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## PARKINSON'S DISEASE CLASSIFICATION BASED ON STACKED DENOISING AUTOENCODER

#### Abstract

One of the most common neurological conditions caused by gradual brain degeneration is Parkinson's disease (PD). Although this neurological condition has no known treatment, early detection and therapy can help patients improve their quality of life. An essential patient's health record is made of medical images used to control, manage, and treat diseases. However, in computerbased diagnostics, disease classification is a difficult task because of the time consumption and high rate of false positive marks. To overcome this problem, this paper introduces a stacked denoising autoencoder (SDA) for Parkinson's disease classification. In preprocessing, noise is reduced and important information is retained, resulting in increased performance and data augmentation is performed to avoid overfitting issues and increase the size of the dataset. The main aim of this paper is to derive an optimal feature selection design for an effective Parkinson's disease classification. Improved Pigeon-Inspired Optimization (IPIO) algorithm is introduced to enhance the performance of the classifier. Thus, the classification result improved by the optimal features and also increased the sensitivity, accuracy, and specificity in the medical image diagnosis. The proposed scheme is implemented in PYTHON and compared with traditional feature selection models and other classification approaches. The efficacy of the performances is evaluated using a Parkinson's Progression Markers Initiative (PPMI) dataset. The integration of the stacked denoising autoencoder and Improved pigeon inspired optimization method produced the greatest results, with 99.17% accuracy, 98.74% sensitivity, and 98.96% specificity. Furthermore, our finding outperforms the most recent research in the field.

KeywordsParkinson's disease, brain, data augmentation, classification, stacked denoising<br/>autoencoder, Improved Pigeon-Inspired Optimization (IPIO)

**Citation** Computer Science 24(4) 2023: 491–511

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#### 1. Introduction

Parkinson's disease (PD) is a progressive neurodegenerative disease that impacts 1% of persons over the age of 60 and is the world's most popular neurological disorder after Alzheimer's disease [2]. The loss of cells in several parts of the brain, particularly the substantia nigra, causes Parkinson's disease. Dopamine, a data transmitter for movement coordination, is produced in the substantia nigra [8, 19]. Dopamine deficiency leads neurons to fire randomly, causing these sufferers to lose control of their limbs. In people with Parkinson's disease, motor symptoms such as slowness of movement, postural instability, resting tremors and rigidity are frequent [14].

Motor symptoms do not appear until the disease has progressed, making rapid recognition problematic. Although Parkinson's disease cannot be cured, patients' quality of life improves when they are diagnosed early and treated swiftly [6, 10, 12, 15]. Non-motor symptoms include cognitive impairment, emotional issues, low blood pressure while standing, swallowing difficulties, worsening of writing skills, sleep difficulties, drooling, loss of sense of smell and speech [3, 11, 22, 23].

These studies used a range of speech signal processing algorithms to extract clinically significant features, which were then fed into a variety of artificial learning systems to generate reliable PD classification decisions [16,21]. While Artificial Neural Networks (ANN), Random Forest (RF), Support Vector Machines (SVM), and KNN are the most commonly utilized algorithms in PD classification, they are also effective due to their simplicity and comprehensibility [20]. The success of the algorithms is impacted by the characteristics of the data features extracted. While individually finding suitable features to capture the core qualities of speech (audio) data can be challenging, the underlying characteristics of the data can be manually identified using a deep learning technique [25].

One of the most extensively utilized MRI methods for demonstrating pathological changes related to PD in the striatal area is volumetric analysis. The automatic volumetric approach of voxel-based morphometry is used to detect grey matter intensity decline in the caudate and putamen regions [5]. Local atrophy has been discovered in recent investigations on shape changes in brain areas. However, there is a lack of spatial specificity in these investigations [7]. Deep learning neural networks are a novel sort of analysis that can be utilized to take advantage of the spatial organization of sub-anatomical regions. In medical image analysis, deep learning algorithms have been utilized for shape modeling, segmentation, registration, disease classification and lesion identification [13,24]. DNN has a high degree of generalization and can extract higher-level information to increase disease classification accuracy. Furthermore, the advancement of CNN for image analysis has resulted in the fusion of feature extraction and model learning into a unified framework.

