A Comparison of Machine Learning Algorithms for Parkinson's Disease Detection

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Abstract— **Parkinson's disease is a progressive condition that impacts the neurological system and the areas of the body that are under the control of the nerves. Detecting and diagnosing PD early and accurately is essential for effective treatment and care. Biomedical speech analysis has emerged as a promising non-invasive approach for detecting and monitoring PD. We collected a data set from the University of California at Irvine (UCI) machine learning repository. The study investigates the utilization of a dataset to assess the suitability of machine learning (ML) algorithms for diagnosing Parkinson's disease. The research employs classification algorithms coupled with feature selection based on Pearson correlation. The data set is comprised of 195 voice recordings obtained from 31 patients during their examinations. Among them, 23 individuals in the study were diagnosed with Parkinson's disease. The age at the time of diagnosis ranged from 46 to 85 years. To handle this data, three methodologies are employed: a train/test split, k-fold cross-validation, and stratified k-fold cross-validation to ensure robust evaluation. Additionally, we use the F1 score, accuracy, and balanced accuracy measures to evaluate our models. The highly correlated selection data combined with data processing methods helps achieve positive results for all machine learning algorithms. Especially, Random Forest consistently outperformed other methods in our project. Random Forest with an accuracy of 95.42%, balanced accuracy of 93.98%, and an f1-score of 0.98. This demonstrates the capability of algorithms to diagnose Parkinson's disease effectively, even when confronted with imbalanced data. In our future research, we aim to integrate additional data on Parkinson's Disease in order to conduct a comprehensive evaluation of this condition.**

Keywords— Machine Learning, Parkinson's disease, Voice Measures, Feature Extraction

I. Introduction

Parkinson's disease (PD) is a common neurodegenerative disorder affecting millions of people worldwide [1]. In the United States, it is estimated that 1.04 million people were diagnosed with Parkinson's disease in 2017, with total economic costs of $51.9 billion. Considering that a significant number of people remain undiagnosed or receive incorrect diagnoses, it is highly probable that the actual figure is considerably larger. PD was more common at age 65 and in men [2]. This disease not only affects the patient's life but also causes difficulties for caregivers. While there is no cure for PD, early detection and timely intervention can significantly improve patient outcomes.

To accurately diagnose the disease, doctors employ a combination of DAT scanning and single-photon emission computed tomography (SPECT) to ascertain whether an individual has dopamine-deficient Parkinson's disease or not [3]. Besides, magnetic resonance imaging (MRI) can enhance the precision of diagnosing Parkinson's disease when distinguishing it from other conditions [4]. Various manual techniques exist, but clinical approaches primarily depend on subjective evaluations conducted by doctors and information provided by patients themselves. This process can be time-consuming and susceptible to inaccuracies [1]. Thus, monitoring the progression of PD can be challenging, especially in the early stages, when symptoms may be mild or non-specific.

With the rapid advancement of artificial intelligence (AI) technology, numerous solutions for supporting the diagnosis of Parkinson's disease (PD) have been researched and developed. Machine learning (ML) offers an economical, non-invasive, and valuable approach to PD diagnosis. Hence, our study aims to investigate the potential of machine learning classifier algorithms for predicting PD using voice recordings' speech features. Our research combines selective correlation features based on Pearson correlation with either k-fold or stratified k-fold cross-validation methods. We examine five common machine learning algorithms—Support Vector Machines (SVM), Decision Trees (DT), Logistic Regression (LR), Random Forest (RF), and Naïve Bayes. We evaluate each model's accuracy, balanced accuracy, and F1 score through careful study. Subsequently, we conduct a comparative analysis, aiming to enhance the efficiency of Parkinson's disease classification.

