Enhancing Parkinson's disease Prediction using Machine Learning Techniques

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Abstract- **A degenerative neurological condition called Parkinson's disease results in problems with mobility and frequently results in stiffness and tremors. Life expectancy can be increased and symptoms can be managed with early identification. Addressing the dataset's multicollinearity problems and lowering the input feature space's size from the pre-processed image using Z score normalization, this paper first applies hybrid feature engineering techniques such as Local Binary Pattern (LBP) and EfficientNet to the featured dataset. The suggested CNN model is then fed the characteristics that were chosen using the chi-squared technique. Several tests are conducted to assess Using previously established techniques, Using the same dataset, the model's performance and outcomes are compared. In terms of AUC, the area under the curve was 0.86% and the accuracy was 88.9%, this 2D CNN model fared better than the traditional CNN model, which achieved 72.22% accuracy with an AUC of 0.50. These findings show that 2D CNNs are a more dependable method for classifying Parkinson's disease (PD) because they can successfully capture intricate spatial relationships in MRI data. By improving automated PD diagnosis, this study opens the door to better early detection, treatment planning**.

Keywords: ***Parkinson's disease, Magnetic Resonance Imaging, DL, Convolution Neural Networks, Preprocessing Techniques, Evaluation Metrics.***

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I. INTRODUCTION

A specific area of the brain's dopamine-producing cells is harmed in PD, a neurodegenerative condition. In addition to evaluating speech patterns, handwriting motions, and gait signals, the researchers presented a number of computer-based methods for Parkinson's disease prediction, including standard medical imaging methods such is signals from Single-Photon Emission Computed Tomography Electroencephalograms and MRI [1].In particular, structural magnetic resonance imaging, which can capture subtle structural changes in the brain and offer high-resolution information on brain tissue structure, is a crucial noninvasive technique for researching changes in brain structure and function [2].Suggest multi-stage CNN architecture for MRI image analysis and feature extraction that is based on the cutting-edge Efficient Net model. With Efficient Net, we integrate transfer learning to improve forecast accuracy, enabling more efficient use of the given data. The model is trained on a large dataset of MRI scans from patients with AD and PD to ensure good generalization using data augmentation, cross-validation, and an adaptive learning rate technique. Our CNN with several stages based on EfficientNetmodel outperforms other models in separating brain MRI images from those with diseases, according to experimental data [3]. Clinical and EEG datasets were preprocessed, with noisy signals undergoing normalization and noise reduction as well as z score normalization-based imputation for missing values. To reduce dimensionality, the feature engineering method included LBP and EfficientNet [4]. The CNN -based DL techniques are this most popular among them for classifying. These techniques are useful for building an end-to-end network because they enable quick, automatic, and thorough feature extraction pictures [5]. This method adjusts the weights and uses the new weights to retrain the model. if the accuracy is below ideal. Until the ideal precision is attained or the predetermined condition limiting the iterations is satisfied, this procedure is continued repeatedly. Ultimately, a vector with the ideal weights for training the chosen model is displayed. After being balanced with the best traits in order to recognize Parkinson's disease, the characteristics are examined during this testing phase [6]. In individuals with AI-based gait assessment has shown potential in lowering the symptoms of Parkinson's disease the likelihood of freeze episodes, enhancing diagnosis, and boosting motor independence. Personalized therapy procedures, ongoing monitoring, and improved diagnostic accuracy are some of its benefits [7]. The problem is formulated as follows

Parkinson's disease diagnostic classification from MRI images is difficult because spatial patterns can be very subtle and MRI has a high-dimensional feature space. The research outlined in this study aims to develop an accurate automated classification model using hybrid feature engineering and 2D CNNs to improve early detection of the disease. The major objectives are as follows

- To analyze MRI images using DL methods, especially 2D CNNs, in order to diagnose Parkinson disease accurately and promptly.
- To improve model performance and MRI data quality, a variety of preprocessing techniques (such as noise reduction, normalization) and hybrid feature extraction (LBP and EfficientNet) should be used.
- To analyze the accuracy of the proposed model's predictions using reliability-ensuring evaluation criteria, such as F1-score, sensitivity, specificity, and accuracy.
- To compare the proposed model's performance with traditional CNN model with loss metrics, AUC and ROC.

