Artificial Intelligence for Parkinson's Disease Prediction

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Parkinson's disease (PD) is a pervasive neurodegenerative disorder with a diverse clinical presentation and a complex etiological landscape. A comprehensive introduction to the current state of PD research, diagnosis, and management, emphasizing the need for early detection and personalized treatment strategies is presented in this paper. Recognizing the multifactorial nature of PD, the genetic and environmental risk factors, highlighting the role of genetics in monogenic and polygenic PD are explored. Furthermore, the clinical diagnosis of PD, encompassing both motor and non-motor symptoms, and underscore the significance of a prolonged prodromal phase preceding clinical manifestations are discussed. The importance of personalized management, including pharmacological and non-pharmacological interventions, is also emphasized. In the quest for disease modification, the potential of emerging therapies and the ongoing research into the genetic basis of PD is explored. Notably, the promising role of machine learning techniques, including Convolutional Neural Networks (CNN), Artificial Neural Networks (ANN), K-Nearest Neighbors (KNN), and fuzzy logic, in early PD detection and diagnosis is investigated. By leveraging these advanced computational approaches, there is potential to revolutionize PD diagnosis, providing earlier interventions and tailored treatment strategies. This paper sets the stage for a comprehensive examination of the application of machine learning in PD research and clinical practice. By amalgamating existing knowledge and cutting-edge technologies, the aspiration of this paper is to advance the understanding and management of Parkinson's disease, ultimately improving the lives of those affected by this challenging condition.

Keywords: SVM, KNN, ANN, Predictive analytics, Voice datasets, CNN, Fuzzy KNN, Fuzzy c-means.

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1. Introduction

Parkinson's Disease (PD) is a multifaceted and progressive neurodegenerative disorder characterized by a range of clinical manifestations. While its increasing global prevalence has raised concerns resembling pandemic trends, it's crucial to note that PD is fundamentally distinct as it is non-infectious in origin. Although genetic factors contribute to some PD cases, a significant proportion is attributed to multifactorial causes. Current research indicates that around 3–5% of PD cases are linked to specific known PD genes, making them monogenic, while 16–36% of the heritable risk of non-monogenic PD can be explained by 90 genetic risk variants. Other noteworthy risk factors include a family history of PD, the presence of tremors, constipation, and non-smoking status, each conferring a two-fold or greater risk of developing the disease.

The clinical diagnosis of PD primarily relies on observable motor symptoms, including bradykinesia (slowness of movement) and the presence of rest tremor, rigidity, or both. However, the clinical presentation extends beyond motor deficits to encompass a variety of non-motor symptoms, making the diagnostic process multifaceted and challenging. To provide accurate prognostic counseling, one must understand the diverse subtypes of PD, as the disease's progression can vary significantly among individuals. Notably, PD often follows a prolonged prodromal phase characterized by subtle symptoms that precede clinical manifestations, which may become more clinically relevant with the advent of disease-modifying treatments.

The management of PD is highly individualized, emphasizing the need for personalized treatment approaches. For individuals with disability due to PD, timely initiation of symptomatic therapy, often beginning with levodopa, is recommended. Optimal PD management extends beyond medication, incorporating an expanding array of non-pharmacological interventions to enhance patients' quality of life.

Presently, there are no therapies capable of halting or slowing the progressive nature of PD. Nevertheless, ongoing research into the genetic underpinnings and mechanisms of neuronal degeneration has yielded promising insights, with several potential disease-modifying strategies in various stages of development and evaluation. Machine learning techniques have recently emerged as powerful tools in healthcare, offering the potential to enhance early PD detection, refine diagnosis, and personalize treatment strategies based on individual disease profiles.

This research paper aims to provide a comprehensive overview of PD, highlighting its multifaceted nature, clinical diagnosis, and management, and ongoing efforts to develop disease-modifying therapies. It also explores the potential of machine learning as a promising avenue for early PD detection and its potential to revolutionize Parkinson's disease research and clinical practice. By synthesizing existing knowledge and emerging technologies, this survey aims to shed light on the role of machine learning in advancing the understanding and management of Parkinson's disease.

