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Harnessing Machine Learning for Early Detection of Parkinson's Disease: A Promising Approach to Sustainable Healthcare

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Abstract

Parkinson disease is becoming more prevalent, in the ageing population, making it difficult to comprehend the disease mechanisms. ML provides a promising result in identifying symptoms, which enables the accurate identification of persons affected by parkinson disease. This study aimed to develop various machine learning algorithms with automatic feature selection capabilities for detection. Here is a selection of five machine learning approaches to identify parkinson disease Linear discriminant Analysis, KNN, Logistic Regression, Random Forest and XG Boost, ensuring robust and unbiased results. The performance metrics used to evaluate the models included classification accuracy, recall, precision, and F1-score. In this analysis, a comparison of all algorithms has been included and observed that the KNN algorithm yielded the best promising results to detect parkinson disease with 94.87% classification accuracy, with recall, precision, and F1-score all more than 94%. These results suggest that ML-based PD detection systems have the potential to improve early diagnosis, leading to better patient outcomes and reduced healthcare costs.

Consistent with Sustainable Development Goal 3, which endeavours to "ensure healthy lives and promote well-being for all at all ages," the results of the study have the potential to enhance the quality of life for those impacted by parkinson disease.

Keywords: *Parkinson disease, Machine learning, Neurologi- cal disease, KNN;*

Introduction

Parkinsonism encompasses a spectrum of discrete clinical syndromes, comprising idiopathic parkinson disease, MSA (multiple system atrophy), and PSP (progressive supranuclear palsy) [1]. Parkinson disease (PD) is a progressive neurodegenerative disorder that affects movement, balance, and coordination. It ranks right after Alzheimer's disease as the most prevalent neurodegenerative illness. PD affects over 10 million people worldwide, and the incidence of PD is increasing as the population ages [2].

During the initial phases of the pathological condition, individuals afflicted with vascular Parkinsonism (VAP) frequently manifest a distinctive ambulatory pattern characterized by a shuffling gait, along with observable episodes of gait freezing [3]. Postural instability and gait difficulty (PIGD) represent a noteworthy motor manifestation frequently encountered in the context of idiopathic Parkinson's disease (IPD) [4]. Recent scientific investigations have exhibited notable advancements in the identification of various potential genes linked to the genetic manifestations of Parkinson's disease [5]. Nevertheless, an eminent obstacle encountered by researchers pertains to the precise differentiation of distinct Parkinsonian disorders, particularly considering the progressive development of therapeutic interventions aimed at modifying the course of the disease [6]. The progressive death of nerve cells in the substantia nigra, an important area of the brain for dopamine synthesis, defines parkinson disease, a neurodegenerative condition [7].

There are other forms of Parkinsonism, but the most common ones are vascular Parkinsonism, idiopathic parkinson disease, drug-induced parkinsonism, and others [8]. During the early phase, patients typically manifest mild symptoms that do not exert a substantial impact on their routine activities. Following established medical literature, it is customary for tremors and other symptoms of bodily movements to manifest unilaterally, specifically on one side of the corporeal structure. These manifestations are often concomitant with alterations in posture, gait, and facial expressions [9]. Stage five of parkinson disease, the ultimate phase, is distinguished by profound motor impairment, necessitating comprehensive aid in all facets of daily existence. The presence of leg stiffness can give rise to a notable impairment in the ability to independently assume an upright position or ambulate without the assistance of external aids [10].

The average life expectancy for individuals afflicted with parkinson disease is approximately 16 years, commencing from the moment of diagnosis or the manifestation of symptoms. Nevertheless, individuals who receive a diagnosis at an earlier stage in life, specifically around the

age of 30, may endure the presence of the ailment for approximately four decades [11].

