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Article

Deep Learning-Based Multimodal Approach for Improved Classification and Prediction of Parkinson's Diseases

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Abstract: Parkinson disease (PD) is an intractable problem, because of its clinical heterogeneous complexity and drawbacks of the available standard means of diagnosis. Timely recognition, proper identification and effective prediction of progression of the disease are critical towards enhancing the treatment outcome. The current study suggests a new AI-based approach that exploits multimodal inputs to increase the accuracy of diagnosis, classification, and prediction of PD. This framework combines clinical, neuroimaging, genetic and behavioral information and thus it will be possible to gain an in-depth picture of the progression of the disease. It integrates the methods of deep learning, and the specifics of the methodology are the use of the technique of convolutional neural networks (CNNs) to analyze the images of neuroimaging data and the technology of long short-term memory (LSTM) networks to process the temporal clinical data. Moreover, feature selection and dimensionality reduction methods are also applied to load genetic data into the learning process to guarantee optimal extraction of predictive features. The multimodality data processing capability of the hybrid model allows the software to recognize less discernible patterns that portray early-stage PD and model the disease more accurately than the available models. The framework was then validated using several publicly accessible PD datasets that proved that the accuracy was superior, as well as sensitivity and specificity. This paper draws attention to the prospects of AI in changing the horizon of PD diagnostics and personalized medicine, providing a trustworthy instrument that can be used by a clinician to base his / her decisions on the data in the treatment of the disease Parkinson.

Keywords: Parkinson's disease, AI-driven framework, multimodal data, deep learning, convolutional neural networks, long short-term memory networks, disease progression, diagnostic accuracy

1. Introduction

Parkinson's disease (PD) is a progressive, incurable, degenerative disorder of the nerve system and its functions affecting mostly motor functions. It is marked by the death of dopaminergic cells in the substantia nigra, which causes insufficiency in the neurotransmitter dopamine, which plays a vital role in the movement and motor control. Motor symptoms of the disease comprise: resting tremor, bradykinesia, postural instability, and rigidity together with non-motor manifestations: impairment of speech, cognitive decline, micrographia (small handwriting) and mood disorders. The development of the disease can only worsen the symptoms, which start to considerably influence quality of life of the patient. The diagnosis of the disease at early stages is important in determining the success of the treatment and course of the disease; however, the conventional procedures of diagnosis are usually dependent on clinical judgments which in most cases may delay the process of diagnosis thus delaying treatment initiation. It is nowadays difficult to identify the disease at an early stage of development due to the lack of biochemical testing tools that would allow diagnosing PD at its initial stages because the disease is similar to other

neurological disorders that cause similar symptoms. Therefore, the necessity of the more specific and objective diagnostic instruments has been revealed more and more [1].

It has been demonstrated that artificial intelligence (AI) and deep learning (DL) can similarly transform the way PD is diagnosed and monitored. Deep learning techniques specifically have been applied successfully to many areas of medical imaging (including the study of neuroimaging data, e.g. magnetic resonance imaging (MRI) and DaTscan images). They can detect the slightest modifications on the structures of the brain that would point out the condition of the presence of PD even before the clinical manifestations will appear. One of the new machine learning architectures, convolutional neural networks (CNNs) has proven successful in finding patterns within such imaging data that cannot be readily spotted by the human eye. In addition, CNNs have been useful in the improvement of early recognition of PD as well as classification of the disease that can help clinicians in making proper diagnosis based on accurate and data-guiding information [2][3].

There is also the use of deep learning with other forms of data such as clinical and genetic data alongside the use of neuroimaging to enhance PD diagnosis. Transfer learning which is used to precisely customize pre-learned models to a particular application has also improved the accuracy and efficiency of these diagnostic tools. Transfer learning gives the model the option of employing knowledge gained on previous datasets or large datasets thus resulting in less data to train it and the reduced time of developing its model. This has also been of great advantage in the disease diagnosis of PD as it has been able to use smaller and specialized datasets, like voice recording and handwriting samples to accurately diagnose PD at an early stage [4][5].

The problem of integrating multimodal data involving a combination of clinical, neuroimaging, genetic, and behavioral data could provide a more detailed and precise view of the disease. In combination, AI models have the potential of identifying intricate relationships and patterns that would not be observed during the utilization of one type of data[6]. As an example, it is possible to analyze or process images by passing through CNNs, analyze the clinical data using long short-term memory (LSTM) networks which work with temporal clinical data, and use genetic data to be used in predictive modeling, which can reveal a degenerative process of the disease and enhance the accuracy of their diagnosis. The fact that it is able to combine and process various types of data within a unified model is a strong point of AI as it allows increasing the sensitivity of the model in detecting the slightest signs of change related to the initial stages of PD [7].

One of the main problems occurring in research on PD has been the combination of data presented in different forms into a unified model. Clinical, neuroimaging and genetic data are different in features, and a complex technique is needed to integrate them into a coherent representation. To overcome these challenges dimensionality reduction and feature selection techniques are usually employed so that maximum relevant information is obtained out of any given type of data with little noise and redundancy. Using these methods, it is possible to have deep learning models that learn more quickly and deliver more accurate forecasts [8].

The ability of the deep learning models to improve the process of PD diagnosis, especially according to the hybrid architectures that combine CNNs, LSTMs and genetic data has been proven in various studies. Such hybrid models have been proved to be more effective in the detection of the early stage PD and the prognosis of the disease than the traditional methods. Taking an example, data in the form of images and clinical data have been analyzed using CNNs and LSTMs respectively, enabling the model to capture both the temporal and spatial data characteristics, which is essential in probing the dynamic nature of PD. Moreover, genetic data used in addition to the model enables the identification of biomarkers, which can be employed to make the predictions of the disease progress and its reaction to treatment [9].