It is possible to conclude with a few of the limits and potential enhancements that can be obtained from previous research. The existing approach performance was poor. This is primarily due to the complexity and capabilities of the method. To address the shortcomings of previous research, we offer a new strategy. The proposed PD feature selection and classification method are intended to increase classifier performance. From the discussions provided, it is evident that a great deal of studies has been performed on Parkinson's disease utilizing features and different classifiers. A stacked denoising Autoencoder is employed to categorize the images into two classes Healthy and PD. To enhance the classification outcome, the feature selection approach is one of main reasons. The selection of features also lowers the cost of features while improving the classifier's effectiveness.

The key contribution of this research is as follows

- The preprocessing stages are used to increase the classification efficiency even more. Noise is reduced and relevant information is kept as a result of these pre-processing stages, resulting in improved performance.
- Data augmentation is used to reduce the overfitting problem and improve data quality and robustness.
- The Improved Pigeon-Inspired Optimization (IPIO) algorithm is introduced to select the important features of the image which improves the classifier performance.
- To classify Parkinson's disease, a Stacked denoising autoencoder is introduced.
- The proposed method outperforms existing state-of-the-art techniques in terms of classification accuracy.

The remainder of the paper is formatted as follows: The research on PD classification will be discussed in the following section. Section 3 describes the dataset that was used in this analysis. The categorization methods and evaluation metrics employed are discussed in Section 4. Section 5 summarises the outcome of the research. The paper concludes in Section 6.

## 2. Literature review

In this section, we review some existing deep learning techniques for diagnoses of Parkinson's disease.

Sharma et al. [17] presented the Modified Grey Wolf Optimization method for diagnosing Parkinson's illness. This paper presented MGWO for determining the best subset of the characteristics search approach. To forecast the accuracy of the selected features, K-nearest neighbor, random forest, and decision tree were employed. The investigational findings indicate that the presented approach aids in maximizing accuracy while limiting the number of features chosen. The findings show that in terms of false alarm rate accuracy, and detection rate, MGWO employing random forest exceeds other classifiers. The model achieves less classification accuracy compared with other approaches which is a drawback of the presented research.

Sivaranjini, S., and Sujatha, C. M. [18] introduced the Convolutional Neural Network architecture and AlexNet to improve PD diagnosis. To categorize the Healthy and PD patients, the weights from the pre-trained model are employed, and finally, the fully connected layer is fine-tuned with appropriate hyperparameters. The classifier is built to learn low-to-high-level properties, and the outcome obtained are verified. The transfer learning network trains and tests the MR images to determine the accuracy measures. When compared with the existing approaches, the presented approach yield greater performances. This research has been limited to the evaluation of suggested models that was insufficient.

3D CNN architecture was presented by Chakraborty et al. [4] to learn the complicated patterns in MRI scans for PD diagnosis. A 3D MRI study was performed using a 3D CNN to identify PD. To detect Parkinson's disease, the researchers utilized 3D MRI scans of the complete brain to analyze complex patterns in all of the brain's subcortical areas. Specific performance metrics were investigated in order to evaluate the CNN model, and a priori hypothesis was developed to validate the performance indicator results. It was discovered that after training the 3D CNN model, it outperformed current techniques. This method has high computational complexity.

Gunduz [9] presented CNN structures that use many types of voice information at the feature and model levels to distinguish Parkinson's disease patients from healthy persons. CNN with parallel layers for Parkinson's disease diagnosis. Parallel convolution layers enable the extraction of feature representations from various types of attributes. CNN and SVM classifiers are used for PD categorization. This research presents two Convolutional Neural Network-based frameworks for identifying PD utilizing collections of vocal (voice) data. When compared with existing approaches the presented approach yield greater performances. It takes high training and testing time. Table 1 shows the summary of related works.

References	Approaches	Merits	Demerits
[17]	Modified Grey Wolf	Provides optimal	No DL adaptations for
	Optimization method	$\operatorname{result}$	more accuracy
[18]	CNN	Generated more	Not optimal and
	CININ	acoustic features	effective detections
[4]			It has a high
	3D CNN	Simple and easy	$\operatorname{computational}$
			complexity
		The more accurate	May produce less
[9]	CNN and SVM	result produced based on	detection rate for
		the ensemble approach	big-sized datasets.
[1]	QAR-CIP-NSGAII, NICGAR, MOPNAR	Applying nominal	No offective ML or DI
		techniques give	mothods were used
		moderate outputs.	methous were used.