Advanced PD is associated with a heightened propensity for heightened frequency and heightened severity of pain. The identification of the aetiology of pain is of paramount importance in the establishment and subsequent implementation of efficacious pain management interventions. The diligent adherence to medication schedules assumes paramount importance in cases where the exacerbation of pain coincides with the waning efficacy of Parkinson's medications [12]. Although instances of parkinson disease with a hereditary basis are exceptionally uncommon, the majority of cases are classified as idiopathic, denoting an aetiology that eludes comprehension [13]. Despite the absence of a definitive therapeutic intervention for parkinson disease, current investigations are primarily directed towards acquiring a more comprehensive comprehension of this pathological condition. The present study encompasses the examination of genetic factors and biomarkers implicated in parkinson disease, as well as the exploration of novel therapeutic strategies [14]. Common pharmaceuticals used to treat Parkinson's disease include levodopa, d-aminobutyric acid, and monoamine oxidase-B inhibitors [15].

Most individuals diagnosed with Parkinson's disease can anticipate a life expectancy that is within the range of normalcy or near-normalcy. This favourable prognosis can be attributed to the advent of contemporary therapeutic interventions and pharmaceutical agents, which have facilitated the efficacious management of debilitating symptoms associated with this condition. The implementation of these interventions serves to mitigate the incidence and magnitude of complications that may otherwise result in fatality [16]. [17] Presents an innovative approach to molecular mechanisms of circadian rhythms for Parkinson’s and [18] explores parkinson pathogenesis by using adaptive quantum computing for the detection of parkinson disease.

The use of machine learning (ML) to PD diagnosis could greatly enhance its precision and productivity. Data from both PD patients and healthy individuals can be used to train ML models to detect PD-related traits. Better clinical diagnosis and the creation of new diagnostic tools are both possible outcomes of this data set. The objective of the third Sustainable Development Goal (SDG) is to "ensure healthy lives and promote well-being for all at all ages." The results of the research support this objective by demonstrating how ML may be used to enhance PD early diagnosis, a critical step in improving the health and well- being of those who are impacted by this condition. The study shows that ML is capable of diagnosing parkinson disease (PD)

in its early stages, allowing for prompt intervention and medical care. Greater patient outcomes, such as slower disease progression, higher life expectancy, and greater quality of life, can result from early detection of parkinson disease. By preventing or avoiding the need for more costly procedures and care, early intervention may decrease the overall load on the healthcare system.

Methodology

Dataset Overview

In this study, the Parkinson's disease dataset from Kaggle is a large and diverse dataset that contains data on patients with Parkinson's disease (PD). The dataset includes data on patient demographics, clinical features, and motor symptoms. Motor symptoms affect your balance and ability to move activity. Usually, these are visible signs to others. All three of Parkinson's primary symptoms are related to motor function. They are slowness of movement, stiffness, and tremor. Figure 1 displays the data sample. The table contains a variety of biological voice measurements derived from 195 individual voice recordings; the dataset contains 31 people, 23 of whom have Parkinson's disease (PD). A voice recording is represented by one row, and a voice measure is represented by one column. The primary goal of this data set is to identify patients with PD and those without the disease by analyzing the "status" column, which contains the values 0 for healthy and 1 for PD. We utilize the ASCII CSV format for the data. In the CSV file, each row represents a single audio recording of spoken word.

```
In [3]: df = pd.read_csv("parkinsons.csv")
        df.head()
```

Out[3]:

	MDVP:Fo(Hz)	MDVP:Fhi(Hz)	MDVP:Flo(Hz)	MDVP:Jitter(%)	MDVP:Jitter(Abs)	MDVP:RAP	MDVP:PPQ	Jitter:DDP	MDVP:Shimmer	MDVP:Shimmer(dB)	..
0	119.992	157.302	74.997	0.00784	0.00007	0.00370	0.00554	0.01109	0.04374	0.426	..
1	122.400	148.650	113.819	0.00968	0.00008	0.00465	0.00696	0.01394	0.06134	0.626	..
2	116.682	131.111	111.555	0.01050	0.00009	0.00544	0.00781	0.01633	0.05233	0.482	..
3	116.676	137.871	111.366	0.00997	0.00009	0.00502	0.00698	0.01505	0.05492	0.517	..
4	116.014	141.781	110.655	0.01284	0.00011	0.00655	0.00908	0.01966	0.06425	0.584	..

