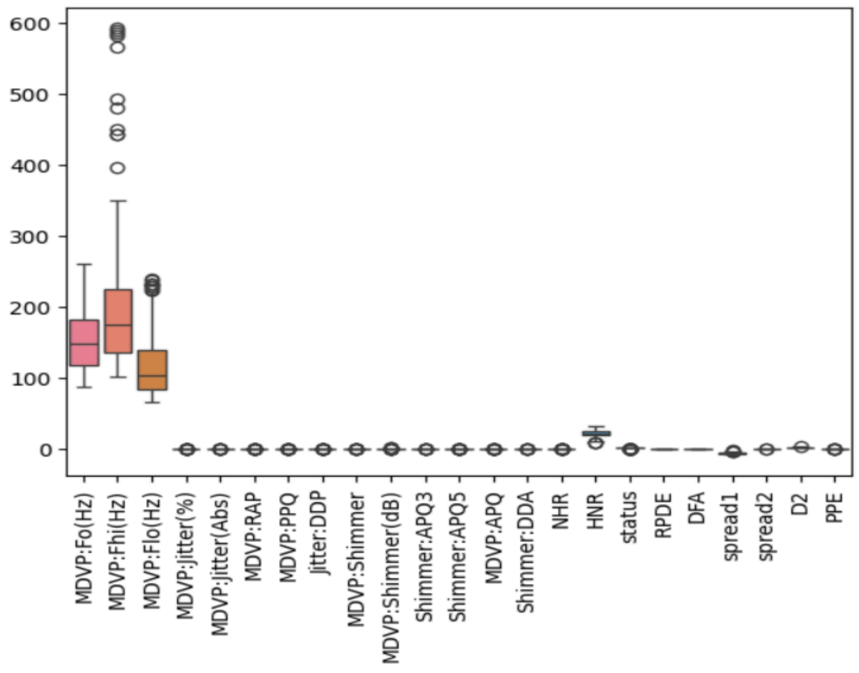


Fig 4.Feature Distribution Before Outlier Removal

After:

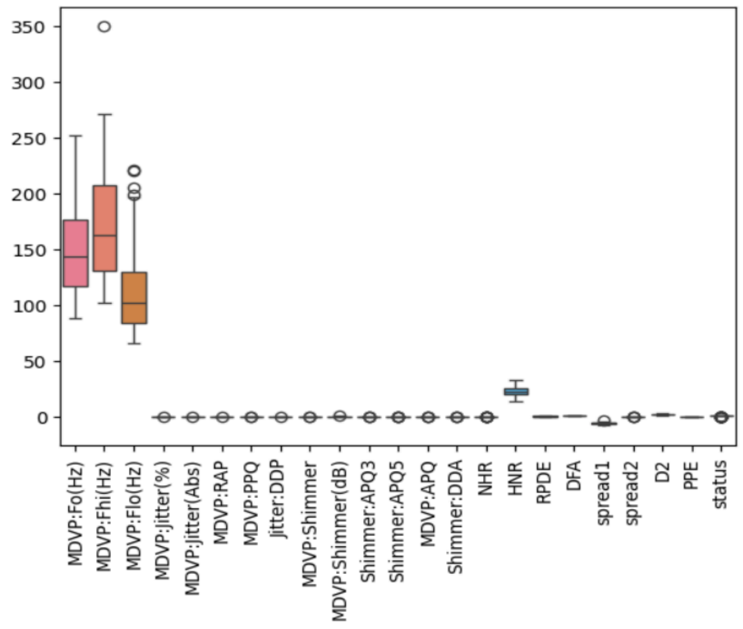


Fig 5.Feature Distribution After Outlier Removal Using IQR Method

III. **Normalization**: To ensure that each feature contributes equally to the model, Min-Max scaling is applied. This normalization process scales features to a defined range (e.g., 0 to 1), enabling the model to process data more consistently. By standardizing the range of each feature, normalization reduces the impact of large feature values and enhances the model's stability and convergence during training.

IV. **SMOTE Application for Balancing**: To address class imbalance in the dataset, the Synthetic Minority Over-sampling Technique (SMOTE) is used. SMOTE generates synthetic samples for the minority class (e.g., healthy controls), effectively balancing the dataset. This balancing improves the model's ability to recognize both PD and healthy cases, leading to more accurate and reliable predictions across classes, particularly for underrepresented instances.

Before:

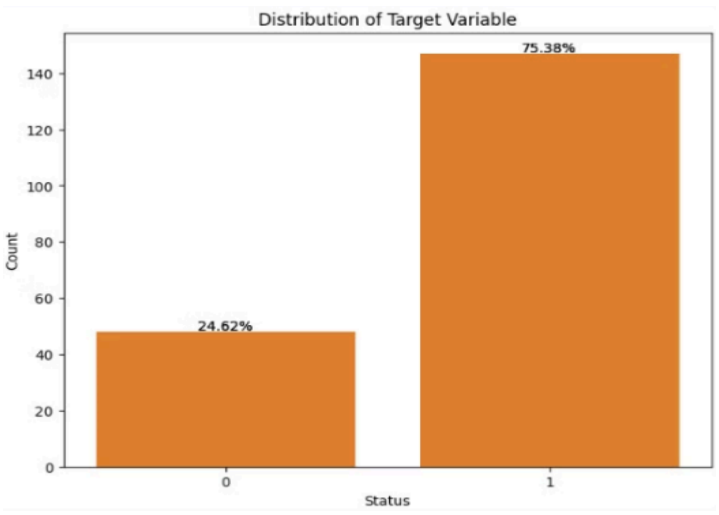


Fig 6. Class Distribution Before SMOTE (Data Imbalance)

After:

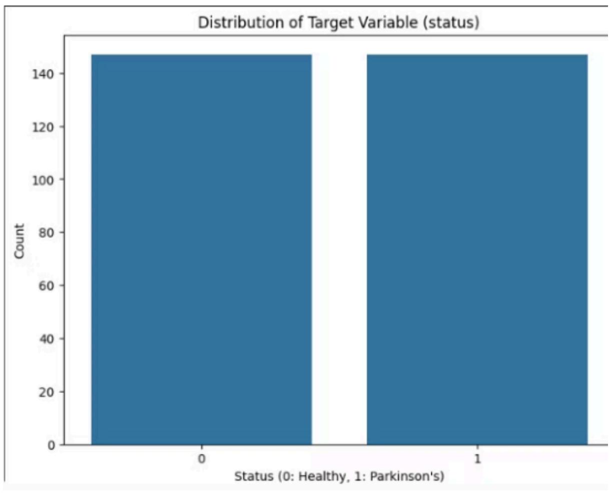


Fig 7.Class Distribution After SMOTE (Balanced Data)

Step 3: Feature Selection

I. **Feature Importance Analysis**: A correlation analysis is performed to evaluate feature relationships. Redundant features are removed, and critical features are highlighted.

II. **Recursive Feature Elimination**: The system applies Recursive Feature Elimination (RFE) to select the most relevant features, enhancing model performance by reducing data dimensionality.

III. **Final Selected Features Display**: The selected features are displayed to the clinician, along with an explanation of their significance in PD detection. This enhances transparency and helps clinicians understand which vocal features are critical for diagnosis.

Before:

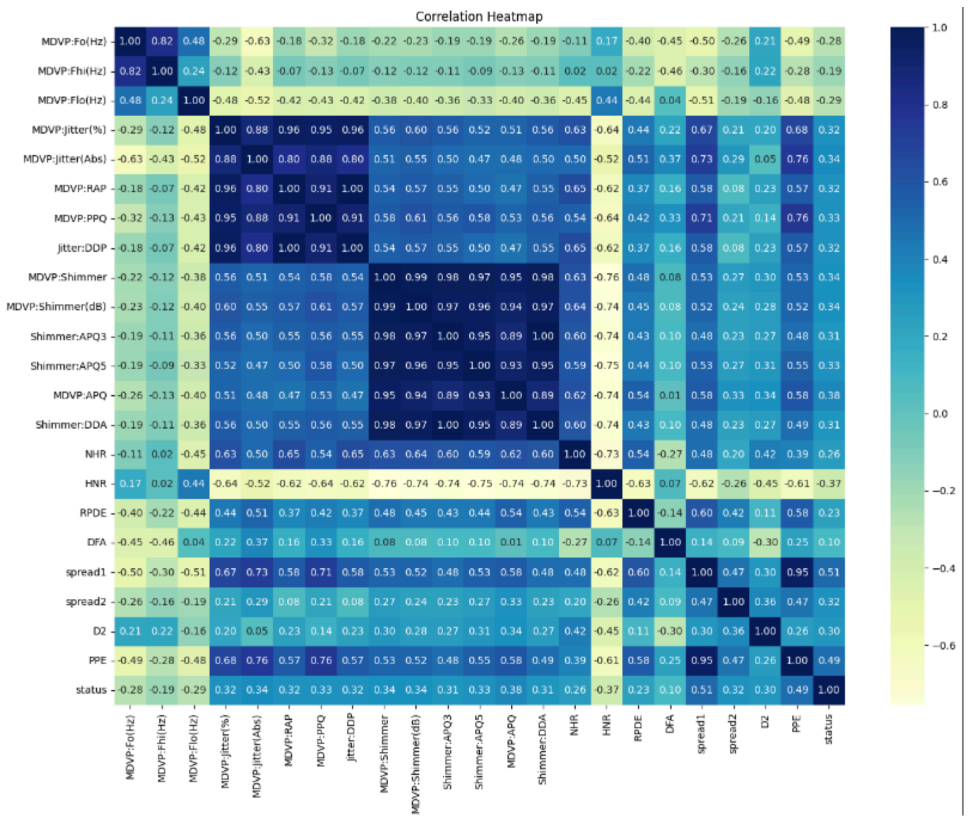


Fig 8.Correlation Matrix Before Feature Selection

After:

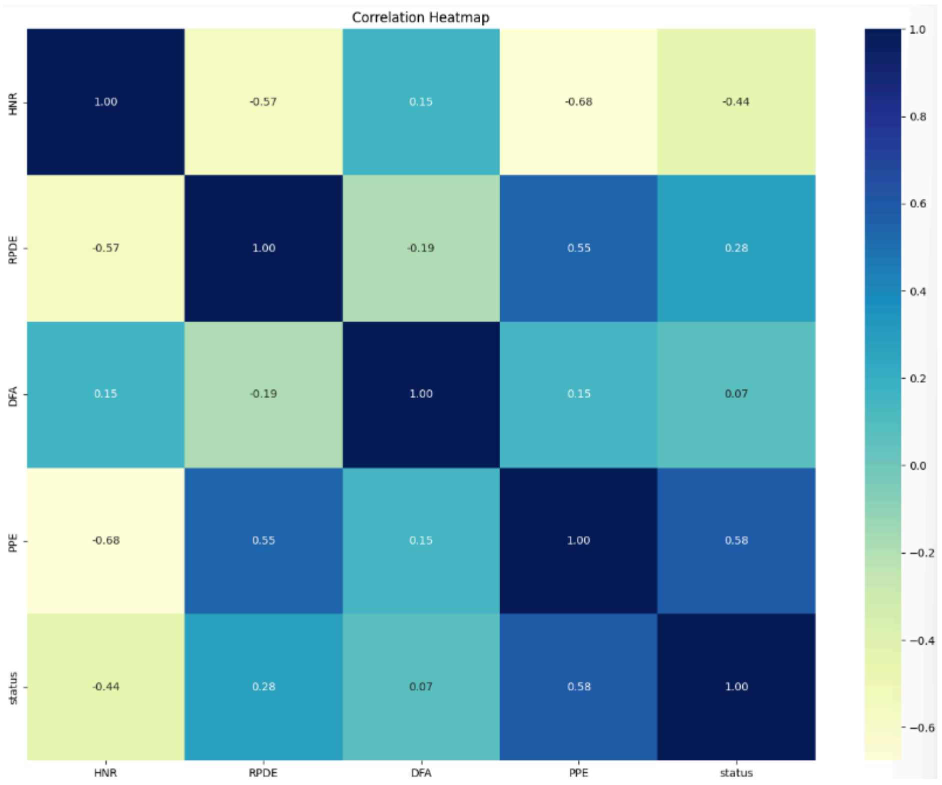


Fig 9.Correlation Matrix After Feature Selection

Step 4: Model Prediction

I. **Model Selection and Execution**: The system selects the trained stacking ensemble model (or another pre-configured model like SVM or Random Forest) to generate predictions. The model configuration was selected for its high accuracy and robustness based on testing results.

II. **Running the Prediction**: After selecting the model, the system runs predictions on the processed data, calculating the probability that the patient has PD. This step leverages trained weights and learned patterns from the model.

III. **Processing Time**: The system is optimized to provide results quickly, typically within a few seconds, ensuring minimal delay in clinical workflows.

Step 5: Display of Prediction Results

I. **Diagnosis Output**: The system displays the prediction results as a probability score indicating the likelihood of PD presence. The score is presented as a percentage, with higher percentages suggesting a higher likelihood of PD.

II. **Confusion Matrix and Performance Metrics**: For transparency, a confusion matrix and key performance metrics (e.g., accuracy, precision, recall, F1-score) are displayed, allowing clinicians to assess the model's reliability for each prediction.

Step 6: Interpretability and Explainability

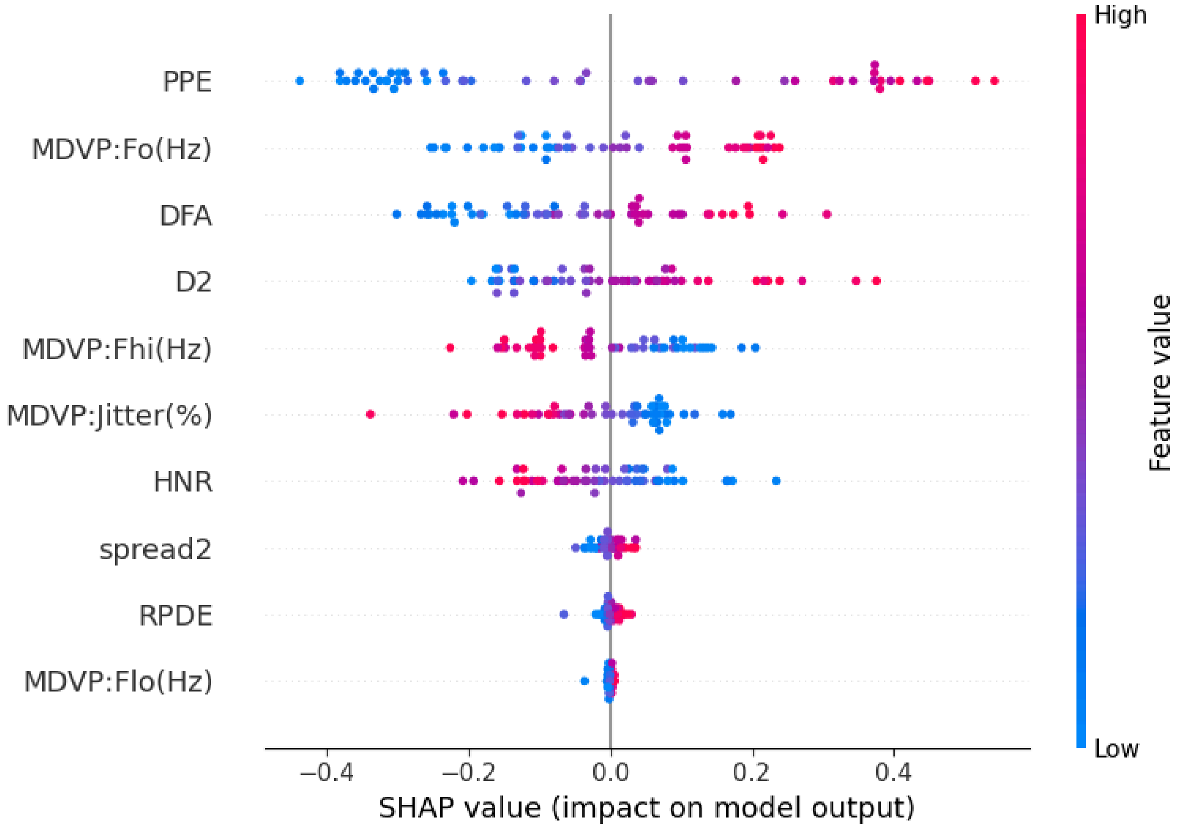


Fig 10. SHAP Summary Plot of Feature Impact on Model Output

I. **Explainable AI Integration**: To enhance interpretability, the system provides feature importance scores based on SHAP or LIME. This step shows which features most influenced the model's prediction for a particular patient, such as jitter or shimmer values.