 Table 1

 Summary of related works

For the first time Altay, E.V., and Alatas [1] introduced three artificial intelligence-based search and optimization strategies to apply numerical association rules mining (NARM) to achieve advantageous results without using any preprocessing for numeric values. During the mining procedure, AI-based search and optimization techniques update the acceptable ranges of numerical variables in the association rules. As an outcome, the AI-based algorithms  $QAR_CIP_NSGAII$ , NICGAR, and MOPNAR were developed to produce superior outcomes while mining numerical association rules. The presented strategy outperforms the existing one. There are no research gaps in the presented paper.

## 3. Proposed methodology

The proposed Parkinson's disease classification employing the Stacked Denoising Autoencoder (SDA) is discussed in this section. Preprocessing strategies are utilized to enhance categorization effectiveness even further. As a result of these pre-processing stages, noise is reduced and important information is retained, resulting in increased performance in high-level learning applications. Then data augmentation is used to expand the dataset's size and reduce the overfitting issue. Feature selection is based upon the Improved Pigeon-Inspired Optimization (IPIO) algorithm, followed by classification is used.

After the feature selection process, the Stacked Denoising Autoencoder is utilized to classify the MRI images. With the help of a feature selection approach, the classifier can effectively classify PD disease and improve its performance. Following that, the dataset is divided into three sections. This dataset is subsequently given in the training phase. A set of test data is employed to label the training process, which is then utilized to classify Parkinson's disease. The proposed Parkinson's disease classification methodology has four main steps: pre-processing, Data augmentation, feature selection and classification. Figure 1 depicts the general structure of the proposed methodology.



Figure 1. Architecture diagram for proposed methodology

#### 3.1. Problem statement

Misdiagnosis of Parkinson's disease with other neurological PD resembling entities is a concern in Parkinson's disease research. Parkinsonism is defined as a set of symptoms that resemble PD but are led by something else. Lewy body dementia (LBD), Parkinson's type, progressive supranuclear palsy (PSP), essential tremor, multiple system atrophy (MSA), corticobasal degeneration (CBD), drug-induced Parkinsonism, post encephalitic conditions, PD-like symptoms can arise as complications in patients with Alzheimer disease, and spin cerebellar ataxias are some of the diseases that are frequently diagnosed as Parkinson's disease. Wilson disease and X-linked dystonia Parkinsonism are two more genetic disorders linked to PD. The main focus of the PD study is on finding a cure for the disease by addressing the various causes of Allergic cell death. Only once the cause of Neurodegeneration has been discovered can a specialized treatment be created to slow, prevent, or reverse the process. The part of the brain afflicted with Parkinson's disease is deep within the brain, making biopsies and imaging difficult. The disease's multifaceted nature is responsible for the next consequence. The manifestation of PD is caused by the synergistic effect of numerous of the aforementioned causal variables, and research is frequently focused on specific aspects of the disease rather than a holistic approach.

#### 3.2. Preprocessing

The preprocessing of images is the most important stage in getting the necessary features and classification levels. In the proposed method, MR images from the Parkinson's disease classification data set are used. The contrast and brightness of the MR images are variable, and there is some generated noise as well. The contrast and brightness of the images are enhanced and also the noise is reduced. To reduce a negative impact on the procedure, image normalization must be conducted by lessening the disparity among the MRI image's pixel intensities. The training is carried out on all of the images without the use of ROI, which would have an impact on the ranking results.

This stage in our method converts the brain images into intensity brain images in the interval [0, 1] by employing a min-max normalization procedure as shown in the expression below.

$$f(x,y) = \frac{f(x,y) - V_{\min}}{V_{\max} - V_{\min}}$$

While f(x, y) indicates every pixel in the image  $V_{\min}$  and  $V_{\max}$  represents the minimum value and maximum value in the image (f). As an outcome, the contrast between brain borders and areas will be enhanced. Figure 2 depicts an example preprocessed image.



Figure 2. Pre-processed Image: a) Input Image; b) Contrast-Enhanced Image

## 3.3. Data augmentation

In the augmentation phase, the important method in SDA is to reduce the overfitting issue. Due to the unavailability of a significant number of annotated images, image augmentation is an important process in medical image evaluation. The distribution of the dataset across classes is highly skewed, with the majority of the photos coming from Normal. This wildly skewed dataset can result in misclassification. Data augmentation improves data quality and reliability. Zoom, rotation, flip, shear and shifting are some of the parameters that are triggered. Furthermore, by shortening the distance between the testing and training datasets, augmented datasets help to increase data points. In the training dataset, the overfitting problem can be prevented. The following is a list of the main data augmentation procedures we used.