II. Related Works

Previous studies have investigated recognizing Parkinson's disease using machine learning. Detailed reviews of previous studies have been presented by Drotar et al. [6] conducted handwriting analysis from both a surface writing and a hand movement perspective when writing in the air. They identified Support Vector Machine (SVM) as the classification model and attained 80% accuracy. To detect disease based on brain tumors, Arjurkar and Ridhorkar [7] conducted an extensive investigation into the effectiveness of machine learning methods in decision support systems for diagnosing Parkinson's disease. Their research revealed that boosted logistic regression outperformed all other algorithms, demonstrating remarkable accuracy in identifying patients with Parkinson's disease. Furthermore, Gait Measures is one of the ways to detect PD. It is diagnosed based on the identification of motor signs of bradykinesia, rigidity, tremor, and postural instability. Alex Li and Chenyu Li [8] used the Gait in Parkinson's Disease data set on PhysioNet. Using different machine learning methods, including Logistic Regression, SVM, Decision Tree, and K-Nearest Neighbors (KNN), has improved impression accuracy.

To detect Parkinson's disease based on voice signals, some research based on data Max A. Little et al. [5] created in their paper. They develop pitch period entropy (PPE), a new measure of dysphonia that is resistant to several uncontrollable confounding factors, such as loud acoustic surroundings and typical, healthy changes in voice frequency. They use a kernel support vector machine to have a high accuracy of 91.4%. Max A. Little was also researched in another paper with Athanasios Tsanas et al. about accurate telemonitoring of PD. This groundbreaking study showcases the ability to quickly and accurately assess the UPDRS (Unified Parkinson's Disease Rating Scale) remotely, with results that closely align with clinicians' evaluations. This achievement is accomplished through uncomplicated, self-administered, and noninvasive speech tests. The significance of this research lies in its potential to contribute to tele-monitoring systems [9]. In their research, Arti Rana et al. [10] investigated the effectiveness of supervised classification algorithms, including SVM, Naïve Bayes, k-nearest neighbor (K-NN), and artificial neural network (ANN), for Parkinson's disease detection. The experimental results demonstrated that the (ANN) achieved the highest level of accuracy among the tested algorithms. Moreover, Deep learning is also used to predict this disease.

Following the machine learning approach, Mehrbakhsh Nilashi et al. [11] predicted PD by employing techniques such as noise reduction, clustering, and prediction methodology. They used Principal Component Analysis (PCA) and Expectation Maximization (EM), then applied the Adaptive Neuro-Fuzzy Inference System (ANFIS) and Support Vector Regression (SVR). The results also indicated that all of the approaches used in this study can significantly improve the accuracy of PD prediction and apply to other classification and prediction problems within the medical domain. In addition to [12], the authors used the Synthetic Minority Over-sampling Technique (SMOTE), and hyperparameter tuning (GridSearchCV) to process data. For this study, the accuracy of Random Forest is 92%. In the same data set, Grover et al. also applied deep learning-based techniques. In their study, which used Deep Neural Network (DNN), they were able to diagnose Parkinson's disease symptoms in individuals with an accuracy of about 81.67% [13]. The author in [14] proposed two deep-learning frameworks to classify speech data. They use two frameworks, and merged features were then classified using a 10-layer CNN, comprising four consecutive convolution layers with each pair followed by a max pooling layer, a fully connected layer, and a final output layer. The two frameworks achieved accuracy of 84.5% and 86.8%, respectively.

III. Dataset and Methodology

A. Dataset

The data set used in the current study was analyzed and published in [5] by Max A. Little. Data published for general voice disorders includes 195 vowel pronunciations. A range of biological voice measurements were collected from 31 patients in this data collection, 23 of whom had Parkinson's disease (PD). There were six voice signal recordings for each patient. The age range for the diagnosis was from 46 to 85 due to the specificity of the condition. Each participant provided an average of six transcriptions, with each one lasting between one and 36 seconds. Every column in the data set represents a specific vocal measurement, while each row corresponds to one of the 195 recorded voices from these individuals, identified by the "name" column. The scatter matrix of some features is shown in Fig. 1.