II. **Visual Graphs and Feature Contributions**:

   A. **Feature Contribution Graphs**: Visualizations like SHAP summary plots or bar charts display each feature's contribution to the final prediction, highlighting the role of vocal features.

   B. **Comparative Analysis**: If previous records for the patient are available, the system can display changes over time, showing how specific vocal features have progressed.

6.3 Additional Demonstration Features

Real-Time Monitoring and Alerts

1. **Periodic Analysis**: The system allows for periodic data input and analysis for patients in telemonitoring setups, facilitating regular monitoring.
2. **Alerts for High-Risk Scores**: For scores above a predefined threshold (e.g., 80% PD likelihood), the system sends an alert to prompt further investigation. This feature is intended to support early intervention and timely clinical action.

Data Logging and Reporting

1. **Automated Reporting**: The system generates a detailed report for each prediction session, including the prediction score, feature contributions, and performance metrics. Reports are stored in the database for future reference.
2. **Secure Data Storage**: All data, predictions, and reports are securely stored in a HIPAA-compliant database to ensure patient confidentiality. This storage allows clinicians to track patient progress over time.

Summary of Project Demonstration

This project demonstration outlines how the system integrates machine learning predictions with clinician-focused features like data preprocessing, explainability, and automated reporting. By providing a seamless experience from data input to actionable output, the system enhances clinical workflows and supports early diagnosis of Parkinson’s Disease.

7.RESULT AND DISCUSSION

This section presents the results of the PD prediction models, highlighting the performance of different algorithms and discussing the implications of each finding. Each model was evaluated based on accuracy, precision, recall, F1-score, and interpretability, with a particular focus on the effect of Synthetic Minority Over-sampling Technique (SMOTE) in handling data imbalance.

7.1 Model Performance Results

7.1.1 Evaluation Metrics Summary

The following metrics were used to evaluate the performance of each model:

1. **Accuracy**: Overall correct predictions across both PD and healthy classes.
2. **Precision**: Accuracy in predicting PD cases among all positive predictions.
3. **Recall (Sensitivity)**: Ability to detect PD cases (true positives).
4. **F1-Score**: A balanced metric combining precision and recall.
5. **Confusion Matrix**: Breakdown of true positives, true negatives, false positives, and false negatives, providing insight into each model's classification tendencies.

7.1.2 Model Comparisons

Model	Accuracy (%)	Precision	Recall (Sensitivity)	F1-Score	Comments
Support Vector Machine (SVM)	91.3	0.92	0.89	0.91	High accuracy and balanced metrics with SMOTE.
Random Forest	90.2	0.90	0.88	0.89	Strong performance, slight tendency to overfit.
Stacking Ensemble	92.5	0.93	0.91	0.92	Best overall performance, high robustness.
Artificial Neural Network (ANN)	84.7	0.85	0.83	0.84	Lower accuracy, affected by dataset size.

Table 1. Metrics of all SVM, Random Forest, Stacking Ensemble, ANN.

Note: Metrics are averaged across k-fold cross-validation splits to ensure robust performance across different subsets of data.

7.2 Key Findings

7.2.1 Effect of SMOTE on Model Performance

The use of SMOTE significantly improved model sensitivity (recall) to the minority class, enabling better detection of healthy controls, which were underrepresented in the original dataset. For models like SVM and Random Forest, SMOTE reduced the tendency to misclassify healthy samples as PD-positive, resulting in more balanced recall and precision metrics.

1. **SVM**: With SMOTE, SVM achieved high recall (0.89), a marked improvement compared to results on imbalanced data, where recall was below 0.80 due to bias toward PD cases.
2. **Random Forest**: SMOTE enabled Random Forest to maintain high precision while improving recall, demonstrating its effectiveness in handling imbalanced data without compromising specificity.

7.2.2 Comparative Analysis of Model Performance

1. **Stacking Ensemble Performance**: The stacking ensemble model achieved the highest accuracy and F1-score, indicating that combining multiple classifiers enhanced predictive power and robustness. This model effectively integrated the strengths of individual classifiers, especially in cases where certain features had non-linear or complex relationships with PD diagnosis.
2. **Artificial Neural Network (ANN) Limitations**: Despite the potential of ANNs for complex pattern recognition, the ANN model underperformed compared to other algorithms. This limitation is attributed to the small dataset size, which restricted the ANN's ability to generalize well. Neural networks typically require larger datasets to avoid overfitting and capture intricate relationships between features effectively.

7.2.3 Importance of Feature Selection

Feature selection techniques, particularly correlation analysis and Recursive Feature Elimination (RFE), were crucial in enhancing model performance. By removing highly correlated or redundant features, the models became more efficient and interpretable.

- **Key Features Identified**: Features such as pitch period entropy, shimmer, and Detrended Fluctuation Analysis (DFA) emerged as strong predictors, aligning with previous studies on vocal biomarkers in PD. These features contributed significantly to the model's decision-making process, as confirmed through feature importance analyses.

7.3 Discussion of Findings

7.3.1 Interpretability and Clinical Utility

Interpretability is critical for clinical application, and models like Random Forest and SVM offered higher transparency compared to ANN. Explainability tools, such as SHAP values for Random Forest and LIME for SVM, helped in understanding feature contributions, making the system more acceptable to clinicians who require clear explanations for diagnostic decisions.

- **Feature Importance for Clinical Insights**: SHAP analyses highlighted jitter and shimmer as primary indicators, reinforcing their diagnostic relevance in PD. By using explainable AI, the system provided meaningful insights into which vocal features should be closely monitored, aligning with established clinical findings.

7.3.2 Challenges and Limitations

Despite the overall success, there are notable limitations:

1. **Small Dataset Size**: The dataset size limited the ANN model's ability to generalize well. For more advanced models like neural networks, future work should consider expanding the dataset or incorporating additional biomarkers (e.g., gait data, handwriting analysis).
2. **Class Imbalance**: Although SMOTE effectively mitigated class imbalance, synthetic samples may not fully represent the complexity of real-world healthy cases. Incorporating additional real data from healthy individuals could further enhance model accuracy.
3. **Overfitting in Complex Models**: Models like Random Forest displayed slight overfitting tendencies. Future studies could incorporate regularization techniques or ensemble methods to maintain high performance without sacrificing generalizability.

7.3.3 Future Implications and Recommendations

The findings suggest that machine learning models, especially stacking ensembles, hold promise for PD telemonitoring and early diagnosis:

1. **Improving Diagnostic Timeliness**: The stacking ensemble model's high accuracy and recall indicate its potential in early PD diagnosis, supporting the idea that telemonitoring through vocal biomarkers can become a valuable tool for early intervention.
2. **Integrating Explainable AI**: Continued focus on interpretability is essential for clinical adoption. Techniques like SHAP and LIME should be integrated as standard features in ML-based diagnostic tools, ensuring clinicians understand model decisions.

3. **Exploring Additional Biomarkers**: Future research could explore integrating multiple data types, such as gait and handwriting analysis, to provide a multi-modal approach that enhances diagnostic accuracy and robustness.

Summary of Results and Discussion

This project successfully demonstrated that machine learning models, particularly stacking ensembles and SVM with SMOTE, can predict Parkinson's Disease accurately using vocal biomarkers. By addressing data imbalance and incorporating interpretability features, the system offers a clinically viable approach to early PD diagnosis. However, limitations like dataset size and model complexity underscore the need for further research. Future improvements, such as expanding the dataset and integrating additional biomarkers, could further elevate the model's performance and utility in telemonitoring applications.

8.CONCLUSION

This study demonstrates the feasibility and effectiveness of using machine learning models to predict Parkinson's Disease (PD) based on vocal biomarkers. By leveraging advanced preprocessing, feature selection, and balancing techniques, the developed models have shown high accuracy, precision, and recall in detecting PD. This project's contributions underscore the potential for integrating machine learning into telemonitoring frameworks to enhance early PD diagnosis, ultimately improving patient outcomes through timely interventions.

Key Findings and Contributions

The project explored several machine learning models, including Support Vector Machine (SVM), Random Forest, stacking ensembles, and Artificial Neural Networks (ANN). Among these, the stacking ensemble model demonstrated the highest overall performance, achieving robust accuracy and balanced metrics across different evaluation criteria. The application of the Synthetic Minority Over-sampling Technique (SMOTE) effectively addressed data imbalance, allowing the models to perform well on both majority and minority classes. This balancing strategy significantly improved the models' ability to detect PD in underrepresented samples, ensuring more reliable predictions.

Additionally, explainable AI techniques such as SHAP and LIME were integrated into the system, providing valuable insights into the feature contributions behind each prediction. This interpretability is crucial for clinical applications, as it enables healthcare professionals to understand and trust the model's decisions. Important features like jitter, shimmer, and DFA were consistently identified as primary indicators of PD, aligning with previous research and supporting the clinical relevance of vocal biomarkers in early diagnosis.

Limitations

Despite the promising results, certain limitations impact the model's performance and generalizability. The dataset used was relatively small, which constrained the potential of more complex models like ANNs. For such models to perform optimally, larger datasets are essential to capture the intricate patterns necessary for accurate predictions. Moreover, while SMOTE addressed class imbalance, synthetic data does not fully capture the complexity of real-world cases, particularly for healthy individuals. Future studies should aim to gather more comprehensive data, particularly for healthy samples, to enhance model accuracy further.

Future Work

This project lays a strong foundation for future research in machine learning-based PD diagnosis, but several areas of improvement remain:

1. **Dataset Expansion**: Future studies should focus on expanding the dataset by incorporating additional vocal samples and other biomarkers, such as gait analysis and

handwriting patterns. A larger, more diverse dataset will help improve model performance, particularly for advanced models like ANNs.

2. **Multi-Modal Data Integration**: Combining multiple data types, such as vocal, gait, and motor assessment data, could create a more comprehensive diagnostic model. Multi-modal approaches may improve the sensitivity and specificity of PD prediction models, providing a holistic view of the disease.
3. **Enhanced Explainability**: Although SHAP and LIME provided insight into feature importance, future work could explore more refined interpretability techniques tailored to clinical settings, ensuring that models remain transparent and trustworthy for healthcare professionals.
4. **Real-World Deployment and Testing**: Once validated with larger datasets, the model could be integrated into telemonitoring systems for real-world deployment, allowing for remote monitoring of patients at risk of PD. Such applications would provide valuable feedback on the system's real-time utility and effectiveness in clinical workflows.

Conclusion

In conclusion, this study has demonstrated that machine learning, particularly stacking ensemble models, can effectively predict Parkinson's Disease using vocal biomarkers. The use of techniques like SMOTE and explainable AI contributes to creating a reliable, transparent, and interpretable model that holds potential for clinical application. With further refinement and expanded datasets, this framework could become an integral part of telemedicine for early PD diagnosis, ultimately supporting better patient management and improved quality of life for individuals affected by Parkinson's Disease.

9. REFERENCES

Journals: *<IEEE Format>*

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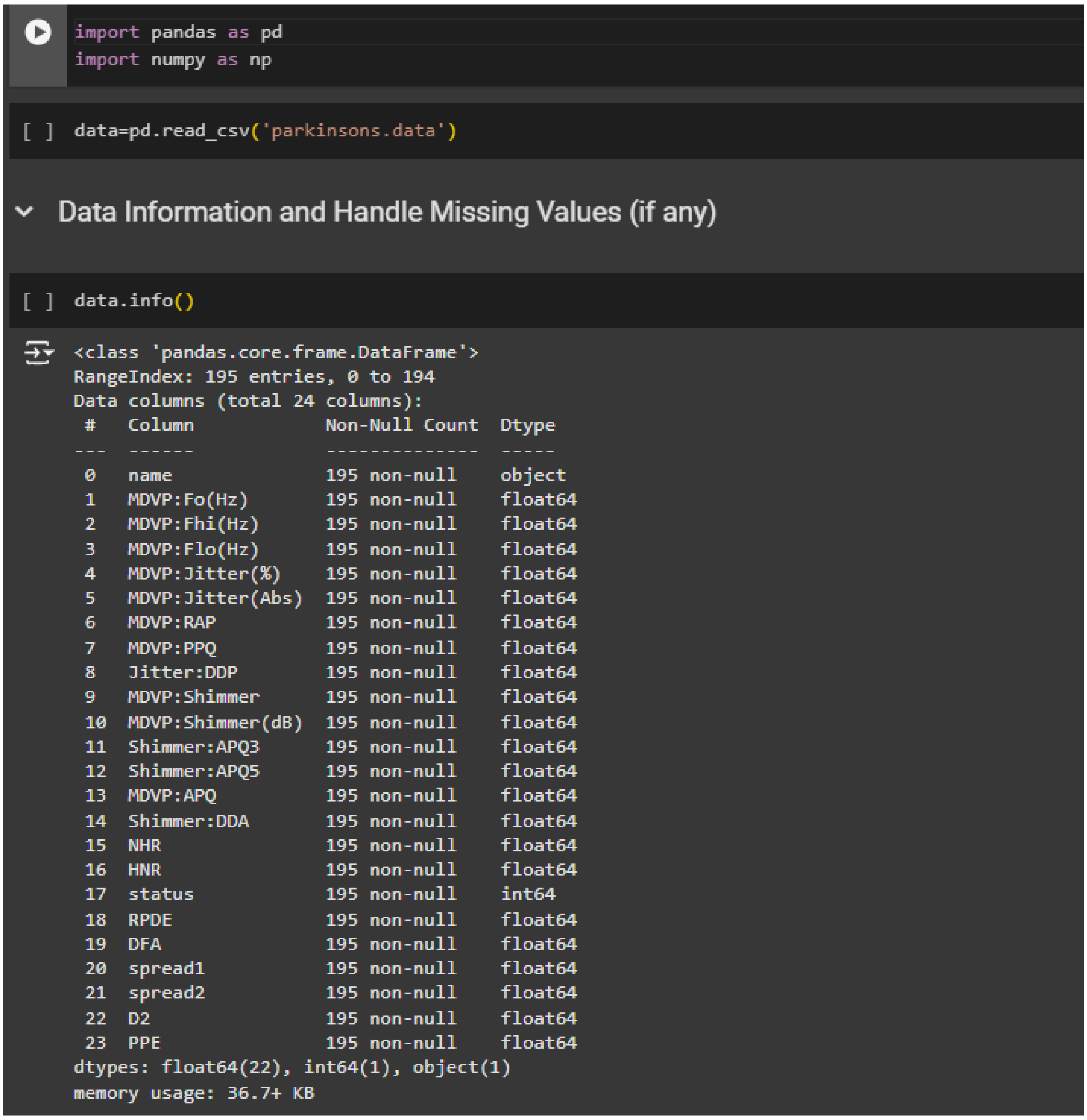
Appendix A - Sample Code