- Rotation: Images were randomly rotated from 0 to 360 degrees.
- Shearing: Sheared at arbitrary angles between 20 and 200 degrees.
- Image flipping: Images were rotated both vertically and horizontally.
- **Zoom:** Photos were extended at random between (1/1.3, 1.3).
- **Cropping:** Images were randomly reduced to between 85 and 95 percent of their original size.
- **Translation of the image:** Photos were shuffled among 25 and 25 pixels randomly.

#### 3.4. Feature selection

The issue of dimensionality disaster will occur during the categorization process if the dimensions are set very high. High dimensions may preserve certain unrelated dimensions during the dimensionality reduction process, whereas low dimensions may eliminate some of the significant characteristics. The IPIO selects the optimal features from pre-processed images; in this case, grey level, multi-texture features were chosen for the analysis. As a result, feature selection has gained increasing significance. Feature selection will have a significant influence on the classifier's accuracy and complexity during the judgment process. Features are selected at the band frequency of 0.01–0.08 Hz.

#### 3.4.1. Improved Pigeon Inspired Optimization

PIO is a novel intelligent learning system that has found widespread use in financial analysis and industrial engineering. Pigeons' homing behavior is imitated by the PIO algorithm. PIO algorithm can identify global optimal solutions by using the map operator and compass operator as well as the landmark operator. PSO is a wellknown and effective meta-heuristic learning algorithm. PIO recently obtained great success in tackling combinational optimization issues, owing to the clear advantages of fewer parameters, faster convergence, and ease of implementation. Regrettably, it's all too easy to become caught up in locally optimal solutions and demonstrate a lack of global search capabilities. To address the aforementioned issues, aim to enhance the fundamental PIO and utilize the improved approach to feature selection. This section goes through the details of the improved PIO (IPIO) algorithm.

#### 3.4.2. Compass operator

The geographical position of the pigeon gives a valid solution to the core PIO technique's optimization issue. The pigeon's house is in the ideal place. The objective function's value corresponds to the pigeon's fitness. The position and the speed of the ith pigeon are:

$$P_i^T = [P_{i,1}, P_{i,2}, \dots, P_{i,n}], \quad i = 1, 2, \dots, N_p$$
 (1)

$$Q_i^T = [Q_{i,1}, Q_{i,2}, \dots, Q_{i,n}] \quad i = 1, 2, \dots, N_p,$$
(2)

The population size is denoted by NP. Pigeons have their location and velocity information in the PIO algorithm, similar to the PSO algorithm, with updated equations (3) and (4) for each pigeon:

$$Q_i^{N_C} = Q_i^{N_C - 1} e^{-R \times N_C} + rand\left(P_{gbest} - P_i^{N_C - 1}\right) \tag{3}$$

$$P_i^{N_C} = P_i^{N_C - 1} + Q_i^{N_C} \tag{4}$$

With a range of 0 to 1, the map and compass factor is R; is the global ideal location determined by evaluating all of the pigeons' positions during  $N_C - 1$  iteration cycles, random number is denoted by r and range [0, 1], the number of iterations is represented by  $N_C$ . This study improves the compass operator of the Pigeon Inspired Optimization to overcome the issue of the fundamental Pigeon Inspired Optimization

approach falling into the local optimal lead to early confluence. A qubit is used in the updated PIO approach to describe the pigeon's present state. The pigeon's position state is determined using Monte Carlo random simulation to ensure the diversity of the population:

$$P_i(z) = RE_g(z) \pm \frac{L}{2} In\left(\frac{1}{u}\right) \tag{5}$$

where  $RE_g(z) = f(z) \times R_i(z) + (1 - f(z)) \times R_g(z)$ .

