Parkinson Disease Prediction and Classification Using Ensemble Stacking Learning Algorithm

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Abstract— Data Mining (DM) is a pragmatic method to find patterns in massive datasets, representing knowledge that is implicitly stored and to focus on problems of feasibility, utility, efficacy, and scalability. Medical data mining is a huge field of study, where techniques are used to address issues on diagnosis, treatment, and to explore the knowledge of disease identification. A neurological disease known as Parkinson Disease (PD) has reportedly affected the majority of people across the world. According to recent studies, voice defects are identified in 90% of PD patients. PD is a disorder of the central sensory system in human body that affects movement and causes tremors. Unfortunately, it can be difficult to identify PD in its early stages. A number of measures available to identify Parkinson Disease. As a result, voice estimations can be utilized to identify the state of impacted persons. This research work proposed a novel method called as Ensemble Stacking Learning Algorithm (ESLA), a classifier for identifying PD on the collected data. To calculate the performance, the proposed ensemble method is compared with other existing technique and shows the improved classification ability of this proposed method. It is exhibited that the proposed methods for PD patients, which creates the most reliable outcomes and accomplishes the highest accuracy. This ensemble approach uses various existing classifiers like Random Forest (RF), XGBoost (Extreme Gradient Boost), Linear Regression, Ada Boost (AB), and Multi-Layer Perceptron (MLP) and compared results with the proposed method for a better prediction of accuracy. Finally, performance of the proposed method among the chosen algorithms is suggested for the prediction of disease and gives future directions.

Keywords- Parkinson Disease, Voice attributes, Classification Algorithms, Ensemble Stacking Learning Algorithm, Stacking Methods.

Introduction

Data Mining (DM) is an approach that focuses on concerns about utility, efficacy, scalability, and practicability. It is a practical way to uncover patterns in large datasets that represent knowledge that is implicitly stored. In the vast field of study known as medical mining, methods are employed to address problems with disease detection, treatment, and understanding. To predict trends, improve outreach, and even more efficiently control the spread of diseases, healthcare analytics is looking at both recent and old data. The amount of healthcare data that needs to be evaluated is expanding every second in today's digital world. Due to the development of electronic records, applications, and other electronic data gathering tools, a significant amount of data is being gathered in real time. The second most common neuro-degenerative disorder in the world, PD is characterized by the gradual degeneration of functions related to damage cells in the brain, producing dopamine. This condition was named after an English surgeon by the name of James Parkinson, who published the first thorough description of the neurological syndrome in 1817 in his article "An Essay on the Shaking Palsy". Over 10 million people worldwide are currently affected with PD (Politis, 2014). The cardinal symptoms of Parkinson disease (PD), abbreviated as TRAP (resting Tremors, Rigidity, Akinesia (or Bradykinesia), and Postural Instability), are associated to impaired non-motor and motor functions because of the Dopamine degeneration network of neurons, known as a Nigrostriatal pathway.

Millions of people worldwide suffer from Parkinson disease (PD), a neurodegenerative brain disorder. It affects the neurons, or nerve cells, that are present in the human brain. Dopamine is a key substance that the Neurons create and regulates movement in the body. A decrease in dopamine levels causes uncontrollable bodily movements. By developing machine learning models that help us with accurate disease prediction, early prediction can be considerably increased. The Parkinson disease dataset for this study was obtained from the Kaggle Web source. The dataset contains 23 numeric attributes. The classification algorithms Random Forest, XGBoost (eXtreme Gradient Boost), Logistic Regression (LR), AdaBoost (AB) and Multi Layer Perceptron (MLP) are used in this research work. These existing machine learning techniques are used to frame stacked models to enhance performance and to significantly aid in the early detection of PD. Finally, a Novel Ensemble Stacking Learning algorithm (ESLA) has been developed to identify it between healthy people and those People with Parkinson (PWP) based on Rank_ Test_Score and confusion matrix. The proposed model ESLA improves the prediction accuracy and the results are compared with the other stacked models.

Parkinson disease is characterized by slower movement, tremor, and difficulty with gait and balance in a human body. The death of nerve cells in the locus niger, is a portion of the nervous system is the main reason for PD. Dopamine and other neurotransmitters are secreted by cells in the substantia nigra, which connect with other brain movement control areas. When cells in the substantia nigra die, the secretion of serotonin is stopped, and the other movements become uncontrolled. Dorsey *et al.* (2007) discussed in their research work, Parkinson disease (PD) is a neurodegenerative condition that affects tremor and bradykinesia, which are two types of recognisable motor symptoms. About 1% to 2% of those over 65 and 4% of people over 80 are affected. The number of Parkinson sufferers will rise as the average lifespan of people increases. By 2030, it is anticipated that this percentage will be greater than 50%. The main motor symptoms of PD are bodily tremors, stiffness and imbalance in various organs, and immobility in movements. Sometimes it's considered as a symptom when only one hand is trembling. PD initially just affects one side of the body, but as the disease progresses, other symptoms start to emerge (Jankovic 2008). There are numerous articles about the diagnosis and therapy of PD in the medical literature. Machine learning techniques are being developed in the engineering industry to diagnose this disease. Voice and walking records of people were obtained for this reason. In the early stages of Parkinson disease, pronunciation problems occur (Tsanas *et al.*, 2010). Predictive analytics is getting important day by day in medicine and healthcare systems by following the age-old saying “Prevention is better than cure”. The World Health Organization has acknowledged the value of knowledge detection and medical data repositories as improving in medical forecasting and disease prediction.

The medical industry generates enormous amounts of data, which includes assessment reports on patients' clinical and physical evaluations, treatments, upcoming visits, and a list of prescribed or over-the-counter medications. It is difficult and time-consuming to organise this data in the necessary way for optimal extraction and effective processing (Kononenko, 2001). Data mining is the process of learning from a database that has been used to recognise patterns or create a prototype that gives the data a useful consequence. ML approaches are the foundation for the creation of intriguing patterns with significant results. Recently, ML has been applied to the diagnosis of Parkinson disease (PD) using a range of data modalities. With the help of ML, it is possible to integrate various modalities and determine whether an unusual form or preclinical phases of PD are present. (Mei *et al.* 2020). The rest of the paper is organized as follows. Section 2 provides related work through literature survey. Section 3 demonstrates material and methods of this research. Experimental work is given in section 4. Finally, the conclusion of this research work is pointed out in section 5.

Literature Survey

Many researchers have done their research in prediction and analyzing of Parkinson disease.