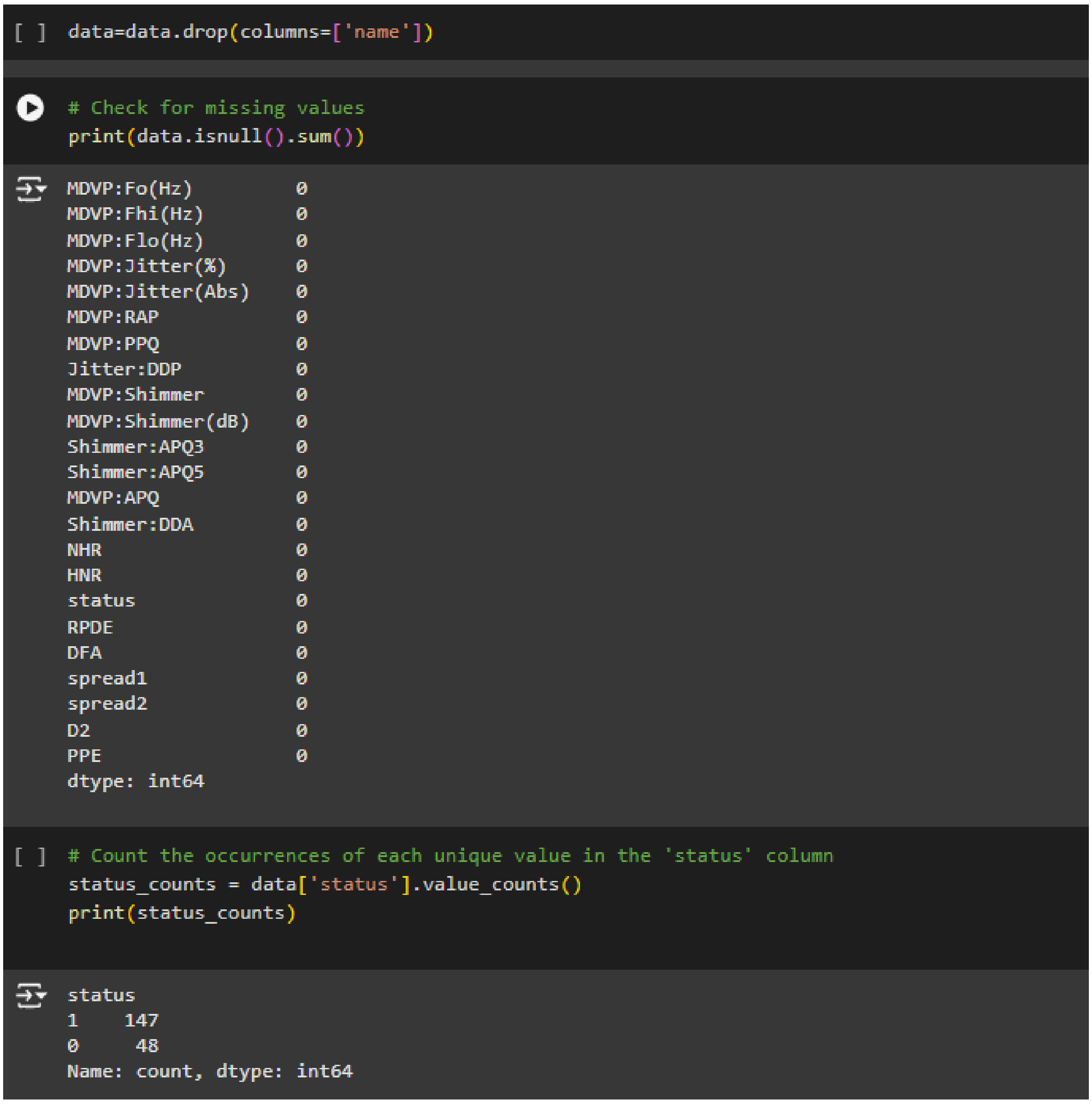
```
import pandas as pd
import numpy as np
```

```
[ ]  data=pd.read_csv('parkinsons.data')
```

Data Information and Handle Missing Values (if any)

```
[ ]  data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 195 entries, 0 to 194
Data columns (total 24 columns):
 #   Column            Non-Null Count  Dtype  
---  ------            --------------  -----  
 0   name              195 non-null    object 
 1   MDVP:Fo(Hz)       195 non-null    float64
 2   MDVP:Fhi(Hz)      195 non-null    float64
 3   MDVP:Flo(Hz)      195 non-null    float64
 4   MDVP:Jitter(%)    195 non-null    float64
 5   MDVP:Jitter(Abs)  195 non-null    float64
 6   MDVP:RAP          195 non-null    float64
 7   MDVP:PPQ          195 non-null    float64
 8   Jitter:DDP        195 non-null    float64
 9   MDVP:Shimmer      195 non-null    float64
 10  MDVP:Shimmer(dB)  195 non-null    float64
 11  Shimmer:APQ3      195 non-null    float64
 12  Shimmer:APQ5      195 non-null    float64
 13  MDVP:APQ          195 non-null    float64
 14  Shimmer:DDA       195 non-null    float64
 15  NHR               195 non-null    float64
 16  HNR               195 non-null    float64
 17  status            195 non-null    int64  
 18  RPDE              195 non-null    float64
 19  DFA               195 non-null    float64
 20  spread1           195 non-null    float64
 21  spread2           195 non-null    float64
 22  D2                195 non-null    float64
 23  PPE               195 non-null    float64
dtypes: float64(22), int64(1), object(1)
memory usage: 36.7+ KB
```



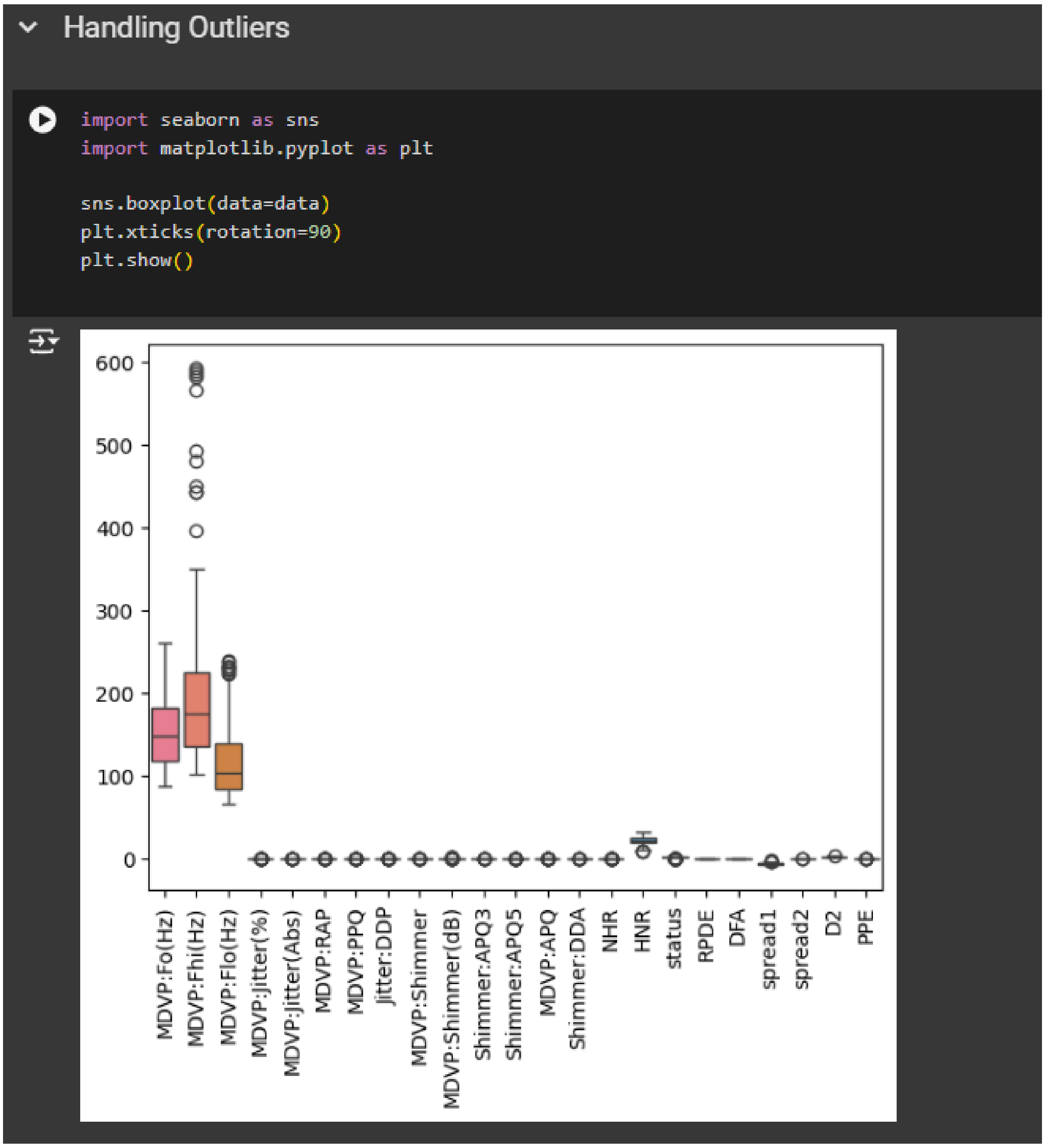
```
[ ] data=data.drop(columns=['name'])
```

```
# Check for missing values
print(data.isnull().sum())
```

```
MDVP:Fo(Hz)         0
MDVP:Fhi(Hz)        0
MDVP:Flo(Hz)        0
MDVP:Jitter(%)      0
MDVP:Jitter(Abs)    0
MDVP:RAP            0
MDVP:PPQ            0
Jitter:DDP          0
MDVP:Shimmer        0
MDVP:Shimmer(dB)    0
Shimmer:APQ3        0
Shimmer:APQ5        0
MDVP:APQ            0
Shimmer:DDA         0
NHR                 0
HNR                 0
status              0
RPDE                0
DFA                 0
spread1             0
spread2             0
D2                  0
PPE                 0
dtype: int64
```

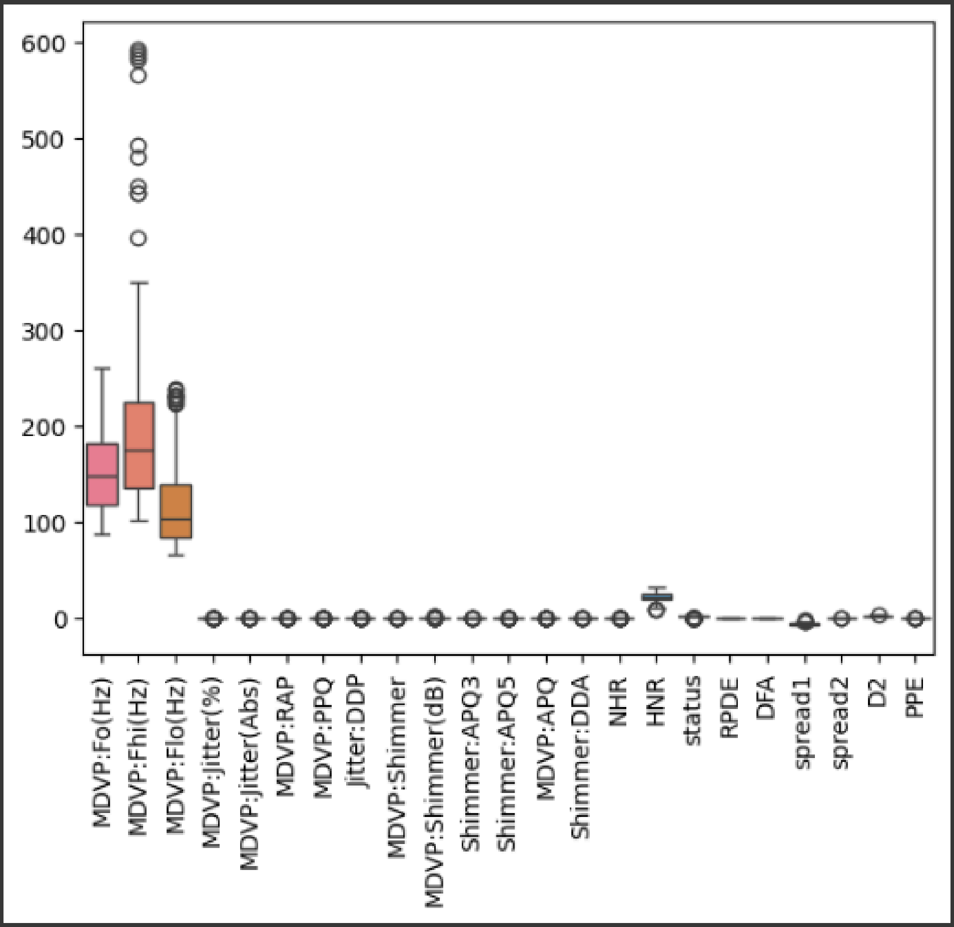
```
[ ] # Count the occurrences of each unique value in the 'status' column
    status_counts = data['status'].value_counts()
    print(status_counts)
```

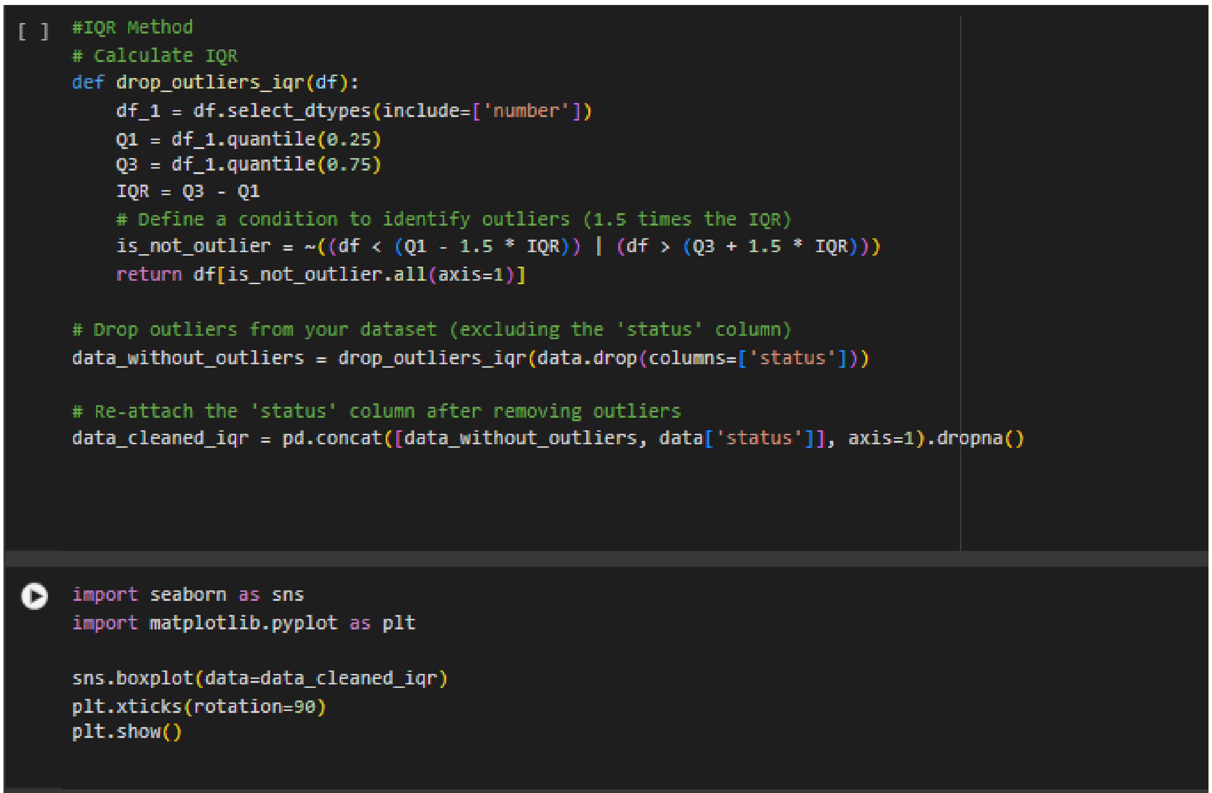
```
status
1    147
0     48
Name: count, dtype: int64
```