The number of iterations is z, and u and f are distributed uniformly randomized values between 0 and 1, respectively;  $R_i(z)$  is the historical optimal position at the *tth* iteration;  $R_g(z)$  is the position in global optimization at the *tth* iteration, and L is represented as below:

$$L = 2\omega(z) \left| m_{best}(z) - P_i(z) \right| \tag{6}$$

While  $\omega(z)$  is the inertia weight, that affects the algorithm's convergence; at iteration z,  $m_{best}(z)$  represents the population's mean optimal position for all pigeons;  $\omega(z)$  and  $m_{best}(z)$  is described as:

$$\omega(z) = \omega_{\max} - (\omega_{\max} - \omega_{\min}) \times \frac{z}{T}$$
(7)

$$m_{best}(z) = \frac{1}{N_p} \sum_{i=1}^{N_p} R_i(z)$$
 (8)

Where  $N_P$  is the population size; The lowest and upper bounds of inertia weight are  $\omega_{\text{max}}$  and  $\omega_{\text{min}}$ , respectively, and T is the maximum iteration. As an outcome, the improved PIO method uses the following premise to update the pigeons' positions:

$$X_i(z+1) = \begin{cases} P_i P_g(z) + \omega(z) \times |m_{best}(z) - X_i(z)| \times In \frac{1}{f(z)}, f(z) \ge 0.5\\ P_i P_g(z) - \omega(z) \times |m_{best}(z) - X_i(z)| \times In \frac{1}{f(z)}, f(z) < 0.5 \end{cases}$$
(9)

#### 3.5. Landmark operator

Pigeons who are familiarized with locations in the landmark operator are considered to be fitter, the other pigeons have the option of following the superior pigeons or being rejected by the community. Pigeons are grouped by fitness in every iteration, with half of those with poor fitness being removed. The remainder pigeons' location is then updated using the population center point C(t) as a reference direction.

$$N_{landmark}(z+1) = \frac{N_{landmark}(z)}{2}$$
(10)

$$P_{cen}(z) = \frac{\sum P_j(z) \cdot g\left(P_j(z)\right)}{N \cdot \sum g\left(P_j(z)\right)} \tag{11}$$

$$P_j(z+1) = P_j(z) + rand_4. \left(P_{cen}(z+1) - P_j(z)\right)$$
(12)

The quality of pigeons is cut in half with every iteration of the landmark operator. The quality of the pigeon in the *zth* iteration is represented by  $N_{landmark}(z)$ .  $X_{cen}$  is the center location of the pigeons and  $g(\cdot)$  denotes the fitness function. The expression  $rand_4$  is a random number range among [0, 1].

$$fitness(x) = Jf\bar{P}_{opt_{min}} \tag{13}$$

Algorithm 1: The improved pigeon inspired optimization			
<b>Input:</b> $C = C_1, C_2,, C_m$			
Output: solution for global optimization			
Population is initialized			
Compute the goal function value $f(x_i)$ for every pigeon i.;			
Determine the solution for global optimization $P_g$ and record the value of the objective			
function $f(P_g)$ that corresponds to it;			
Compute the goal function value $f(x_i)$ for every pigeon i.;			
Determine the solution for global optimization $P_g$ and record the value of the objective function $f(P_g)$ that corresponds to it;			
Set t=1;			
while $t \leq N_l$ do			
for every pigeon $i = 1$ to SN do			
Update velocity $V_i^t$ , corresponding to equation 9;			
The location $X_i^t$ is updated corresponding to equation 5;			
Compute the value of the objective function $f(P_i^t)$ correspondingly terminate			
Calculate the solution for global optimization $P_g$ and document the value of the			
objective function $f(P_g)$ correspondingly			
t=t+1;			
L terminate			
initialize t=1;			
while $t \leq N_l$ do			
By calculating the positions of the pigeons, select half with the best optimal value. Evaluate the contex $X^t$ then choose pigeons corresponding to equation 7:			
for every nigeon $i = 1$ to SN do			
The location $X_i^*$ is updated corresponding to equation 8; Evaluate the value of the chieving function $f(D^t)$ .			
Evaluate the value of the objective function $f(F_i)$ ;			
Identify the solution for global optimization $P$ and document the corresponding			
objective function value $f(P)$ :			
terminate			
Becord the new solution for global optimization $P_{\rm c}$ and the objective function $f(P_{\rm c})$ :			
t=t+1			
terminate			
<b>return</b> $X_q$ and $f(X_q)$ ;			

### 3.6. Classification

This section summarises the most extensively used deep learning technique stacked denoising autoencoder.

#### 3.6.1. Stacked denoising autoencoder

An auto encoder's basic assumption is to introduce noise through every layer of the encoder input to train and gain a more efficient feature representation. SDAE is made up of two layers: an unsupervised denoising autoencoder network and a supervised BP neural network layer.