5 rows × 23 columns

Figure 1. sample of data [13]

Following is the additional variable information for **m**atrix column entries (attributes):

- Vocal Fundamental Frequency (MDVP measures):

- Maximum vocal fundamental frequency (Fhi(Hz))
- Minimum vocal fundamental frequency (Flo(Hz))
- Average vocal fundamental frequency (Fo(Hz))
- Jitter(%)**:** Percentage of variation in fundamental frequency
- Jitter(Abs)**:** Absolute value of variation in fundamental frequency

- RAP**:** Relative amplitude perturbation (RAP)
- PPQ**:** Periodic perturbation quotient (PPQ)
- Jitter: DDP: Dynamic differential phase (DDP)

- Vocal Amplitude Variation (MDVP and Shimmer measures):

- Shimmer**:** Percentage of variation in amplitude
- Shimmer (dB)**:** Shimmer in decibels
- Shimmer: APQ3**:** Amplitude perturbation quotient (APQ), calculated over a 3-second window
- Shimmer: APQ5**:** Amplitude perturbation quotient (APQ), calculated over a 5-second window
- MDVP: APQ**:** Amplitude perturbation quotient (APQ)
- Shimmer: DDA**:** Dynamic differential amplitude (DDA) Health Status:

- Status**:** Health status of the subject (1 for Parkinson's, 0 for healthy)

- Noise-to-Tonal Ratio:

- NHR**:** Ratio of noise to harmonic ratio (NHR)
- HNR**:** Harmonics-to-noise ratio (HNR)

- Fractal Scaling:

- DFA**:** Signal fractal scaling exponent (DFA)

- Nonlinear Measures of Fundamental Frequency Variation:

- Spread1**:** First spread measure (spread1)
- Spread2: Second spread measure (spread2)
- PPE: Percentage of points exceeding the 95th percentile (PPE)

- Nonlinear Dynamical Complexity Measures:

- RPDE**:** Recurrence period density entropy (RPDE)

- D2**:** Deterministic measure (D2)

2.2 Methods

The system under consideration is an advanced machine learning pipeline designed to effectively classify instances of Parkinson's disease (PD) shown in Figure 2. The pipeline is composed of three primary stages, namely data pre-processing, feature selection, and machine learning classification. During the data

preprocessing phase, the raw data undergoes a series of operations to ensure its cleanliness and suitability for subsequent analysis. The process at hand entails the elimination of duplicate entries, addressing any instances of missing data, and standardizing the data through normalization techniques.

