Parkinson's Disease Medical Image Diagnosis Using Deep Learning and Optimize Features

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***Abstract*—Growing population increases the load of medical practioner and they need some assistance to improve the work quality. Man power has its limitation hence many of researchers provides various solutions to reduce the work load and increase quality. This paper has resolved the Parkinson disease detection by optimizing the input data and train a mathematical model. Proposed model has processed the input data by Group Search Optimization algorithm by clustering the image into features and noise region. Identified feature region image was used for the feature extraction. Extracted features were used for the training of the spiking neural network. As Parkinson have complex image structure hence spiking neural network give a clear and precise prediction class of the model. Experiment was done on real dataset have all set of classes and results shows that proposed Parkinson disease detection by Group Search optimization (PDDGSO) improve the accuracy by % as compared to comparing models.**

***Index Terms*—Genetic Algorithm, Image Processing, Machine Learning, Parkinson Detection.**

I. INTRODUCTION

Parkinson's disease (PD) is a progressive neurological condition characterized by the gradual loss or dysfunction of specific neurons in the midbrain and is widely classified as a movement-related disorder. The primary pathological cause of PD is the degeneration of dopamine-secreting neurons located in the substantia nigra (SN) [1]. As these neurons deteriorate, dopamine levels in the brain decline sharply, impairing the regulation of motor functions. This deficiency results in hallmark symptoms such as resting tremors, muscle stiffness, slowed movements (bradykinesia), poor balance, and gait disturbances. Dopamine functions as a vital neurotransmitter that ensures smooth and coordinated movement by transmitting signals between the substantia nigra and the striatum [2]. This communication pathway, known as the nigrostriatal pathway, plays a central role in controlling motor circuitry and enabling the initiation and execution of voluntary movements. With disease progression, PD may also manifest non-motor complications, including cognitive impairment, depression, and dementia.

Conventional approaches to predicting Alzheimer's disease (AD) risk have largely depended on predefined health and demographic indicators. These include sociodemographic attributes such as age, gender, and education level; lifestyle factors like physical activity; midlife health parameters including systolic blood pressure, body mass index (BMI), and cholesterol levels [3]; along with cognitive performance measures [4]. However, a key challenge remains whether such limited-variable models can adequately capture the complex and multifactorial nature of AD in real-world clinical environments. Evidence from meta-analytic research indicates that models incorporating multiple interacting risk factors offer superior predictive accuracy for dementia, while single-factor models demonstrate weak performance [5]. This suggests that reliable AD risk prediction requires the inclusion of a broader and more diverse feature set.

Recent developments in machine learning (ML) have introduced powerful tools for enhancing diagnostic

accuracy in neurological disorders. By processing large-scale datasets encompassing clinical records, genetic data, and neuroimaging results, ML algorithms can uncover subtle and complex patterns that may not be readily apparent to human clinicians [6]. These capabilities support earlier diagnosis, enable individualized treatment planning, and improve predictions of disease progression. As artificial intelligence (AI) and ML technologies continue to evolve, their integration into neurological diagnostics is expected to significantly improve precision, efficiency, and patient-specific care.

In related research, Lang et al. [7] explored factors predictive of deep brain stimulation (DBS) surgery candidacy in patients newly diagnosed with PD. Their findings identified several key indicators, including age at symptom onset, Hoehn and Yahr (H&Y) disease stage, tremor severity scores, and the cerebrospinal fluid ratio of tau to Aβ42. Although patients who initially received DBS exhibited a slower rate of cognitive decline, they experienced a more rapid worsening of motor symptoms. It is important to note that, due to the absence of detailed postoperative response data, the study focused on predicting DBS eligibility rather than evaluating specific clinical outcomes.

II. LITERATURE REVIEW

Güven et al. [8] explored the application of artificial intelligence for disease classification by utilizing advanced transformer-based deep learning models, including the Swin Transformer, Vision Transformer (ViT), and Bidirectional Encoder Representations from Image Transformers (BEiT). Their study employed a publicly available dataset consisting of 450 images, equally representing healthy individuals, Alzheimer's disease, and Parkinson's disease cases. The dataset was systematically divided into training and validation sets, with 80% (390 images) used for training and 20% (90 images) reserved for validation. The models achieved classification accuracies exceeding 80%, demonstrating the strong potential of transformer architectures for neurological disease identification. The authors further suggested exploring hybrid and ensemble approaches that combine multiple transformer-based models to enhance diagnostic performance in future work.