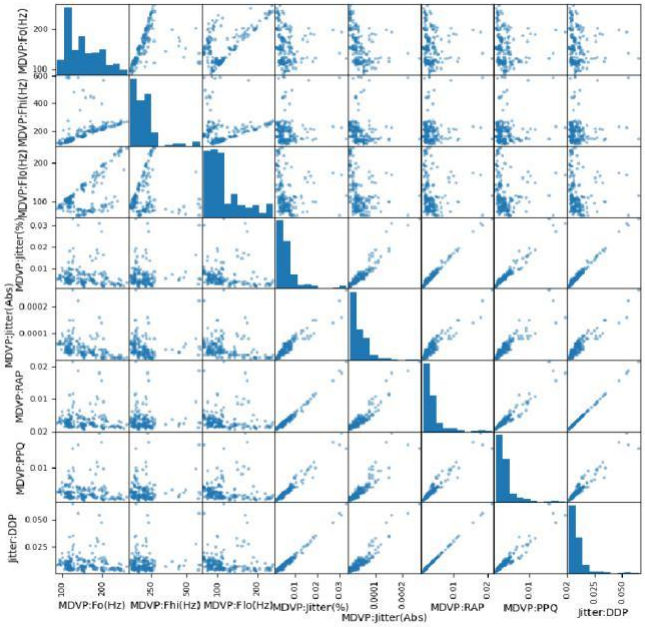

Fig. 1. Scatter matrix some features

Details on the information regarding data collection have been described in [5]. Briefly, the Computerized Speech Laboratory 4300B hardware was used to directly record the voice signals at a sample rate of 44.1 kHz and a 16-bit resolution. Before calculating the measures, all samples underwent digital amplitude normalization. The data set used consists of several attributes. These include the subject's name and recording number. Many measures of fluctuation in the fundamental frequency and amplitude are among the features. Jitter pertains to the degree of variation in speech F0, while shimmer relates to the extent of variation in speech amplitude from cycle to cycle. In particular, the data contains pitch cyclic entropy (PPE), a dysphonia measurement that can detect changes in each patient's voice. Noise to harmonics ratio (NHR) and harmonics to noise ratio (HNR) indicate the proportion of noise to tonal components present in the voice. The status attribute indicates the health status of the subject, with a value of one indicating Parkinson's disease and zero indicating a healthy status. The attributes recurrence period density entropy (RPDE) and detrended fluctuation analysis (DFA) were used and demonstrated their effectiveness in identifying common voice disorders. Finally, some other measures of fundamental frequency variation are recorded.

B. Methodology

The flow chart in Fig. 2 illustrates the process of the proposed algorithm. The first stage involves obtaining and importing the data set, which serves as the foundation for the entire process. Subsequently, the data goes through a feature

selection process where we clean, extract relevant features, and prepare it for analysis. In the next step, we employ both stratified k-fold cross-validation and k-fold cross-validation techniques to ensure robust model evaluation. In the stratified k-fold cross-validation approach, the data is stratified to maintain the class distribution, a crucial consideration when dealing with imbalanced datasets. Meanwhile, using k-fold cross-validation, we divide the data into subsets for training and testing in a systematic manner. The goal of our project is to classify them based on their ”status” value. A ”status” value of 0 corresponds to healthy individuals in 48 samples. On the other hand, a ”status” value of 1 indicates patients with Parkinson’s disease. Once the data has been appropriately divided and validated, we proceed to train the classification model, which is a pivotal stage in our algorithm’s development. Subsequently, the model advances to the evaluation phase, where we measure its accuracy and F1 score to gauge its effectiveness. Before outputting the most desirable algorithm, we fine tune the algorithm and perform evaluation multiple times. Multiple models are trained using the dataset to identify the most suitable algorithm.