The remainder of the paper is organized into important sections that are explained as follows: Section II lists the current research projects in Enhancing Parkinson's Disease Prediction that have been completed by different authors. Section III outlines the workflow of the proposed method. The comparison results of proposed model with traditional model for Parkinson disease Prediction shown in Section IV. In Section V, together with references, is the conclusion of the suggested work that will be undertaken in a future scope.

II. LITERATURE SURVEY

Wang et al., (2020) This study includes data from cerebrospinal fluid, fast eye movement, olfactory loss, and signs of dopaminergic imaging. Comparing the suggested deep learning model with twelve machine learning and ensemble learning methods on a relatively small dataset reveals that the developed model outperforms the others in detection, with the highest average accuracy of 96.45%. Apart from PD detection, we also offer feature importance for the Boosting-based PD detection procedure[8].

Das et al., (2024) By creating a prediction method especially suited to PD datasets, our research seeks to lessen these difficulties. We do this by methodically investigating several ML methods for binary classification tasks and evaluating how well they predict Parkinson's disease. Our results highlight how crucial it is to use machine learning approaches for creating efficient decision support systems for PD prediction. In addition to addressing current research gaps, our work offers practical insights for the creation of cutting-edge medical applications by combining the output of many algorithms[9].

Keserwaniet al., (2024) Since artificial intelligence can manage enormous volumes of data and produce precise statistical predictions, many academics have lately been drawn to study in this area. In order to meet this requirement, scientists are now concentrating on AI as a potential solution. This article's objective is to present a thorough overview and in-depth examination of several AI-based strategies. These methods help forecast PD by utilizing ML, DL, and meta-heuristic algorithms[10].

Rakesh Arya et al., (2024) The These biomarkers are the subject of the study and were selected for their contribution to the field, methodological excellence, and significance. Glial fibrillary acidic protein and α-synuclein are two examples of biochemical biomarkers that can forecast the severity and course of a disease. The development of PD has been linked to a large number of genes and genome wide association study sites[11].

Zhang et al., (2023) In order to enable thorough evaluation, we first categorized PD-related parameters according to their accessibility and cost before progressively incorporating them into risk assessments that were created using eight popular ML models. Lastly, the contributions of each element were examined using the Shapley Additive Explanations approach. In terms of prediction, the polygenic risk score was the most effective, and the addition of invasive biomarkers did not increase its accuracy further[12].

Shohreh Abdollahiet al., (2024) Machine learning approaches provide the possibility of creating effective and trustworthy diagnostic instruments in the context of this neurological condition. This study examines the effectiveness of three popular algorithms for identifying Parkinson's disease using speech-related features: LR, SVM, ANN. According to the investigation, the ANN outperforms the SVM and Logistic Regression with the maximum accuracy of 92.4%[13].

Srinivasan et al., (2024) The KNN and FNN models are two ML and DL techniques that we apply in this work to use speech signal features to distinguish between people with Parkinson's disease (PD) and healthy people. We have 195 voice recordings from the University of UCI and 31 patients in our dataset. We use a variety of techniques to maximize model performance, such as Randomized Search CV for hyperparameter estimation, Feature Selection for finding the most pertinent features, and SMOTE for class imbalance weakening[14].

Hussain et al., (2023) This study proposes a machine learning-based ensemble classifier-based strategy for PD detection. Parkinson's disease patients and healthy controls are the two groups we examine. Our methodology combines feature extraction, feature selection, and classification techniques to provide a reliable and accurate model. Our results show how well the suggested approach may detect PD and emphasize the value of machine learning techniques in supporting PD early diagnosis and detection[15].