Some of the research works are taken and their results are analyzed in this paper. Voice analysis reveals significant improvement in the progression of PD. As a result, voice-related characteristics take part in a significant division in the automated diagnosis of Parkinson disease. Hughes AJ *et al*. (1992) Hughes AJ et al. published a paper titled "Accuracy of clinical diagnosis of idiopathic Parkinson disease: a clinico-pathological study of 100 cases", There are a-synuclein-immuno reactive inclusions made up of a number of neuro filament proteins together with proteins responsible for proteolysis. To identify PD, different signs have been explored, including EEG, step and discourse. This paper proposes another calculation for diagnosing of Parkinson sickness dependent on voice examination. In the initial step, Genetic Algorithm (GA) is attempted for choosing streamlined highlights from all extricated highlights.

Sakar and Kursun (2010) achieved 92.75% classification accuracy by combining support vector machine classifier with feature selection approaches for the diagnosis of Parkinson disease. Shahbaba and Neal's (2009) proposed nonlinear model for the classification of PD produced, when compared to SVM, multinomial log it models, and decision trees, the best classification accuracy of 87.7%. PD can be brought on by polygenic and environmental causes. It has been discovered that a single gene contributes to the development of the disease in 1%–2% of instances of Parkinson disease (mainly hereditary) Ozkan (2016) offered hybrid methodology based on vocal indicators based on Principle Component Analysis with K-NN result of the research that indicates the robustness of the proposed approach with an precision of 99.1%. Parisi *et al*. (2018) suggested a hybrid approach based on SVM (Multi Layer Perceptron - LSVM). The deployed method presented the highest accuracy in comparison with other techniques for PD diagnosis.

Breiman *et al*. (2001) suggested that Random Forest is an extended version of bagging algorithm with randomness property injected. The algorithm requires two parameters to set before starting. The first one is the number of variables (m) used in every node for determining the best split. The second one is the number of trees (N) to be extended. Random Forest uses CART (Classification and Regression Tree) algorithm to produce trees. Archer *et al.* (2008), Random Forest splits every node to branches using the best one from randomly selected variables on every node instead of using the best branch through all variables. Each dataset is generated from the original one by replacement. Random feature selection is used to extend trees. Extended trees are not pruned. This strategy makes Random Forest's accuracy. Random Forest is also very fast and robust to overfitting that takes its source from decision trees' nature. Chen *et al*. (2016) have defined the XGBoost algorithm has good scalability, so that it runs more rapidly than available famous machine learning algorithm, besides it consumed less memory. In the KDD Cup 2015, XGBoost was used by every victorious team. Between the victorious teams, there are only slightly using ensemble method which is beat the single well-configured XGBoost method. Other than that, in the Kaggle's competition 2015, between 29 nomination of the winner, 17 using XGBoost, which is 17 using only XGBoost, while the others using ensemble methods by combining XGBoost with neural networks, and 11 solutions used deep neural networks. It is a Machine Learning algorithm which is used the model of classification. Modeling was using the xgboost algorithm. Training and testing data were formed from the dataset with the data testing were 0.33 part of the available dataset, and the rest were used as data training Brownlee J (2016).

Challa *et al*. (2016) developed automated diagnostic models using Multilayer Perceptron, BayesNet, Random Forest and Boosted Logistic Regression. It has been observed that Boosted Logistic Regression provides the best performance with an impressive accuracy of 97.159 % and the area under the ROC curve was 98.9%. Thus, it is settled that this methods can be used for early prediction of Parkinson disease. Psorakis I (2010) introduced a novel convergence measures, sample selection strategies and model improvements, it is demonstrated that mRVMs can produce state-of-the-art results on multiclass discrimination problems. In addition, this is achieved by utilizing only a very small fraction of the available observation data. The author examined the sparsity and acknowledgment abilities of two surmised Bayesian order calculations, the multi-class multi-kernel relevance vector machines (mRVMs) that have been as of late proposed experimentation on an enormous scope of genuine world datasets yielded 89.47% (10-overlay CV) accuracy. Richa Mathur *et al.* (2019), suggested a method for predicting the PD. They used a weka tool for implementing the algorithms to perform preprocessing of data, classification and the result analysis on the given dataset. They used k-NN along with Adaboost.M1, bagging, and MLP. It was observed that k-NN + Adaboost.M1 yielded the best classification accuracy of 91.28%. Muhtasim Billah *et a.l* (2014) applied Ada-Boost algorithm to classify the Parkinson disease on the basis of Voice measurements data of PD patients. Then, Support vector Machine with Sequential Minimal Optimization classifier, is used to make the comparison with the result of Ada-Boost classifier to find out the best classifier. In addition, six other best classifiers such as Naïve bayes, J48 Tree, LogitBoost, ADTree, BFTree, and Decision Stump Tree are used to make comparison with Parkinson dataset and to select the best classifier. Ali Asghar Heidari *et al.* (2019) proposed a new hybrid stochastic training algorithm using the recently proposed Grasshopper Optimization Algorithm (GOA) for Multilayer Perceptron (MLP) neural networks. The GOA algorithm is an emerging technique with a high potential in tackling optimization problems based on its flexible and adaptive searching mechanisms. It can demonstrate a satisfactory performance by escaping from local optima and balancing the exploration and exploitation trends. The proposed GOAMLP model is then applied to five important datasets: breast cancer, parkinson, diabetes, coronary heart disease, and orthopedic patients. The results are deeply validated in comparison with eight recent and well-regarded algorithms qualitatively and quantitatively. It is shown and proved that the proposed stochastic training algorithm GOAMLP is substantially beneficial in improving the classification rate of MLPs. Omer Eskidere (2012) studied the performance of SVM, least square SVM, General Regression Neural Network and Multilayer Perceptron Neural Network for tracking the progressiveness of PD. Results indicated that among all this four methods, lease square SVM provides the best performance.