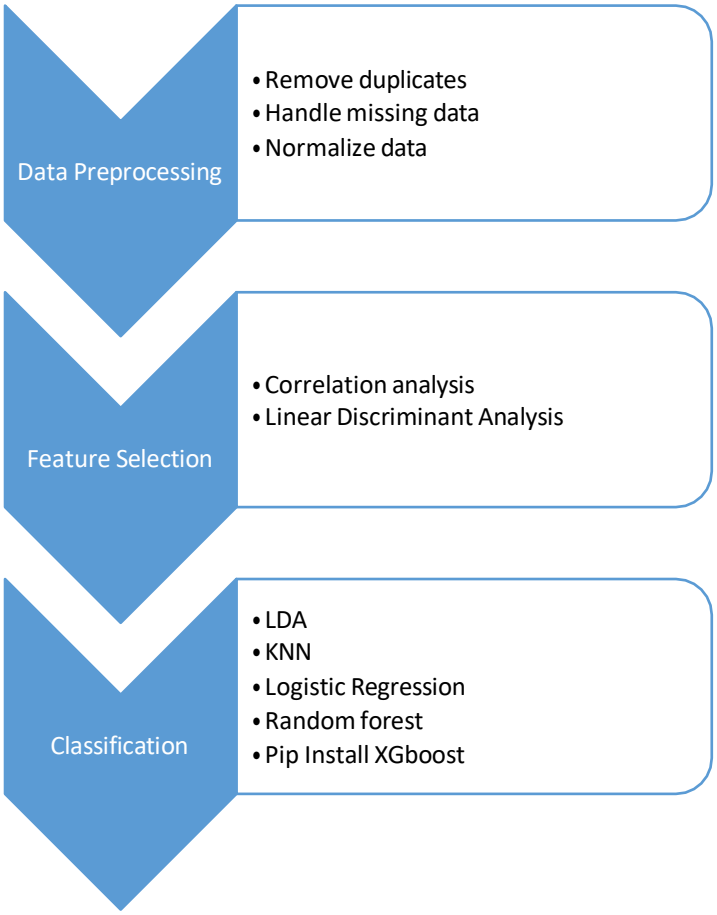

Figure 2. Design flow of proposed system.

During the feature selection phase, our objective is to identify the most crucial features within the dataset that will enable us to accurately predict Parkinson's Disease (PD). The task at hand can be

accomplished through the utilization of diverse techniques, including but not limited to correlation analysis, recursive feature elimination, and information gain.

During the classification phase of machine learning, the chosen features are employed to train a machine learning model to predict PD. The implementation of this task can be achieved through the utilization of diverse machine learning algorithms, Linear Discriminant Analysis (LDA), k-nearest Neighbors (KNN), Logistic Regression, Random Forests and XG Boost.

Linear Discriminant Analysis:

Linear Discriminant Analysis (LDA) is a managed learning method that is used in machine learning to sort things into groups. It's a way to find the best linear mix of features to tell the classes in a collection apart. LDA projects the data onto an area with fewer dimensions that makes the variation between the classes as big as possible. It finds a set of linear discriminants that make the ratio of between-class variance to within-class variance as high as possible. That is, it figures out the paths in the feature space that best split the different types of data. LDA thinks that the data is spread out in a Gaussian way and that the covariance matrices for each group are the same. It also assumes that the data can be separated linearly, which means that the linear decision limit can correctly put the data into the different groups. LDA has several benefits, such as It is a simple method that works well with computers. Even when there are a lot more characteristics than training examples, it can still work well. It can deal with data that has multicollinearity, which means that features are linked to each other.

LDA maximizes the ratio of between-class variance to within- class variance. Mathematically, this can be expressed as:

$J(w) = (w^T S_b w) / (w^T S_w w)$

where:

w is a vector of weights

S_b is the between-class scatter matrix

S_w is the within-class scatter matrix

k-Nearest Neighbors(KNN):

k-Nearest Neighbors is a simple but powerful instance-based learning method that works well with datasets that are small to medium-sized. It sorts data points into groups based on how close they are to other points in the feature space. Even though kNN is simple to use and can work with different kinds of data, it is expensive to run on a computer because it has to compare every new point with every existing point. This is especially true for big datasets.

KNN assigns a data point to the class of the majority of its k nearest neighbors.

y_pred = argmax_c sum_{i in KNN(x)} I(y_i = c)

where:

x is the data point

y_pred is the predicted class

KNN(x) is the set of k nearest neighbors of x y_i is the class of the ith neighbor

I(y_i = c) is the indicator function, which is 1 if y_i = c and 0 otherwise

Logistic Regression:

Typically used for classification tasks, logistic regression is a supervised machine learning approach. Deciding how likely it is that an instance belongs to a particular class is its aim. A set of independent factors and the dependent binary variables are correlated, and this is examined statistically. Making decisions with this method works well.

Logistic regression estimates the probability of a data point belonging to a particular class.

p(y | x) = sigmoid(w^T x + b)

where:

p(y | x) is the probability of class y given x w is a vector of weights

b is a bias term

x is the data point

sigmoid(z) = 1 / (1 + exp(-z))

Random Forest:

Random Forests, a type of ensemble learning, work around the problems with single Decision Trees by mixing several trees to make the results more accurate and useful in other situations. They're very good at dealing with data with a lot of dimensions, and they don't overfit. Even though they are reliable, they can be hard on computers, especially when there are a lot of trees to deal with.