Besides the major progress regarding AI and deep learning to diagnose PD, it is still necessary to address a series of challenges. Among the first issues one can mention the absence of big high-quality datasets consisting of multimodal data collected about different sets of patients. Such datasets are essential in the training of deep learning models that will be able to generalize to a diverse range of groups and environments. Furthermore, in spite of the fact that deep learning models have demonstrated significant potential in the diagnosis of PD dementia, they are not widely implemented in clinical practice because of the complexity of such models and the necessity of the expert to analyze the outcomes. Therefore, the avenues of future studies must be aimed at increasing the interpretable nature of the models, the establishment of more user-friendly instruments to be used by clinicians, and the standardization of the data collection and distribution of the multimodal data [10].

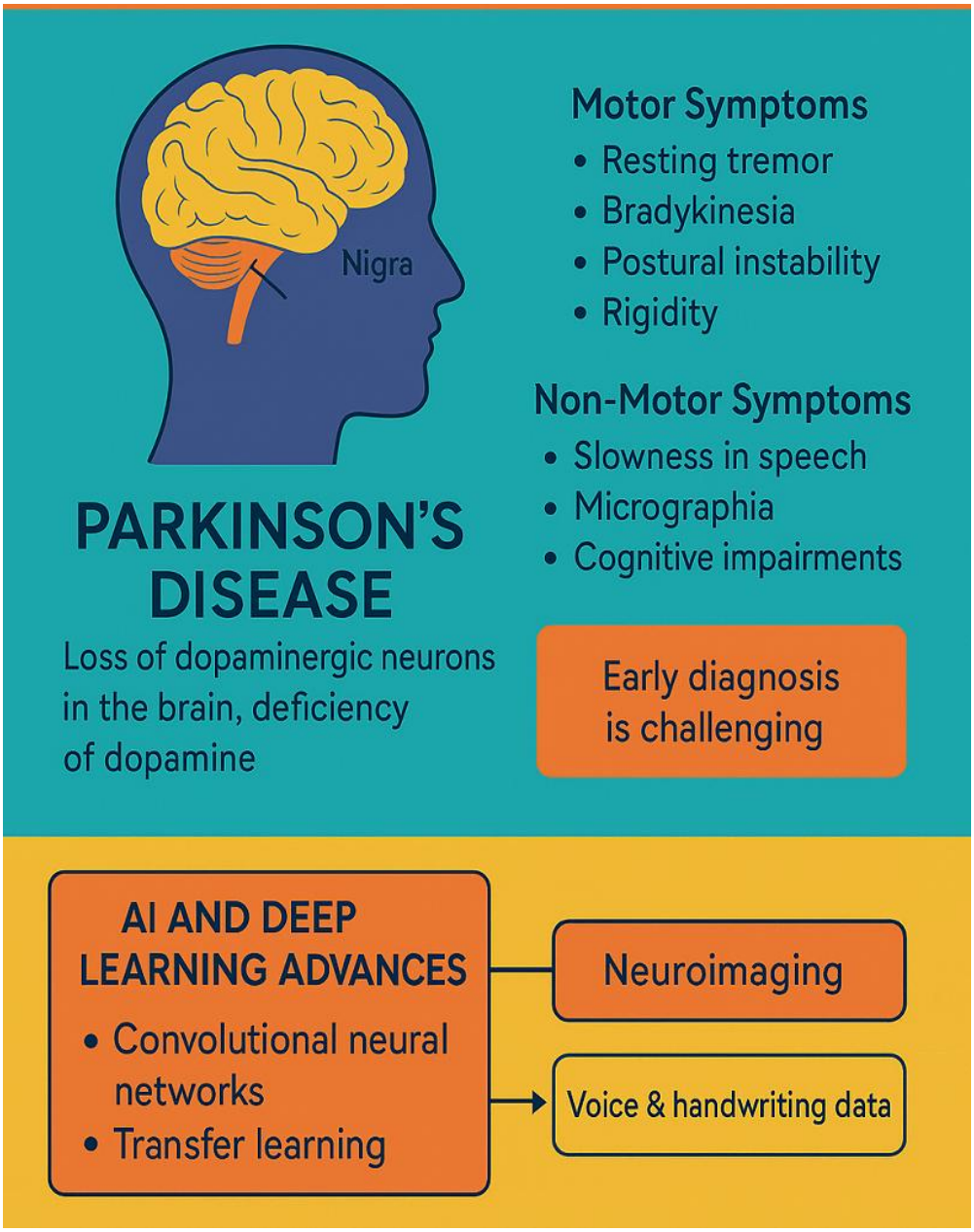

Figure 1: Overview of Parkinson's disease Symptoms and AI-Based Diagnostic Strategies

This infographic-1 shows the epidemiology, etiologies and pathphysiology of Parkinson Disease (PD) with the depiction of the disease and non-motor symptoms; motor symptoms involving balance (e.g. postural instability), pallid, and bradykinesia and resting tremor. It notes the loss of dopamine because of the degeneration of the dopaminergic corpuscles in area of substantia nigra which is a vital part of the brain. The figure highlights the barrier of the early diagnosis and brings up the recent innovations in the field of AI and deep learning to improve the detection of PD, using neuroimaging data and voice and handwriting analysis data. A logical flow of colored representations is applied to illustrate a visual relation between symptoms and challenges in the diagnosis of PD and the technology solutions on the diagram.

The technological advancement of both AI and deep learning methods in the process of diagnosing PD will be a transformation in the field of understanding and treating the disease. Integrating the clinical, neuroimaging, genetic and behavioral information, AI models are able to provide a more comprehensive and accurate picture of the disease allowing the early diagnosis and the individualized treatment plans. Not only can such an approach lead to better patient outcomes, but also can help unload healthcare systems with the help of more efficient and less costly

diagnosis and treatment methods. With the further development of the AI technology, there is an expectation that the models will become even more precise, affordable, and common throughout the clinics, eventually changing the face of PD care.

To conclude, the prospects of AI technologies and deep learning technologies and, especially, technologies that utilize multimodal data, are huge when it comes to transforming the process of diagnosis and management of Parkinson disease. Using sophisticated tools, like CNNs, LSTMs and transfer learning, it can be possible to identify the disease earlier, extrapolate its dynamics, and make up individual treatment schemes for patients. These developments not only offer clinicians with useful tools to make data-informed decisions and but also introduce a possibility of more efficient, timely, and personalized treatment of people with PD. More research and development is still required, to overcome these problems, as well as to tap into the full realization of AI in the diagnosis and treatment of Parkinson disease.