Nazmun Nahar et al. [9] proposed a machine learning–driven framework for Parkinson's disease detection that integrates feature selection and classification techniques. The study employed Boruta, Recursive Feature Elimination (RFE), and Random Forest (RF) methods to identify the most relevant features. For classification, four algorithms—gradient boosting, extreme gradient boosting, bagging, and Extra Trees—were evaluated. Among these, the combination of bagging and recursive feature elimination delivered the best performance, outperforming the other models considered in the study.

C.-M. Kim et al. [10] introduced an ensemble-based convolutional neural network (CNN) framework designed to classify different stages of Alzheimer's disease based on brain morphology. The proposed architecture combines the convolutional layers of the Visual Geometry Group network (VGGNet), known for its effectiveness in image recognition, with a one-dimensional CNN pipeline. In this approach, MRI images are processed using a Line Feature Analysis (LFA) algorithm to convert visual line segment information into vector representations that capture key brain shape characteristics. These vectors are then analyzed using a 1D CNN with multiple parallel convolutional layers, enabling detailed observation of structural brain patterns. The extracted brain shape features are subsequently fused with image-based features from VGGNet, resulting in improved classification performance compared to existing approaches.

Singh et al. [11] presented a sparse feedforward deep neural network architecture for encoding and decoding the structural connectome of the human brain. Their model incorporates sparsely connected element-wise multiplication in the first hidden layer and a fixed transformation layer at the output, significantly reducing the number of trainable parameters and training time relative to conventional feedforward networks. Using diffusion tensor imaging (DTI) brain scans, the authors demonstrated superior performance in encoding structural connectivity patterns associated with Alzheimer's and Parkinson's diseases. For the decoding phase, they employed Recursive Feature Elimination (RFE) guided by DeepLIFT, Layer-wise Relevance

Propagation (LRP), and Integrated Gradients (IG) to eliminate irrelevant features and identify critical biomarkers linked to AD and PD.

To address the challenge of integrating heterogeneous data sources, another study proposed by R. Guo et al. in [12], is a novel graph-based fusion (GBF) framework. This approach includes an imaging–genetic fusion module that uses attention mechanisms to extract both modality-specific and shared representations from imaging and genetic data. In addition, a multi-graph fusion module was introduced to incorporate clinical information, which plays a vital role in diagnosing neurodegenerative disorders. This module employs a learnable graph construction strategy along with graph ensemble techniques to effectively combine imaging, genetic, and clinical features, thereby enhancing diagnostic accuracy.

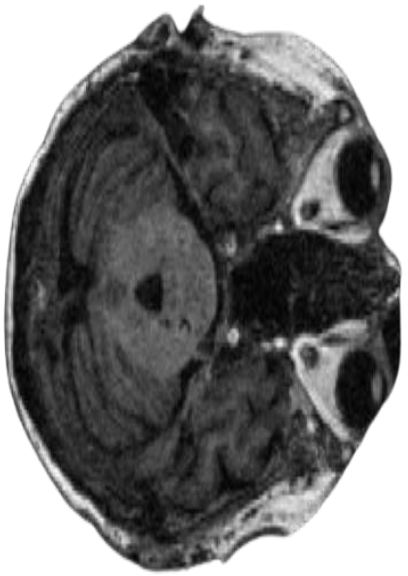
Katako et al. [13] focused on constructing machine-based imaging biomarkers using fluorodeoxyglucose positron emission tomography (FDG-PET) data from the Alzheimer's Disease Neuroimaging Initiative (ADNI). The study applied several analytical techniques, including the General Linear Model (GLM), Subprofile Modeling (SSM), and Support Vector Machine (SVM). GLM was used as a foundational statistical approach for classification, while SSM—an extension of principal component analysis (PCA)—proved effective for differential diagnosis and prognosis in neurodegenerative diseases. SVM, a widely adopted machine learning algorithm for binary classification tasks, was utilized to enhance diagnostic performance on large-scale datasets.

III. PROPOSED MODEL

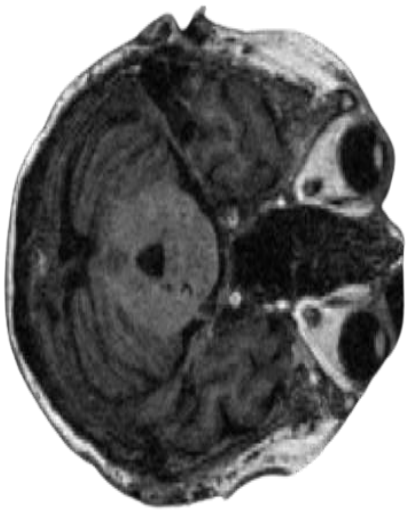
Disease detection at primary level is very helpful to the patient and doctor. Most of this depends on the diagnosis hence this paper work on the Parkinson disease detection by Group Search optimization (PDDGSO) model. Input medical image processing is done by Group Search Feature Optimization algorithm and features were extract for the training of spiking neural network model. Proposed model flow is shown in fig. 1. Various notation used for the explanation of model is list in table 1. Input to the model is training images and out is trained spiking neural network.