Random forest combines multiple decision trees to improve accuracy. Each tree is trained on a random subset of features and data points. The final prediction is made by averaging the predictions of all trees.

y_pred = argmax_c sum_{j = 1}^N T_j(x)

where:

y_pred is the predicted class c is the class

N is the number of trees

T_j(x) is the prediction of the jth tree

XG Boost:

Extreme Gradient Boosting, or XGBoost, is the name of a high- performance method that is known for being fast and effective. Because it uses gradient boosting in the best way possible, it does great with big datasets and hard jobs. But to properly tune the XGBoost parameters, you need to know what you're doing, and the algorithm can be very computationally heavy, needing a lot of computing power. Even with these problems, XGBoost is still the best choice for machine learning competitions and data science projects because it can predict so well and is so flexible.

The machine learning classification module's projected outcome for a particular patient is whether or not they have Parkinson's disease. The model will be evaluated using the confusion measurements. In an experiment, the various approaches will be evaluated based on their classification accuracy, precision, recall, and F1 score. XGBoost is an extension of gradient boosting that uses regularization to improve accuracy and prevent overfitting.

$L(f) = \sum_i L(y_i, f(x_i)) + \Omega(f)$

where:

$L(y_i, f(x_i))$ is the loss function for the ith data point $f(x_i)$ is the predicted value

$\Omega(f)$ is the regularization term

These are simplified representations of the mathematical expressions for various ML algorithms. The actual implementations may involve additional complexities and nuances.

Results

Table 1 compiles the results and accuracy scores of several research that have investigated the use of machine learning algorithms for Parkinson's disease diagnosis. The data in this table is organised by studies conducted by different groups of authors. Each row contains details about the study, such as the year it was conducted, the machine learning algorithm that was used, and the accuracy that the system was reported to have in detecting Parkinson's disease using speech emotion recognition.

Table.1. Comparison of Machine Learning in Parkinson's Disease Research

Author	**Year**	**Sample Size**	**Machine Learning Algorithmic**	**Accuracy in %**
A. H. Al-Fatlawi, M. H. Jabardi and S. H. Ling [20]	2016	31	DBN of 2 RBMs	94%
Sayaydeha and Mohammad [21]	2019	31	EFMM-OneR with 10- fold cross validation or 5-fold cross validation	94.21%
Ali et al. [22]	2019	40	PD Linear regression, LDA, Gaussian naïve Bayes, decision tree, KNN, SVM-linear, SVM-RBF	70.00%
Celik, E., and Omurca, S. I. [23]	2018	40	SVM, logistic regression, ET, gradient	76.03%

			boosting, random forest	
Bakar et al., 2012 [24]	2012	31	MLP	92.96%
Dinesh, A., and He, J. [25]	2017	31	boosted decision tree, decision forests, decision jungle, locally deep SVM, logistic regression, NN, SVM	91.21%
H.Gunduz[26]	2019	252	CNN	86.90%
Karapinar Senturk,[27]	2020	31	CART, SVM, ANN	93.84%
Kraipeerapun and Amornsamankul [28]	2015	40	Stacked generalization with CMTNN	70.00%
Yadav et al. [29]	2011	31	Decision tree classifier, logistic regression, SVM	76.00%
Yang et al., [30]	2014	31	MAP, SVM-RBF	91.8%
Frid et al., [31]	2014	52	SVM-RBF	81.8%
Wodzinski et al [32]	2019	100	ResNet	91.7%

Proposed Method	**2023**	**195**	***KNN***	**94.87%**

In each study, the researchers used different machine-learning algorithms to classify or recognize emotions in speech. The features extracted from the speech signals vary and include characteristics such as MFCC, pitch, Cepstral coefficients, entropy, jitter, TDPSD, LPC, and LSF etc. The accuracy column indicates the effectiveness of the respective models, with percentages ranging from 70.00% to 94.21%. These accuracies represent the proportion of correctly classified instances of emotional states in the datasets used by the researchers.