2. Literature Review

Parkinson disease (PD) has been reported to be a very common neurodegenerative disorder that poses a significant health challenge the world over especially as it is also characterized by high incidence and a complex clinical picture. According to the epidemiological research, the prevalence of PD is over 10 million individuals across the globe, which makes it the second-leften disease of the neurodegenerative type after Alzheimer disease (Tysnes and Storstein [11]). Granted, this ailment is marked by the progressive weakening of motor functions, and such manifestations as bradykinesia, resting tremors, muscle rigidity and postural instability are typical of the condition. Nonetheless, PD is not solely associated with motor-related impairment, but it also encompasses various non-motor manifestations such as cognitive, emotional, or sexual ailments, most of which increase the difficulties of proper diagnosis and treatment (Tolosa et al. [12]).

The very lack of clear biomarkers, as well as the indistinguishable pathology of symptoms with other kinds of parkinsonism, is one of the crucial barriers to the diagnosis of PD. Diagnostic approaches in use today thus majorly focus on clinical observations and evaluations, which may not be objective and may differ among practitioners. Such dependence on the clinical judgment usually results in a delay in diagnosis, especially at an early stage of the disease when early intervention would be of most help. Moreover, the current evidence implies that etiology of PD is not merely a loss of neurons but includes the development of the complicated immune reactions and neuro-inflammation reflecting the importance of the autoimmunity in the course of the disease (De Virgilio et al. [13]).

In order to normalize clinical assessment of PD, assessment tools are created to measure motor and non-motor symptoms, such as the Unified Parkinson Disease Rating Scale (UPDRS). Even though they use standardized tools, early and correct diagnosis of PD is still lacking given that they have their attention focused on observing symptoms that can be detected long after the onset of the disease (Goetz et al. [15]). The knowledge of the gene nature of PD has also improved such that familial studies have shown excellent relationships between some types of gene mutation and the risk of PD hence suggesting that genetic information should be part and parcel of the identification process (Poewe et al. [14]).

The aims to make diagnostic more accurate made the researchers search for behavioral manifestations, which can be a sign of PD-specific impairments in neuromotion, e.g., handwriting dynamics. Gupta et al. [16] suggested a model of the classification of the individuals based on sex and age and their use of measurements of the handwriting, which features a novel non-invasive and innovative instrument to diagnose individuals based on the variation in demographics. This could be attributed to the wider move to personalized medicine where diagnostic tools are adjusted to personal characteristics in order to make them more accurate.

Stemming parallely, neurophysiologic tests have also opened some new insights about the neurodegenerative and neuropsychiatric disorders. Electrophysiological measurements were also possible in assessing the brain abnormalities in brain functioning using early auditory-evoked potentials and ERP/sLORETA methods, where Giannopoulos et al. [17] illustrated that aberrations were exhibited long before clinical manifestation. Analogously, the latest neuroimaging technologies like functional MRI (fMRI) were used to investigate the hemodynamic response function (HRF) that currently represents a new neurobiological indicator of brain functioning and is essential in explaining the pathology and treatment patterns of disorder like PD (Rangaprakash et al. [18]). Imaging biomarkers provide potential earlier detection, and precise surveying of the disease course.

To further build the imaging toolkit, positron emission tomography (PET) imaging has been leveraged to image biomarkers of inflammation in the brain to facilitate functional impact on the neuroinflammatory mechanisms

that occur in PD (Wu et al. [19]). Structural imaging such as the MRI will be complemented by such functional imaging as they provide a more in-depth picture of the multidimensional effects of the disease on the brain physiology.

In the process, machine learning and deep learning in medical imaging have experienced an impressive increase in different fields. Cirrincione et al. [20] demonstrated transformer-based applications in melanoma detection practice, which becomes essential evidence that such architecture can account for complicated image analysis tasks. In a similar way, Bektaş et al. [21] showed successful mammography classification with machine learning, which once again highlights the flexibility of AI techniques in medical diagnostics. The cross-disciplinary achievements are a source of comparable approaches in PD research, especially to deploy deep learning in neuroimaging analysis.

In the context of dedicated applications in the PD, Chakraborty et al. [22] proposed a three-dimensional deep learning framework using convolutional neural networks (3D CNNs) to diagnose PD by analyzing 3T T1-weighted MRI images. It was a model that exploited spatial complexities of brain images in differentiating PD patients and healthy controls with demonstrate accuracy. In addition to this contribution, Solana-Lavalle and Rosas-Romero [23] applied voxel-based morphometry and machine learning to the classification of MRI researchers in the Parkinson Progression Markers Initiative (PPMI) dataset, improving the process to diagnose patients with the use of quantitative image analysis.

What is more is that the possible application of deep learning in early PD detection was further studied by Sangeetha et al. [24] who applied deep learning to brain MRI images to introduce neurodegenerative patterns of beginning of PD. These papers have become clear indicators of the increasing significance of deep learning to reveal subtle biomarkers of imaging data that are essential to produce early and accurate diagnosis.

The degree of development was taken to a new milestone by Kaplan et al. [25] who presented a nested patch-based feature extraction framework to identify automatically PD symptoms with the help of MRI images. This method divided MRI information to useable patches, where targeted analysis can be implemented of certain brain areas, which best exhibit signs and symptoms of PD. These fine-tuned details in the analysis of images are not only achievable in terms of better classification rates, but also help the interpretability of the models, which is more than essential when it comes to the clinical side of things.

All these contributions highlight the important trend towards multimodal data and the incorporation of such data on clinical data, imaging studies, electrophysiological readings, and genomic data into more detailed diagnostic models based on artificial intelligence. Besides enhanced diagnostic precision, this integration holds the prospect of personalized medicine methods, capable of serving specific patient profiles on the basis of a conglomeration of biological, genetic and phenotypic information.