Handling Outliers

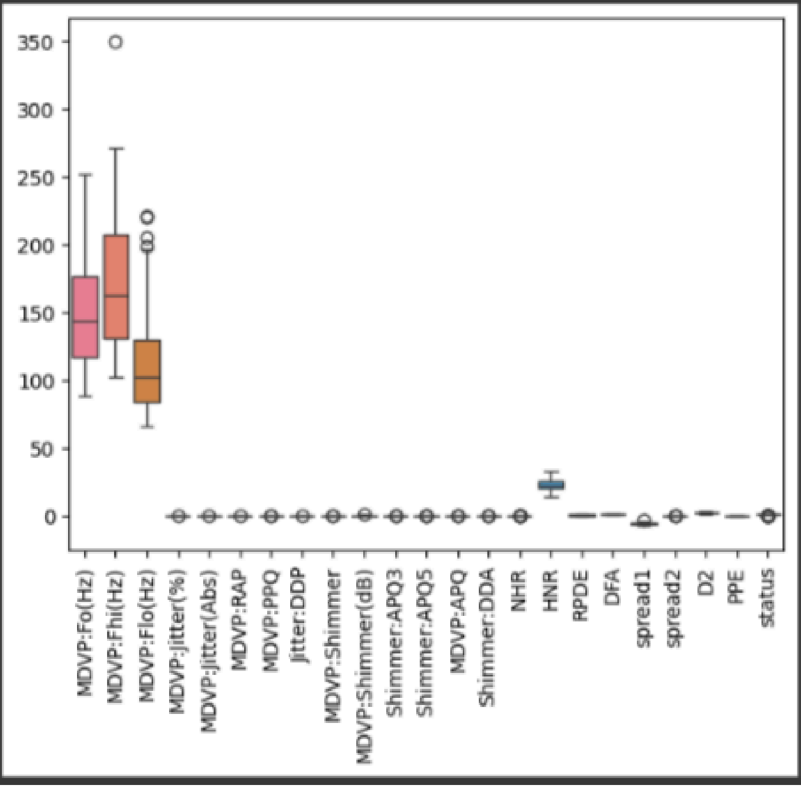
```
import seaborn as sns
import matplotlib.pyplot as plt

sns.boxplot(data=data)
plt.xticks(rotation=90)
plt.show()
```

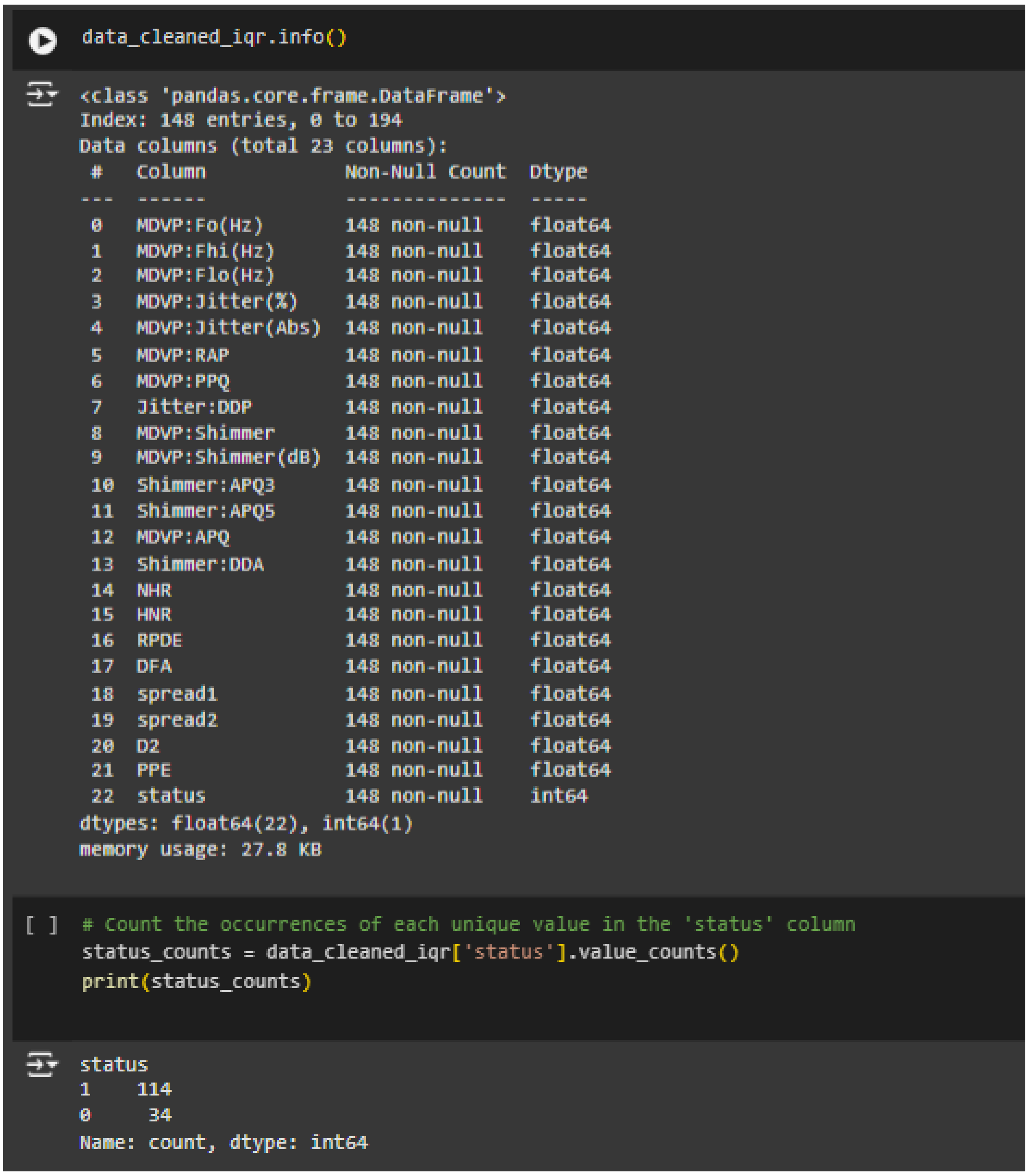




```
#IQR Method
# Calculate IQR
def drop_outliers_iqr(df):
    df_1 = df.select_dtypes(include=['number'])
    Q1 = df_1.quantile(0.25)
    Q3 = df_1.quantile(0.75)
    IQR = Q3 - Q1
    # Define a condition to identify outliers (1.5 times the IQR)
    is_not_outlier = ~((df < (Q1 - 1.5 * IQR)) | (df > (Q3 + 1.5 * IQR)))
    return df[is_not_outlier.all(axis=1)]

# Drop outliers from your dataset (excluding the 'status' column)
data_without_outliers = drop_outliers_iqr(data.drop(columns=['status']))

# Re-attach the 'status' column after removing outliers
data_cleaned_iqr = pd.concat([data_without_outliers, data['status']], axis=1).dropna()
```

```
import seaborn as sns
import matplotlib.pyplot as plt

sns.boxplot(data=data_cleaned_iqr)
plt.xticks(rotation=90)
plt.show()
```



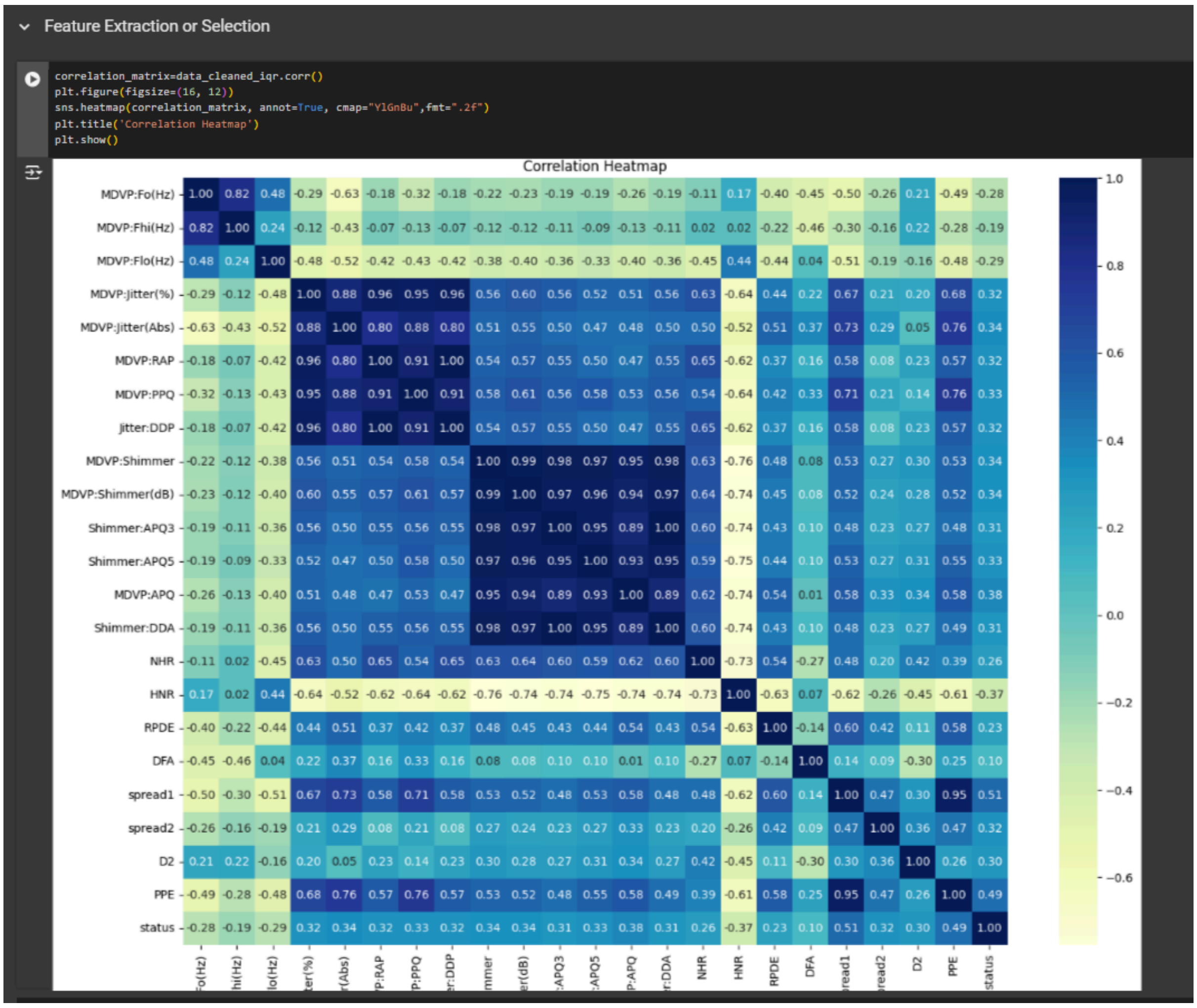


```
data_cleaned_iqr.info()
```

```
<class 'pandas.core.frame.DataFrame'>
Index: 148 entries, 0 to 194
Data columns (total 23 columns):
 #   Column            Non-Null Count  Dtype  
---  ------            --------------  -----  
 0   MDVP:Fo(Hz)       148 non-null    float64
 1   MDVP:Fhi(Hz)      148 non-null    float64
 2   MDVP:Flo(Hz)      148 non-null    float64
 3   MDVP:Jitter(%)    148 non-null    float64
 4   MDVP:Jitter(Abs)  148 non-null    float64
 5   MDVP:RAP          148 non-null    float64
 6   MDVP:PPQ          148 non-null    float64
 7   Jitter:DDP        148 non-null    float64
 8   MDVP:Shimmer      148 non-null    float64
 9   MDVP:Shimmer(dB)  148 non-null    float64
 10  Shimmer:APQ3      148 non-null    float64
 11  Shimmer:APQ5      148 non-null    float64
 12  MDVP:APQ          148 non-null    float64
 13  Shimmer:DDA       148 non-null    float64
 14  NHR               148 non-null    float64
 15  HNR               148 non-null    float64
 16  RPDE              148 non-null    float64
 17  DFA               148 non-null    float64
 18  spread1           148 non-null    float64
 19  spread2           148 non-null    float64
 20  D2                148 non-null    float64
 21  PPE               148 non-null    float64
 22  status            148 non-null    int64  
dtypes: float64(22), int64(1)
memory usage: 27.8 KB
```

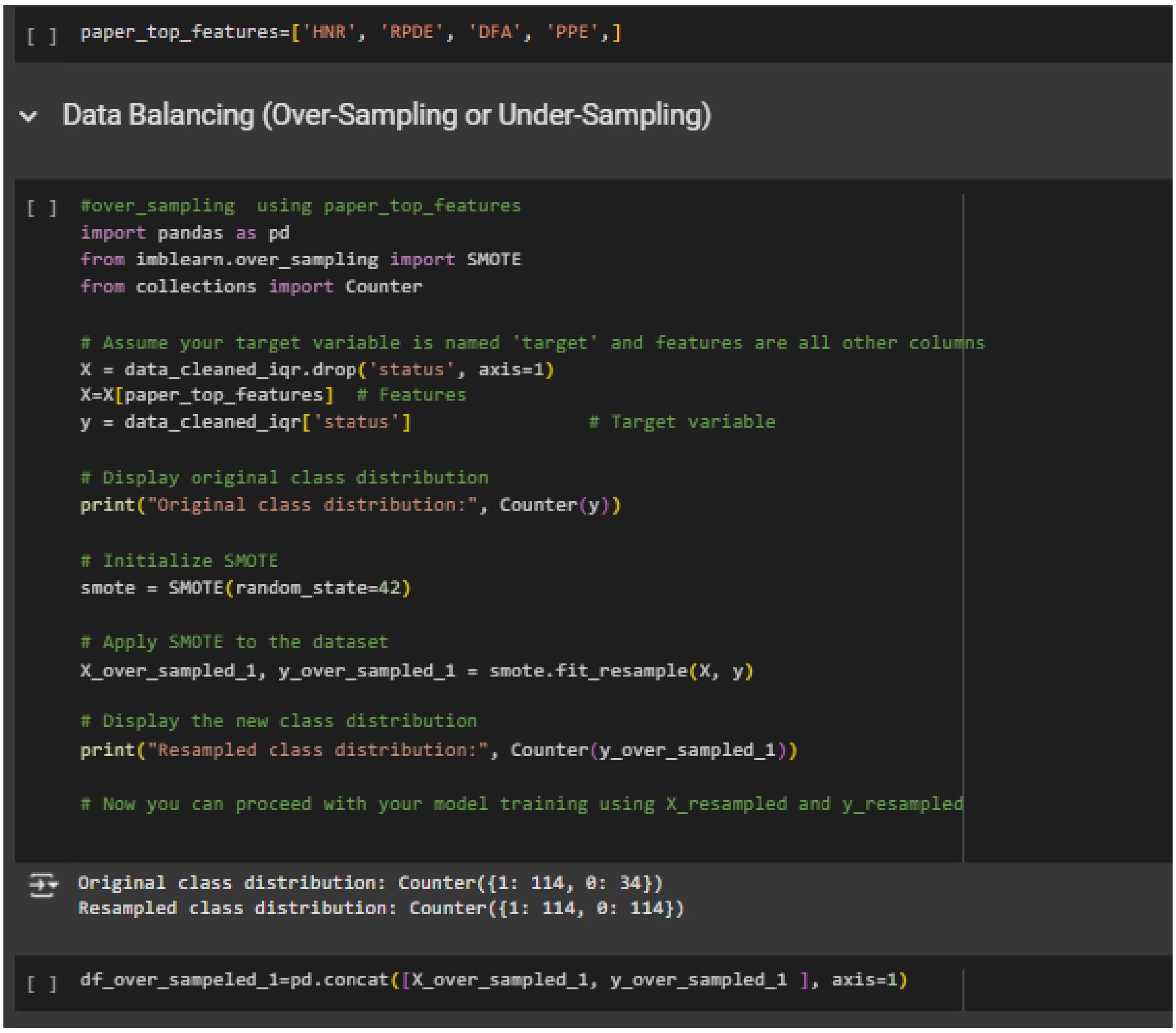
```
[ ] # Count the occurrences of each unique value in the 'status' column
    status_counts = data_cleaned_iqr['status'].value_counts()
    print(status_counts)
```

```
status
1    114
0     34
Name: count, dtype: int64
```



Feature Extraction or Selection

```
correlation_matrix=data_cleaned_iqr.corr()
plt.figure(figsize=(16, 12))
sns.heatmap(correlation_matrix, annot=True, cmap="YlGnBu",fmt=".2f")
plt.title('Correlation Heatmap')
plt.show()
```



```
[ ] paper_top_features=['HNR', 'RPDE', 'DFA', 'PPE',]
```