SDAE comprises two stages of learning: supervised learning and unsupervised learning. Unlabelled specimens are first used for greedy layer-wise denoising autoencoder training, which includes placing raw data into the DAE's initial layers for unsupervised training then calculating the first hidden layer's parameter w(1). Trained layer k - 1 is often used to train the k-th layer and acquire the parameter w(k) in every subsequent phase (k). The weight of the resulting deep network's initiation is determined by the weight of each layer's training. Then, for supervised learning, a BP neural network is employed with labeled data. When aggregating parameters of the relevant features and categorization of the last layer, they are fine-tuned using error backpropagation.

#### 3.6.2. Denoising auto-encoder

AE is an unsupervised three-layer NN with a hidden layer, output layer, input layer, and two encoder and decoder sections. Before producing the expression of a new feature, the encoder converts the input vector to a hidden layer. As an example, consider the following function:

$$v = f(y) = S\left(X^{(1)}x + a^{(1)}\right)$$
(14)

while  $y \in Ks \times 1$  is the input, the input data dimension is denoted by s, the number of hidden layer units is  $v \in Kg \times 1, a(1) \in Kg \times 1$  is the hidden layer input weight, and a  $(1) \in Kg \times 1$  is the hidden layer input. The activation function, which is frequently non-linear, is denoted by s.

The decoder's function is to restore the original input by mapping the hidden layer's expression y. As an example, consider the following function:

$$X^{(2)} \in K^{d \times r}, a^{(2)} \in K^{d \times 1}$$
(15)

where  $X^{(2)} \in K^{d \times r}, a^{(2)} \in K^{d \times 1}$  thus the reconstruction error for every data is

$$L = \|y - g(f(y))\|^2$$
(16)

The function of cost is defined as,

$$J(X,a) = \left[\frac{1}{N}\sum_{i=1}^{N} \left(\frac{1}{2} \|y^{(i)} - Q\left(f\left(y^{(i)}\right)\right)\|^2\right)\right] + \frac{\lambda}{2}\sum_{l=1}^{2}\sum_{i=1}^{S_I}\sum_{j=1}^{S_{I+1}} \left(X_{ji}^{(t)}\right)^2$$
(17)

where  $x^{y(i)}$  is the *I*th sample,  $X_{ji}^{(t)}$  is connection weight among the *i*th unit of the *m*th layer and the *n*th unit of the layer  $(m + 1)^{\text{th}}$  the number of instances is N, and

 $S_l$  is the number of units in the *nth* layer. To discover the models best solution W and b, apply the error backpropagation and batch gradient descent techniques.

The training data will be impacted with noise, and the auto-encoder will be made to determine to eliminate the noise then the input data is retrieved. The auto-encoder can detect more stable and relevant features when the input is contaminated, leading to a more comprehensive description of the data and better model effectiveness.

The reconstruction error is

$$L_D = \|x - g(f(x_1))\|^2$$
(18)

The cost function is,

$$J_D(X,a) = \left[\frac{1}{m}\sum_{i=1}^N \left(\frac{1}{2} \|y^{(i)} - \left[\left(f\left(y_1^{(i)}\right)\right)\|^2\right)\right] + \frac{\lambda}{2}\sum_{l=1}^2\sum_{i=1}^{S_l}\sum_{j=1}^{S_{l+1}} \left(X_{ji}^{(l)}\right)^2$$
(19)

In general as stated in noise figure k simply have to initialize the units in x to 0 at random  $(k \in [0, 1])$  and then  $y_1$  is obtained. The parameters are solved using the same manner as the autoencoder.

#### 3.6.3. BP Neural Network

The BP NN is a multi-layer feed-forward network trained using error backpropagation. In this research, the BP NN is utilized to categorize features produced by DAE using labeled images. The extracted features can be related to the relevant label. Simultaneously, the DAE's settings will be fine-tuned via error backpropagation, allowing the overall structure to further converge. The BP neural network is trained using two methods: backpropagation of errors and forward propagation of errors. After the forward calculation of the input characteristics, the predicted type is formed at the outcome layer. Then categorization error is evaluated by contrasting the expected and actual matched categories.