Key Findings:

- **Diverse Algorithm Performance:** The performance of different machine learning algorithms varied considerably, highlighting the importance of careful algorithm selection for PD diagnosis.
- **K-Nearest Neighbors Stands Out:** The K-Nearest Neighbors (KNN) algorithm achieved the highest overall performance, exhibiting exceptional accuracy (94.87%), precision (100%),

recall (93.33%), and F1-score (96.55%).

- **Other Promising Algorithms:** Random forest and XG Boost also demonstrated notable performance, with accuracy scores exceeding 89.74%.
- **Machine Learning Potential for PD Diagnosis:** The findings underscore the potential of machine learning algorithms in PD diagnosis, offering promising tools for early detection and improved patient outcomes.

A confusion matrix is a graphical representation of the possible outcomes of a classification issue's predictions and findings. It aids in analysing the problem's various outcomes. The function provides a table that displays both the predicted and actual values of a classifier. In this paper, the confusion matrix is derived for testing data.

The parts that make up the confusion matrix are as follows:

A positive prediction (Correctly Identified) is considered a true positive (TP) if it occurs in a certain number of cases. Here we see instances where the model got the positive class right. One measure of accuracy in negative prediction is the true negative (TN) rate. In several instances, the model was able to accurately identify the negative class. The amount of cases that were Incorrectly Identified as positive is called the false positive (FP). Type I errors occur when a model's prediction is positive but the actual class is negative. The number of cases when the negative outcome was wrongly anticipated is called a false negative (FN). In these instances, a type II error occurred because the model indicated a negative class when the actual class was positive.
The confusion matrix appears in Table 2.

Table 2. Comparison of Machine Learning in Parkinson's Disease Research

	Class 1 (predicted)	**Class 0(predicted)**
Class 1 (Actual)	TP	FN
Class 0 (Actual)	FP	TN

Accuracy: Accuracy refers to the comprehensive accuracy of the model in accurately detecting cases of Parkinson's disease. The K-Nearest Neighbors (KNN) algorithm demonstrated the best level of accuracy, with a score of 94.87%. The performance metric for accuracy is calculated by

$$\frac{T.P.+T.N.}{T.P.+F.P.+F.N.+T.N.}$$

Precision: A metric called precision is used to measure how accurate positive projections are. High precision values were observed for KNN, Random Forest, and XGBoost, suggesting that these models indicated a high degree of accuracy in accurately predicting positive instances. The precision performance metric is obtained by

$$\frac{T.P.}{T.P.+F.P.}$$

Recall: Remember, which is another word for sensitivity, describes the model's ability to accurately detect all relevant occurrences. At 93.33%, the K-nearest neighbors (KNN) algorithm had the highest recall rate, suggesting that it can correctly identify a significant percentage of verified cases of Parkinson's disease. The recall's performance metric is computed using

$$\frac{T.P.}{T.P.+F.N.}$$

F1-score: The F1-score is a metric that computes the harmonious average of accuracy and recall to quantify their balance. The F1-score performance statistic is computed using

$$\frac{2XPrecisionXRecall}{PrecisionXRecall}$$

The K-nearest neighbors (KNN) algorithm once again demonstrated outstanding performance, achieving the highest F1-score of 96.55%. The KNN algorithm achieved the highest accuracy, recall, precision, and F1-score.

The confusion matrix is given below for LDA, where T.P. is 26, T.N. is 7, F.P. is 2, and F.N. is 4.