Hashim et al., (2024) This study uses well-known ML methods to increase the precision of the diagnosis. Numerous individual and ensemble artificial intelligence models, such as On two popular benchmark datasets, three scenarios are utilized to test the RF, DT, LR, Gradient Boosting, SVM, Stacking, and Bagging Ensemble classifiers; the Stacking Ensemble classifier yields the best results is used, which uses Logistic Regression to classify Parkinson's disease and Support Vector Machine and Gradient Boosting to extract features[16].

Pratihara et al., (2024) This study offers a thorough analysis of current biomarker research, improvements in healthcare infrastructure, and technology developments for objective evaluation. Using machine learning algorithms, it provides a thorough evaluation of many biomarkers' use in diagnosing Parkinson's disease across numerous datasets. The performance, advantages, and drawbacks of several diagnostic techniques are also examined in this study, offering important new information on how well they diagnose Parkinson's disease[17].

Rana et al., (2022) Giving a thorough rundown of the artificial intelligence techniques and data modalities used in Parkinson's disease investigation and diagnosis. This study examined the objectives, data sources, types of datasets, machine learning approaches, and associated outcomes of 112 academic articles in total. The findings indicated that novel biomarkers and machine learning techniques hold great potential for application in clinical decision-making, perhaps leading to a more thorough and knowledgeable diagnosis of Parkinson's disease[18].

Mei et al., (2021)Early non-motor symptoms of Parkinson's disease (PD) can be caused by a number of different conditions and can be quite mild. Because of this, these symptoms are usually ignored, which makes it challenging to make an early diagnosis of Parkinson's disease. Machine learning techniques have been applied to the classification of Parkinson's disease (PD) and healthy controls or patients with similar clinical in order to overcome these challenges and improves the diagnosis and evaluation processes of PD[19].

Priyadharshini et al., (2024) In order to prevent misdiagnosis, this project aims to create a technique that not only detects Parkinson's disease (PD) early on but also gives doctors a tool to understand the AI models' conclusions. The MRI data is pre-processed using techniques such as segmentation, normalization, bias correction, image registration, and brain extraction [20].

III. METHODOLOGY

This study presents an advanced methodology for enhancing Parkinson’s disease prediction using deep learning techniques. The dataset consists of MRI images, which undergo preprocessing using Z-score normalization to standardize pixel intensity values and reduce multicollinearity. This ensures that all features contribute equally to the model, improving the stability and accuracy of predictions. A hybrid feature engineering approach is applied by combining Local Binary Pattern (LBP) and EfficientNet. LBP captures texture-based features, which are crucial for identifying patterns in MRI images, while EfficientNet extracts deep spatial features that enhance feature representation. This combination ensures a comprehensive extraction of both low-level and high-level features, improving the classification accuracy. To refine the feature set, the chi-square algorithm is used for feature selection. This statistical method identifies the most relevant features, reducing dimensionality and eliminating irrelevant or redundant data, which optimizes computational efficiency. The selected features are then fed into a 2D Convolutional Neural Network (CNN) model for classification. CNNs are particularly effective in medical imaging tasks as they can capture intricate spatial relationships within MRI data, leading to more accurate predictions. These findings highlight the effectiveness of 2D CNNs in early Parkinson's disease detection, contributing to improved diagnostic accuracy and better treatment planning. Figure shows the workflow of the proposed method.