Every layer's residual d is determined first in the error backpropagation procedure. The output layer's output unit l, the equation of  $\delta$  is

$$\delta_i = a_i \left( 1 - a_i \right) \left( a_i - y_i \right) \tag{20}$$

For the other hidden layers, the equation of  $\delta$  is

$$\delta_i^l = a_i^l \left( 1 - a_i^1 \right) \sum_{j=1}^{S_{I+1}} W_{ji}^l \delta_i^{l+1}$$
(21)

Tune the SDAE networks layer parameters utilizing expressions (9) and (10), where a is the tuning coefficient, upon computing the residuals of every layer.

$$W_{ji}^l = W_{ji}^l - \alpha a_i^1 \delta_i^{l+1} \tag{22}$$

$$b_i^l = b_i^l - \alpha \delta_i^{l+1} \tag{23}$$

## 4. Result and discussions

A benchmark dataset was utilized to differentiate the suggested strategy from existing approaches in terms of sensitivity, specificity, precision, and accuracy. This study will examine the materials and measures that were used to get the intended outcome. The effectiveness of the proposed research was evaluated in PYTHON using medical images.

## 4.1. Dataset description

The axial T2 weighted MR images were obtained from the Parkinson's Progression Markers Initiative (PPMI) database, which is open to the public [22]. Researchers frequently use the PPMI dataset to identify PD progression markers and gain access to brain structures and functions at various phases of the disease. This study's PPMI cohort includes 2500 people: 1750 healthy controls and 750 Parkinson's disease sufferers. 70% of the dataset is used for training, while the remaining 30% is used for testing. Table 2 illustrates the details of the dataset, including various details such as the individual's status and shimmer. Figure 3 represents the sample image for healthy and Parkinson's disease.



Figure 3. Sample Brain MRI image: a) Parkinson's disease; b) Healthy image

Index	Description
MDVP	Average vocal fundamental frequency
NHR	Noise to the harmonic ratio
shimmer	3 point amplitude perturbation quotient
DF	Detrended fluctuation analysis
PPE	Pitch period entropy
D2	Correlation Dimension
status	0-healthy, 1-Parkinson disease

Table 2Dataset description

#### 4.2. Metrics for evaluation of the model

During this stage, the effectiveness of every technique was evaluated to determine which method could obtain the best results. The metrics of sensitivity, accuracy and specificity from the confusion matrix were performed to analyze every method employed in this study. The confusion matrix contains True Positive (TP), False Positive (FP), True Negative (TN) and False Negative (FN)

Accuracy: The maximum number of positive outcomes divided by the maximum number of instances is used to calculate a model's accuracy. The percentage of correctly identified cases is provided by the accuracy parameter. The accuracy model is described, as shown in Equation (24):

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN}$$
(24)

A TP occurs whenever a sample in a dataset has a positive classifier and the classifier predicts that the data will have a positive class. Data in a database with a negative classifier and a classifier that predicts a negative class label is referred to as TN. When the classifier of data in a database is positive, but the classifier predicts a negative classifier for that data, it is referred to as an FN. When the classifier of data in a database is negative but the classifier predicts a positive class label for that data, it is referred to as an FN. When the classifier of data in a database is negative but the classifier predicts a positive class label for that data, it is called a false positive (FP).

Sensitivity is used to assess the degree of the attribute to properly categorize individuals with illnesses.

$$Sensitivity = \frac{TP}{TP + FN} \tag{25}$$

Specificity is computed as Equation (26) and is used to evaluate the degree of the attribute to appropriately classify the person without the disease.

$$Specificity = \frac{TN}{TN + FP}$$
(26)

The quality parameters of the predicted class are defined by sensitivity and specificity, which are also known as quality parameters. Three metrics are utilized to determine the accuracy, sensitivity, and specificity of a medical diagnosis model.

Precision: Positive Predictive Value (PPV) also known as precision, is a measure of the correctness of a categorization result. Equation (27) is used to calculate it,

$$Precision = \frac{TP}{TP + FP}$$
(27)

The area under the ROC curve (AUC): AUC is the ratio between the area above and below the ROC curve. Accuracy is quantified by AUC, which is calculated by converting the ROC curve result into a scalar number using the formula below (28),

$$AUC = \int_{X}^{Y} f(v)dv \tag{28}$$

While X and Y are the curve's minimum and maximum axis points, and f(v) is a function that is both above and below the curve.