Wibawa *et al.* (2017), developed machine learning method using ensemble learning and feature selection to improve the quality of Chronic Kidney Disease (CKD) diagnosis. The CKD dataset was taken from UCI machine learning repository, it contain 400 instances. CKD dataset have 24 attributes including signs, symptoms and risk factors that might appear due to CKD. In this study, features were selected using a Correlation-based Feature Selection (CFS) and AdaBoost was used for ensemble learning to improve the detection of CKD. KNN, NBs and SVM were used as base classifier. Overall, the best result was achieved by combination of KNN classifier with CFS and AdaBoost, with 0.981 accuracy rates, 0.980 recall rates and 0.980 f-measure rates. Highest precision rate was achieved by the combination of NBs classifier with CFS and AdaBoost, with 0.981 precision rates. Zeynu and Patil (2018) proposed an ensemble model that uses Information gain attributes evaluator with ranker search engine and wrapper subset evaluator with best first engine to predict CKD. In this work, K-Nearest Neighbor(KNN), J48, Artificial Neural Network(ANN), NBs and SVM classification techniques were used to identify CKD. InfoGain, AttributeEval with ranker and Wrapper Subset Evaluator with Best first search were used for selecting the important features. Experimental results of this research work reveal that Wrapper Sub set Evaluator with Finest first search engine feature selection method evaluated against KN classification algorithm has shown an accuracy of 99%, J48 with Info Gain Attribute Evaluator with ranker search engine has shown an accuracy of 98.75%, ANN is comparison to other methods with and without feature section method, SVM with Info Gain Attribute Evaluator with ranker has 98.25% accuracy in prediction of CKD, NBs with Wrapper Sub set Evaluator with Best first search engine has 99% accuracy, and NBs with Wrapper Sub set Evaluator with Best first search engine has 99.5% accuracy.

Alelyani *et al.* (2021), proposed an ensemble approach based on the bagging technique to improve feature selection stability in medical datasets via data variance reduction. An experiment is conducted using four real-world medical datasets each of which suffers from high dimensionality and relatively small sample size. On each dataset, five well-known feature selection algorithms namely four filter approaches - Fisher Score, ReliefF, Information Gain, Chi-Square score and one wrapper approach - l1SVM are employed to select varying number of features. In order to evaluate selection quality, two classification algorithms, K-Nearest Neighbor (KNN) and Support Vector Machine (SVM) are used. Bagging technique is used in this method to reduce data variance which improves the stability of the feature selection algorithm. The proposed technique shows a significant improvement in selection stability while maintaining the classification accuracy. The Stability improvement ranges from 20 to 50 percent in all cases. This implies that the likelihood of selecting the same features increased 20 to 50 percent more. This is accompanied with the increase of classification accuracy in most cases, which signifies the stated results of stability.

Hoque *et al.* (2018) have used an ensemble method for feature selection known as EFS-MI based on the feature-class and feature-feature mutual information in order to derive the optimal feature subset. The authors have validated the feature selection results using decision tree, SVM, random forests and KNN. The datasets that have been used in carrying out the experiment belong to three different applications which are network security, gene expression dataset and datasets from the UCI. In this method, the authors have used mutual information as a measure to find the information gain among all features and between feature and attributes of class. The results the EFS-MI feature selection method is compared with other feature selection methods viz., Symmetric Uncertainty (SU), Info Gain (IG), Chi-Square (CS), Gain Ratio (GR), and ReliefF (RF) methods. Experimental results on network security dataset indicate that the proposed EFS-MI method achieves highest accuracy of 92-98% compared to the other feature selection methods when K-NN and decision tree classification algorithm are employed. Results validated on gene expression dataset indicate that the ensemble feature selection method, EFS-MI achieves high accuracy for all the four classifiers. The authors have validated EFS-MI on 14 UCI datasets and have given the comparison results of this method with other feature selection methods and four classifiers. Sunitha and Geethanjali (2018) proposed an Ensemble Feature Selection (EFS) that combines the output of two selection methods namely Bat Algorithm (BA), and Firefly Algorithm (FA) which could obtain approximation at better level. In newly introduced system, the presence of heart related diseases can be denoted using 1 and the absence could be represented using 0 which is found out in heart data samples. Parallel Deep Learning Algorithm (PDLA) Classifier which is proposed in this system has been evaluated in UCI repository.

Materials And Methods

There are a few approaches available for the analysis of PD in the research areas of information technology. Herewith, it is discussed as to how some of the techniques which are used by most of the researchers in their work are taken into account through some existing methods. The existing methods RF, XGBoost, Linear Regression, AB, and MLP are used in this work to analyze the Parkinson data. Motivated by the previous ensemble works, in this study, an ensemble PD classifier is proposed by combining both Random Forest and Extreme Gradient Boosting (XGBoost) algorithms with Linear Regression and AdaBoost (AB) ensemble methods. This study used four stacking models to improve the prediction precision.

Description of Dataset

The dataset was taken from kaggle online repository [1] from the centre of machine learning and intelligent systems which were created by Max Little of the University of Oxford, in collaboration with the National Centre for Voice and Speech, Denver, Colorado. This dataset is composed of a range of biomedical voice measurements. Each column in the table is a particular voice measure, and each row corresponds one of 1170 voice recordings from these individuals. The last column represents the status of the people i.e., “0” for normal and “1” for PD. The step to derive the attributes from the ARFF file is given at the end of the appendix. The Characteristic features of PD dataset are shown in table 1.

Architecture of the Proposed Work

In this research work, as a first step, the dataset is preprocessed to obtain clean and relevant data. Next, the existing machine learning classification algorithms are implemented on the preprocessed data and the results are compared. After this work, an Ensemble Stacking Learning Algorithm is developed using various classifiers. Finally, the performance of the proposed model is compared with the other stacked models and various performance metrics have been calculated and interpreted. The overview of the research is presented in Figure 1.

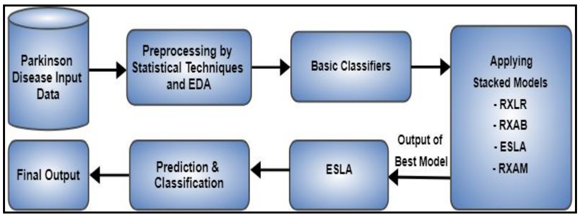


Table 1: Description of Dataset

Feature Name	**Description**
P: Fo(Hz)	Average vocal fundamental
MDVP: Fhi(Hz)	Maximum vocal fundamental
MDVP: Flo(Hz)	Minimum vocal fundamental
MDVP: Jitter(%)	Kay Pentax MDVP jitter as
MDVP:Jitter (Abs)	Kay Pentax MDVP absolute jitter in microseconds
MDVP: RAP	Key Pentax MDVP Relative Amplitude Perturbation
MDVP: PPQ	Kay Pentax MDVP five-point Period Perturbation Quotient
Jitter: DDP	Average absolute difference of differences between cycles, divided by the average period
MDVP:Shimmer	Key Pentax MDVP local shimmer
MDVP:Shimmer (dB)	Key Pentax MDVP local shimmer in decibels
Shimmer: APQ3	3 Point Amplitude Perturbation Quotient
Shimmer: APQ5	5 Point Amplitude Perturbation Quotient
MDVP: APQ	Kay Pentax MDVP eleven-point Amplitude Perturbation
Shimmer: DDA	Average absolute difference between consecutive
NHR	Noise to Harmonic Ratio
HNR	Harmonics to Noise Ratio
RPDE	Recurrence Period Density
DFA	Detrended Fluctuation Analysis
Spread1	Non-Linear measure of fundamental frequency
Spread2	Non-Linear measure of fundamental frequency
D2	Correlation Dimension
PPE	Pitch Period Entropy
Status	Health Status 1- Parkinson; 0-