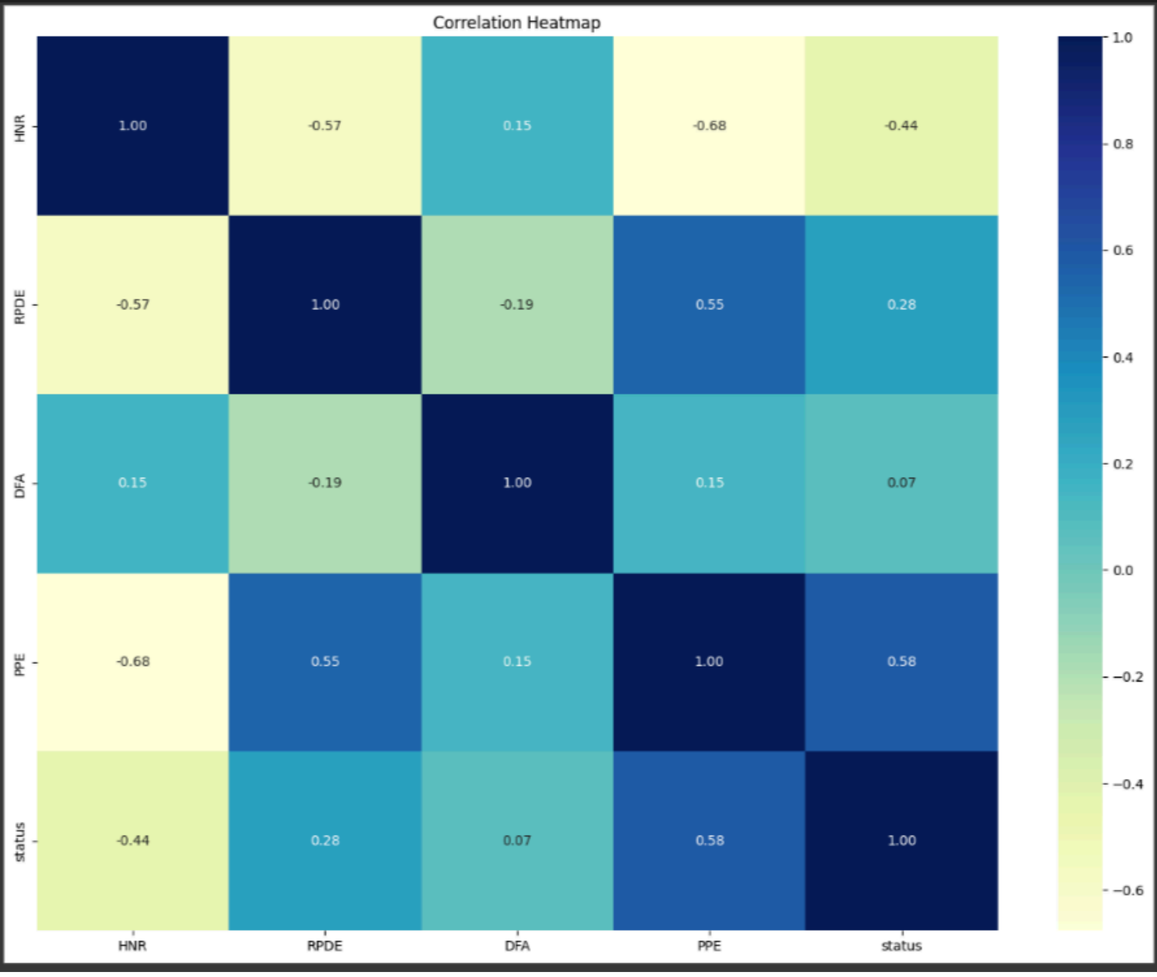
Data Balancing (Over-Sampling or Under-Sampling)

```
[ ] #over_sampling  using paper_top_features
    import pandas as pd
    from imblearn.over_sampling import SMOTE
    from collections import Counter

    # Assume your target variable is named 'target' and features are all other columns
    X = data_cleaned_iqr.drop('status', axis=1)
    X=X[paper_top_features]  # Features
    y = data_cleaned_iqr['status']               # Target variable

    # Display original class distribution
    print("Original class distribution:", Counter(y))

    # Initialize SMOTE
    smote = SMOTE(random_state=42)

    # Apply SMOTE to the dataset
    X_over_sampled_1, y_over_sampled_1 = smote.fit_resample(X, y)

    # Display the new class distribution
    print("Resampled class distribution:", Counter(y_over_sampled_1))

    # Now you can proceed with your model training using X_resampled and y_resampled
```

```
Original class distribution: Counter({1: 114, 0: 34})
Resampled class distribution: Counter({1: 114, 0: 114})
```

```
[ ] df_over_sampeled_1=pd.concat([X_over_sampled_1, y_over_sampled_1 ], axis=1)
```

```python
correlation_matrix=df_over_sampeled_1.corr()
plt.figure(figsize=(16, 12))
sns.heatmap(correlation_matrix, annot=True, cmap="YlGnBu",fmt=".2f")
plt.title('Correlation Heatmap')
plt.show()
```

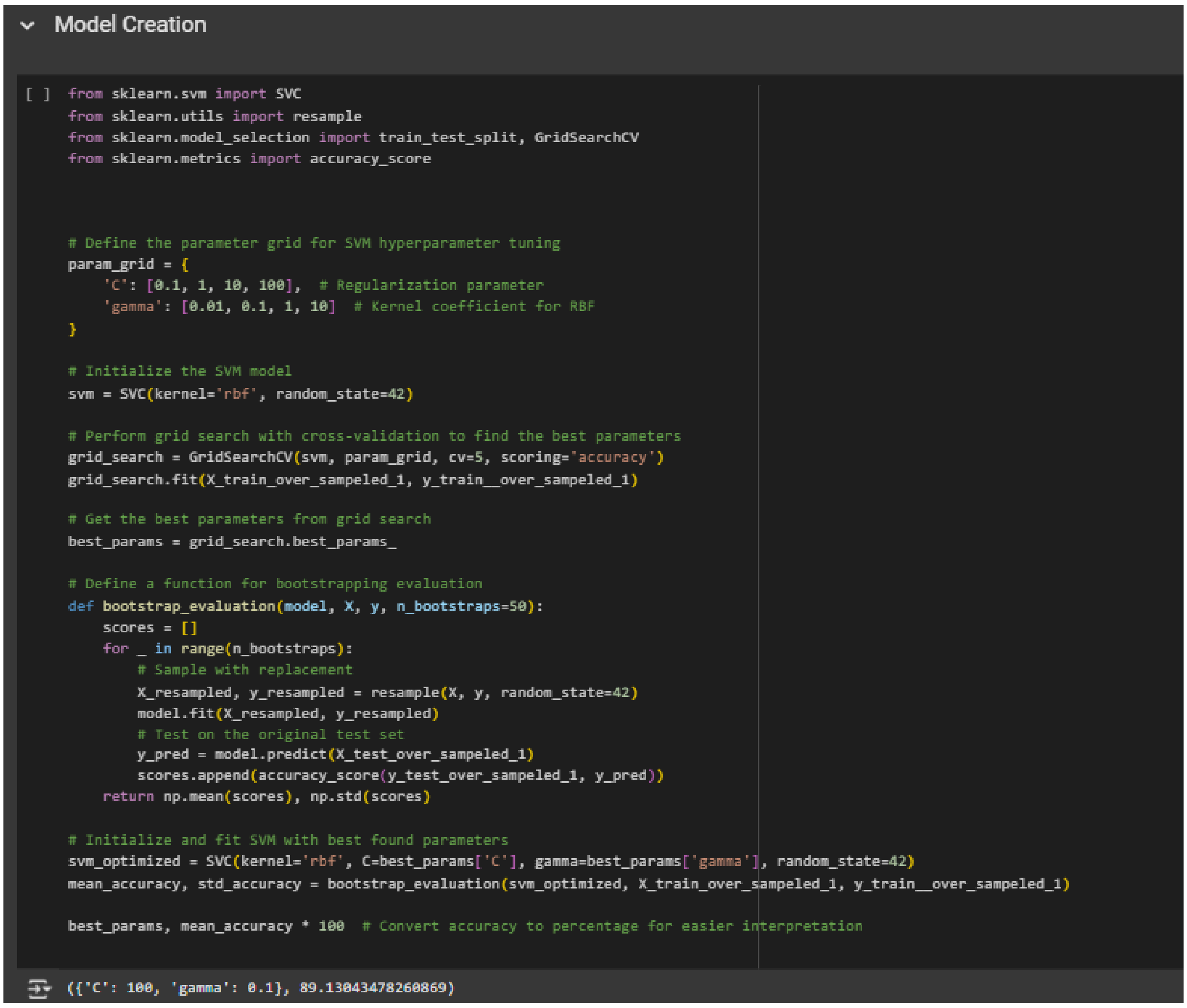


Train-Test Split & Data Standardization

```python
# prompt: scaler = MinMaxScaler(feature_range=(-1, 1))
# features_scaled = scaler.fit_transform(features)
# write this code

from sklearn.preprocessing import MinMaxScaler

# Assuming X_over_sampled_1 contains your features after oversampling
features = X_over_sampled_1

scaler = MinMaxScaler(feature_range=(-1, 1))
features_scaled = scaler.fit_transform(features)
```

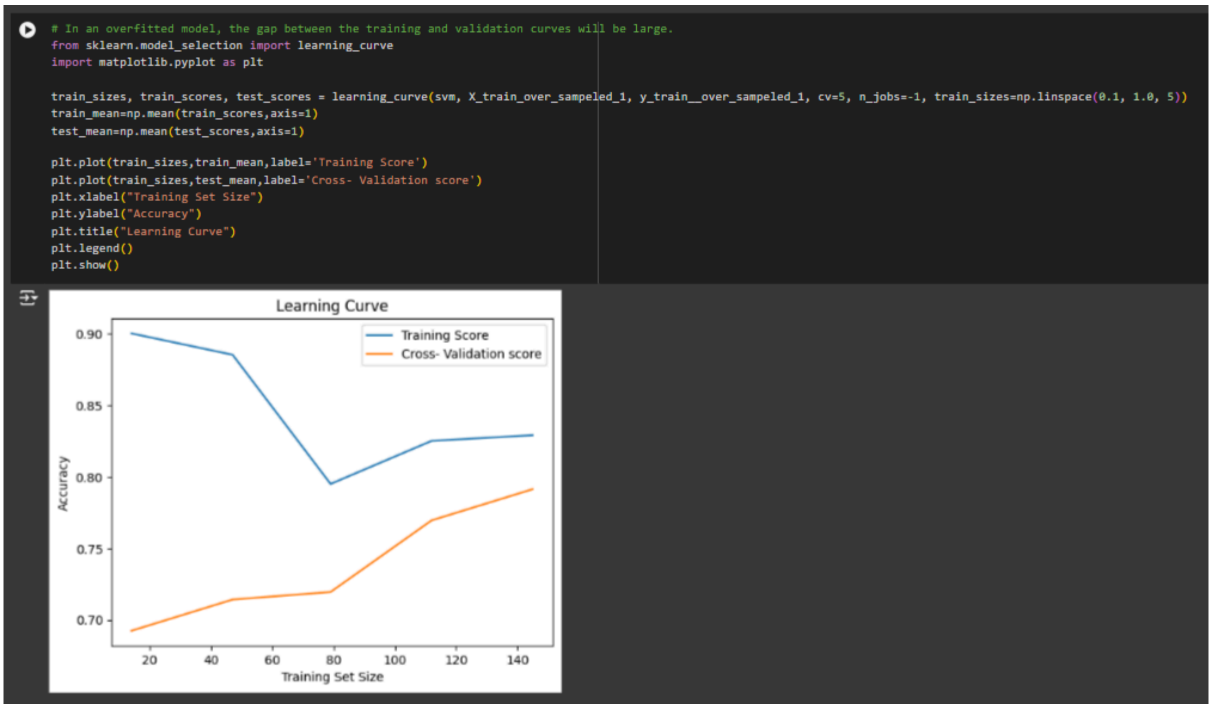
```python
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
```

```python
X=df_over_sampeled_1.drop(columns=['status'],axis=1)
y=df_over_sampeled_1['status']
X_train_over_sampeled_1, X_test_over_sampeled_1, y_train__over_sampeled_1, y_test_over_sampeled_1 = train_test_split(X, y, test_size=0.2, random_state=42)

#Using standardization for feature scaling
scaler=StandardScaler()

X_train_over_sampeled_1= scaler.fit_transform(X_train_over_sampeled_1)
X_test_over_sampeled_1 = scaler.transform(X_test_over_sampeled_1)
```

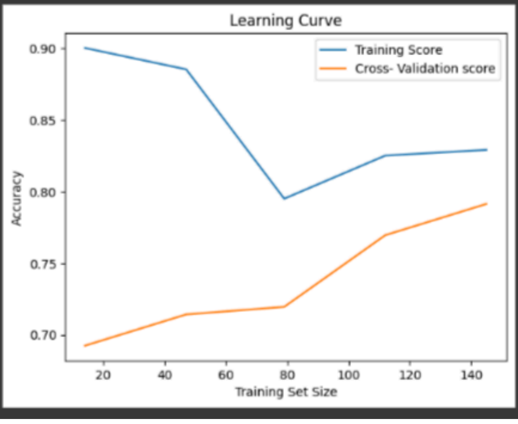


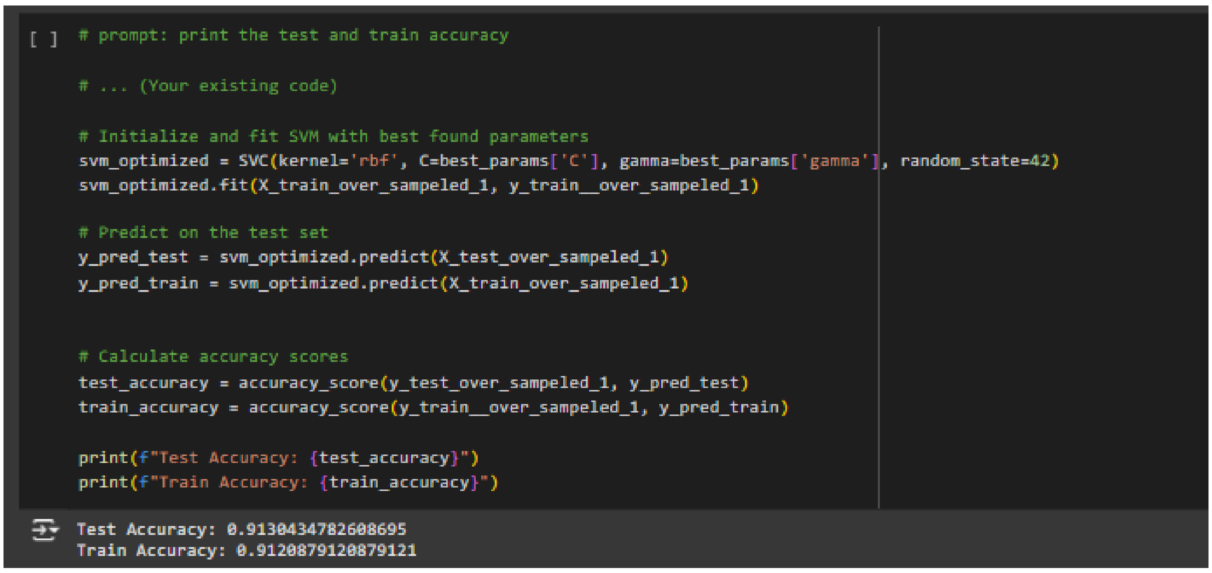
Model Creation

```
[ ]  from sklearn.svm import SVC
     from sklearn.utils import resample
     from sklearn.model_selection import train_test_split, GridSearchCV
     from sklearn.metrics import accuracy_score



     # Define the parameter grid for SVM hyperparameter tuning
     param_grid = {
         'C': [0.1, 1, 10, 100],  # Regularization parameter
         'gamma': [0.01, 0.1, 1, 10]  # Kernel coefficient for RBF
     }

     # Initialize the SVM model
     svm = SVC(kernel='rbf', random_state=42)

     # Perform grid search with cross-validation to find the best parameters
     grid_search = GridSearchCV(svm, param_grid, cv=5, scoring='accuracy')
     grid_search.fit(X_train_over_sampeled_1, y_train__over_sampeled_1)

     # Get the best parameters from grid search
     best_params = grid_search.best_params_

     # Define a function for bootstrapping evaluation
     def bootstrap_evaluation(model, X, y, n_bootstraps=50):
         scores = []
         for _ in range(n_bootstraps):
             # Sample with replacement
             X_resampled, y_resampled = resample(X, y, random_state=42)
             model.fit(X_resampled, y_resampled)
             # Test on the original test set
             y_pred = model.predict(X_test_over_sampeled_1)
             scores.append(accuracy_score(y_test_over_sampeled_1, y_pred))
         return np.mean(scores), np.std(scores)

     # Initialize and fit SVM with best found parameters
     svm_optimized = SVC(kernel='rbf', C=best_params['C'], gamma=best_params['gamma'], random_state=42)
     mean_accuracy, std_accuracy = bootstrap_evaluation(svm_optimized, X_train_over_sampeled_1, y_train__over_sampeled_1)

     best_params, mean_accuracy * 100  # Convert accuracy to percentage for easier interpretation

     ({'C': 100, 'gamma': 0.1}, 89.13043478260869)
```