2. Data Preprocessing

There are various data preprocessing techniques available to handle data and help in optimal parameter selection with respect to machine learning for the problem statement. Few of them are mentioned as follows,

2.1 Synthetic Minority Over-sampling Technique (SMOTE)

SMOTE[13] can be applied when there are more examples of one class in the dataset than samples of other classes. One method for addressing unequal classes is to oversample samples in the minority class. This can be achieved by using duplicate instances from the minority class in the training dataset. Although it might balance out the distribution of classes, this doesn't reveal anything new. Another technique for enhancing minority data based on prior samples is called SMOTE, or Synthetic Minority

Oversampling Technique. Using close features, the SMOTE method creates a linear link and then chooses a new sample from the minority class along that line.

2.2 Hyperparameter Tuning (GridSearchCV)

Variables known as hyperparameters are typically set by the user while creating the machine learning model[1]. Utilizing GridSearchCV to find the ideal hyperparameter values is necessary to obtain the greatest performance out of the model. The simplest search technique that yields the most precise predictions is grid search. Because each trial in a grid search runs independently without regard to time sequence, it is easy to conduct in parallel (Yu and Zhu, 2020). It primarily accepts arguments, such as estimator, parameter grid, and CV. The descriptions of each argument are as follows: Estimator: the item being utilized for the estimator A K-fold cross-validation folds are represented by an integer in the parameter grid, which is a list of parameter values together with their names.

2.3 Principal Component Analysis (PCA)

Essentially, principal component analysis is a statistical process that transforms a collection of observations of variables that may be correlated into a corresponding collection of values for variables that are linearly uncorrelated. All of the primary components are orthogonal to one another and are selected so as to describe the majority of the remaining available variance. The first principal component has the highest variance among all the other principal components.

PCA is used to determine the relationships between variables in the data. It helps with data visualization and interpretation. Reduction in the number of variables simplifies additional analysis. It is frequently used to show genetic relatedness and distance between populations.

Basically, a square symmetric matrix is used for them. It might be a matrix with only sums of squares and cross-products. A matrix of correlation or covariance. If the variance of each variable varies significantly, a correlation matrix is employed.

In order to maximize variance from the variables, PCA essentially looks for a linear combination of variables. After this procedure is finished, it is eliminated and a new linear combination that explains the largest percentage of residual variance—basically, orthogonal factors—is found. This approach analyzes the overall variance [13].

2.4 Data Reduction: Autoencoder

An autoencoder[3][8] is a type of neural network design that uses feature compression to attempt to learn a deep representation of the input. As seen in Fig.1, In order to do this, a symmetric design with the same number of input neurons as output neurons and fewer neurons in the middle layer than in the input and output layers is constructed. Latent space refers to this intermediate layer as a bottleneck. The network is able to learn a compact and deep representation of the data in the latent space when one attempts to extract the net's output directly from the input. The term "encoder" refers to any layer that is present prior to the bottleneck, while "decoder" refers to all layers that are present thereafter.

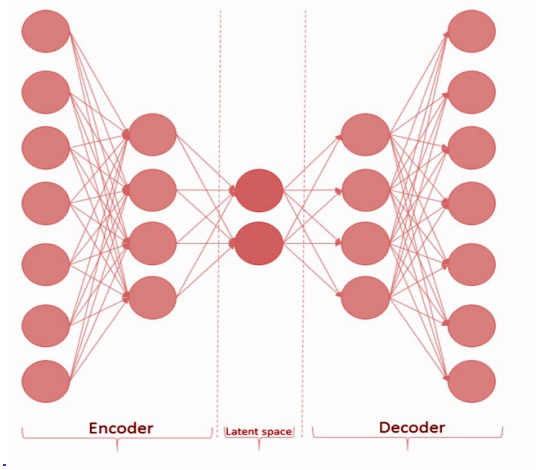

Fig. 1. Layers in Autoencoder.