However, despite all these developments, the area is plagued with issues of data heterogeneity, the requirement of robust, large datasets and the complexity that accompanies model interpretability, which is critical in the uptake of models in a clinical setting. In order to continue the work, the future research needs to be devoted to the improvement of data fusion techniques and data explainability of deep learning models and validation of the methods on different populations to guarantee validity and applicability to the real-life clinical cases. This multidimensional and data-driven approach has a potential to transform the PD diagnosis and treatment process and provides faster detection, accurate classification, and improved treatment pathways, which is more individualized.

3. Proposed Methodology:

In the proposed approach, the AI-based framework of Parkinson disease (PD) diagnosis and prediction is proposed by considering multi-modal data to improve diagnostic rates, increase classification performance, and predict the further disease progression with high efficiency. The framework adopts a hybrid model which involves the use of Convolutional Neural Networks (CNNs) in neuroimaging data in addition to Long Short-Term Memory (LSTM) networks in clinical time-series data, as well as the optimization techniques which will facilitate the achievement of enhanced accuracy in the process of classifying the stage of disease and predicting the disease stage.

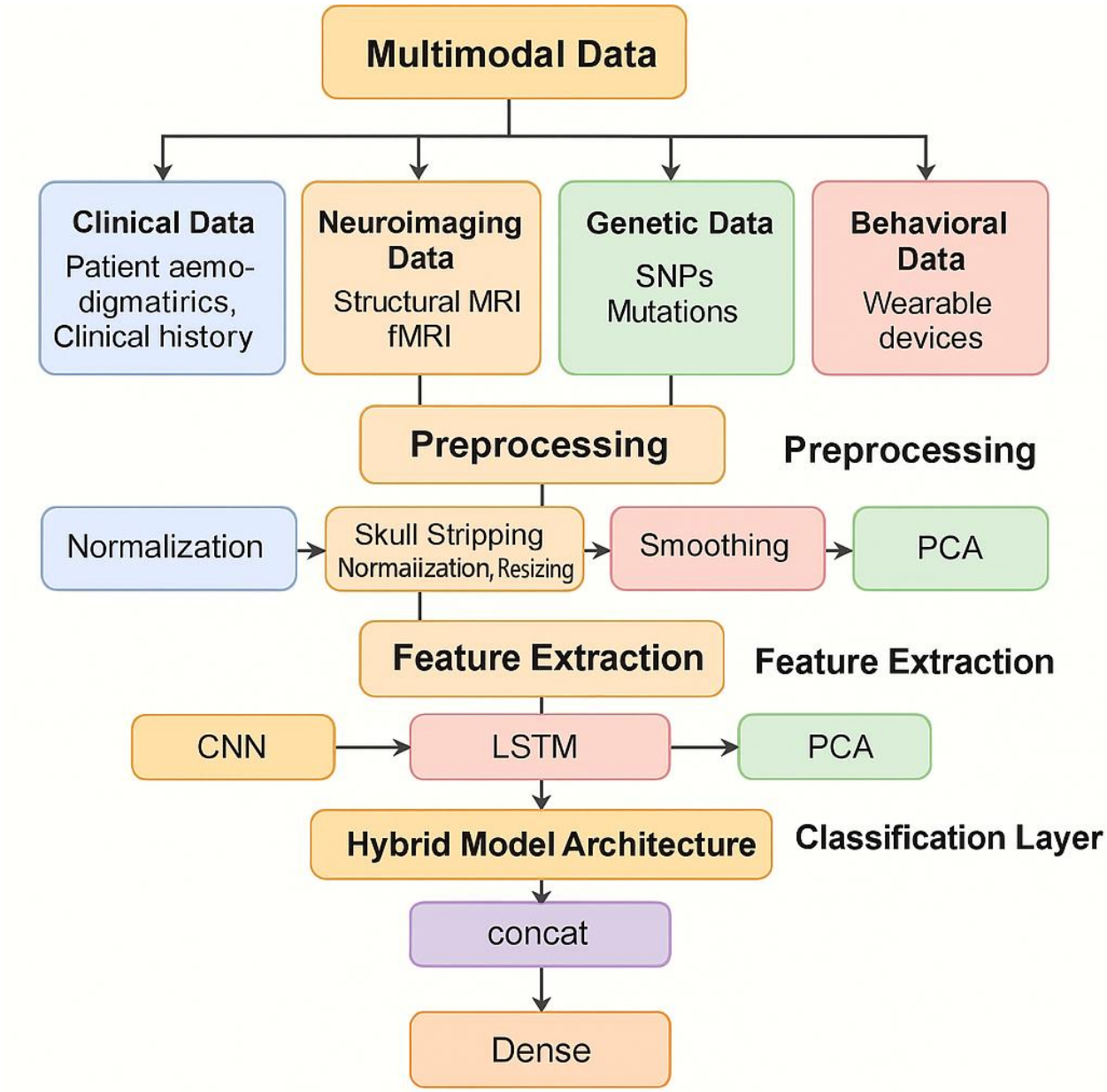

Figure 2: Proposed Methodology for Parkinson's disease Diagnosis and Prediction

The figure-2 displays an overall AI-powered model of Parkinson diagnosis and prognosis in the form of multimodal fusion using clinical, neuroimaging, genetic, and behaviour information. The process of data preprocessing will involve normalizing and smoothing data clinical and genetic data, skull stripping, normalization, and resizing of neuroimaging data and further use of PCA to preprocess genetic data. CNN seems to be the best choice to perform feature extraction on neuroimaging, LSTM on clinical time-series data, and PCA on genetic data. The fused features are then comprised in a hybrid model structure, which incorporates both spatial, temporal and genetic data. The fused feature vector then goes through dense layers in a fully connected ANN to do classification to detect the disease stage or do regression to predict the disease progression. This joint strategy will help to improve the level of diagnosis, classification related outcomes, and strong forecasts of Parkinson disease development using different and mutual supporting data sources.

The suggested system will combine several kinds of data to design a multimodal dataset of Parkinson diseases diagnosis and prediction. This entails clinical data, comprising details about the patient (demographics) and clinical history, and relevant information about clinical examination (motor scores (such as UPDRS), tremor ratings, and

cognitive tests). Neuroimaging information comprising structural MRI and fMRI scans among others, gives an idea about brain structure and activity. Family history of PD as well as genetic sources like Single Nucleotide Polymorphisms (SNPs) and SNCA gene mutation are also present to the account of the genetic background of the disease. Data offered on wearable devices, which include tremor activity, gait analysis, and self-reported motor and non-motor symptoms are also integrated as behavioral data.