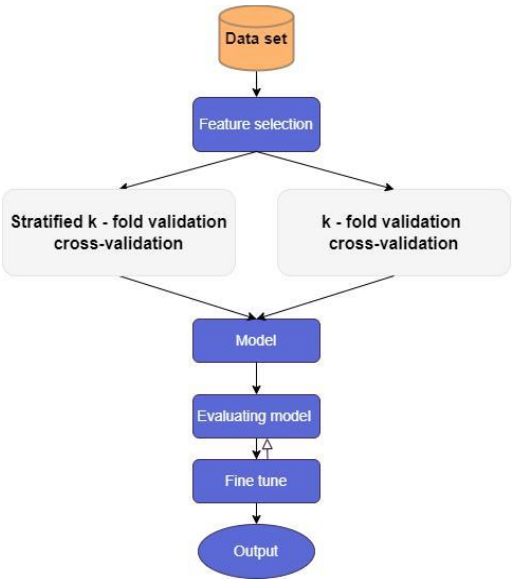

Fig. 2. The flow chart of the proposed model

♦ Feature extraction

In our research, we calculate Pearson’s correlation coefficient in equation (1). Developed by Pearson in 1895, it is the common way of measuring linear correlation, represented as a value between -1 and 1, quantifying the intensity and direction of the connection between two variables.

$$\rho = \frac{cov(X,Y)}{\sigma_X \sigma_Y} \quad (1)$$

Using the correlation between multiple variables to remove features with correlation. Multidimensional voice program (MDVP) features exhibit a positive association with another. This indicates that variables have a linear relationship. High correlation features have approximately equal effects on the dependent variable since they are more linearly dependent. The removal of highly correlated features helps the linear model work better, avoiding bias between features. The extracted features that were utilized for model training are listed in the Table I.

TABLE I. DESCRIPTION AND STATISTIC OF EXTRACTED FEATURES

No.	Feature	Mean	Max	SD
1	MDVP:Fo(Hz)	154.2	260.1	41.39
2	MDVP:Fhi(Hz)	197.1	592.0	91.49
3	MDVP:Flo(Hz)	116.3	239.2	43.52
4	MDVP:Jitter(%)	0.006	0.033	0.005
5	MDVP:Jitter(Abs)	0.00004	0.0003	0.00003
6	MDVP:RAP	0.003	0.021	0.003
7	MDVP:PPQ	0.003	0.019	0.003
8	Jitter:DDP	0.010	0.064	0.009
9	MDVP:Shimmer	0.030	0.119	0.019
10	MDVP:Shimmer(dB)	0.282	1.302	0.194
11	Shimmer:APQ3	0.016	0.056	0.010
12	Shimmer:APQ5	0.018	0.079	0.012
13	MDVP:APQ	0.024	0.138	0.017
14	Shimmer:DDA	0.047	0.169	0.030
15	NHR	0.025	0.315	0.040
16	spread1	-5.684	-2.434	1.090
17	status	0.754	1	0.432
18	PPE	0.207	0.5273	0.090

♦ Cross-validation

Cross-validation is a statistical method used when optimizing model hyperparameters to estimate the skill of machine learning models. This method also helps to detect overfitting, and the data sets utilized are split into multiple subsets of equal size through the process of cross-validation.

1) K-fold: In our research, we initially use k-fold cross-validation with k = 5. This approach is widely used because of its simplicity and its ability to yield less biased evaluations compared to other methods like a traditional train and test split. This approach utilizes a technique known as k-fold cross-validation, which involves randomly partitioning the observations into k-folds. The first fold serves as the validation set, while the model is trained on the remaining k = 1 folds.

2) Stratified k-fold : During the research, we found out that the data is largely imbalanced, with 23 patients and 8 healthy individuals. Due to this reason, we chose stratified k-fold cross-validation. It is an enhancement of the traditional k-fold cross-validation method designed to address issues related to imbalanced datasets and ensure a robust assessment of a predictive model’s performance. Stratified k-fold takes the concept of non-stratified k-fold a step further by ensuring that each fold maintains the same class distribution as the original dataset, thus preserving the proportion of different classes within each fold. The benefits of stratified k-fold cross-validation

include better representation of data and enhanced model robustness [15].

- **Classification based on machine learning**

The desired output variable in classification issues is discrete and divided into various classes or groups. In our study, for instance, this may entail designating '1' for patients and '0' for people in good health. We carried out experiments using some available algorithms but have chosen to present results for only the five performing ones. The algorithms we have reported are Support Vector Machines, Decision Trees, Logistic Regression, Random Forests, and Naïve Bayes. These algorithms are commonly utilized in the field due to their user-friendliness and the limited number of parameters that require tuning.