3. Machine Learning Algorithms and Techniques

There are ample different types of machine learning and deep learning models that are already available which can be utilized in the problem statement[19]. After reviewing different algorithms, here is a summarization of some significant techniques,

3.1 Support Vector Machine (SVM)

One potent machine learning technique that is frequently used in the field of medical diagnostics, particularly the diagnosis of Parkinson's disease (PD), is Support Vector Machine (SVM)[9]. Based on a variety of input data sources, including clinical, genetic, and imaging data, SVM's ability to do binary classification has shown to be useful in differentiating between people with Parkinson's disease (PD) and healthy controls.

SVM is a member of a new class of learning systems that draws on recent developments in statistical learning theory. This data algorithm works with both linear and non-linear data. By transforming the initial data into a higher dimension, machine learning techniques to detect Parkinson's disease using voice signal features may be able to use this information to build a hyperplane for data separation utilizing support vectors, which are essential training tuples[2].

3.2 K- Nearest Neighbour (KNN)

Parkinson's disease (PD) identification is one of the many uses for the well-liked machine learning technique K-Nearest Neighbors (KNN)[2][22]. PD is a multifaceted neurodegenerative illness that manifests as both motor and non-motor symptoms. Based on unique input variables, including clinical evaluations, genetic markers, or imaging data, KNN is especially well-suited for binary classification tasks, which makes it a useful tool for differentiating between people with PD and healthy controls.

KNN is an instance-based learning algorithm, which means it makes predictions based on the similarity of input data points to training examples. In the context of PD detection, KNN assesses the similarity between individuals' feature vectors to determine their PD status.

The choice of the "K" value, representing the number of nearest neighbors to consider, is a critical aspect of KNN. Proper selection of K can significantly impact the algorithm's performance and should be determined through cross-validation or other optimization techniques.

3.3 Convolution Neural Network (CNN)

CNNs[23] are designed to automatically learn hierarchical features from images. This ability enables them to capture complex patterns and relationships in medical images, such as brain scans or pathological tissue samples, that might be indicative of PD[33].

CNNs use convolutional layers to scan images at multiple spatial scales, allowing them to detect features of varying sizes. This is particularly advantageous for capturing abnormalities in medical images that can manifest at different scales.

For both purposes, an MLP architecture is employed, which underwent several modifications to tailor it to specific requirements.

An input layer, an output layer, and one or more hidden layers make up this neural network [11]. Multiple layers are commonly used in deep learning[4] to efficiently capture the complex patterns found in the input data. Every neuron in layer n of an MLP is tightly coupled to every other neuron in layer n + 1[5].
When it comes to binary classification, like this one, the most common method uses one output neuron in conjunction with a sigmoid activation function.

This function calculates the probability of the input, denoted as x, belonging to the positive class and is expressed as:

$$f(x) = 1 / (1 + e^{(-x)}) \quad (1)$$

In the case of regression, the activation function for the output layer is defined as "RELU," following the equation:

$$f(x) = \max(0, x) \quad (2)$$

VGG16 stands as a prominent architecture, highly acclaimed for its exceptional performance in the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) of 2014, where it achieved an impressive test accuracy of 92.7% on the ImageNet dataset. This model comprises a total of 16 layers, thoughtfully organized into various components, including:

Convolutional Layers: VGG16 incorporates a total of 13 convolutional layers, responsible for extracting intricate features from the input data.

Fully Connected Layers: The model includes 3 fully connected layers, enabling it to make sense of the features extracted by the earlier layers and establish complex relationships.
Max Pooling Layers: In addition, there are 5 max pooling layers that downsample the spatial dimensions of the data, aiding in feature reduction and abstraction. Softmax Layer: To adapt the architecture for the specific binary classification task at hand, a final Softmax activation layer has been added.