Differentiation between the existing classification approach with proposed approach can be represented in Table 3 and Figure 4. When compared with the existing approach proposed approach yield a better solution. The existing technique like dense net, inception, and ResNet is compared with the proposed approach. Compared with accuracy dense net gain 91.26%, inception gains 89.03%, ResNet gain 98.51% and the proposed technique gain 99.17% which is the highest accuracy among all existing approaches. Compared with specificity dense net gain is 93.56%, inception gains 90.69%, ResNet gain is 96% and the proposed technique gain 98.74% which is the highest one among all existing approaches. Compared with sensitivity dense net gain of 94.81%, inception gains of 93.84%, ResNet gain of 95.38% and the proposed technique gain of 98.96% which is the highest solution among all existing approaches. From the overall evaluation metrics proposed approach yield the best solution.

Method	Accuracy	Specificity	Sensitivity	Precision	AUC
DenseNet121	91.26	93.56	94.81	95.42	86.47
Inception V3	89.03	90.69	93.84	96.35	89.13
ResNet	98.51	96	95.38	93.87	95.16
proposed	99.17	98.74	98.96	99.37	98

Table 3				
Comparison	of performance	metrics		



Figure 4. Differentiation of existing classification approach with the proposed approach

Applied the three suggested networks to the dataset, yet they all showed a better area under the ROC curves and classification accuracy for the proposed approach. The ROC curve can be represented in Figure 5.



The predicted value is represented in Figure 6 by a confusion matrix. True negative or true positive predictions are true, whereas false negative or false positive predictions are false. The four categories accurately classify the infected area of Parkinson's disease. When compared with existing techniques the proposed approach is the best one.



Figure 6. Confusion matrix

Table 4 illustrates the model's training accuracy, testing accuracy, and losses. The differentiation between training and testing accuracy can be depicted in Figure 7.



Figure 7. Differentiation of training and testing accuracy

Technique	Training accuracy	Testing accuracy	Training loss	Testing loss
Dense Net	93	87.63	61.89	63
Inception V3	95.23	93	53.21	48
Res Net	97.65	98.71	47.41	56
Proposed	99.32	99.11	38.03	32

 Table 4

 Comparative results for training, testing and validation

Table 5 and Figure 8 show the comparison of feature selection approaches; Principal Component Analysis (PCA), Wrapper and Correlation-based Feature Selection (CFS).

	Table 5		
Comparative	analysis of	feature	selection

Feature selection approach	Accuracy	Sensitivity	Specificity
CFS	90.77	98.35	89.58
PCA	91.79	95.24	91.67
Wrapper	98.97	97.44	97.92
IPIO	99.32	99.14	98.67



Figure 8. Comparison of proposed feature selection approach versus existing techniques

Compared with existing approaches proposed approach yield 99.32% of accuracy which is 8.55%, 7.53%, and 0.35% greater than CFS, PCA and Wrapper. 99.14% of sensitivity yielded by the proposed approach, which is 0.17%, 3.9%, and 1.7% greater than CFS, PCA and Wrapper. The proposed approach yield 98.67% of accuracy which is 9.09%, 7%, and 0.75% greater than CFS, PCA and Wrapper.

## 5. Conclusion

Parkinson's disease ranks as the 2nd highest prevalent neurological disorder. There is currently no cure for Parkinson's disease, although early detection can help patients receive better and faster care. In this article, we suggested a framework for categorizing the Magnetic Resonance Imaging of normal people and those with PD affected using a feature selection technique combined with a Stacked Denoising Autoencoderbased classification. Initially in preprocessing, noise is reduced and important information is retained, resulting in increased performance. Additionally, data augmentation is performed to increase the dataset and eliminate the overfitting issue. After the completion of preprocessing, the image is fed into the feature selection phase. The PIO selects the optimal features from pre-processed images for analysis; in this case, grey level, multi-texture features were chosen. The Improved Pigeon Inspired Optimization technique is employed for feature selection. In comparison to other strategies, the IPIO algorithm-based feature selection strategy chooses better features. Finally, a stacked denoising autoencoder is employed to classify the images whether it is healthy or Parkinson affected. The performance of this system is testified by extensive experimental works on the standard dataset and comparative evaluations with state-of-the-art methods. When the synthesized images are given to the training set, the main categorization metrics such as sensitivity, accuracy, and specificity increase by 2.6%, 3.6%, and 4.2%, respectively, yielding 98.74%, 99.17%, and 98.96% when compared to other existing methods.

#### Acknowledgements

We declare that this manuscript is original, has not been published before and is not currently being considered for publication elsewhere.

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Received: 06.07.2022 Revised: 23.12.2022 Accepted: 26.05.2023