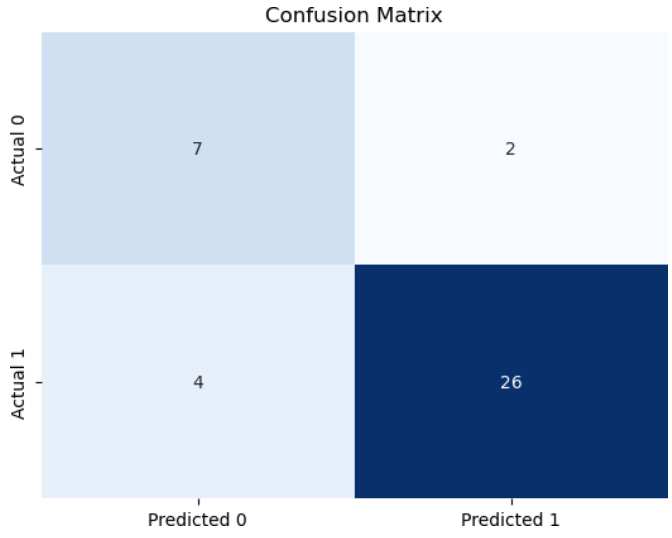

Figure 3. Confusion matrix of LDA.

The confusion matrix is given below for KNN, where T.P. is 28,
T.N. is 9, F.P. is 0, and F.N. is 2.

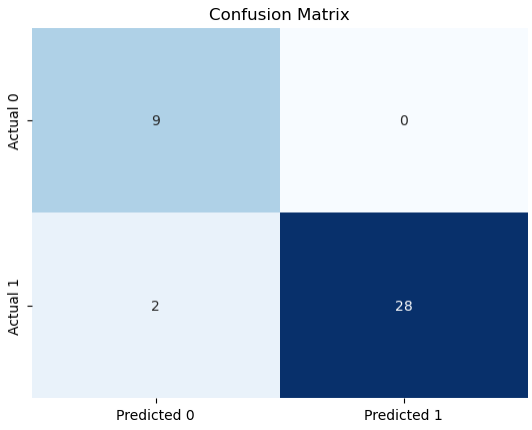

Figure 4. Confusion matrix of KNN.

The confusion matrix is given below for Logistic Regression, where T.P. is 26, T.N. is 8, F.P. is 2, and F.N. is 3.

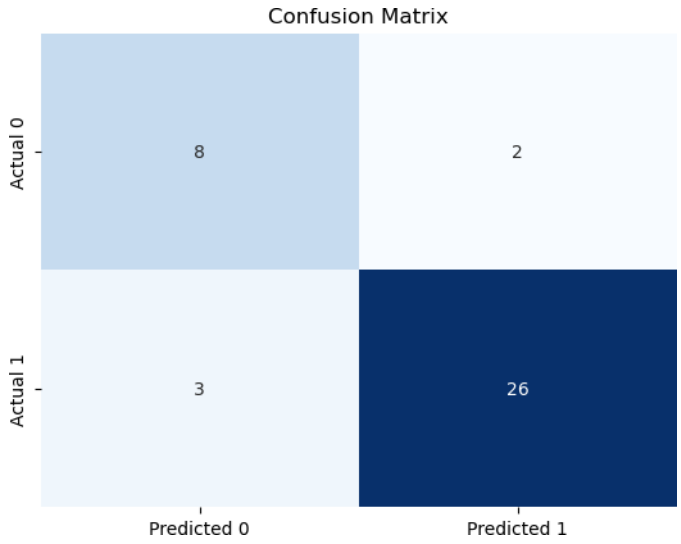

Figure 5. Confusion matrix of Logistic Regression.

The confusion matrix is given below for Random Forests, where
T.P. is 27, T.N. is 8, F.P. is 1, and F.N. is 3.