Throughout the hidden layers of this model, the Rectified Linear Unit (ReLU) serves as the activation function. The utilization of ReLU contributes to accelerated learning and mitigates the issue of vanishing gradients, enhancing the model's training efficiency.

Inception-V3, as extensively applied in image classification tasks, emerges as a prominent model [28]. This model exhibits a distinctive composition, encompassing both symmetric and asymmetric components. Within its architecture, you'll find an array of essential layers, including convolutional layers, average pooling layers, max pooling layers, and fully connected layers.

Notably, Inception-V3 boasts an impressive 42-layer architecture and encompasses approximately 12 million parameters. Despite its depth and complexity, this model demonstrates exceptional computational efficiency, surpassing the efficiency of the VGGNet model.

3.4 Fuzzy KNN

Fuzzy k-Nearest Neighbors (Fuzzy KNN)[7] is an extension of the traditional k-Nearest Neighbors (KNN) algorithm, designed to handle uncertainty and imprecision in classification tasks. It incorporates fuzzy[6] set theory into the KNN framework, allowing it to make more nuanced decisions when assigning data points to classes. Fuzzy KNN[27] is particularly useful when dealing with datasets that exhibit overlapping or ambiguous boundaries between classes.

Fuzzy algorithm takes a training set X with labeled patterns and a test pattern y as input. Its goal is to determine the class label for y and provide a confidence level for each class label. It does this by finding the k nearest neighbors in the training set to the test pattern y based on Euclidean distance. If a nearest neighbor is closer to y than any previous ones, it replaces the farthest neighbor. Then, membership values for each class are computed, and the class label for y is assigned to the one with the highest membership value[30].

3.5 Fuzzy C-Means

A unique viewpoint on data clustering is provided by fuzzy clustering, often known as soft clustering or soft k-means. Unlike traditional clustering methods, such as K-means, fuzzy clustering allows data points to have a nuanced relationship with multiple clusters rather than rigidly assigning them to a single cluster[29][30].

In contrast to traditional clustering techniques, fuzzy clustering introduces a more flexible approach to data grouping. Instead of rigidly assigning each data point to a single cluster, as seen in conventional clustering methods like K-means, fuzzy clustering acknowledges that data points may exhibit varying degrees of affiliation with multiple clusters simultaneously. This nuanced perspective allows for a more accurate representation of the inherent complexity and uncertainty present in many real-world datasets.

By adopting fuzzy clustering, analysts can capture the subtleties and nuances within their data, leading to more comprehensive and insightful cluster assignments. This approach proves particularly valuable in scenarios where data points may not fit neatly into discrete clusters and instead possess multifaceted relationships with various cluster centroids.

In summary, fuzzy clustering represents a sophisticated and versatile approach to cluster analysis, enabling a more nuanced understanding of data relationships. It embraces the idea that data points can belong to multiple clusters to varying degrees, offering a powerful tool for tackling complex datasets with intricate similarities and affiliations.

4. Performance Metrics of Various Machine Learning Algorithms

There are various techniques and metrics to analyze the performance of a machine learning model. These metrics evaluate the effectiveness of a model. Following are the metrics used to analyze and compare various algorithms.

4.1 Recall

The recall[2] is a measure of how well the model identifies True Positives. Thus, recall informs how many people were accurately identified as having Parkinson's disease out of all those who truly have Parkison's disease.

Recall = TruePositive/(TruePositive + FalseNegative) (3)

4.2 Precision

Precision[2], as defined by the ratio of True Positives to all Positives, represents the proportion of correctly diagnosed Parkinson's disease patients among all individuals detected with the condition by the algorithm.

Precision = TruePositive/ (TruePositive + FalsePositive) (4)

4.3 Accuracy

The ratio of the overall number of accurate predictions to the total number of forecasts is known as accuracy[4].