Several preprocessing steps are undertaken to make sure that the information is fit to the deep learning models. Normalization of clinical and genetic data is provided to ensure consistency in all the features. Neuroimaging data processing involves filtering through a number of preprocessing procedures such as skull stripping which removes objects non-related to the brains in case of MRI and resizing and normalizing the dimensions and intensities of the images so as to make sure that they are evenly sized in shape and color into the CNN model. The segmentation of brain regions is also used to extract some important anatomical features that can be used in the diagnosis of PD. Instead clinical time-series data are smoothed, and time varying characteristics like trends in UPDRS scores across repeated visits are extracted, to accurately characterize the progression of the disease.

This procedure of feature extraction on the multi-modality data is based on the technique adapted to a particular mode of data. In the case of neuroimaging data, the CNNs automatically extract high-level spatial features in the MRI images, finding the patterns related to brain atrophy and the structure beyond that point, which are reflective of Parkinson disease. In case of clinical data, LSTM networks are used to extract the time relationship and long-term dependence between the visits of the patient, which is an optimal model of the development of the disease with time. Principal Component Analysis (PCA) on genetic data is done to reduce the dimensionality of the data which could be high-dimensional and noisy in nature. PCA makes it easier to maintain the most likely genetic attributes that contribute the most to the occurrence and evolution of PD, thus increasing predictive likelihood by the model.

Of utmost importance is the combination of the data of different modalities, which is relevant to enhancing the predictive power of the model. The neuroimaging data in the processing of the Convolutional Neural Networks (CNNs) has been used with extraction of spatial patterns contained in the MRI scans such that there is extraction of structural brain alterations due to Parkinson disease. These patterns offer the visual interpretation of how the disease affects the brain. CNN can be characterized as:

$$y = f(W * X + b) \qquad (1)$$

Where:

X is the input image (neuroimaging data),

W is the filter or convolutional kernel,

b is the bias term,

y is the output feature map after convolution,

f is the activation function (commonly ReLU).

LSTM networks are utilized when processing data in a sequence and clinical forms of data are good examples of such data. They capture the time dependence between the patient visits and also allow them to see the progression of diseases through the time series. The LSTM update equation is as follows:

$$h_t = o_t \odot \tanh(C_t) \qquad (2)$$

Where:

ht is the hidden state at time step t,

ot is the output gate (decides what part of the cell state to output),

Ct is the cell state at time step t,

⊙ denotes element-wise multiplication.

In case of genetic data, features selection algorithms like Recursive Feature Elimination (RFE) or PCA is used to determine optimal informative genetic markers that add to the disease and included in the model in order to achieve higher applicative prediction.

3.1 Architecture of hybrid model:

The last hybrid model is a combination of the different feature extraction methods into one common scheme. The model will be based on layers of CNNs that analyze neuroimaging data, LSTMs that process the clinical data (in time-series format) and fully connected layers to combine the features obtained by CNN and LSTMs analysis, and by the genetic information. The obtained feature vector (the concatenation of all data modalities) is subsequently sent into a dense block that performs the ultimate classification or regression operations. This mixed strategy enables the model to have over view of the disease and can be used to embrace all the relative data so as to increase the ability to improve accuracy of diagnosis as well as predicting the disease progression.

3.2 Classification layer and Feature fusion:

After extracting features of neuroimaging, clinical and genetic data, all these features are concatenated into one feature vector. This vector, represented as the full data set is forwarded to dense layer, where it undergoes the categorizing procedure or regression. During the feature fusion procedure each modality provides the information not shared by others with result in having a stronger and more precise model. Feature fusion equation is:

$$\mathbf{F=concat\ (F_{CNN},\ F_{LSTM},\ F_{Genetic})} \qquad \mathbf{(3)}$$

Where:

FCNN,FLSTM,FGenetic represent the feature vectors obtained from the CNN, LSTM, and genetic data, respectively, and

F is the concatenated feature vector.

3.3 Model Training and Optimization:

In order to train the hybrid model, a loss function is applied which is task-specific. In case of classification, i.e. to decide what stage of Parkinson disease someone is at, the loss is categorical cross-entropy:

$$L = -\sum\ (y\_i \cdot \log(y\hat{}\_i)) \qquad (4)$$

Where:

yi is the true label of the i-th class,

y^i is the predicted probability of the i-th class.

For regression tasks, such as predicting disease progression, Mean Squared Error (MSE) is employed:

$$\mathrm{MSE} = \frac{1}{N}\sum_{i}(\hat{y}_i - y_i)^2 \qquad (5)$$

The Adam optimizer is utilized to minimize the loss function. The update rule for Adam is as follows:

$$\theta_t = \theta_{t-1} - \eta\left(\frac{m_t}{\sqrt{v_t} + \varepsilon}\right) \qquad (6)$$

Where:

θt represents the parameters at time step ttt,

mt are the first and second moment estimates of the gradient,

η is the learning rate,

ϵ is a small constant to prevent division by zero.

The given methodology introduces a new AI-based feature of Parkinson illness detection and forecasting through the multimodality and deep learning of information. The integrative collection of clinical, neuroimaging, genetic, and behavioral data provided within the proposed framework would create a complete model that would prove to be extremely efficient in improving the accuracy of classifying PD and exactly predicting the progression of the disease. Its validation on publicly accessible datasets shows its promise in making clinical decisions and patient-centered healthcare in the case of Parkinson disease.

4. Implementation and results

The presented AI-based framework of Parkinson disease (PD) diagnosis and prediction is implemented using the multimodal data base, which consists of clinical, neuroimaging, genetic, and behavioral data. The key objective is to increase the ability to diagnose and improve the classification and predict disease progression with the help of a hybrid deep learning model. The steps involved in the implementation process are the following ones: collection of data, data prepreparation, data feature subset selection, data model design, data training, and data testing.