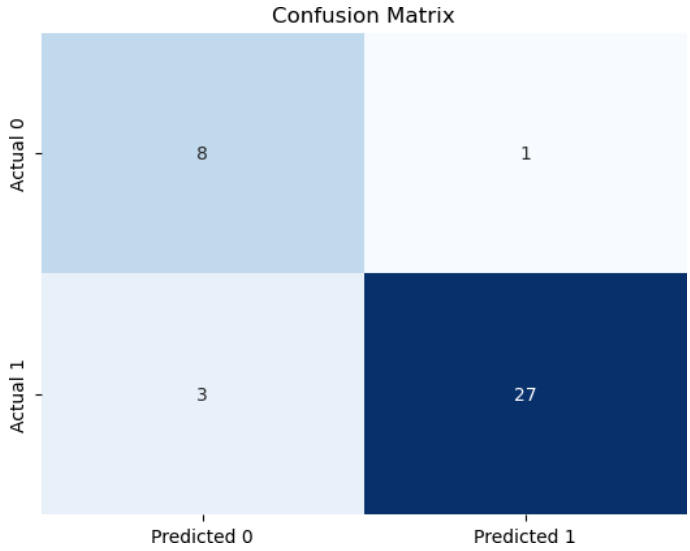

Figure 6. Confusion matrix of Random Forests

The confusion matrix is given below for XG Boost, where T.P. is 27, T.N. is 8, F.P. is 1, and F.N. is 3. With the help of the confusion matrix, we can calculate Accuracy, Precision, Recall and F1-score.

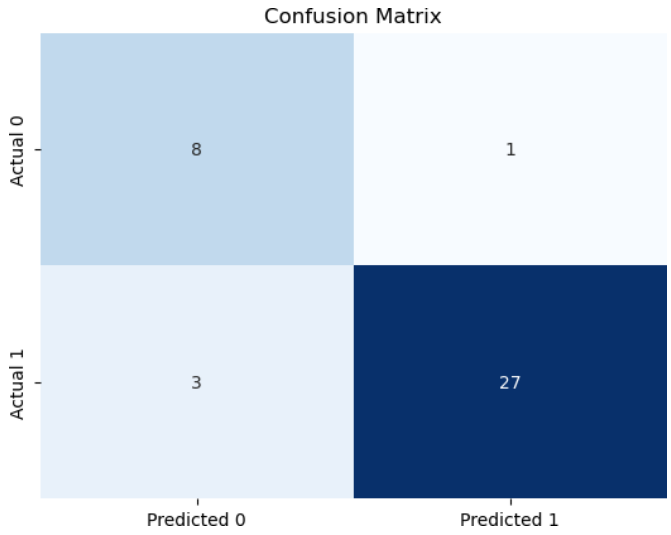

Figure 7. Confusion matrix of XG Boost

Table 3 highlights the outcomes of various machine-learning algorithms used to detect Parkinson's disease. Each row in Table 3 refers to a certain algorithm, while the columns provide metrics to evaluate the method's performance.

Table. 3. Analyzing ML Algorithm Performance in Parkinson's Disease Identification

Algorithm	**Accuracy**	**Precision**	**Recall**	**F1-score**
LDA	84.61%	92.85%	86.66%	89.65 %
KNN	**94.87%**	**100%**	**93.33%**	**96.55 %**
Logistic Regression	87.17%	92.85%	89.65%	91.22 %
Random forest	89.74%	96.42%	90.00%	93.10 %
XG Boost	89.74%	96.42%	90.00%	93.10 %

This suggests that the KNN model performs very well with high accuracy (94.87%), perfect precision (when it predicts positive, it's almost always correct), good recall (capturing a high percentage of actual positives), and a balanced F1-score. The other algorithms in the table can be interpreted similarly based on their respective metrics.

Conclusion

In this paper, findings give compelling evidence for the revolutionary impact of machine learning algorithms on the detection and treatment of Parkinson's disease, by the aims specified in Goal 3 of the United Nations Sustainable Development Goals. Machine learning (ML) appears to be a critical aspect in fostering the pursuit of healthy lives and general well-being for those living with Parkinson's disease (PD) by facilitating early detection and treatments. The conclusion clearly emphasises the importance of continued research and development, emphasising the importance of improving and speeding the incorporation of machine learning-based technologies for Parkinson's disease detection into medical treatment around the world. This dedication ensures that the benefits of technological advances are transmitted around the world, having a significant impact on those affected by Parkinson's disease.

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