Accuracy = (True Positive + True Negative)/(True Positive + True Negative + False Positive + False Negative) (5)

4.4 Specificity

Specificity[4] is a statistical measure that quantifies the proportion of true negatives correctly predicted as negatives. In other words, it represents the accuracy in identifying actual negative cases as negative (referred to as true negatives). Conversely, there is a complementary proportion of actual negatives incorrectly predicted as positive (known as false positives), which can also be described as the false positive rate[28].

Specificity = TrueNegative/(TrueNegative + FalsePositive) (6)
= probability of a negative test given that the patient is well

4.5 Confusion Matrix

A confusion matrix serves as a tabular representation that summarizes a machine learning[20] model's performance when evaluated against a set of test data. Its primary application lies in assessing the effectiveness of classification models, specifically those designed to predict categorical labels for input instances[24].

Within this matrix, one can observe and quantify the following key metrics produced by the model during its evaluation on the test data:
True Positives (TP) are occasions in which the model forecasts the positive class properly.
True Negatives (TN) are instances in which the model correctly forecasts the negative class.
False Positives (FP) occur when the model forecasts the positive class wrongly (a sort of inaccuracy).

False Negatives (FN) are situations where the model forecasts the negative class incorrectly (another form of mistake).

The confusion matrix has the shape of a 2x2 table in the context of binary classification as shown in figure 2. In the case of multi-class classification, however, the dimensions of the matrix correspond to the count of unique classes contained in the collected dataset. For n classes, the matrix takes the form of a nXn table, allowing for a thorough examination of the model's performance across multiple class differences.

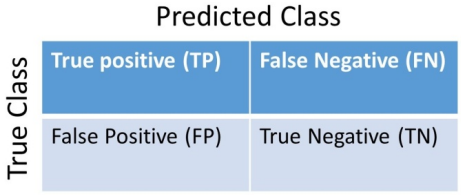

Fig. 2. Confusion Matrix

The confusion matrix assists in computing various model parameters like accuracy, precision, and more. It not only reveals classifier errors but also categorizes them as either type one or type two errors.

A comparative study of different deep learning and machine learning algorithms with their performance metrics and key highlights is shown in Table 1.

Table 1. Summarization of different Deep Learning and Machine Learning Techniques

Authors	Methodology	Highlights	Dataset used	Performance
Mathur et al.[1]	SVM, KNN, ANN(Artificial Neural Networks)	WEKA (Waikato Environment for Knowledge Analysis) is used to construct data mining methods for preprocessing, classification, clustering, and result analysis. To evaluate the worth of an attribute, "cfsSubsetEval" attribute evaluator and the "BestFirstSearch" technique has been utilized, which takes into account the particular predictive ability of each feature.	Voice datasets	Accuracy: 91.88%
Zhang et al.[5]	TQWT-DRSN(Tunable Q-factor wavelet transform with deep residual shrinkage network), WPT-DRSN	Combining time–frequency analysis with deep learning To categorize four types of clinical sleep EEG data, the wavelet packet transform with deep residual shrinkage network (WPT-DRSN) is used.	Signal dataset: EEG	Classification accuracy: 99.92% WPT-DRSN accuracy: 97.81% and 92.59%