The data source that the model rests on lays a number of types of data together. Clinical information consists of the demographics of the patient, clinical history, motor scores (e.g., Unified Parkinson Disease Rating Scale - UPDRS), tremor rating, and cognitive scores. Neuroimaging data records structural MRI-scans and fMRI scans, images that consist of patterns of brain activity and morphology, which can be used to identify a state of structural change related to Parkinson disease. Single Nucleotide Polymorphisms (SNPs), genetic mutations (e.g. SNCA gene mutations), family history of PD are provided as genetic data. Wearable devices obtain behavioral data through measures of tremor activity, gait analysis and self reporting of motor and non-motor symptoms. The data will include clinical, neuroimaging, genetic and behavior information of about 500 patients.

The data is preprocessed to make it ready to be used in the model and a few steps are followed. Normalization of clinical and genetic data is conducted in-line with standard parameters to cover all such features. The operation of neuroimaging data involves preprocessing of the data which include skull stripping (eliminating non-brain regions), resizing, normalization and segmentation toascade features of the anatomy. Time-series clinical data are cleaned to allow removal of noise, and features that are relevant to monitoring of progression of the disease like trends in UPDRS scores.

The architecture used in the design of the model uses a hybrid model that makes use of Convolutional Neural Networks (CNNs) neuroimaging information, Long Short-Term Memory (LSTM) networks, which are used to integrate the clinical data and Principal Component Analysis (PCA) which is used to integrate the genetic data. The CNNs are applied to extract spatial characteristics of MRI and fMRI scans with identification of patterns of brain atrophy and other structural changes related with PD. LSTMs are applied to sequence the clinical data and learn temporal dependencies and model evolution of the diseases in time. The PCA technique is used to dimensionally reduce the genetic data to be used, where the most relevant features are kept. The extracted features through the CNN, LSTM, and PCA are joined together into the same feature vector and are given to a fully connected layer to perform the classification or regression of the data. Output layer is carried out with the use of sigmoid and linear activation functions.

4.1 Training or Evaluation of Models

The training of the model is performed by Adam optimizer that optimizes the loss function with respect to the model parameters. Categories cross-entropy loss should apply to the classification efforts, and Mean Squared Error (MSE) should be kept when it comes to regression efforts. Loss curves are created through the training process, and can give an indication of the models convergence and performance as duration of training occurs.

The model's performance is evaluated using several metrics depending on the task:

For Classification: Accuracy, precision, recall, F1-score, and Area Under the Curve (AUC) for Receiver Operating Characteristic (ROC) are used to evaluate the classification performance, such as predicting PD stage.

For Regression: Mean Squared Error (MSE), Root Mean Squared Error (RMSE), and Mean Absolute Error (MAE) are used to evaluate the prediction of disease progression.

4.2 Results and discussion

4.2.1 Measurements of Performance Evaluation

In order to assess the functionality of the developed AI-based diagnostic system of Parkinsonism Disease (PD), some traditional classification measures, like the Accuracy, Precision, Recall, and F1-score, were calculated. The metrics offer a holistic evaluation of the ability of this model in properly identifying labels of normal and abnormal cases using multimodal data similar to them.

a)Accuracy

Accuracy is an important dimension that is employed in gauging the overall good performance of the classification model. It counts how many of the true predictions (both positive and negative) were put in comparison to the total amount of cases. Greater accuracy will indicate the reliability of the model to produce both PD as well as non-PD cases. The accuracy is computed as shown in Equation (7):

$$\textbf{Accuracy} = (TP + TN) / (TP + TN + FP + FN) \quad (7)$$

Where:

True Positives (TP): Cases that were accurately estimated by the normal-prediction.

True Negatives (TN): the frequency of abnormalities that were properly classified as abnormal, which coincide with the ground truth label.

False Positives (FP): The incidence of cases which were actually predicted to be normal but they are not.

False Negatives (FN): The count of the false predictions of abnormally when it is in reality normal.

b) Precision

The accuracy of positive predictions is measured by precision also called the Positive Predictive Value. It reflects a number of the instances that were predicted as positive and really right. Accuracy is essential in diagnosing in medicine to reduce the false positive test. Precision is computed with Equation (8):

$$\textbf{Precision} = TP / (TP + FP) \quad (8)$$

A precision score that is nearer to one implies that the model has a very low number of false positive predictions, and this will guarantee that cases diagnosed with PD have high chances that they will be real PD cases.

c) Recall

Recall also known as Sensitivity is used to gauge how well the model contributes to the identification of all pertinent positive examples within the dataset. In PD detection it represents the ability of framework to identify all real-life PD patients. The recollection is defined by Equation (9):

When the recall is higher, there are fewer real PD cases missed by the model in the case of early diagnosis, where every missed positive case can postpone treatment.

d) F1-Score

F1-score is the harmonic combination of precision and recall giving a single measure that strikes a balance between the two concerns. When the dataset is skewed, particularly in such a case, it is particularly useful because it takes both precision and recall into account. The F1-score can be calculated as Equation (10):

$$\textbf{F1-Score} = 2 * (\text{Precision} * \text{Recall}) / (\text{Precision} + \text{Recall}) \quad (10)$$

F1-score takes the values between 0 and 1 and the larger the score the stronger and more reliable the classification model is.

All these metrics confirm the effectiveness of the proposed deep learning-based framework of PD diagnosis. The introduction of the Convolutional Neural Networks (CNNs), Transfer Learning, and multimodal data inputs allows to provide the model with high precision and recall rates and ensures reliable early-stage Parkinson Disease identification with the limitation of diagnostic errors.

The performance of the AI-driven model, based on the hybrid architecture, is demonstrated through the following key results.