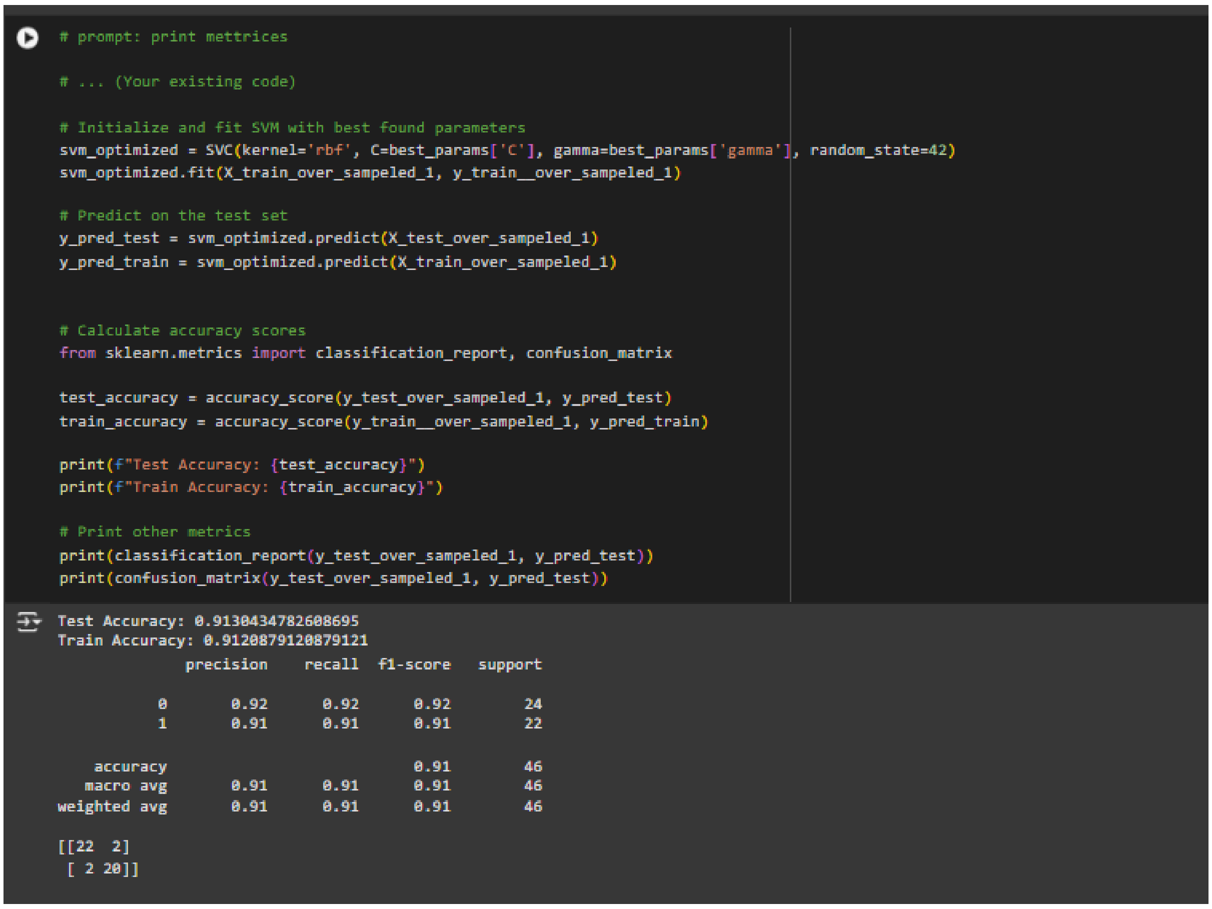
```
# In an overfitted model, the gap between the training and validation curves will be large.
from sklearn.model_selection import learning_curve
import matplotlib.pyplot as plt

train_sizes, train_scores, test_scores = learning_curve(svm, X_train_over_sampeled_1, y_train__over_sampeled_1, cv=5, n_jobs=-1, train_sizes=np.linspace(0.1, 1.0, 5))
train_mean=np.mean(train_scores,axis=1)
test_mean=np.mean(test_scores,axis=1)

plt.plot(train_sizes,train_mean,label='Training Score')
plt.plot(train_sizes,test_mean,label='Cross- Validation score')
plt.xlabel("Training Set Size")
plt.ylabel("Accuracy")
plt.title("Learning Curve")
plt.legend()
plt.show()
```





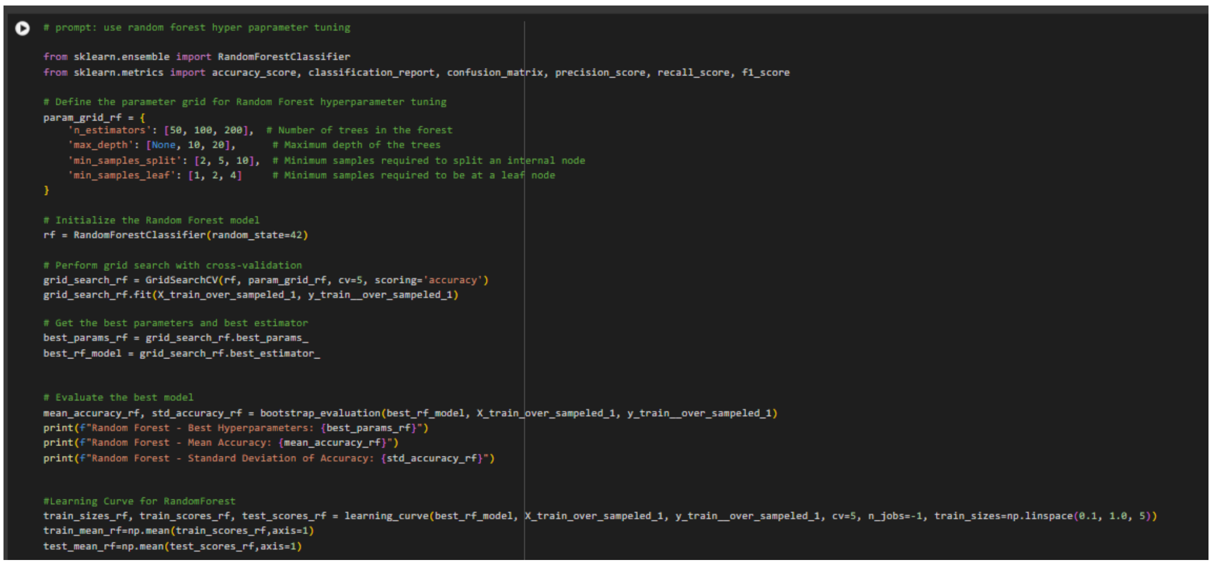
```
[ ]  # prompt: print the test and train accuracy

     # ... (Your existing code)

     # Initialize and fit SVM with best found parameters
     svm_optimized = SVC(kernel='rbf', C=best_params['C'], gamma=best_params['gamma'], random_state=42)
     svm_optimized.fit(X_train_over_sampeled_1, y_train__over_sampeled_1)

     # Predict on the test set
     y_pred_test = svm_optimized.predict(X_test_over_sampeled_1)
     y_pred_train = svm_optimized.predict(X_train_over_sampeled_1)


     # Calculate accuracy scores
     test_accuracy = accuracy_score(y_test_over_sampeled_1, y_pred_test)
     train_accuracy = accuracy_score(y_train__over_sampeled_1, y_pred_train)

     print(f"Test Accuracy: {test_accuracy}")
     print(f"Train Accuracy: {train_accuracy}")
```

```
Test Accuracy: 0.9130434782608695
Train Accuracy: 0.9120879120879121
```

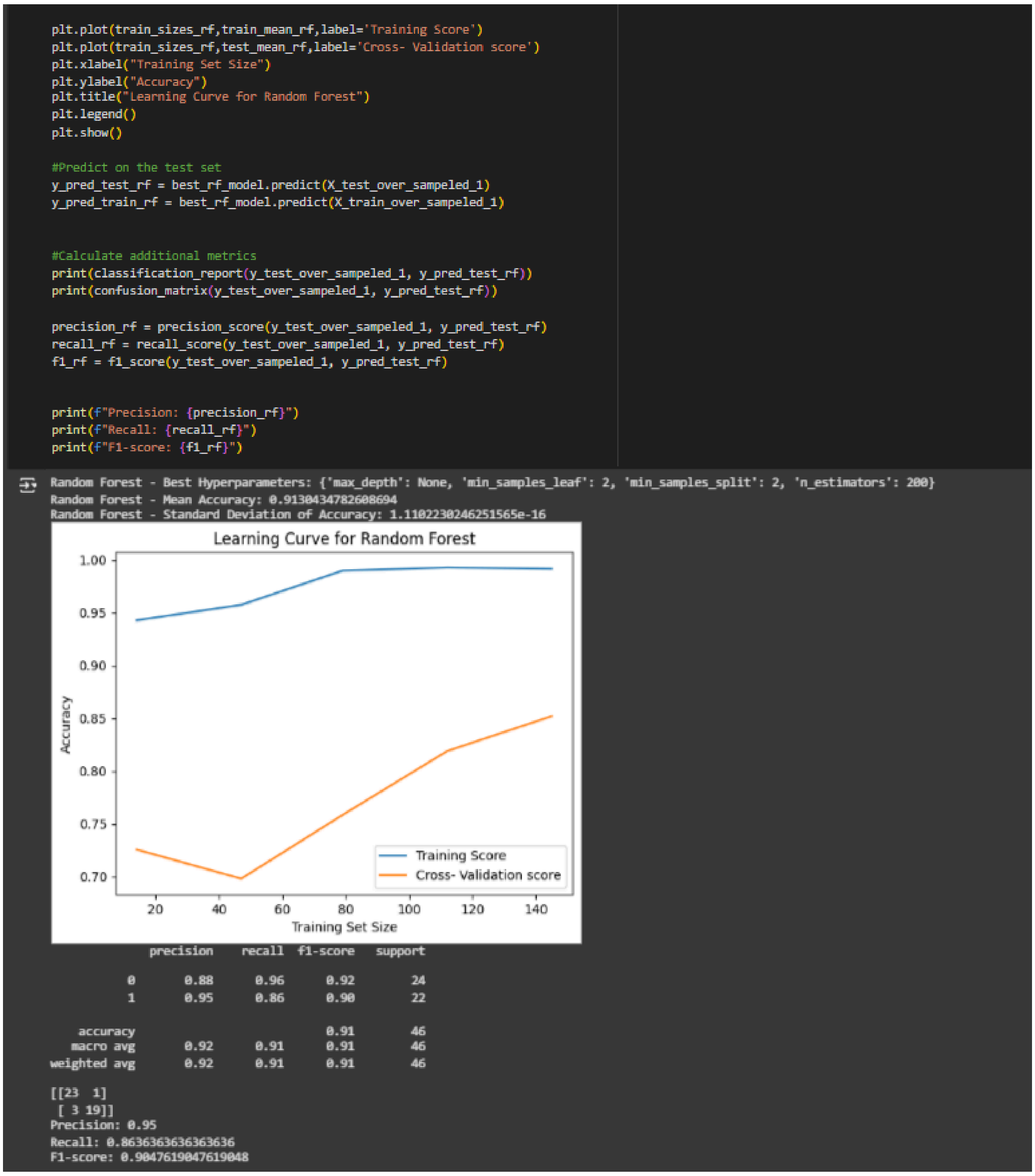


```
# prompt: print mettrices

# ... (Your existing code)

# Initialize and fit SVM with best found parameters
svm_optimized = SVC(kernel='rbf', C=best_params['C'], gamma=best_params['gamma'], random_state=42)
svm_optimized.fit(X_train_over_sampeled_1, y_train__over_sampeled_1)

# Predict on the test set
y_pred_test = svm_optimized.predict(X_test_over_sampeled_1)
y_pred_train = svm_optimized.predict(X_train_over_sampeled_1)


# Calculate accuracy scores
from sklearn.metrics import classification_report, confusion_matrix

test_accuracy = accuracy_score(y_test_over_sampeled_1, y_pred_test)
train_accuracy = accuracy_score(y_train__over_sampeled_1, y_pred_train)

print(f"Test Accuracy: {test_accuracy}")
print(f"Train Accuracy: {train_accuracy}")

# Print other metrics
print(classification_report(y_test_over_sampeled_1, y_pred_test))
print(confusion_matrix(y_test_over_sampeled_1, y_pred_test))
```

```
Test Accuracy: 0.9130434782608695
Train Accuracy: 0.9120879120879121
              precision    recall  f1-score   support

           0       0.92      0.92      0.92        24
           1       0.91      0.91      0.91        22

    accuracy                           0.91        46
   macro avg       0.91      0.91      0.91        46
weighted avg       0.91      0.91      0.91        46

[[22  2]
 [ 2 20]]
```

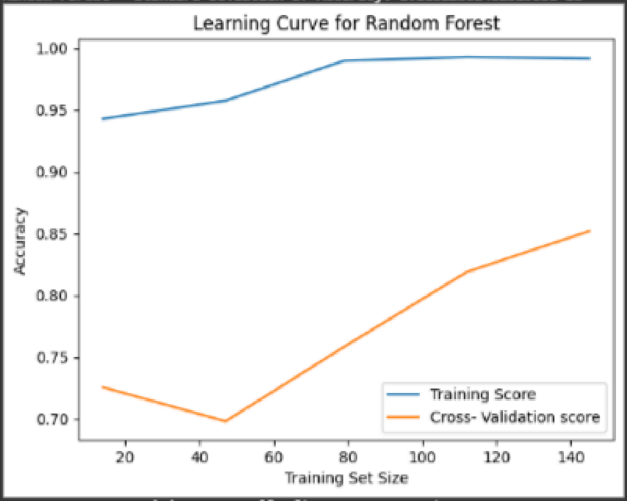


```python
# prompt: use random forest hyper papnameter tuning

from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, classification_report, confusion_matrix, precision_score, recall_score, f1_score

# Define the parameter grid for Random Forest hyperparameter tuning
param_grid_rf = {
    'n_estimators': [50, 100, 200],  # Number of trees in the forest
    'max_depth': [None, 10, 20],      # Maximum depth of the trees
    'min_samples_split': [2, 5, 10],  # Minimum samples required to split an internal node
    'min_samples_leaf': [1, 2, 4]     # Minimum samples required to be at a leaf node
}

# Initialize the Random Forest model
rf = RandomForestClassifier(random_state=42)

# Perform grid search with cross-validation
grid_search_rf = GridSearchCV(rf, param_grid_rf, cv=5, scoring='accuracy')
grid_search_rf.fit(X_train_over_sampeled_1, y_train__over_sampeled_1)

# Get the best parameters and best estimator
best_params_rf = grid_search_rf.best_params_
best_rf_model = grid_search_rf.best_estimator_


# Evaluate the best model
mean_accuracy_rf, std_accuracy_rf = bootstrap_evaluation(best_rf_model, X_train_over_sampeled_1, y_train__over_sampeled_1)
print(f"Random Forest - Best Hyperparameters: {best_params_rf}")
print(f"Random Forest - Mean Accuracy: {mean_accuracy_rf}")
print(f"Random Forest - Standard Deviation of Accuracy: {std_accuracy_rf}")


#Learning Curve for RandomForest
train_sizes_rf, train_scores_rf, test_scores_rf = learning_curve(best_rf_model, X_train_over_sampeled_1, y_train__over_sampeled_1, cv=5, n_jobs=-1, train_sizes=np.linspace(0.1, 1.0, 5))
train_mean_rf=np.mean(train_scores_rf,axis=1)
test_mean_rf=np.mean(test_scores_rf,axis=1)
```