Preprocessing by Statistical Techniques and Exploratory Data Analysis

In this research work Statistical techniques and Exploratory Data Analysis (EDA) approach are used. Preprocessing is a prominent approach in research activity to obtain the high precision in predictions. Statistical methods are used to analyze the information and to apply it in various types of factual issues. Some of the statistical methods are mean, median, standard deviation and so forth. EDA is central to hypothesis generation that would aid in the subsequent choice of Machine Learning techniques, if need be, to develop a solution for a problem. There are many tools and frameworks that can be used to do EDA. However, a custom-built framework built on top of Python facilitates a natural extension of this approach to include Machine Learning to enhance knowledge discovery. The correlation coefficient is a statistical indicator of how closely two variables move in respect to one another. The range of values is -1.0 to 1.0. A computation result in the correlation is shown by a value that is either bigger than 1.0 or smaller than -1.0. A correlation of -1.0 indicates a perfect negative correlation, whereas a correlation of 1.0 indicates a perfect positive correlation. A correlation of 0.0 indicates that there is no linear relationship between the two variables' movements. The correlation coefficient is calculated by dividing the covariance by the sum of the standard deviations of the two variables. The standard deviation is a measure of how far apart the data are from the mean. A measure of the relationship between two variables is called covariance. The correlation co-efficient heatmap represents the relationship between the attributes in the Parkinson Disease dataset.

IV **CLASSIFICATION ALGORITHMS**

Random Forest Algorithm: A random forest is a supervised machine learning method for tackling classification and regression problems. It makes use of ensemble learning, a method for solving complicated issues by combining a number of classifiers. Based on the predictions of the decision trees, this algorithm determines the result. Root nodes serve as the starting point, while the leaves make the final decision. The value of Gini Index is used in decision trees to split the population into two equal halves. Mathematically Gini index can be written as:

$$Gini\ Index = 1 - \sum_{i=1}^{n} (Pi)\hat{}2 = 1 - \{(P_+)^2 + (P_-)^2\}$$

(1)

Where P+ is the probability of a positive class and P_ is the probability of a negative class.

Extreme Gradient Boost (XGBoost) Algorithm: XGBoost stands for Extreme Gradient Boosting. An enhanced Library for gradient boosting in machine learning is called XGBoost. XGBoost does not employ entropy or Gini indices, instead it uses gradient (the error term) and hessian to build the trees. To make a prediction for a new data point, the constructed trees or models are used to obtain all the values needed to solve the problem and the equation is given by:

$$F2(X) = \sigma(0 + 1 * h1(X) + 1 * h2(X)) \quad (2)$$

Where, F2(X) is resulting value of XGBoost model.

Logistic Regression Algorithm: Logistic regression predicts the probability of an outcome that can only have two values. One or more predictors are used to make the prediction. Using a logistic regression, a logistic curve is created, which can only contain values between 0 and 1. Similar to a linear regression, a logistic regression builds its curve using the natural logarithm of the target variable's "odds" rather than the probability. The logistic regression equation can be written in terms of an odds ratio as follows:

$$\ln\left(\frac{p}{1-p}\right) = b_0 + b_1 x \quad (3)$$

- Where ln is the natural logarithm, p is the probability, b0 is the coefficient of the constant term, b1 is the coefficient on the independent variable, and x is the independent variable.

Adaptive Boost (AdaBoost) Algorithm: AdaBoost algorithm, is the acronym for Adaptive Boosting. This is a Boosting technique used as an Ensemble Method in Machine Learning. It works on the principle of learners growing sequentially. Except for the first, each subsequent learner is grown from previously grown learners. In simple words, weak learners are converted into strong ones. The Mathematical formula for AdaBoost is given in the following equation.

$$H(x) = sign\left(\sum_{t=1}^{T} \alpha_t h_t(x)\right)$$

(4)

Where ht(x) is the output of weak classifier t for input x and αt is weight assigned to classifier.

Multi-Layer Perceptron (MLP): Multi-Layer Perceptron (MLP) is a supplement of feed forward neural network. It consists of three types of layers namely the Input layer, Output layer and Hidden layer. The input layer receives the input signal to be processed. The required task such as prediction and classification are performed by the output layer. An arbitrary number of hidden layers that are placed in between the input and output layer are the true computational engine of the MLP. The computations taking place at every neuron in the output and hidden layer are as follows:

$$o(x) = G(b(2) + W(2)h(x))$$

(5)

$$h(x) = \phi(x) = s(b(1) + W(1)x)$$

(6)

Where b(1) and b(2) are bias vectors, W(1) and W(2) are weight matrices, G and s are activation functions, and ***Φ*** is the sigmoid function.

Rank_test_score: It indicates the rank of a grid search parameter combination based on the mean¬¬_test_score. If there were N parameter combinations in grid search, the rank_test_score reaches from 1 to N. Grid search refers to a technique used to identify the optimal hyperparameters for a model. Unlike parameters, finding hyperparameters in trained data is unattainable. As such, to find the right hyperparameters, we create a model for each combination of hyperparameters. Exhaustive search was done over specified parameter values for an estimator. GridSearchCV implements a “fit” and a “score” method. The parameters of the estimator used to apply these methods are optimized by cross-validated grid-search. The mean_fit_time is the average time of training between different folds. The correlation coefficient values 0.5 to 0.35 were taken for this research work.

Confusion Matrix: Confusion matrix prediction outcomes are compiled in a confusion matrix. Count values are used to describe the number of accurate and inaccurate predictions for each class. In a number count, a confusion matrix prints both the accurate and inaccurate values. It facilitates effective data visualization for predicting the data. Confusion matrix for a two-class classifier is written as True Positive, True Negative, False Positive, and False Negative and comprises information about the actual and predicted classifications made by a classification system. The total of diagonals is the total of cases that were accurately categorized.