1) Decision Tree (DT): A decision tree is a supervised learning algorithm employed for performing classification and regression tasks in machine learning. It involves a tree structure consisting of a root node, branches, internal nodes, and leaf nodes by recursively partitioning the data based on a set of decision rules.

2) Random Forest (RF): A random forest can be described as a classification model that comprises a set of tree-based classifiers {h(x, k), k = 1,...} [16], where the {k} are independent distribute each tree casts a unit vote for the most popular class at input x. The hyperparameters of the random forest algorithm consist of the node size, which determines the minimum number of samples required to form a node, the number of trees in the forest, and the number of features randomly selected for each tree during training.

3) Logistic Regression (LR): Logistic Regression is another supervised machine learning algorithm used for binary classification tasks. Despite its name, logistic regression is primarily used for classification, not regression tasks. The algorithm models the relationship between the input features and the probability of the binary outcome using the logistic function, also known as the sigmoid function.

4) Naïve Bayes Classifier: Naive Bayes is a probabilistic machine learning algorithm commonly used for classification tasks. It is based on Bayes' Theorem, which calculates the probability of an event given prior knowledge or evidence. The Bayes' Theorem is described mathematically in the form of the following equation (2):

$$P(Y|X) = \frac{P(X|Y)\times P(Y)}{P(X)} \quad (2)$$

Through the application of this theorem, the probabilities P (X|Y) and P (Y) can be calculated from the training data. However, as the number of features increases, this process becomes much more difficult and requires more processing power.

5) Support Vector Machine (SVM): Support Vector Machines (SVM) are a class of supervised learning algorithms used for classification and regression tasks. They are widely used for their effectiveness in handling complex datasets by finding the optimal decision boundary, or hyperplane, that maximizes the margin between different classes.

$$w*x + b = 0 \quad (3)$$

The mathematics behind this process is described in the following equation (3), where w is the weight vector, x is the feature vector, and b is the bias term.

IV. Result and Discussion

A. Results

An overview of the results for some of the models above can be seen in Fig. 3. A chart comparing the results presents the results for algorithms trained on normal train/test split data. For these metrics, Logistic Regression, Random Forests (RF), and Decision Tree have an accuracy greater than 90%. This evaluation shows that RF gives us the best percentage of correctly classified, while Naïve Bayes has 67.80% accuracy. The experimental outcomes show that the F1-score of SVM is 0.92, RF is 0.98, SVM is 0.92, and LR is 0.94.

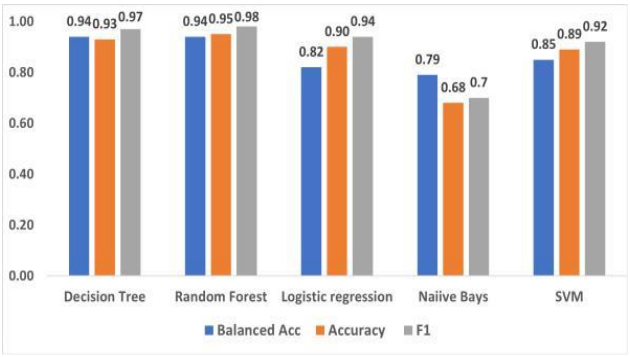

Fig. 3. Performance comparison on train/test split data

To account for imbalanced data, we employ balanced accuracy, which proves beneficial when tackling the challenge of uneven class distributions, where one class prevails over the other. Interestingly, when assessing this accuracy, we observe that DT and RF consistently exhibit the highest accuracy, with SVM following closely behind. It is concluded that the RF is the most accurate one, with the highest both accuracy and F1-score.