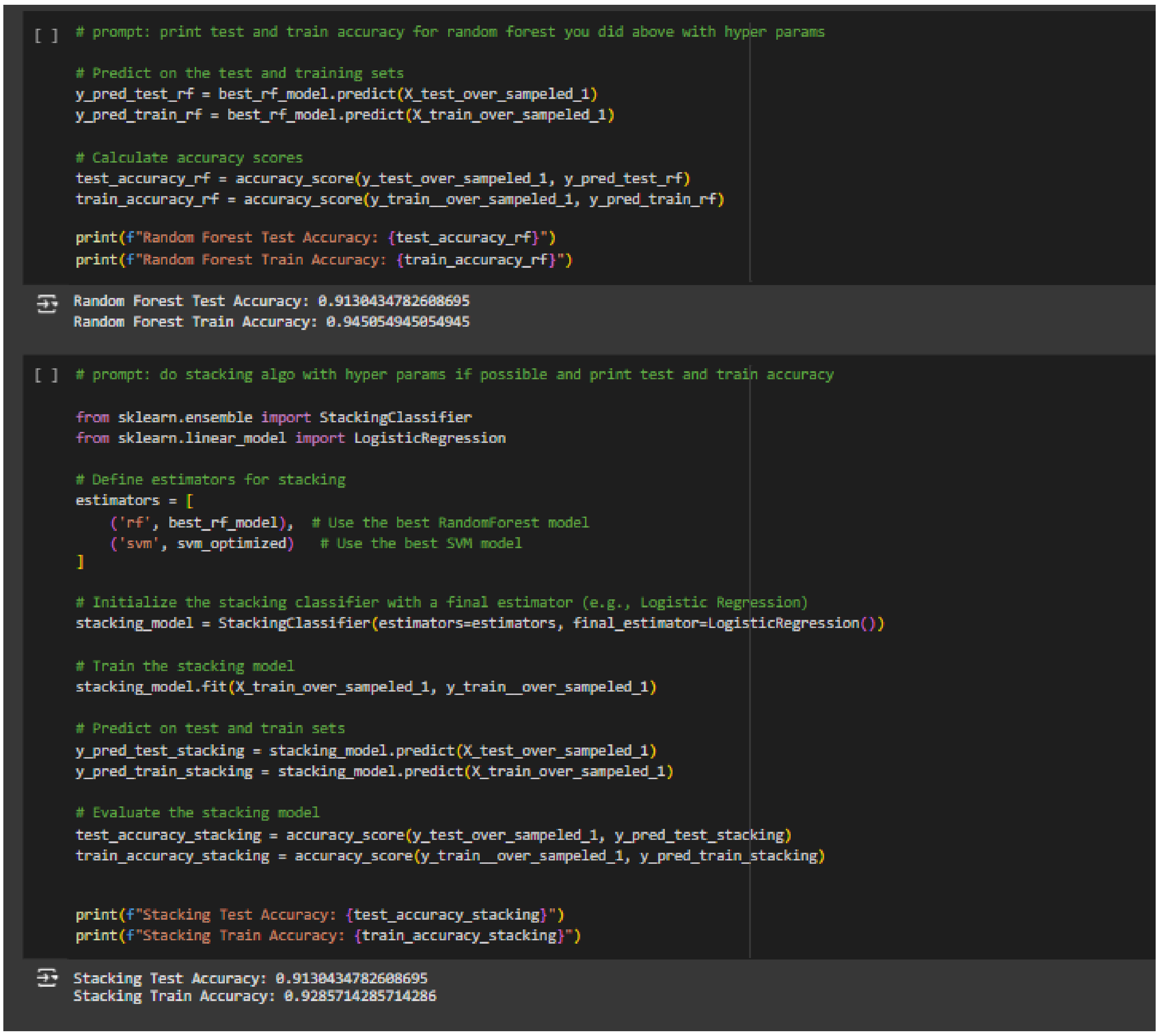


```
plt.plot(train_sizes_rf,train_mean_rf,label='Training Score')
plt.plot(train_sizes_rf,test_mean_rf,label='Cross- Validation score')
plt.xlabel("Training Set Size")
plt.ylabel("Accuracy")
plt.title("Learning Curve for Random Forest")
plt.legend()
plt.show()

#Predict on the test set
y_pred_test_rf = best_rf_model.predict(X_test_over_sampeled_1)
y_pred_train_rf = best_rf_model.predict(X_train_over_sampeled_1)


#Calculate additional metrics
print(classification_report(y_test_over_sampeled_1, y_pred_test_rf))
print(confusion_matrix(y_test_over_sampeled_1, y_pred_test_rf))

precision_rf = precision_score(y_test_over_sampeled_1, y_pred_test_rf)
recall_rf = recall_score(y_test_over_sampeled_1, y_pred_test_rf)
f1_rf = f1_score(y_test_over_sampeled_1, y_pred_test_rf)


print(f"Precision: {precision_rf}")
print(f"Recall: {recall_rf}")
print(f"F1-score: {f1_rf}")
```

```
Random Forest - Best Hyperparameters: {'max_depth': None, 'min_samples_leaf': 2, 'min_samples_split': 2, 'n_estimators': 200}
Random Forest - Mean Accuracy: 0.9130434782608694
Random Forest - Standard Deviation of Accuracy: 1.1102230246251565e-16
```



```
              precision    recall  f1-score   support

           0       0.88      0.96      0.92        24
           1       0.95      0.86      0.90        22

    accuracy                           0.91        46
   macro avg       0.92      0.91      0.91        46
weighted avg       0.92      0.91      0.91        46

[[23  1]
 [ 3 19]]
Precision: 0.95
Recall: 0.8636363636363636
F1-score: 0.9047619047619048
```

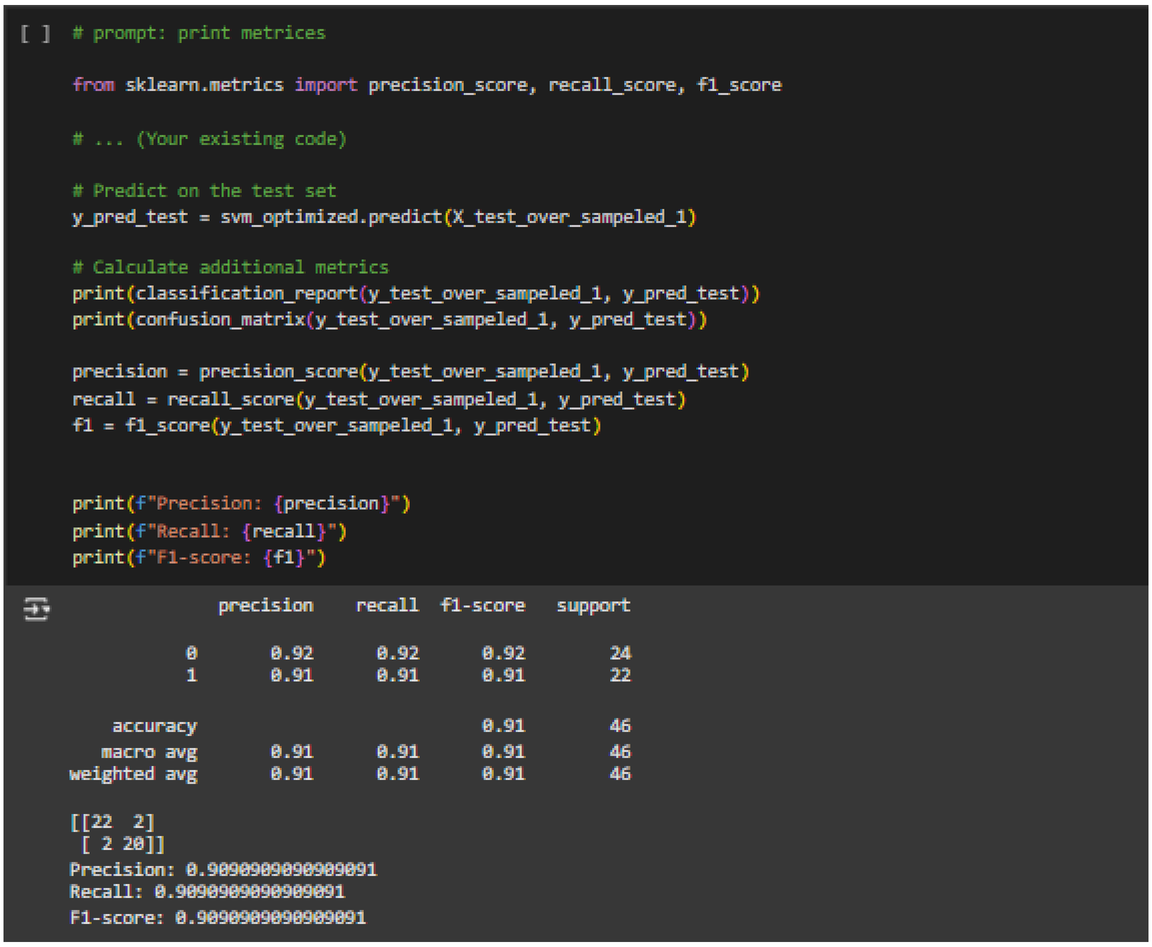


```
[ ] # prompt: print test and train accuracy for random forest you did above with hyper params

    # Predict on the test and training sets
    y_pred_test_rf = best_rf_model.predict(X_test_over_sampeled_1)
    y_pred_train_rf = best_rf_model.predict(X_train_over_sampeled_1)

    # Calculate accuracy scores
    test_accuracy_rf = accuracy_score(y_test_over_sampeled_1, y_pred_test_rf)
    train_accuracy_rf = accuracy_score(y_train__over_sampeled_1, y_pred_train_rf)

    print(f"Random Forest Test Accuracy: {test_accuracy_rf}")
    print(f"Random Forest Train Accuracy: {train_accuracy_rf}")
```

```
Random Forest Test Accuracy: 0.9130434782608695
Random Forest Train Accuracy: 0.945054945054945
```

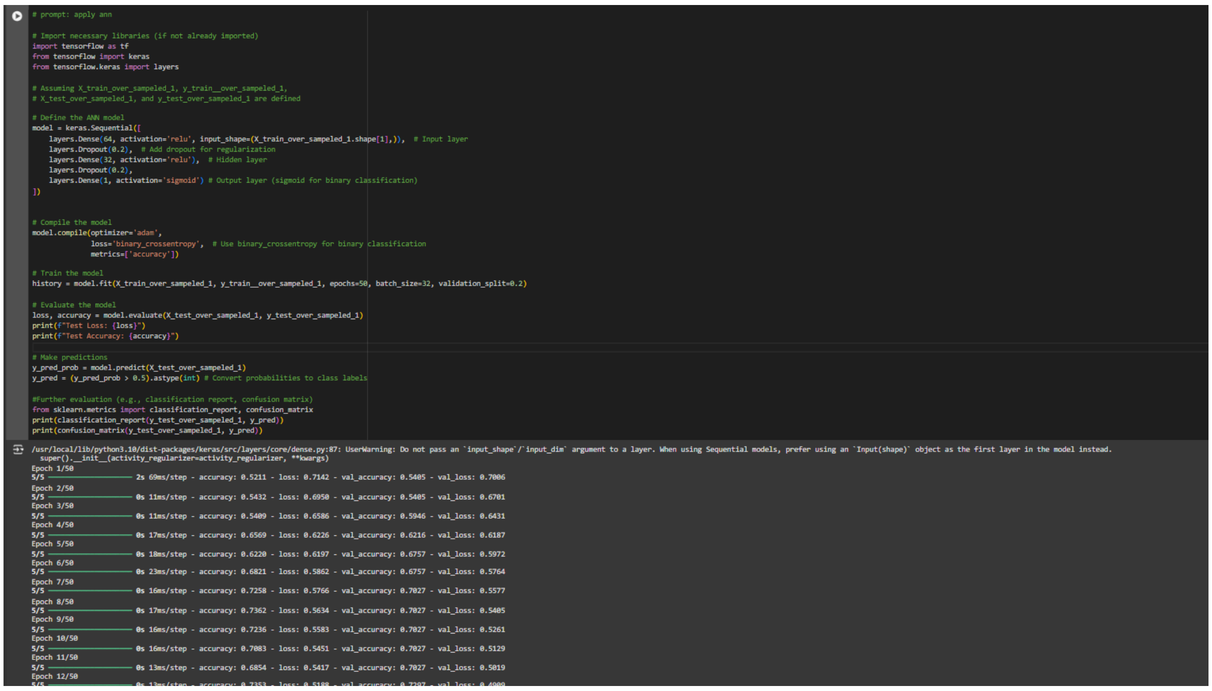
```
[ ] # prompt: do stacking algo with hyper params if possible and print test and train accuracy

    from sklearn.ensemble import StackingClassifier
    from sklearn.linear_model import LogisticRegression

    # Define estimators for stacking
    estimators = [
        ('rf', best_rf_model),  # Use the best RandomForest model
        ('svm', svm_optimized)   # Use the best SVM model
    ]

    # Initialize the stacking classifier with a final estimator (e.g., Logistic Regression)
    stacking_model = StackingClassifier(estimators=estimators, final_estimator=LogisticRegression())

    # Train the stacking model
    stacking_model.fit(X_train_over_sampeled_1, y_train__over_sampeled_1)

    # Predict on test and train sets
    y_pred_test_stacking = stacking_model.predict(X_test_over_sampeled_1)
    y_pred_train_stacking = stacking_model.predict(X_train_over_sampeled_1)

    # Evaluate the stacking model
    test_accuracy_stacking = accuracy_score(y_test_over_sampeled_1, y_pred_test_stacking)
    train_accuracy_stacking = accuracy_score(y_train__over_sampeled_1, y_pred_train_stacking)


    print(f"Stacking Test Accuracy: {test_accuracy_stacking}")
    print(f"Stacking Train Accuracy: {train_accuracy_stacking}")
```

```
Stacking Test Accuracy: 0.9130434782608695
Stacking Train Accuracy: 0.9285714285714286
```