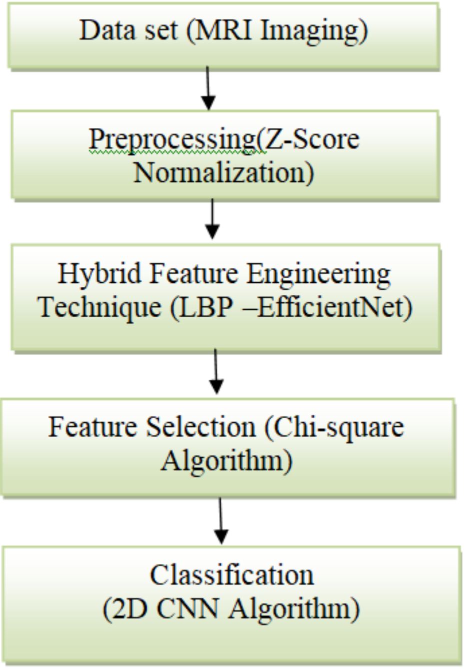

Figure 1 Proposed flow diagram

A. Dataset (MRI Imaging)

Comprehensive information on the records we gathered and our data source is given in this area. Between 2022 and 2023, a total of 7,500 MRI samples are gathered the clinical assessment samples as well. Patients, aged 40 to 85, both male and female, are included in these samples. Table 1 provides an extensive breakdown of MRI samples. Table: 1 lists the summary of the MRI samples that were gathered

Table 1 Demographic Distribution of Study Participants

Collected information	PD	Healthy
No. of samples	3500	4000
Male	40≤Age≤85	40≤ Age≤ 80
Female	40≤ Age≤ 80	45 ≤ Age≤ 80

B. Pre - Processing Z-Score Normalization

Z-score normalization (also known as standardization) is a widely used preprocessing technique in MRI image analysis to ensure that intensity values are standardized across different images or modalities. This helps improve model performance in machine learning and deep learning applications by reducing variations caused by scanner settings, patient differences, and acquisition protocols. Let x_i concretely represent the i-th component of each feature vector x ∈R^D, where i = 1, 2…, D. First, we determine these D components' mean and standard deviation.

$$\mu_x = \frac{1}{D}\sum_{i=1}^{D} x_i \,, \sigma_x = \sqrt{\frac{1}{D}}\sum_{i=1}^{D}(x_i - \mu_x)^2 \qquad (1)$$

Next, Z-score normalization is used as

$$X^{(zn)} = ZN(x) = \frac{x-\mu_x 1}{\sigma_x} \in \mathrm{R}^{\mathrm{D}} \qquad (2)$$

Where 1 is equal to [1, 1, 1]. The components of T, a D-dimensional vector, are all ones. Using the z-score feature normalization definition given above, we can determine that

$$\|X^{(zn)}\| = \sqrt{\sum_{i=1}^{D}\left(\frac{x_i-\mu_x}{\sigma_x}\right)2} = \sqrt{\frac{\sum_{i=1}^{D}(x_i-\mu_x)^2}{\frac{1}{D}\sum_{i=1}^{D}(x_i-\mu_x)^2}} = \sqrt{D} \qquad (3)$$

$$< x^{(zn)}, 1 > \sum_{i=1}^{D}\frac{x_i-\mu_x}{\sigma_x}.1 = \frac{\sum_{i=1}^{D}(x_i-D\mu_x}{\sigma_x} = 0 \qquad (4)$$

C. Hybrid Feature Engineering Technique (LBP & Efficient Net)

The picture of the MRI image of brain has been scaled to 512 × 512 pixels. Each block (subimage) of the pictures is prepared as an image input for the uniform LBP feature extraction step. The circular neighborhood (P) with radius (R) serves as the basis for calculating the LBP coefficients. Figure 2 shows the concatenation of the pre-established LBP values from the preceding block with the uniform LBP features that were retrieved from each block.