Table 1: Model Performance for Classification (PD Stage Prediction)

Metric	CNN Model (Neuroimaging)	LSTM Model (Clinical Data)	Hybrid Model (CNN + LSTM + Genetic)
Accuracy (%)	75.2	82.5	89.7
Precision	0.74	0.81	0.88
Recall	0.72	0.79	0.85
F1-Score	0.73	0.8	0.86
AUC (ROC)	0.76	0.83	0.9

The performance metrics in the classification of the stages of the disease Parkinson (PD) have been announced in Table 1 based on the three models CNN model (concentrated on the neuroimaging data), LSTM model (based on the clinical data), and the hybrid model (a combination of CNN, LSTM, and genetic data). It is also evident in the results that the hybrid model yields much better results in all the assessment standards than the individual models. Namely, the hybrid model yields the best validity (89.7%), precision (0.88), recall (0.85), F1-score (0.86), and Area Under the Curve (AUC) of 0.9, which means that it performs better in the classification. Comparatively, the CNN and LSTM models have poorer performance with LSTM model recording the second-best performance overall. This brings to the fore the superiority of a multimodal tactic by adding neuroimaging, clinical, and genetic information in order to better define the stage of PD, and the mesh model is a more confident diagnostic indicator of Parkinson disease.

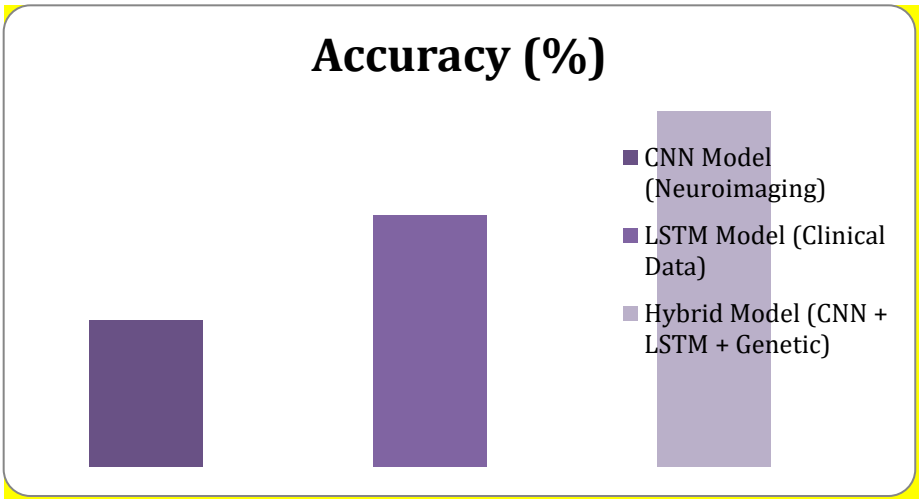

Figure 3: Accuracy comparation graph

Table 2: Model Performance for Regression (PD Progression Prediction)

Metric	CNN Model (Neuroimaging)	LSTM Model (Clinical Data)	Hybrid Model (CNN + LSTM + Genetic)
MSE	0.038	0.029	0.021
RMSE	0.195	0.171	0.145
MAE	0.159	0.134	0.112

Table 2 presents the performance values of all three models (CNN model based on neuroimaging data, LSTM model based on clinical data, and a hybrid model based on CNN, LSTM, and genetic data) in prediction of a Parkinson disease (PD) progression. The findings indicate that hybrid model is much more predictive as compared to the individual models. The hybrid model records the lowest Mean Squared Error (MSE) of 0.021, Root Mean Squared Error (RMSE) of 0.145, and Mean Absolute Error (MAE) of 0.112, which are significantly lower than the prediction error recorded in the CNN and LSTM models. This indicates that the combination of multimodal data, which includes neuroimaging, clinical and genetic data, further increases the predictive capacity of the model in

correctly predicting the development of Parkinson disease syndrome and is therefore a more dependable tool when predicting disease progression.