Input Image Pre-Processing Raw input image need to pre-process that help in improving the data quality. As image is matrix hence this work transform each image into square matrix [12]. Further image was transform into gray scale. Image is collection of pixel and during communication some noise may come in original data. To reduce the noise weiner filter [14] was adopt by the work.

PID←PreProcessing(RID)



(a)



(b)

Fig. 1 Raw input image (a), pre-processed image data (b).

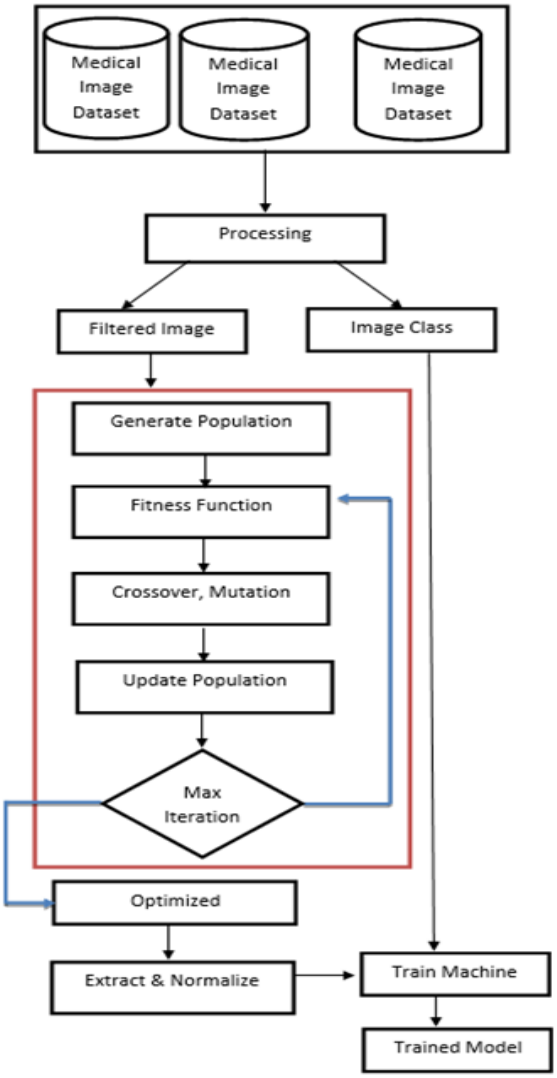


Fig.2 Proposed work block diagram.

Table 1 Notation used in the proposed model explanation.

Notions	Meaning
RID	Raw Input Data
PID	Processed Image Data
m	Number of Member
C	Cluster
P	Producer
r	Random Position
Pr, Po	Synaptic Value
w	Weight
E	Error
O	Desired Output Class

Data Optimization

In order to improve the data quality, image is cluster into two region by Group search Optimization algorithm. One region is selected for the training and other region is removed from the work as useless pixel values. The refined dataset obtained after clustering is then subjected to feature selection. Since the performance of the learning model depends heavily on the chosen feature subset, evaluating all possible feature combinations is computationally expensive and time-consuming. To overcome this limitation, a Group Search–based genetic optimization strategy is adopted to identify an optimal subset of features efficiently. GSO is inspired by animal foraging behavior, where individuals search for food in three distinct roles: producer, scrounger, and ranger. In the proposed work, a food source represents a candidate feature subset encoded as a binary vector, where 1 indicates feature selection and 0 denotes feature exclusion [15]. The primary objective of the foraging process is to identify a food source (feature subset) that maximizes classification performance.

Food Source:

A one-dimensional binary vector representing a feature subset. Any modification in the vector generates a new food source in the search space.

Member: A chromosome representing a candidate solution that points to a specific food source. A member may explore different food sources across iterations.

Group (Population): A collection of members forming the population. Each member initially points to a randomly generated food source. The population is mathematically represented as:

GM←Gaussian_Feature_Set(m,c)

where m denotes the number of members and c represents the total number of clusters. Random food sources are initialized using a Gaussian distribution.

Producing In this phase, all members evaluate their assigned food sources. This process is equivalent to fitness evaluation in genetic algorithms. The fitness value reflects the classification performance achieved using the selected feature subset.