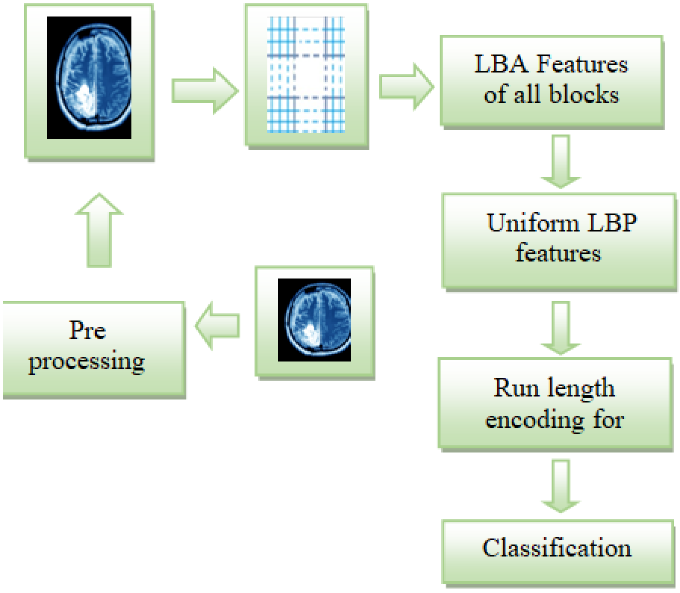

Figure 2 : Proposed technique of extracting and forming the encoded uniform LBP

Selecting this Choosing the right block size to process for LBP extraction is essential is dependent on the fundus image's smallest lesion, which is reliant on the image's size. At a 512 × 512 image resolution, our manual examination of the fundus image showed that the smallest lesion (microaneurysm) is around 5 × 5 pixels. Less than one percent of aneurysms are microaneurysms. Since the block size should be small to match the tiniest lesion, experiments were started using R = 2 and a block size of 5 × 5 pixels. In order to preserve local information, it is not advised to expand the block size above what is required. The block size needs to be within the immediate vicinity of the processing pixel's neighbors. The block's size needs to surpass the circular neighborhood's (2 × radius (R)). Equation (5). Next, using Equation (6), the picture partitions into blocks are computed.

$$Block\ size = 2 \times R + (5) \qquad (5)$$

$$Divisions = 5 \times floor(imagesize/(5 \times Block\ size)) \qquad (6)$$

Equation (7) states that the quantity of returned LBP coefficients for every block was initially significantly influenced by the number of neighbors P.

$$Num\ of\ uniform\ LBP\ coefficients\ for\ each\ block = P \times (P-1) + \qquad (7)$$

Due to the encoding of zero values, the suggested LBP encoded zeros approach altered the situation, and P no longer affects the dimensions of the characteristics vector. Radius R is the primary parameter that has an inverse relationship with feature vector size. The number of picture divisions, the quantity of extracted features and the number of blocks per picture that require processing will all drop as R increases since it will increase the block size. In order to eliminate duplicate data, the features extraction procedure will mask off any block or portion of the picture that is part of the black backdrop at the corners. Additionally, this is seen as a feature vector size decrease. Once zero values are encoded, the retrieved characteristics vector is once again reduced in size. It is established that this feature size is at its largest. experimentally after removing zeros from the features vector, as seen in Table 2 below.

Table 2 Effect of radius R on feature size.

R	Block Size	Divisions	Features size
2	5×5	100 × 100	16,150
3	7×7	70 × 70	8200
4	9×9	55 × 55	4950
5	11×11	45 × 45	3300

Our model's core makes use of the EfficientNet architecture, which is renowned for its computational speed and parameter usage economy. Squeeze-and-excitation blocks and depth wise separable convolutions are used to create each EfficientNet variation, which enables improved feature extraction at a minimal computational cost. To improve the focus on the most essential aspects, we incorporate the CBAM modules at different stages of the EfficientNet design. A Global Average Pooling (GAP) layer is then applied to the output from the last layer, reducing the dimensionality while maintaining crucial spatial information Equation (8).

$$F_{GAP} = GAP(\acute{F}_s) \tag{8}$$

In order to ensure that the model successfully captures both local and worldwide data, The output of the GAP layer is then sent into layers that are fully connected for classification tasks. By utilizing both channel and spatial attention processes, the combination of CBAM and EfficientNet offers a strong framework for the computationally efficient categorization of pictures related to breast histopathology.