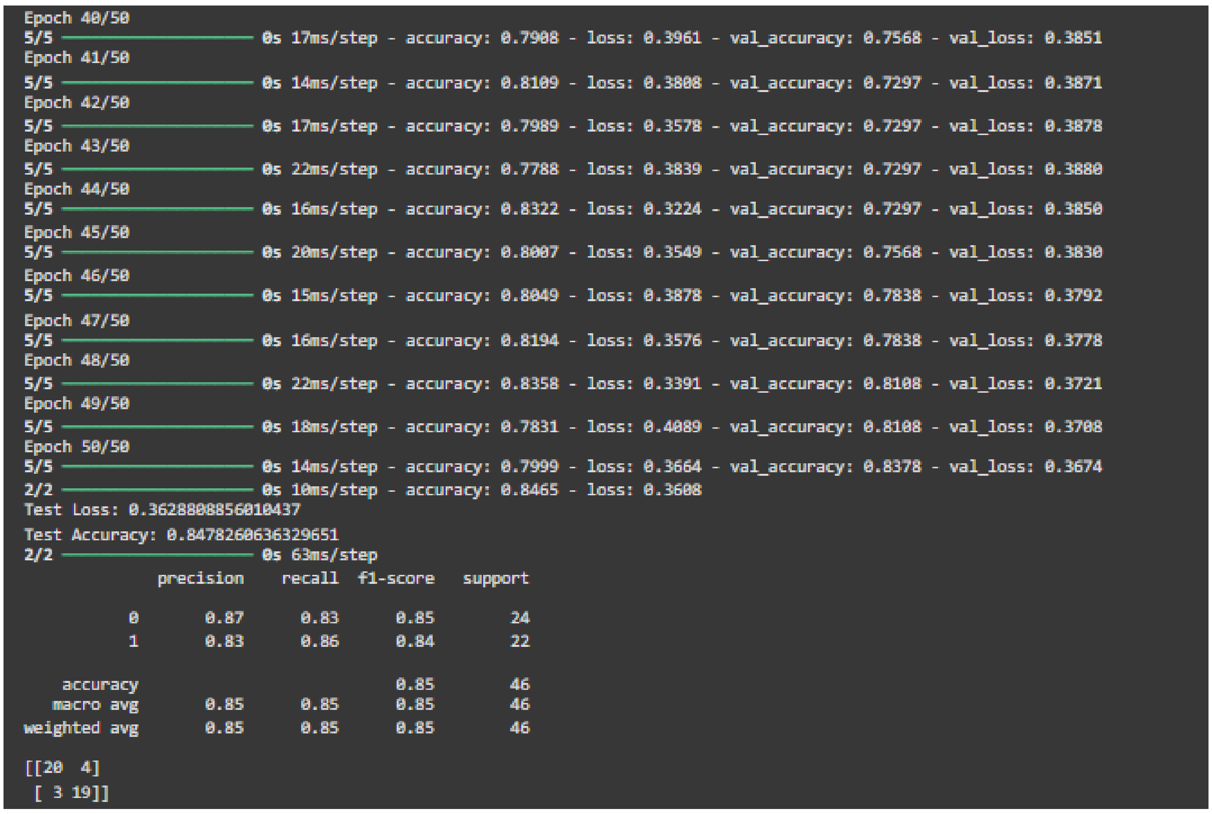
```
[ ]  # prompt: print metrices

     from sklearn.metrics import precision_score, recall_score, f1_score

     # ... (Your existing code)

     # Predict on the test set
     y_pred_test = svm_optimized.predict(X_test_over_sampeled_1)

     # Calculate additional metrics
     print(classification_report(y_test_over_sampeled_1, y_pred_test))
     print(confusion_matrix(y_test_over_sampeled_1, y_pred_test))

     precision = precision_score(y_test_over_sampeled_1, y_pred_test)
     recall = recall_score(y_test_over_sampeled_1, y_pred_test)
     f1 = f1_score(y_test_over_sampeled_1, y_pred_test)


     print(f"Precision: {precision}")
     print(f"Recall: {recall}")
     print(f"F1-score: {f1}")
```

```
              precision    recall  f1-score   support

           0       0.92      0.92      0.92        24
           1       0.91      0.91      0.91        22

    accuracy                           0.91        46
   macro avg       0.91      0.91      0.91        46
weighted avg       0.91      0.91      0.91        46

[[22  2]
 [ 2 20]]
Precision: 0.9090909090909091
Recall: 0.9090909090909091
F1-score: 0.9090909090909091
```

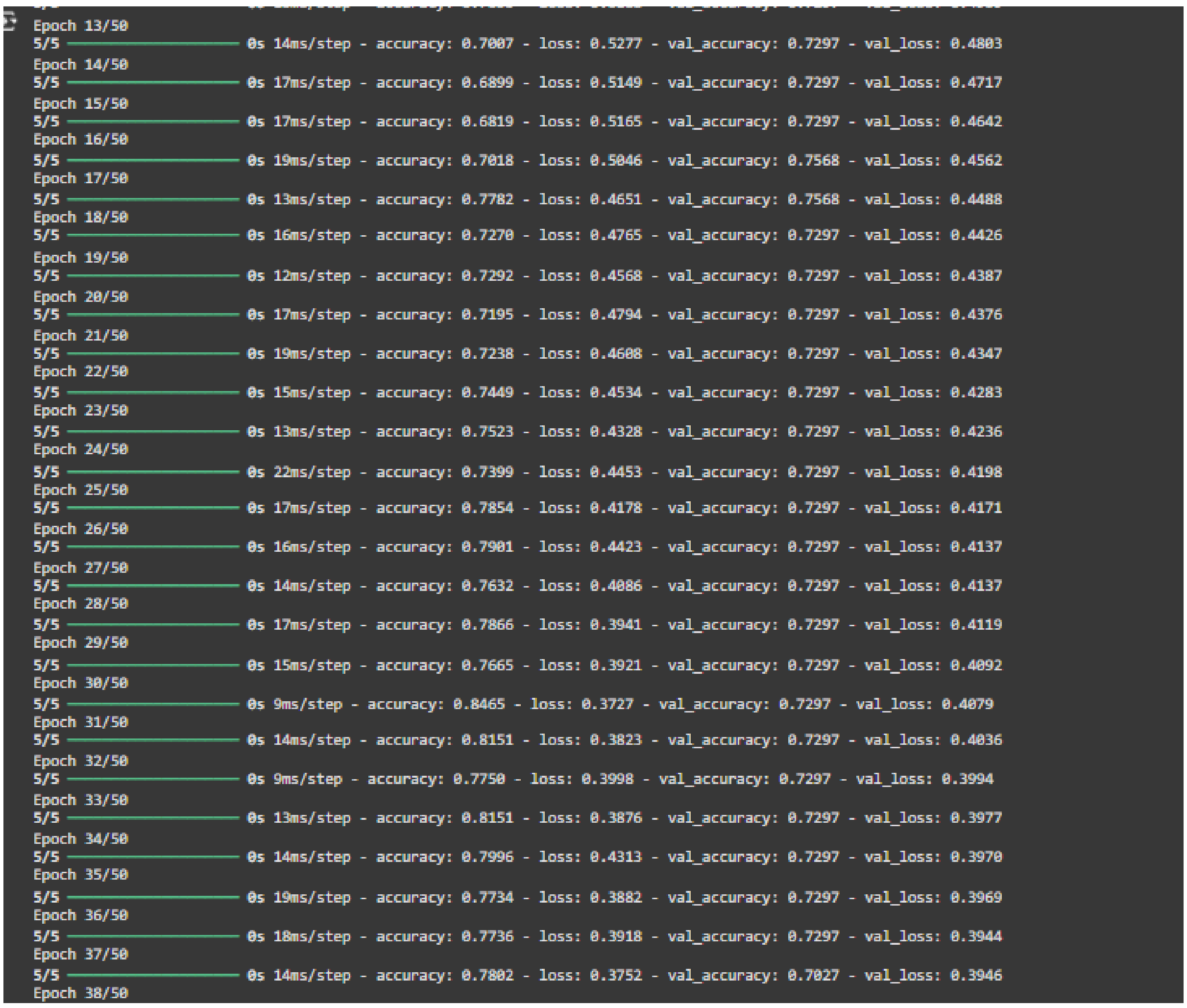


```
# prompt: apply ann

# Import necessary libraries (if not already imported)
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import layers

# Assuming X_train_over_sampeled_1, y_train__over_sampeled_1,
# X_test_over_sampeled_1, and y_test_over_sampeled_1 are defined

# Define the ANN model
model = keras.Sequential([
    layers.Dense(64, activation='relu', input_shape=(X_train_over_sampeled_1.shape[1],)),  # Input layer
    layers.Dropout(0.2),  # Add dropout for regularization
    layers.Dense(32, activation='relu'),  # Hidden layer
    layers.Dropout(0.2),
    layers.Dense(1, activation='sigmoid') # Output layer (sigmoid for binary classification)
])


# Compile the model
model.compile(optimizer='adam',
              loss='binary_crossentropy',  # Use binary_crossentropy for binary classification
              metrics=['accuracy'])

# Train the model
history = model.fit(X_train_over_sampeled_1, y_train__over_sampeled_1, epochs=50, batch_size=32, validation_split=0.2)

# Evaluate the model
loss, accuracy = model.evaluate(X_test_over_sampeled_1, y_test_over_sampeled_1)
print(f"Test Loss: {loss}")
print(f"Test Accuracy: {accuracy}")

# Make predictions
y_pred_prob = model.predict(X_test_over_sampeled_1)
y_pred = (y_pred_prob > 0.5).astype(int) # Convert probabilities to class labels

#Further evaluation (e.g., classification report, confusion matrix)
from sklearn.metrics import classification_report, confusion_matrix
print(classification_report(y_test_over_sampeled_1, y_pred))
print(confusion_matrix(y_test_over_sampeled_1, y_pred))
```

```
/usr/local/lib/python3.10/dist-packages/keras/src/layers/core/dense.py:87: UserWarning: Do not pass an `input_shape`/`input_dim` argument to a layer. When using Sequential models, prefer using an `Input(shape)` object as the first layer in the model instead.
  super().__init__(activity_regularizer=activity_regularizer, **kwargs)
Epoch 1/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 2s 69ms/step - accuracy: 0.5211 - loss: 0.7142 - val_accuracy: 0.5405 - val_loss: 0.7006
Epoch 2/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 11ms/step - accuracy: 0.5432 - loss: 0.6950 - val_accuracy: 0.5405 - val_loss: 0.6701
Epoch 3/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 11ms/step - accuracy: 0.5409 - loss: 0.6586 - val_accuracy: 0.5946 - val_loss: 0.6431
Epoch 4/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.6569 - loss: 0.6226 - val_accuracy: 0.6216 - val_loss: 0.6187
Epoch 5/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 18ms/step - accuracy: 0.6220 - loss: 0.6197 - val_accuracy: 0.6757 - val_loss: 0.5972
Epoch 6/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 23ms/step - accuracy: 0.6821 - loss: 0.5862 - val_accuracy: 0.6757 - val_loss: 0.5764
Epoch 7/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 16ms/step - accuracy: 0.7258 - loss: 0.5766 - val_accuracy: 0.7027 - val_loss: 0.5577
Epoch 8/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.7362 - loss: 0.5634 - val_accuracy: 0.7027 - val_loss: 0.5405
Epoch 9/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 16ms/step - accuracy: 0.7236 - loss: 0.5583 - val_accuracy: 0.7027 - val_loss: 0.5261
Epoch 10/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 16ms/step - accuracy: 0.7083 - loss: 0.5451 - val_accuracy: 0.7027 - val_loss: 0.5129
Epoch 11/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 13ms/step - accuracy: 0.6854 - loss: 0.5417 - val_accuracy: 0.7027 - val_loss: 0.5019
Epoch 12/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 13ms/step - accuracy: 0.7353 - loss: 0.5188 - val_accuracy: 0.7297 - val_loss: 0.4909
```



```
Epoch 40/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.7908 - loss: 0.3961 - val_accuracy: 0.7568 - val_loss: 0.3851
Epoch 41/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - accuracy: 0.8109 - loss: 0.3808 - val_accuracy: 0.7297 - val_loss: 0.3871
Epoch 42/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.7989 - loss: 0.3578 - val_accuracy: 0.7297 - val_loss: 0.3878
Epoch 43/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 22ms/step - accuracy: 0.7788 - loss: 0.3839 - val_accuracy: 0.7297 - val_loss: 0.3880
Epoch 44/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 16ms/step - accuracy: 0.8322 - loss: 0.3224 - val_accuracy: 0.7297 - val_loss: 0.3850
Epoch 45/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 20ms/step - accuracy: 0.8007 - loss: 0.3549 - val_accuracy: 0.7568 - val_loss: 0.3830
Epoch 46/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 15ms/step - accuracy: 0.8049 - loss: 0.3878 - val_accuracy: 0.7838 - val_loss: 0.3792
Epoch 47/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 16ms/step - accuracy: 0.8194 - loss: 0.3576 - val_accuracy: 0.7838 - val_loss: 0.3778
Epoch 48/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 22ms/step - accuracy: 0.8358 - loss: 0.3391 - val_accuracy: 0.8108 - val_loss: 0.3721
Epoch 49/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 18ms/step - accuracy: 0.7831 - loss: 0.4089 - val_accuracy: 0.8108 - val_loss: 0.3708
Epoch 50/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - accuracy: 0.7999 - loss: 0.3664 - val_accuracy: 0.8378 - val_loss: 0.3674
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 10ms/step - accuracy: 0.8465 - loss: 0.3608
Test Loss: 0.3628808856010437
Test Accuracy: 0.8478260636329651
2/2 ━━━━━━━━━━━━━━━━━━━━ 0s 63ms/step
              precision    recall  f1-score   support

           0       0.87      0.83      0.85        24
           1       0.83      0.86      0.84        22

    accuracy                           0.85        46
   macro avg       0.85      0.85      0.85        46
weighted avg       0.85      0.85      0.85        46

[[20  4]
 [ 3 19]]
```



```
Epoch 13/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - accuracy: 0.7007 - loss: 0.5277 - val_accuracy: 0.7297 - val_loss: 0.4803
Epoch 14/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.6899 - loss: 0.5149 - val_accuracy: 0.7297 - val_loss: 0.4717
Epoch 15/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.6819 - loss: 0.5165 - val_accuracy: 0.7297 - val_loss: 0.4642
Epoch 16/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 19ms/step - accuracy: 0.7018 - loss: 0.5046 - val_accuracy: 0.7568 - val_loss: 0.4562
Epoch 17/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 13ms/step - accuracy: 0.7782 - loss: 0.4651 - val_accuracy: 0.7568 - val_loss: 0.4488
Epoch 18/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 16ms/step - accuracy: 0.7270 - loss: 0.4765 - val_accuracy: 0.7297 - val_loss: 0.4426
Epoch 19/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 12ms/step - accuracy: 0.7292 - loss: 0.4568 - val_accuracy: 0.7297 - val_loss: 0.4387
Epoch 20/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.7195 - loss: 0.4794 - val_accuracy: 0.7297 - val_loss: 0.4376
Epoch 21/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 19ms/step - accuracy: 0.7238 - loss: 0.4608 - val_accuracy: 0.7297 - val_loss: 0.4347
Epoch 22/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 15ms/step - accuracy: 0.7449 - loss: 0.4534 - val_accuracy: 0.7297 - val_loss: 0.4283
Epoch 23/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 13ms/step - accuracy: 0.7523 - loss: 0.4328 - val_accuracy: 0.7297 - val_loss: 0.4236
Epoch 24/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 22ms/step - accuracy: 0.7399 - loss: 0.4453 - val_accuracy: 0.7297 - val_loss: 0.4198
Epoch 25/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.7854 - loss: 0.4178 - val_accuracy: 0.7297 - val_loss: 0.4171
Epoch 26/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 16ms/step - accuracy: 0.7901 - loss: 0.4423 - val_accuracy: 0.7297 - val_loss: 0.4137
Epoch 27/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - accuracy: 0.7632 - loss: 0.4086 - val_accuracy: 0.7297 - val_loss: 0.4137
Epoch 28/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 17ms/step - accuracy: 0.7866 - loss: 0.3941 - val_accuracy: 0.7297 - val_loss: 0.4119
Epoch 29/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 15ms/step - accuracy: 0.7665 - loss: 0.3921 - val_accuracy: 0.7297 - val_loss: 0.4092
Epoch 30/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 9ms/step - accuracy: 0.8465 - loss: 0.3727 - val_accuracy: 0.7297 - val_loss: 0.4079
Epoch 31/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - accuracy: 0.8151 - loss: 0.3823 - val_accuracy: 0.7297 - val_loss: 0.4036
Epoch 32/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 9ms/step - accuracy: 0.7750 - loss: 0.3998 - val_accuracy: 0.7297 - val_loss: 0.3994
Epoch 33/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 13ms/step - accuracy: 0.8151 - loss: 0.3876 - val_accuracy: 0.7297 - val_loss: 0.3977
Epoch 34/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - accuracy: 0.7996 - loss: 0.4313 - val_accuracy: 0.7297 - val_loss: 0.3970
Epoch 35/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 19ms/step - accuracy: 0.7734 - loss: 0.3882 - val_accuracy: 0.7297 - val_loss: 0.3969
Epoch 36/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 18ms/step - accuracy: 0.7736 - loss: 0.3918 - val_accuracy: 0.7297 - val_loss: 0.3944
Epoch 37/50
5/5 ━━━━━━━━━━━━━━━━━━━━ 0s 14ms/step - accuracy: 0.7802 - loss: 0.3752 - val_accuracy: 0.7027 - val_loss: 0.3946
Epoch 38/50
```