Scrounging (Crossover) Scroungers Once the producer identifies a promising food source, the remaining members act as scroungers. During this phase, scroungers modify their feature vectors by partially adopting the producer's feature configuration [15]. This operation resembles the crossover mechanism in genetic algorithms.

Let P be the producer and Mm be the mth member. The feature update is performed as:

$GM'_m[1\ r] \leftarrow GM_m[1\ r] + P[1,r]$

where r r is a randomly selected feature index within the range 1 to f. The newly generated food source is evaluated using the fitness function, and the member retains the better-performing solution.

Ranging (Mutation) Rangers In this phase, all members except the producer behave as rangers, independently exploring new regions of the search space. Each ranger randomly flips the state of one or more features in its binary vector, simulating mutation [16].

$GM'_m[1\ r] \leftarrow Flip\ (GM_m[1\ r])$

This flip operation changes a feature state from 1 to 0 or vice versa. The modified solution is evaluated, and the member adopts it only if it yields improved fitness.

Filter Region

The algorithm iterates through producer, scrounging, and ranging phases until a predefined stopping criterion—such as a maximum number of iterations or convergence threshold—is met. The final output is an optimized feature subset that significantly improves model accuracy while reducing computational complexity.

Machine Learning

In the proposed framework, the selected feature vectors extracted from Parkinson's disease data are used as inputs for training, while the corresponding class labels (Parkinson's / Healthy) serve as target outputs. These input–output pairs are fed into a three-layer Spiking Neural Network (SNN) to learn discriminative patterns associated with Parkinson's disease.

Neurons in the SNN communicate through synapses, where incoming spike signals first pass through the pre-synaptic region and are then processed at the post-synaptic junction [17]. The pre-synaptic response is modeled as:

$$P_{rs}(t) = \int_0^{\infty} K_{syn}(t - t^f) e^{\frac{-t}{\tau}}$$

where Ksyn controls the peak synaptic conductance, t represents time, tf denotes the firing time, and τ is the synaptic time constant. This formulation enables spatio-temporal integration of the input spike trains.

The total post-synaptic current is computed as:

$$P_{os}(t) = \int_0^{\infty} P_{os}(t) - V(t) \int_0^{\infty} P_{os}(t)$$

Based on these synaptic responses, the synaptic weights are initialized and updated using the learning rule [18]:

$$\frac{d}{dx} w_{ij}(t) = a_o + a_1 P_{rs}(t) + a\ \ P_{os}(t) + a_3 P_{rs}(t) P_{os}(t) + a_4 P_{rs}(t) P_{os}(t)$$

where

$wi(t)$ represents the weight between the ith and jth neurons, and a_0–a_4 are learning coefficients controlling synaptic adaptation.

The SNN architecture consists of input, hidden, and output layers. The neuron output is computed as:

$$X_j = \sum x_i \,.\, w_{ij}\, b_j$$

where

xi is the input spike, wij is the synaptic weight, and bj is the bias term. The network output is compared with the desired Parkinson's disease label, and classification error is calculated using a loss function. Gradient-based learning and the chain rule are applied to compute weight updates:

$$\frac{\partial E_i}{\partial W_i} = \frac{\partial E_i}{\partial O_i} * \frac{\partial O_i}{\partial H_i} * \frac{\partial H_i}{\partial W_i}$$

All synaptic weights are updated iteratively as:

$Wij = Wij + \partial Wij$

Training continues until the output error converges to a predefined threshold (e.g., 0.0001), ensuring accurate and stable classification of Parkinson's disease.

Proposed Algorithm

Input: RID

Output: SNN

PID ⟵ PreProcessing(RID)

For Each Image in PID

GM ⟵ Gaussian_Feature_Set(m, f)
Loop 1 : MaxIter
FV[m] ⟵ Fitness(GM)
P ⟵ MemberWithMaxFitness(FV)
GM⟵Scounging(GM,P)
GM⟵ Ranger(GM)
EndLoop
OF ⟵ BestFeatureSubset(GM)
CI<--Cluster_Image(OF,
EF ⟵ FeatureExtraction(FR)
EndLoop
SNN ⟵ TrainSNN(EF, T)

IV. EXPERIMENT AND RESULTS

The experimental evaluation of the proposed PDDGSO model was carried out using MATLAB on a computer system equipped with 8 GB of RAM, running the Windows operating system, and powered by an Intel i3 processor. The performance of the proposed approach was assessed by comparing its results with those produced by an existing algorithm reported in [10].

Dataset

This study makes use of the OASIS MRI dataset, which contains approximately 80,000 brain MRI images. The images are organized into four distinct categories, each representing a different stage of Alzheimer's disease progression. Due to its large scale and detailed annotations, the OASIS dataset provides a valuable foundation for examining brain structural changes and identifying early signs of Alzheimer's disease [19].