D.Feature Selection (Chi-Square Algorithm)

By computing each feature's score based on its association with the target features, the Select K Best approach finds the kth top features. The Chi-Square statistical test is used in this investigation, and k is set at 10. The equation for the computation is shown in (9), and the chi-squared test establishes if two category variables are strongly connected.

$$X^{2c} = \sum \frac{(O_i - E_i)}{E_i} \tag{9}$$

A baseline method for feature selection is threshold, which eliminates features whose variance is less than a certain amount. Features that have the same value in every sample—known as zero-variance features are removed. The threshold value in our case is 0.7. To lessen bias error, the Gradient Boosting ensemble approach is then applied. in order to perform Tree-based feature selection. It refines its methodology and fixes errors caused by previous assumptions. In classification tasks, it also employs MSE as a cost function. Last but not least, a method called "forward feature selection" progressively adds significant characteristics to a prediction model, adding others according to their efficacy after the most crucial one. Until a stopping condition is satisfied or further features don't substantially enhance the model's functionality, this procedure keeps going. To choose the optimal characteristics for our investigation, we employed a Sequential Feature Selector.

E. Classification (2D CNN)

The field of machine vision has been dominated by CNN. A CNN is composed of many hidden layers, an input layer, and an output layer. Layers for normalizing, pooling, convolution, and complete connectivity are the usual components of a CNN's hidden layers. Extra. For more intricate models, layers can be employed. An illustration of a standard CNN is shown in Figure 3.

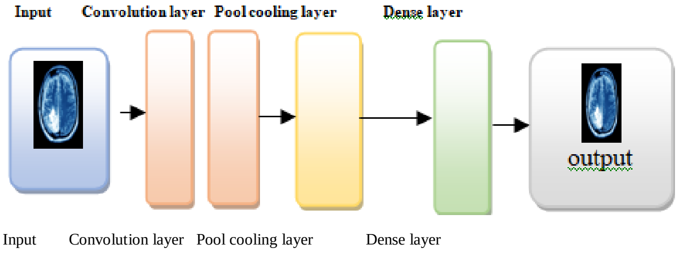

Figure 3 Convolutional Neural Networks Architecture

In several computer vision and machine learning fields, the CNN design has demonstrated exceptional performance. CNN uses an abstract level of training and prediction, saving the specifics for subsequent portions. Because of its consistent record-breaking efficacy, this CNN model is widely utilized in contemporary DL applications. These CNNs operate on the foundation of linear algebra. The foundation of representing Weights and data is matrix vectors multiplied. Every layer has an own set of attributes for a collection of images. For example, a CNN's early layers will learn certain fundamental features like borders, bright spots, dark spots, forms, etc. if it receives a face picture as input. Shapes and identifiable things from the image, such eyes, noses, and mouths, will make up the next layer set. The next layer has features that resemble real faces, i.e., objects and forms information might be used by the network to describe a human face.

CNN divides the image classification process into smaller components (features) by matching certain regions of the picture instead of the entire image. The features that the CNN gathers for assessment are represented by a 3x3 grid. Lining the feature with the picture patch is the next step, referred to as filtering. The total number of pixels in the feature space is then divided by the sum of the outcomes after each pixel is multiplied by its matching feature pixel one at a time. The feature patch is then updated with the feature's final value. A convolution filter is repeatedly used after this process for the remaining feature patches in an attempt to find every match.

Chain rule and vector calculus can be used in the CNN learning process. Let y∈If z is a scalar and R H is a vector, then z ∈ R. If zis is a function of y, then the partial derivative of z with respect to y is a vector, which is defined as follows.

$$(\partial z \ \partial yi) = (\frac{\partial z}{\partial yi}) \tag{10}$$

This study's objective is to retrain this model utilizing a fresh dataset and assess the outcomes. Because it would be a computationally demanding job that may take days or even weeks, it is decided not to train the model from scratch. Furthermore, several GPUs and/or a large number of computers would be needed. Rather, we will use the results of the suggested retrained model to support our assertion by comparing them to those of comparable publications.

IV. FINDINGS AND DISCUSSION

An extensive summary of the experiment and the results achieved using the methods we use for this investigation is given in this part.