V Proposed Stacked Models

In stacking model, the predictions were handled using a number of distinct models rather than just one, and then those predictions are used as features in a higher-level meta-model. It involves combining the predictions from multiple machine learning models on the same dataset. The architecture of a stacking model consists of two or more base models, also known as level-0 models, and a meta-model, or level-1 model, which integrates the predictions of the base models. There are different machine learning models proficient on the same dataset but in various ways, stacking is the suitable method. Stacking is intended to boost modeling efficiency. The important steps for implementing stacking models are as follows:

- Split training datasets into n-folds as this is the most common approach to preparing training datasets for meta-models.
- The first fold, which is n-1, has now been fitted to the base model, and it will now generate predictions for the nth folds.
- The x1_train list is expanded to include the prediction from the previous step.
- To produce an array of x1_train of size n, repeat steps 2 and 3 for the remaining n-1 folds
- The model has now been trained on all n parts and can now predict the results of the sample data.
- Add this prediction to the y1_test list.
- In a similar manner, by employing Models 2 and 3 for training, we may determine x2_train, y2_test, x3_train, and y3_test to obtain Level 2 predictions.
- Now, train the Meta model using level 1 prediction. The model will use these predictions as features.
- Finally, the stacking model can now predict test data using Meta learners.

Table 2: Base and Stacked models

Levels	Models	Ensemble algorithms
Level - 0	Random Forest (RF), XGBoost, AdaBoost, Logistic Regression, MLP	Base Classifiers
Level – 1	RXLR	RF + XGBoost + Logistic Regression
Level – 1	RXAB	RF + XGBoost + AdaBoost
Level – 1	ESLA	RF + XGBoost + Logistic Regression + MLP
Level – 1	RXAM	RF + XGBoost + AdaBoost + MLP

This research work has proposed 4 stacking models for the classification of PD in the chosen data set. A stacking learning algorithm is developed to create four stacked models. Along with the base classifiers RF and XGBoost, Logistic Regression, AdaBoost, and Multi-layer Perceptron (MLP) are ensembled to obtain the highest accuracy in PD prediction. These models are named as RXLR, RXAB, ESLA and RXAM. These are actually known and identified as META models which are used for the prediction in the medical dataset. Out of these four models, one of the models yields the best results which is to be visualized for the prediction of disease. Based on the evaluation criteria of these models, the obtained results are analysed.

RXLR Model (Random Forest, XGBoost, Logistic Regression)

The RXLR stacking model is a hybrid model that combines Logistic Regression, Random Forest, and XGBoost. In this research, the Random Forest classifier's primary parameters were max_depth, min_sample_leaf, and n_estimators. The knowledge to manage for XGBoost classifier are max depth, learning_rate, n_estimators, and min_child_weight. Max_iter and random state are the key features that have been used for logistic regression. The primary motivation for employing this RXLR ensemble strategy was to reduce the error rate. When compared to a single contributing classifier, an ensemble can generate better predictions and produce better results. The models results are merged to get the final prediction for any instance x_i. For learning the weights α_j of the level-0 predictors, stacking adds a level-1 method called meta-learner. That is, for the level-1 learner, the prediction *y (xi)* of each training instance xi is training data which can be defined in the following formula

$$y(x_i) = \sum_{j=1}^{3} \alpha_j h_j(x_i) \qquad (7)$$

Where, x_i - instances - Optimal weights of level-0 predictors and h_j -Base models.

RXAB Model (Random Forest, XGBoost, AdaBoost)

The RXAB stacking model is the hybrid model which is combination of Random Forest, XGBoost and AdaBoost. For Random Forest classifier, the main features used in this study are max_depth, min_samples_leaf and n_estimators. For XGBoostclassifier, the important features used are max_depth, learning_rate, n_estimators and min_child_weight. For AdaBoost, the main features used in this study are random_state and n_estimators. Using this ensemble RXAB method was primarily done to lower the error rate. An ensemble can produce better findings and make better predictions when compared to a single contributing model. The models' results are merged to get the final prediction for any instance x_i. For learning the weights λ_j of the level-0 predictors, stacking adds a level-1 method called meta-learner. That is, for the level-1 learner, the prediction *y* (x_i) of each training instance x_i is training data which can be defined in the following formula

$$y(x_i) = \sum_{j=1}^{3} \lambda_j h_j(x_i)$$

(8)

Where, x_i – instances - Optimal weights of level-0 predictors and h_j -Base models.

ESLA Model (Ensemble Stacking Learning Algorithm)

The proposed ESLA model is the hybrid model which is combination of Random Forest, XGBoost, Logistic Regression and Multi-layer Perceptron. In this proposed ESLA stacking model, four models are being trained on 188 samples of data. The models results are merged to get the final prediction for any instance xi. For learning the weights β_j of the level-0 predictors, stacking adds a level-1 method called meta-learner. That is, for the level-1 learner, the prediction *y* (x_i) of each training instance x_i is training data which can be defined in the following formula

$$y(x_i) = \sum_{j=1}^{4} \beta_j h_j(x_i)$$

(9)Where, x_i - instances - Optimal weights of level-0 predictors and h_j -Base models.

Although any machine learning approach can be employed, logistic regression is commonly utilised to solve the optimization problem. It is depicted using the following formula,

$$\beta^* = \arg\min_{\beta} \sum_{i=1}^{188} (y(x_i) - \sum \beta_j h_j^{(-i)}(x_i))^\wedge 2$$

(10)The leave-one-out prediction derived by training h_j across the subset of *i-1* occurrences with the i^{th} sample left aside is denoted by $h_j^{(-i)}$. Here, *i* refers to the total number of samples. In this case, *i*=188. Base models h_j are re-trained throughout the whole dataset and utilised to assess previously unknown examples and appropriate weights β_j are calculated.

For Random Forest classifier, the main features used in this study are max_depth, min_samples_leaf and n_estimators. For XGBoostclassifier, the important features used are max_depth, learning_rate, n_estimators and min_child_weight. For Logistic Regression, the main features used in this study are max_iter and random state. The Multi Layer Perceptron (MLP) is a category of feed forward neural network. It has three layers: an input layer, a hidden layer and an output layer. For MLP, the main features used in this work are alpha and max_iter. This ESLA stacking model is to improve the prediction accuracy.