Aşuroğlu et al.[4]	Combination of CNN and LWRF	Multiple gait sensors that measure GRF(Ground Reaction Force) value are used to process gait signals. The proposed framework is a hybrid deep learning strategy that uses data relations by combining CNN and LWRF architectures. This hybrid deep learning model outperformed previous regression models by translating time and frequency information from GRF sensors and feeding them into CNN + LWRF architecture	Signal dataset: Physionet Gait in PD	accuracy: 99.5% sensitivity: 98.7% specificity: 99.1%
Cai et al.[7]	FKNN, chaotic bacterial foraging optimization with Gauss mutation (CBFO), bacterial foraging algorithm (BFO),10 fold cross validation	Using 10 fold cross validation, divide the data into training and testing datasets. Data is fed into two models: Fuzzy-KNN and CBFO. CBFO is used for inner model selection based on criteria. The outer model FKNN, is used to decide and group the data.	Voice dataset	Best results FKNN with CBFO
Alshammri et al.[2]	KNN, SVM, DT, RF and MLP	Used Hyperparameter tuning (GridSearchCV) and Synthetic Minority Over-sampling Technique (SMOTE) to resolve unbalanced data.	Signal dataset: Physionet Gait in Parkinson's Disease	KNN accuracy: 88%
García-Ordás et al.[3]	Multilayer perceptron, autoencoder	Used an autoencoder to split data into two sections to detect different features. Send both data to MLP independently Combined outputs to get best results	Voice datasets : https://archive.ics.uci.edu/datasets?search=Parkinsons	Results : 99.15% accuracy (but they had small testing dataset)
Dheer et al.[12]	Acoustic characteristics KNN, NN, LDA, Decision tree classifier, GB, UPDRS are examples of statistical pooling.	The first stage is extracting features from Parkinson's audio dataset. The second stage involves picking the most important qualities from the numerous feature vectors generated. The final step is to use data from the UPDRS, such as motor symptoms, to help identify Parkinson's disease.	Voice datasets: Oxford Dataset	Results: The UPDRS settings achieved the highest success rate.

Polat.[13]	SMOTE, Random Forests Classification	Characteristics extracted from voice signals. Early identification and diagnosis of Parkinson's disease are critical for understanding disease progression and therapy planning. The dataset utilized in this work for Parkinson's disease analysis was available from the UCI machine learning repository. The proposed hybrid machine learning approach is divided into two parts: classification and data pre-processing by over-sampling.	PD two class dataset: UCI machine learning repository	Random forest: 87.037% Combination of SMOTE and Random Forest: 94.89%
Khorasani et al.[15]	HMM with Gaussian Mixtures	In this work, the Hidden Markov Model (HMM) using Gaussian Mixtures was used to identify between Parkinson's disease patients and healthy participants.	Data on 16 healthy and 15 PD participants' gaits.	Result: HMM : 90.3%
Shahsavari et al.[17]	Extreme Learning Machine(ELM) with Hybrid Particle Swarm Optimization (PSO)	Extreme Machine Learning (ELM), a single hidden layer feed-forward neural network, was used. To select relevant feature components, Hybrid Particle Swarm Optimization (PSO) was used.	PD two class dataset: UCI machine learning repository	ELM proves to better than other learning models
Kurmi et al.[28]	CNN Model, ensemble method	To forecast Parkinson's disease, ensemble deep learning systems were used. VGG16, ResNet50, Inception-V3, Xception are the models used. The logic-driven ensemble approach Fuzzy Fusion	PPMI (Parkinson's Progression Markers Initiative)	Accuracy : 98.45%, Precision : 98.84%, Sensitivity : 98.8%, Specificity : 97.6%
Haq et al.[11]	Logistic Regression and Deep Neural Network, Support Vector Machine,	Logistic regression, Support vector machines, and Deep Neural Networks were used. The dataset was divided among 70% training and 30% testing.	The Parkinson disease dataset : UCI machine learning repository	Deep neural classification performance was superior to typical machine learning classifiers.
Xuchen et al.[14]	XGBoost (Extreme Gradient Boosted Algorithm)	A second-order Taylor expansion on the loss function was used to improve optimisation. Incorporated regularization to control model complexity and prevent overfitting	Voice dataset	Accuracy : 90.76%.