A. Performance Evaluation

F1-score, confusion matrix, sensitivity other criteria used to evaluate the neural-based model system's efficacy include recall, accuracy, specificity, and precision. A brief description of these measurements is given below. Accuracy is the percentage of data instances that are properly categorized overall.

$$\text{Accuracy } = \frac{TN+TN}{TP+FP+FN+TN} \tag{11}$$

Precision indicates what percentage of identifications is actually correct

$$\text{Precision} = \frac{TP}{TP+FP} \tag{12}$$

This proportion of correctly identified true positives recognized is known as recall.

$$Recall = \frac{TP}{TP+TN} \tag{13}$$

The accuracy and recall metrics' harmonic mean are used to get the F1 scoretwo classifiers' performances are compared using it.

$$\text{FI Score } = \frac{\text{Precision}}{\text{Precision+Recall}} \tag{14}$$

Table 3Accuracy Comparison Table

Model	Accuracy (%)	AUC	Precision	Recall	F1-Score
2D CNN Model	88.9	0.86	90	92	85
CNN Model	72.22	0.50	85	87	72

The Accuracy Comparison Table 3 displays the classification performance of the proposed CNN model and the traditional 2D model in predicting Parkinson's disease (PD). The CNN model's significantly greater accuracy of 88.9% with an area under the curve (AUC) of 0.86 shows how well it can distinguish between PD and non-PD cases. However, the 2D CNN model shows weaker classification performance with a much lower AUC of 0.50, accuracy of 72.22%, precision of 90%, recall of 92%, and F1 score of 85%. These results show how using deep learning-based feature extraction and selection techniques may help the CNN model better represent intricate spatial relationships in MRI images.

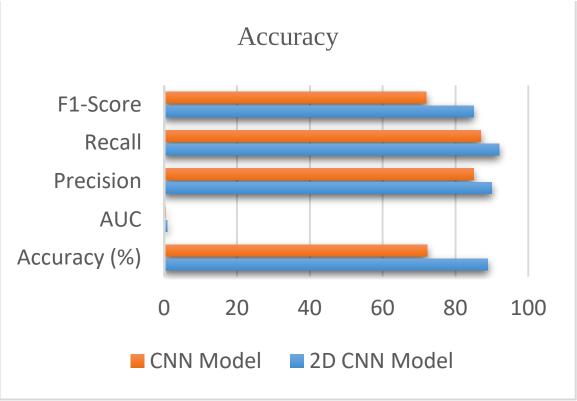

Figure 4 Accuracy Comparison

The accuracy comparison of the suggested CNN model and the conventional 2D CNN model in predicting Parkinson's disease (PD) is shown graphically in Figure 4. The bar graph makes it evident that the CNN model outperforms the 2D CNN model, with an accuracy of 88.9% vs 72.22%, precision of 90%, recall of 92%, and F1 score of 85%. The notable variation in accuracy demonstrates how well deep learning methods—like CNN-based categorization and hybrid feature engineering capture intricate spatial patterns in MRI data.

Table 4: ROC Curve

Threshold	CNN Model TPR	CNN Model FPR (1-Specificity)	2D Model TPR (Sensitivity)	2D Model FPR (1-Specificity)
0.1	0.98	0.50	0.85	0.65
0.3	0.95	0.30	0.78	0.50
0.5	0.90	0.20	0.70	0.45
0.7	0.85	0.12	0.60	0.35
0.9	0.75	0.05	0.50	0.25

The CNN and 2D models are compared at various thresholds in Table 4 of the ROC Curve Table, which displays sensitivity (TPR) and false positives (FPR). With a higher AUC (0.86) and better classification accuracy for Parkinson's disease over a range of decision thresholds, the CNN model routinely beats the 2D model.