RXAM Model (Random Forest, XGBoost, AdaBoost, Multi Layer Perceptron)

This stacking model is the mixture model which is grouping of Random Forest, XGBoost, AdaBoost and MLP. For Random Forest classifier, the main features used in this study are max_depth, min_samples_leaf and n_estimators. For XGBoostclassifier, the important features used are max_depth, learning_rate, n_estimators and min_child_weight. For AdaBoost, the main features used in this study are random_state and n_estimators. For MLP, the main features used in this work are alpha and max_iter. The primary motive for employing this RXAM ensemble strategy was to reduce the error rate. The models' results are merged to get the final prediction for any instance x_i. For learning the weights ω_j of the level-0 predictors, stacking adds a level-1 method called meta-learner. That is, for the level-1 learner, the prediction $y(x_i)$ of each training instance x_i is training data which can be defined in the following formula

$$y(x_i) = \sum_{j=1}^{4} \omega_j h_j (x_i) \quad (11)$$

Where, x_i - instances - Optimal weights of level-0 predictors and h_j -Base models.

Vi Results and Discussion

EDA was done on the Parkinson disease; the dataset contains totally 23 attributes and it was converted from .XLSX format into .CSV format and the inconsistent dataset were transformed into the desired format which was used for this research work. Where the data was cleaned, accounted for missing information and then explored Correlation Analysis, was performed to identify highly correlated variables. For this high dimension, histogram plot visualization for each attribute is very difficult. So, the irrelevant attributes have been removed using the preprocessing steps. The 10 relevant attributes taken are namely, MDVP:Fo(Hz), MDVP:Flo(Hz), DVP:Shimmer,MDVP:Shimmer(dB), Shimmer:APQ5, MDVP:APQ, HNR, spread1, spread2, PPE where the value ranges from (0.5 to 0.35) and the attributes are standardized. The reduction of attributes will result in maximizing the accuracy and using heat map, correlation coefficient values are taken into account.

After the preliminary analysis of the data, Classification algorithms – Random Forest, XGBoost, AdaBoost, Logistic Regression were trained on the data to compare their performance analysis to execution complexity. The proposed research work has combined the existing machine learning algorithms and then developed an Ensemble Stacking Learning Algorithm for the classification and prediction of PD. In order to distinguish between Healthy people and People with Parkinson (PWP) samples, this research effort suggested a stacked model based on chosen dataset. This research paper has proposed 4 stacking models for the classification of PD in the chosen data set. These models are named as RXLR, RXAB, ESLA and RXAM. These are actually known and identified as META models which are used for the prediction in the medical dataset. Out of these four models, one of the models yields the best results which is to be visualized for the prediction of disease. Based on the evaluation criteria of these models, the obtained results are analyzed.

The Python Software was used to apply classification methods to the dataset in this research work. In each classifier model, 80% of the data set was used to train the model and 20% was used to test the model. The datapoints are split into training data and testing data. In Overall 1170 records, 936 records are stored in training data and 234 records in testing data and it is stored in X_train, X_test, Y_train, Y_test. As a first step, the basic and simple classification models are developed by using RF, XGBoost, AdaBoost, Logistic Regression and MLP algorithms. This approach adapts a unique way that it may be used for both regression and classification type of problems. In all these Classification Algorithms parameter tuning are done using rank_test_score method. The method rank_test_score indicates the rank of a grid search parameter combination based on the mean_test_score. The parameter combination that results in the lowest mean_test_score will have a rank_test_score of N and the parameter combination with the highest mean_test_score will have a rank_test_score of 1. For this work, four stacked models are created for Parkinson disease prediction. Stacking is an ensemble machine learning algorithm and learns how to integrate predictions from two or more basic machine learning algorithms using a meta-learning method. Stacking model architecture includes two or more base models, also called as level-0 model, and a meta-model that combines the predictions of the base models, also known as a level-1 model. The primary motivation for employing this ensemble strategy was to reduce the error rate. When compared to a single contributing model, an ensemble can generate better predictions and produce better results.

Result of RXLR Model

The parameters of the estimator used to apply these methods are optimized by cross-validated grid-search over a parameter grid. Table 3 shows the rank_test_score of RXLR model which indicates the parameter tuning Grid Search CV results. Sample input values are chosen randomly. MeanFitTime, StdFitTime, MeanScoreTime, StdScoreTime, MeanTestScore and StdTestScore results are obtained. For the mean_fit_time it is clear that it's the average time of training between different folds. Based on the Rank_test_score method parameter tunings are done and the predictions of Parkinson disease are performed well.

Table 3: Sample Results of Rank_Test_Score in RXLR Model **Fig.**

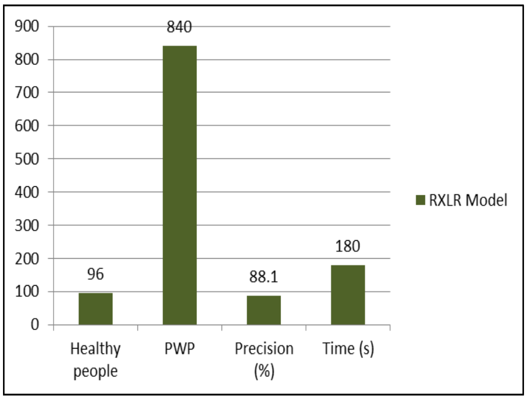
S. No	MeanFit Time	StdFit Time	MeanScore Time	StdScore Time	MeanTest Score	StdTest Score
1	0.128	0.009	0.013	0.002	0.895	0.112
2	0.185	0.019	0.012	0.001	0.873	0.115
3	0.199	0.022	0.012	0.005	0.895	0.123
4	0.169	0.012	0.010	0.007	0.887	0.123
5	0.195	0.020	0.013	0.002	0.862	0.112

In this research work, the ensemble RXLR stacking model used to find the prediction of PD based on confusion matrix and rank_test_score. Table4 shows the healthy people, People with Parkinson (PWP) and Precision. The count of healthy people and PWP are 96 and 840 respectively. Finally, the RXLR model yields precision is 88.10 percent and the time taken for the process is 180 seconds.

Table 4: Result of RXLR Model

Model	Healthy people	PWP	Precision (%)	Time (s)
RXLR Model	96	840	88.10	180

Figure 2 shows the performance analysis by means of Precision, and Time of RXLR model. Error metric is a way to quantify the performance of a model and provides a way for the forecaster to quantitatively compare different models.



Result of RXLR Model

Table 5 shows the residual value of R square yields 0.47565, Root mean square logarithmic error got the minimum value of 0.29912, The MAE shows the value 7.12494 and MSE yields the value 2.84344.