Leung et al.[16]	Deep learning, ensemble methods	A comparison was made between eleven different networks trained in Stage 1 for evaluating image feature extraction techniques. InceptionV3, ResNet50, DenseNet121, and VGG16, all pre-trained on ImageNet, were employed by these networks to extract distinct sets of image features. A collection of image characteristics known as "All ImageNet imaging features" was also used. The MDS-UPDRS-III and case-specific clinical measures in the network were also used as inputs.	PPMI (Parkinson's Progression Markers Initiative)	MAPE : 18.36% MAE : 4.7, Pearson's Correlation Coefficient : 0.84.
Noor et al.[33]	Image registration, deep learning	In recent decades, neuroimaging, notably magnetic resonance imaging (MRI), has played a pivotal role in enhancing the comprehension of brain function and related disorders. State-of-the-art MRI images have revolutionized the ability to detect neurological issues, facilitated by advanced computational tools and cutting-edge machine learning algorithms.	Dataset : MRI Data	CNN : 99%
Alam et al.[21]	Random Forest	Sorted characteristics using one or more appropriate ranker algorithms Highly ranked features are then utilized by the Random Forest classifier	10 different datasets	Accuracy : 82.2%
Pepa et al.[29]	Fuzzy logic based system	By integrating data on the freeze index, energy, cadency fluctuation, and the ratio of the derivative of the energy, a fuzzy logic-based technique is produced.	Dataset : Freezing of Gait(FOG)	Accuracy : 85%
Murthy et al.[31]	Neural Networks	The research combines many CNN designs, including the Efficient-Net B0 and Mobile-Net V2 models, as well as a bespoke CNN architecture. These architectures were first trained on ImageNet before being fine-tuned via transfer learning. By integrating these designs with a bilinear pooling approach, three Bilinear CNN (BCNN) models are created.	Dataset: Gait	Deep semantic networks (DNNs) are preferred for test opportunities.

Shinde et al.[26]	Convolutional Neural Networks	Parkinson's disease (PD) is known for the loss of dopaminergic neurons in the substantia nigra pars compacta (SNc), which makes neuromelanin sensitive magnetic resonance imaging (NMS-MRI) a useful method for detecting SNc abnormalities. Current diagnostic approaches identify Parkinson's disease patients from healthy people by estimating contrast ratios of the SNc seen in NMS-MRI images.	Dataset : MRI Imaging	Accuracy: 80%
Wang et al.[25]	Multimodal model	The purpose of this study was to address the issue of FOG (freezing of gait), which can lead to unintentional falls in patients with PD. PD patients performed in-place movements while researchers captured physiological indicators such as accelerometer and EEG readings. The research entailed creating a multimodal model that integrated accelerometer data with EEG brain activity, proving to be more successful in identifying FOG than single-modal models.	Electroencephalography (EEG) and accelerometer signals	Matthews Correlation Coefficient (MCC) = 0.211
Khachnaoui et al.[32]	Convolutional neural networks, Medical diagnostic imaging	The aim of this study was to create a computerized method for the prediction of Parkinson's Disease(PD) prediction using DaTSCAN imaging.	SPECT DaTSCAN images	Accuracy= 98.47%
Pianpanit et al.[10]	Deep Convolutional Neural Networks model	• Parkinson's disease's SPECT imaging and DCNN models assist diagnosis. • Interpretability challenges in DCNNs are addressed via various visualization methods explored in this tutorial for reliable medical AI diagnostics.		
Thapa, S. et al[18]	Twin Support Vector Machines and Feature Selection methods	• Parkinson's Disease (PD) prompts ML models leveraging speech, gait, and tremor-based features. Naive Bayes, SVM, and Relief-based selection achieve up to 92.7% accuracy in early PD detection, emphasizing speech patterns for swift diagnosis.		Precision= 94% f1 score= 94%

5. Conclusion

This paper summarizes key research with Deep learning and Machine learning techniques to detect Parkinson's disease. It is difficult to collect datasets in the Indian regions owing to the lack of advancements necessary to gather data, thus, frequently the research is relying on freely accessible data. The majority of prior research is concentrated on one form of data, thus opening a wide scope for multi-modal datasets of audio, image and signal characteristics for prediction using advanced tools.
From this survey, it has been understood that accuracy plays a key role on the dependency of an algorithm. As each approach and techniques mentioned above had their own features and drawbacks, a

multi-model or a hybrid approach would be best suited to automate the process of Parkinson's detection and make a reliable system.

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