Results

Table 2 Precision value-based Parkinson disease models comparison.

Testing Image Set	PDDGSO	VGGNet
Set1	1	0.5
Set2	0.875	0.9194
Set3	0.9844	0.5926
Set4	0.9875	0.45
Set5	0.9998	0.4368

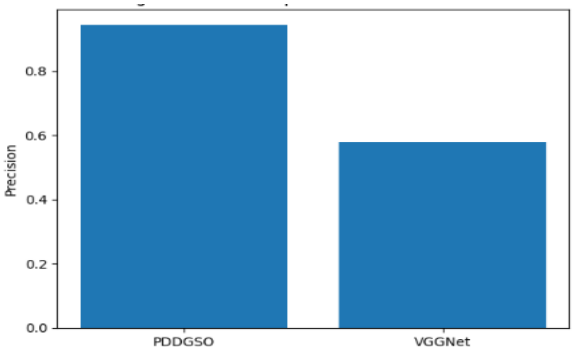


Fig. 2 Average precision values of comparing models.

Table 2 shows the Parkinson disease detection models precision values for various testing sets. It was found that group search optimization has improved the work precision value by 0.3895. Further its shows that use of visual content feature after the optimized image has increased the detection performance.

Table 3 Recall value-based Parkinson disease models comparison.

Testing Image Set	PDDGSO	VGGNet
Set1	1	1
Set2	1	1
Set3	1	1
Set4	1	1
Set5	1	1

Table 3 shows Recall value of comparing models shows that all set of desired class is correctly identified by the models. This shows that testing dataset has similar classet and makes an similar effect on both the models.

Table 4 F-Measure value-based Parkinson disease models comparison.

Testing Image Set	PDDGSO	VGGNet
Set1	1	0.6667
Set2	0.9333	0.958
Set3	0.9921	0.7442
Set4	0.9937	0.6207
Set5	0.9999	0.6081

F-Measure value shown in table 4 for Parkinson disease detection models. It was found that detection of correct class of image f-measure values is high. It was found that use of spiking neural network f-measure value was increased by 0.264 as compared to existing model.

Table 5 Accuracy value-based Parkinson disease models comparison.

Testing Image Set	PDDGSO	VGGNet
Set1	100	51.22
Set2	87.23	93.75
Set3	98.25	65.89
Set4	98.25	52.17
Set5	99.88	46.77

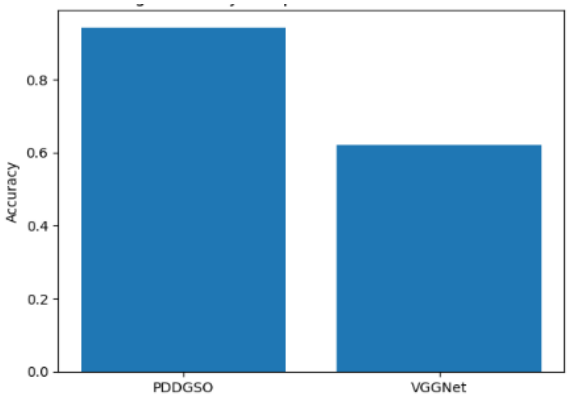


Fig. 3 Average accuracy-based comparisons of models.

Accuracy value shown in table 5 for disease detection has improved the work accuracy by 34.82%. This enhancement in performance shows that group search optimization algorithm has effectively identify the featured region in image for spriking neural network training.

Table 6 Accuracy value based Multiclass Parkinson image disease models comparison.

Testing Image Set	PDDGSO	VGGNet
Set1	100	50
Set2	87.5	93.75
Set3	98.44	65.63
Set4	98.75	51.87
Set5	99,99	46.5

This work train the multiclass image of Parkinson disease. It was shown in table 6 that use of spiking neural network for multiclass disease detection has increase the accuracy by 34.62%. Further proposed PDDGSO model shows that input image processing steps effectively improved the work.

V. CONCLUSIONS

Losing a memory is a tough situation for the human and its family. Hence detection of such disease at early stage help everyone to overcome. This paper has proposed a Parkinson disease detection model that resolves the feature optimization issue. It was found that use of grop search optimization algorithm has increases the feature quality as noise region were removed. Use of content feature in the model has improved the detection accuracy of the work. Experiment was done on real Parkinson image dataset have four classes of images. Result shows that proposed model has increases the precision value by 0.3895 and single class accuracy value by 34.82%. This model classify the multiclass image data and result shows that proposed work has increases correct class detection accuracy by 34.62%. In future scholars can classify the image as per disease age.

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