Table 5: Error Metrics of RXLR

R^2	0.47565
RMSLE	0.29912
MAE	7.12494
MSE	2.84344

Result of RXAB Model

The parameters of the estimator used to apply these methods are optimized by cross-validated grid-search over a parameter grid. Table 6 shows the rank_test_score of RXAB model which indicates the parameter tuning Grid Search CV results. Sample input values are chosen randomly. MeanFitTime, StdFitTime, MeanScoreTime, StdScoreTime, MeanTestScore and StdTestScore findings are produced. For the mean_fit_time it is clear that it's the average time of training between different folds. Based on the Rank_test_score method parameter tunings in RXAB models are produced and the PD predictions are successfully carried out.

Table 6: Sample Results of Rank_Test_Score in RXAB Model

S. No.	Mean Fit Time	Std Fit Time	Mean Score Time	Std Score Time	Mean Test Score	Std Test Score
1	0.328	0.011	0.033	0.007	0.899	0.144
2	0.116	0.008	0.014	0.007	0.889	0.096
3	0.141	0.012	0.076	0.009	0.872	0.155
4	0.716	0.050	0.772	0.033	0.893	0.155
5	0.637	0.034	0.035	0.008	0.896	0.144

RXAB stacking model is the combination of random forest, xgboost and adaboost algorithms. It is used to find the prediction of PD based on confusion matrix and rank_test_score. Table 7 shows the healthy people, People with Parkinson (PWP), precision and time. The count of healthy people and PWP are 90 and 846 respectively. Finally, The RXAB model produces 90.35% of precision and tends to take 175 seconds to complete.

Table 7: Result of RXAB Model

Model	Healthy people	PWP	Precision (%)	Time (s)
RXAB Model	90	846	90.35	175

Figure 3 shows the performance analysis by means of Precision, and Time of RXAB model.

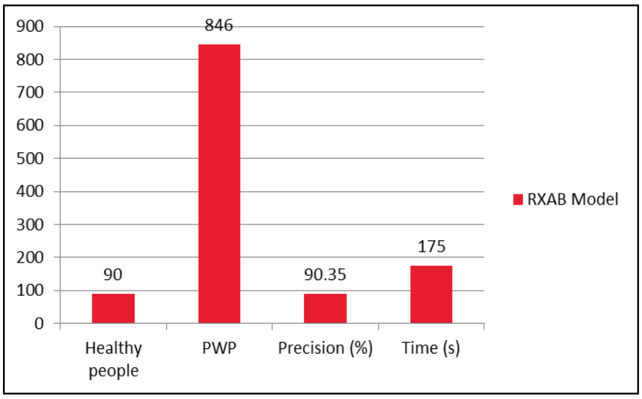


Fig. 3: Result of RXAB Model

Table 8 shows the error metric is a way to quantify the performance of a model. The residual value of R square got 0.36754, Root mean square logarithmic error obtained the minimum value of 0.24145, The MAE yields the value of 6.36448 and Mean Square Error yields 3.41256 of value.

Table 8: Error Metrics of RXAB

R^2	0.36754
RMSLE	0.24145
MAE	6.36448
MSE	3.41256

Result of ESLA Model

The parameters of the Estimator that are used to apply these methods are optimized by cross-validated grid-search over a parameter grid. Table 9 shows the rank_test_score of the proposed ESLA model which indicates the parameter tuning Grid Search CV results. Sample input values are chosen randomly. MeanFitTime, StdFitTime, MeanScoreTime, StdScoreTime, MeanTestScore and StdTestScore results are obtained. For the mean_fit_time it is clear that it's the average time of training between different folds. Based on the

Rank_test_score method parameter tunings are done and the predictions of Parkinson disease are performed well.

Table 9: Sample Results of Rank_Test_Score in ESLA Model

S. No	Mean Fit Time	Std Fit Time	Mean Score Time	Std Score Time	Mean Test Score	Std Test Score
1	0.569	0.027	0.016	0.003	0.883	0.143
2	0.993	0.056	0.015	0.005	0.896	0.130
3	0.734	0.394	0.015	0.006	0.895	0.170
4	0.976	0.050	0.013	0.009	0.885	0.139
5	0.730	0.392	0.016	0.002	0.855	0.159
6	0.814	0.094	0.016	0.004	0.875	0.133
7	0.996	0.030	0.012	0.009	0.881	0.134
8	0.834	0.064	0.012	0.010	0.877	0.160
9	0.996	0.130	0.013	0.008	0.882	0.180
10	0.976	0.070	0.016	0.005	0.876	0.175

In this research work, the ESLA stacking model is used to find the prediction of PD based on confusion matrix and rank_test_score. Table 10 shows the healthy people, People with Parkinson (PWP), precision and time. The count of healthy people and PWP are 60 and 876 respectively. The ESLA model yields precision is 92.60% and the time taken for the process is 160 seconds.

Table 10: Result of ESLA Model

Model	Healthy people	PWP	Precision (%)	Time (s)
ESLA Model	60	876	92.60	160

Figure 4 shows the performance analysis by means of Precision, and Time of ESLA model.

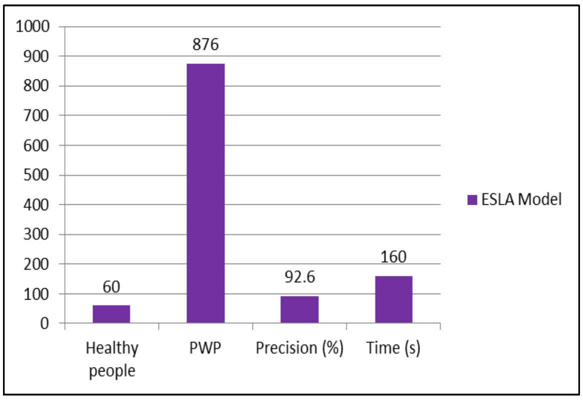


Fig. 4: Result of ESLA Model

Error metric is a way to quantify the performance of a model and provides a way for the forecaster to quantitatively compare different models. Table 11 shows the residual value of R square yields least value 0.72787, the RMSLE got the minimum value of 0.11543, The Mean Absolute Error obtained the value 5.12765 and MSE yields the value 1.78340.

Table 11: Error Metrics of ESLA

R^2	0.72787
RMSLE	0.11543
MAE	5.12765
MSE	1.78340

Result of RXAM Model

The parameters of the Estimator used to apply these methods are optimized by cross-validated grid-search over a parameter grid. Table 12 shows the rank_test_score of RXAM model which indicates the parameter tuning Grid Search CV results. Sample input values are chosen randomly. MeanFitTime, StdFitTime, MeanScoreTime, StdScoreTime, MeanTestScore and StdTestScore findings are produced. For the mean_fit_time it is clear that it's the average time of training between different folds. Based on the Rank_test_score method parameter tunings in RXAM model are produced and the PD predictions are successfully carried out.