TABLE II. Comparing Highest Models Outcome with Data Processing Approaches

No.	Model	70-30 train/test	k-fold	Stratified k-fold
1	Decision Tree	93.22	89.11	87.69
2	**Random Forest**	**95.42**	**91.79**	**91.28**
3	Logistic Regression	89.83	84.10	84.11
4	SVM	88.83	81.54	82.05
5	Naïve Bayes	67.80	68.21	68.72

Additionally, Table II shows the results of different models on the training and test data sets. This table displayed results encompassing five models evaluated using three methods: a 70-30 train/test split, a 5-fold cross-validation, and a stratified 5-fold cross-validation approach. The table illustrates that the Random Forest algorithm attains the highest accuracy, 95.42% using the first split approach and 96.61% with k-fold validation.

Following closely in performance are the DT, LR, and SVM algorithms. Conversely, Naïve Bayes initially exhibited the lowest accuracy at 67.8% and 68.21%, but this improved slightly. In summary, the stratified k-fold method consistently yields lower accuracy compared to the other two methods. Nonetheless, it proves valuable when dealing with unbalanced data. In future work, we plan to perform an extensive analysis of all methodologies on this data set.

B. Discussion

In our research, we employed three different data-splitting approaches, and both of them yielded favorable outcomes. When we selected data and specifically selected highly related features, we obtained a higher level of accuracy compared to using the entire data set. The Random Forest model achieved the best performance with an accuracy rate of 95.42% and an F1-score of 0.98, representing the highest outcome for our research. Random forests are renowned for their accuracy and effectiveness due to the utilization of multiple decision trees. Although each decision tree in the Random Forest algorithm utilizes a subset of the training data, which may result in potential underfitting, the aggregation of predictions from numerous decision trees compensates for this limitation. Furthermore, the Naïve Bayes algorithm exhibits the least accuracy and F1-score measurements. It belongs to a cluster of algorithms that utilize Bayes' theorem under a rather simplistic presumption that assumes all input features are mutually independent. Consequently, for our specific problem, numerous features and correlations are likely to yield unfavorable outcomes. Furthermore, while the Stratified K-fold approach produces less favorable outcomes compared to other methods, it holds significance in the context of data processing.

TABLE III. COMPARING OF RESULT WITH OTHER RESEARCHES

References	Method	Accuracy
[17]	ANN	94.87%
	Random Forest	87.17%
	Naïve Bayes	71.79%
[18]	Decision tree	85.08%
[19]	Random Forest	90.26%
[20]	SVM	82.47%
	Neural Networks	85.03%
	Boosted Decision Tree	91.21%
Our Research	Decision Tree	**93.22%**
	Random Forest	**95.42%**
	Logistic Regression	89.83%
	SVM	**88.83**
	Naïve Bayes	67.80

Numerous researchers used the UCI Parkinson's data set in classification processes. The result is compared with those of previous works that made use of the same data shown in Table III. Moreover, the F1 score offers additional benefits for our problem. A high F1 score signifies excellent precision and recall, indicating a commendable balance between the two. This makes it particularly valuable for addressing unbalanced classification problems and delivering favorable outcomes. Despite employing an identical data set, the studies achieved inferior accuracy compared to our group. It shows that [18] a Decision Tree accuracy of only 85.08%, our study achieved a significantly higher accuracy index of 93.22%. This outcome further strengthens the validity and effectiveness of our data processing techniques.

V. CONCLUSION

Parkinson's Disease is a widespread neurodegenerative disorder that can severely affect the patient's living condition and is currently incurable. We employ machine learning for voice-based analysis in disease diagnosis, enhancing both efficiency and accuracy. Given the data imbalance between individuals with the illness and those who are healthy, we employ three data processing methods. Additionally, we utilize three key metrics—accuracy, F1 score, and Balanced Accuracy —to assess model performance.

Overall, our findings revealed that the Random Forest algorithm achieved the highest prediction accuracy among the evaluated models, and thus was chosen as the output model. Additionally, we employed the stratified k-fold cross-validation technique to mitigate the risk of overfitting and ensure the robustness of our models. However, improving the models is still likely to produce improved performance and greater accuracy. There are other metrics that can be implemented in the evaluation model. In the future, we want to combine other data to make a comprehensive diagnosis of this disease.

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