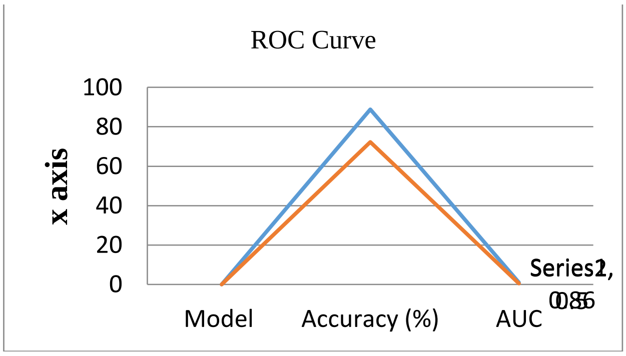

Figure 5 ROC Curve

The CNN and 2D CNN models for Parkinson's disease classification are compared using the Receiver Operating Characteristic (ROC) Curve, which is shown in Figure 5. The True Positive Rate (TPR) is shown on the Y-axis, while the False Positive Rate (FPR) is shown on the X-axis. The ROC curve for the CNN model stays above the 2D CNN model's curve, indicating superior classification performance. The CNN model's AUC of 0.86, which is much higher than the 2D CNN model's AUC of 0.50, shows better prediction accuracy. The CNN model's curve changes toward the top-left corner, confirming higher sensitivity and specificity. According to these results, CNNs are a more effective way to identify Parkinson's disease in its early stages.

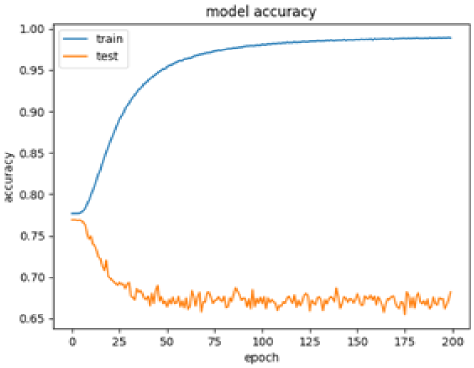

Figure 6 Convolutional neural network model

Figure 6 The CNN classification findings are highlighted in this section. The CNN model's training process and the associated variations in accuracy measures are shown in Figure 6. Accuracy was one of the other rating factors that were questioned.

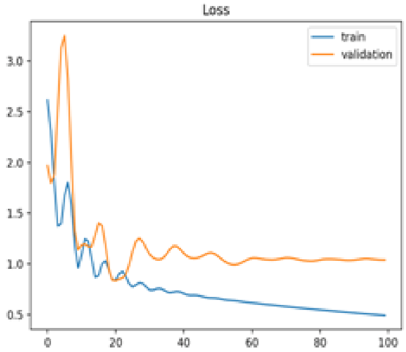

Figure 7 2D Convolutional Neural Network

The outcomes of the classification using the 2D CNN model are highlighted in this section. Figure 7 shows the 2D CNN model's training progress along with the associated variations in loss measures. The loss was one of the several evaluating factors that were questioned.

V. CONCLUSION

This study demonstrates the effectiveness of DL, particularly Convolution Neural Networks in enhancing Parkinson's disease prediction. By leveraging advanced feature extraction techniques such as Local Binary Pattern (LBP) and EfficientNet, and selecting key features using the chi-squared method, the proposed CNN model significantly outperforms traditional 2D CNN models. The 2D CNN model achieved 88.9% accuracy with an AUC of 0.86, while the 2D CNN model lagged with 72.22% accuracy and an AUC of 0.50. These results indicate that deep learning models can better capture spatial relationships in MRI data, improving classification performance. The ROC curve analysis further confirms the superior predictive capability of the CNN model, maintaining higher sensitivity and specificity across various decision thresholds. The study underscores the importance of automated PD diagnosis, allowing for early detection and better treatment planning. Future research should focus on expanding datasets, integrating multi-modal medical imaging, and exploring explainable AI techniques to improve model interpretability. Additionally, implementing real-world clinical validationwill ensure that these AI-based models can be effectively applied in medical practice. In conclusion, machine learning, and particularly CNN-based models, enhances Parkinson's disease prediction, offering a reliable and efficient diagnostic tool. This research contributes to advancing early detection strategies, ultimately improving patient outcomes and treatment effectiveness.

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