Table 12: Sample Results of Rank_Test_Score in RXAM Model

S. No	Mea nFit Time	Std Fit Time	Mean Score Time	Std Score Time	Mean Test Score	Std Test Score
1	0.769	0.029	0.036	0.007	0.886	0.175
2	0.924	0.045	0.017	0.001	0.888	0.111
3	0.676	0.384	0.079	0.009	0.873	0.202
4	1.524	0.087	0.775	0.033	0.876	0.171
5	0.637	0.003	0.035	0.008	0.896	0.144

RXAM stacking model is the combination of random forest, xgboost, adaboost and mlp. It is used to find the prediction of PD based on confusion matrix and rank_test_score. Table 13 shows the healthy people, People with Parkinson (PWP), precision and time complexity. The count of healthy people and PWP are 72 and 864 respectively. Finally, The RXAM model produces 91.40% of precision and tends to take 165 seconds to complete.

Table 13: Result of RXAM Model

Model	Healthy people	PWP	Precision (%)	Time (s)
RXAM Model	72	864	91.40	165

Figure 5 shows the performance analysis by means of Precision, and Time of RXAM model.

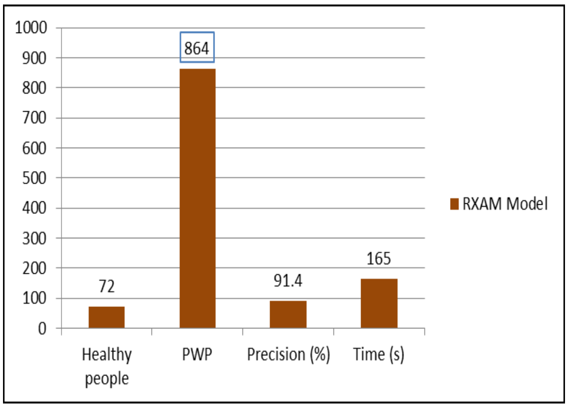


Fig.5: Result of RXAM Model

Table 14 shows the error metric is a way to quantify the performance of a model. The residual value of R square got 0.68198, Root mean square logarithmic error obtained the minimum value of 0.26954, The MAE yields the value of 8.43556 and Mean Square Error yields 3.79688 of value.

Table 14: Error Metrics of RXAM

R^2	0.68198
RMSLE	0.26954
MAE	8.43556
MSE	3.79688

Discussion

The performance of the Algorithms is analyzed after executing the source code which is written in Python programming language. The evaluations of all metrics are carried out in this research work and are explained as follows. Evaluation of performance is critical in classification to justify the accuracy of the study of findings. Many performance evaluation approaches have been followed in classification for a long time and have become standard performance evaluation metrics in related areas. Table 15 shows the results of stacked models where the metrics are healthy people, PWP, Precision and Time taken. The graphical representation of Table 15 is shown as Figure 6 illustrating the metrics of stacked models.

Table 15: Results of stacked models

Models	Healthy people	PWP	Precision (%)	Time taken (in sec)
RXLR	96	840	88.10	180
RXAB	90	846	90.35	175
ESLA	**60**	**876**	**92.60**	**160**
RXAM	72	864	91.40	165

According to the obtained results through its findings, the RXLR algorithm yields the precision 88.10% and 180 seconds of time was taken for the process. RXAB model yields 90.35% of precision and 175 sec time was taken. 91.40 percent of precision was obtained by the RXAM stacking model and the time was taken for the process is 165 seconds. From the obtained results and through the findings, the ESLA model outperformed the other models are obtained 92.60% of precision and time taken was 160 sec. ultimately, by using an ensemble-based strategy. The suggested method was able to attain acceptable results.

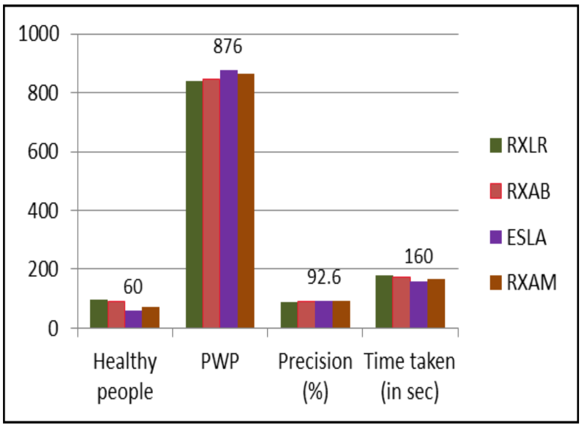


Fig. 6: Metrics of Stacked Models

To evaluate the performance, proposed ensemble method is compared with other stacked models and shows that the proposed method is better implemented. The above table and figure indicates that the results produced by this research work, is of 92.60 percentage of accuracy. It is very clear from the result obtained by this research that the proposed method ESLA model yields better results compared with all other methods through its performance metrics and time complexity.

VII Conclusions

In the recent days, medical data analysis has many approaches and uses a different number of methods for the diagnostics of diseases. Most of the approaches available in today's world have used multiple methods. One of such method proposed in this research work uses prediction and classification of PD from the data set which is available in public. Numeric attributes were taken for the prediction of disease. While identification of Parkinson Disease have been proven to be effective, current approaches do not have the capacity to evaluate speech samples, which is essential for enhancing Parkinson Disease classification effectively. Due to the difficulty of medical diagnosis and the prevalence of PD, it is critical to propose a simple and affordable solution for its accurate and early identification. Parkinson disease prediction is an important area in medical diagnosis. In this research work RF, XGBoost, AdaBoost, Logistic Regression and MLP classification methods are used for developing four stacking models. The Stacking models are namely RXLR, RXAB, ESLA and RXAM. The ensemble stacking models are used to find the prediction of PD based on confusion matrix and rank_test_score. The comparison with the proposed algorithm is done by means of time complexity and accuracy via precision. The results obtained from this research proved clearly that the proposed ESLA model yields better results compared with all other models through its performance metrics and time complexity. The proposed ESLA model yields results that are more accurate empirically and technically. It also identifies the patients affected by Parkinson disease more accurately from the medical data than the other stacked models. From this approach, it is identified the Parkinson disease effectively. The same method may be extended to identify other diseases in future.

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