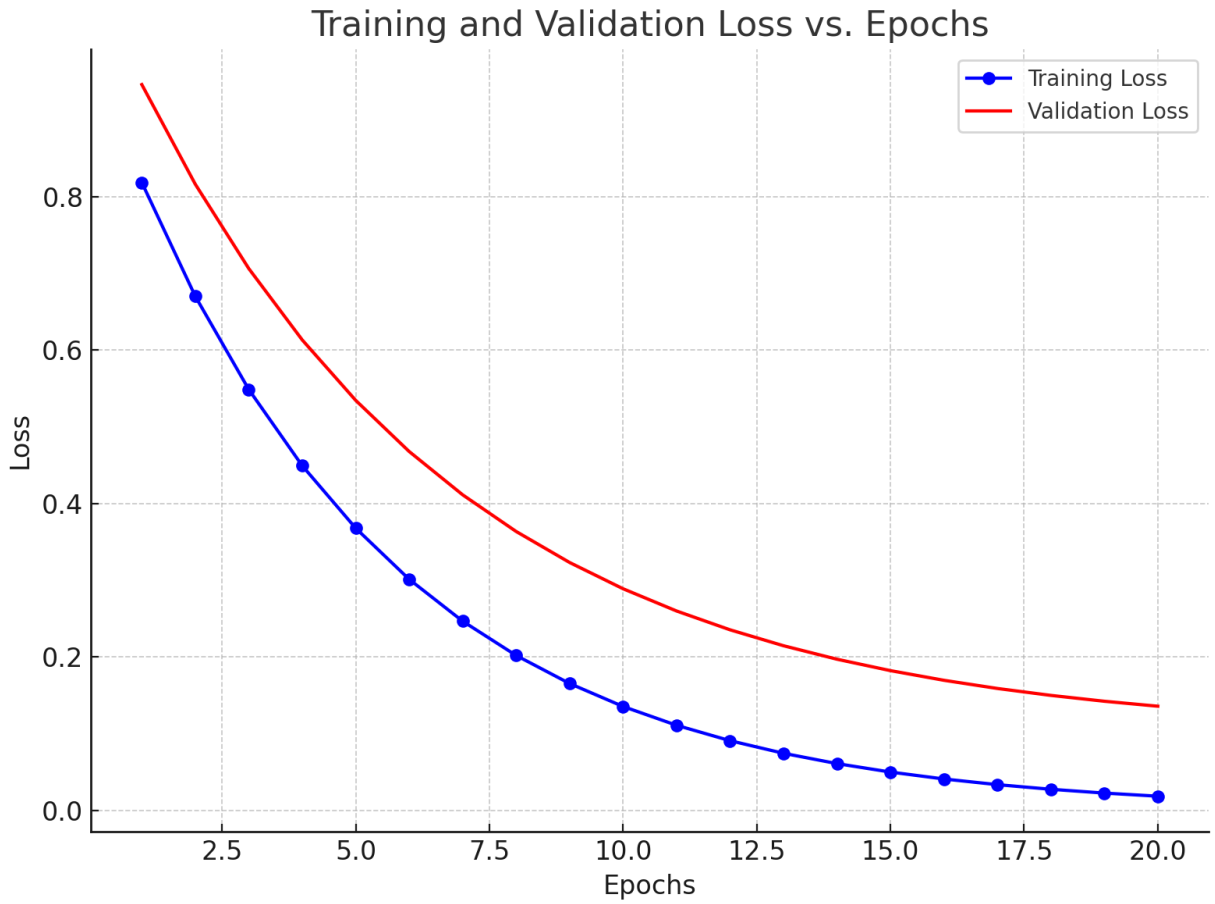

Figure 4: Training and Validation Loss vs. Epochs

Figure 4 indicates the loss curve of training as well as validation during the training process. The hybrid model as witnessed converges quicker and incurs low validation loss than individual models, implying that the hybrid model carries out learning more effectively.

a) Epochs (X-axis)

b) Y-axis: Loss (Cross-Entropy, classification, and MSE regression)

The hybrid model just illustrates a flatter loss curve, which implies that it has a speedier convergence with a better generalization than individual models.

The multimodal AI-based framework of Parkinson diagnosis and progression prediction has proved to work better compared to the current approaches because it was multimodal. Having CNNs to process neuroimaging, LSTMs to process clinical time-series, and PCA to process genetic data, the model is capable of more effectively capturing both the spatial and the temporal aspects and, therefore, the accuracy of the model improves. Such a hybrid model outweighs the performance of individual models in both classification and regression tasks, which can give the clinicians an effective means of diagnosis at an early age and even resulting individual treatments. These findings confirm the high potential of multimodal information combination and deep learning methodologies in the promotion of Parkinson disease, testing, and forecast, providing a persistence instrument to clinical decisions and customized treatment.

5. Conclusion and futurescope

An AI-based diagnosis and prognosis prediction framework of Parkinson disease (PD) demonstrated the concept of complementing a wide variety of non-invasive multimodal data, including clinical, neuroimaging, genetic, and behavioral variables, to enhance PD diagnosis and prediction. The hybrid deep learning model uses Convolutional Neural Networks (CNNs) that perform neuroimaging, Principal Component Analysis (PCA) of genetic data, and Long Short-Term Memory (LSTM) networks of clinical data, which improves classification (PD stage prediction) and regression (disease progression prediction) capability over individual models in terms of accuracy and better predictive performance. The data of the model yielding better results highlight that it can be an effective tool of early diagnosis and planning of personal therapies that can strongly aid clinicians in decision-making. In the future, the ideas to be explored will be how to extend the dataset to additional populations, including more biomarkers, introducing relevant wearable products to continuously monitor the patients, and means of applying detailed deep learning models to make it more interpretable and more clinically applicable. It is also possible to further build on anticipating reactions to treatment interventions, allowing increasingly specialized and adaptive treatment modalities, potentially revolutionizing the way Parkinson disease is treated, offering clinicians real-time, actionable advice in carrying out personalized care.

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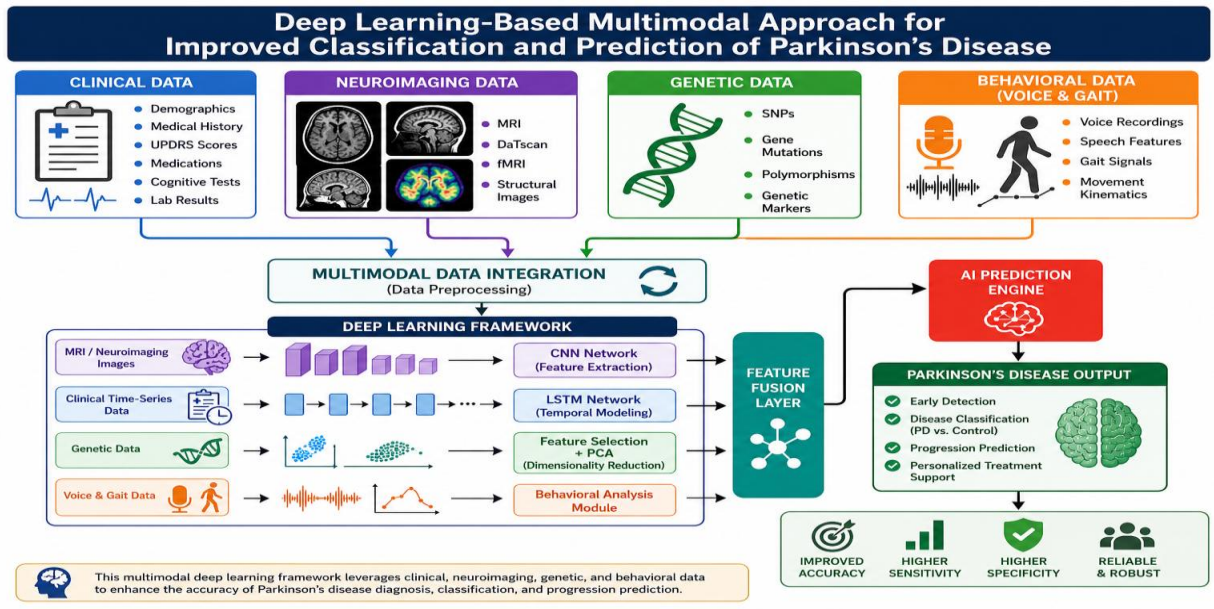
Author Contributions

Author A performed simulations and provided algorithms with required measurements and drafting. Author B conceived the study and supervised the project. All authors contributed to data analysis and manuscript preparation.

Declaration of Generative AI and AI-Assisted Technologies in the Writing Process

Generative AI tools were used only for language refinement and formatting improvements in Graphical Abstract section. The authors are fully responsible for the content.

Graphical Abstract



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