

A CNN Approach to Detect Parkinson's Disease using T1-Weighted, T2-Weighted, and Flair MRI

Neeraj Dhiman
Department of Mathematics
Graphic Era Hill
University
Dehradun, India
ndhiman@gehu.ac.in

Robin Singh
Department of Mathematics
Graphic Era Hill
University
Dehradun, India
robinsingh@gehu.ac.in

Anand Chauhan
Department of Mathematics
Graphic Era Deemed to be
University
Dehradun, India
dranandchauhan83@gmail.com

Aashiya Bi
Department of Mathematics
Graphic Era Hill
University
Dehradun, India
aashiya.saifi999@outlook.com

Abstract— Parkinson's disease (PD) has always been under the category of incurable disease to date. This neurodegenerative disease is generally caused by the deficiency of dopamine-developing nerve cells in the brain. The primary symptom of PD is a tremor, or shaking, in one or both hands. Other symptoms may include harshness of the limbs and trunk, slow movement (bradykinesia), poor balance and coordination, and a change in speech or writing (dysarthria or micrographia). As the senior citizen population is mounting, the patients of Parkinson's are also increasing. Unfortunately, there is absolutely no effective treatment for Parkinson's disease. Therefore, the task at hand is to enhance the timely identification of the illness. This research study has developed a novel 2D convolutional neural network to learn the intricate patterns in three different types of MR Images (MRI) to detect Parkinson's disease, which is thought to be brought on by minor, undetected strokes in the brain or the severity of white matter lesions, using a sizable dataset available on Kaggle. Through this model, a high accuracy of 94% has been achieved. Next, transfer learning is applied by using InceptionV3. The proposed model demonstrates an overall accuracy of 95.29% by leveraging a pre-trained model. Moreover, the precision, recall, and F1-score stand at 95%, 100%, and 97% correspondingly and are higher for the large dataset.

Keywords—Parkinson's disease, silent strokes, magnetic resonance images, dopamine, convolutional neural network architecture

I. INTRODUCTION

Millions of people throughout the world are affected by Parkinson's disease, a well-known movement illness [1-2]. The occurrence of the condition tends to rise in correlation with advancing age, with only 4% of people being projected before age 50 [1]. The deficiency of dopamine-developing nerve cells in the brain is the indication [2] of Parkinson's disease. Chemically, dopamine is a substance that is essential for many body processes. Parkinson's disease symptoms are caused by abnormal brain processes that are brought on by dopamine loss[5][6]. People who have been diagnosed with Parkinson's disease frequently experience tremors, handshaking, poor balance, or lack of coordination[7]. PD is the result of neuron decay in the substantia nigra that no longer produces dopamine [3]. The dopamine-producing neurons located in the substantia nigra region send signals to other parts of the brain, including the basal ganglia, which control muscle movement. When these neurons die or become damaged, the brain can no longer produce enough dopamine.

As a result, there is a reduction in dopamine levels, leading to the motor symptoms associated with PD.

People with PD may benefit from a variety of treatments and drugs that can help them manage their symptoms and live better overall.[9]. However, early detection is challenging, particularly for underdeveloped countries, in rural areas, access to trained neurologists and specialized healthcare can be limited. As an alternative, an MRI scan gives us a detailed look at the smaller parts of the brain. This helps doctors check for any balloon-like bulges or silent strokes [4]in the blood vessels, which can be an early warning sign that leads to dopamine loss. A silent stroke may diagnose by observing white spots, scarred tissue, or tiny areas of bleeding vessels [5]. White spots or white matter lesions [6] can potentially manifest as signal hyperintensities on T2-weighted MR images and are correlated with mobility impairments. Changes in the size of brain tissue, differences in MRI signals, and a build-up of iron can all be signs of brain damage and may mean that brain cells are dying, causing the immune system to go into overdrive [7]. T1, T2-weighted, and FLAIR MR image samples are shown in Fig. 1Fig. 1.

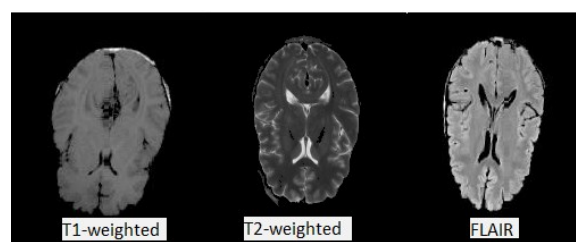


Fig. 1. Axial images of T1-weighted, T2-weighted, and FLAIR MRI [8]

To address this diagnostic challenge in terms of identifying changes in the nigral structure [9], blood vessels or around basal ganglia, or the presence of white matter lesions, a deep learning model or computer vision [10] framework can be used for detecting PD patients by classifying MR images as the analysis of textural tissue is able to perform identification of grey level patterns [11] [12]. The proposed system has achieved a high accuracy rate of 94.88% on test data in classifying MR scans to detect PD from large data than used in existing studies.

This manuscript is divided into six sections that are all well-organized. A review of pertinent studies with an

emphasis on Parkinson's disease early diagnosis is presented in Section II. The specifics of the data used here are described in Section III. Section IV discusses about the approaches used for the creation and improvement of neural network models. Section V elaborates on the outcomes of the suggested strategy. The thorough analysis and summary of the full study is included in Section VI.

II. RELATED WORK

The outcomes of deep learning and machine learning-based models for the prediction of Parkinson's disease have been the subject of studies all across the world up until this point. On various datasets, every machine learning model generates a different set of results. In this section, a concise overview is provided, highlighting a selection of the approaches utilized in the study. Kurmi et al. [13] has proposed an ensemble of deep learning models VGG16 [14], Xception [15], ResNet50 [16] and Inception-V3 [17]. The model's overall performance in detecting Parkinson's disease is enhanced through the application of an ensemble approach in conjunction with Fuzzy Rank Level Fusion (FRLF) using DaTscan images on the PPMI dataset [18] on a total of 645 images, which is 1/7th of the data set we have used and they achieved 98.45% accuracy. To capture intricate patterns in MRI scans, a 3D convolutional neural network is employed by Chakraborty et al. [19] specifically for 3T T1-weighted MRI data and plotted an accuracy of 95.29%. Rumman et al. [20] proposed an artificial neural network for 200 SPECT images and 94% accuracy was achieved by them. Abos et al. [21] achieved 86.96% accuracy by training a support vector machine [22] on selective features via randomized logistic regression with leave-one-out-cross-validation.

Amoroso et al. [23] performed feature selections using the random forest algorithm [24] followed by the application of a support vector machine for accurate classification of Parkinson's disease after defining a network model and got 93% accuracy. In another study by Lei et al. [25] achieved a 78.37% accuracy score on PPMI data by applying Fisher's linear discriminant analysis (LDA) and locality preserving projection (LPP). Salvatore et al. [26] analysed magnetic resonance imaging (MRI) scans of individuals who are considered healthy, have Parkinson's disease (PD), and have Steele-Richardson-Olszewski syndrome. They utilized features extracted from these images and employed Principal Component Analysis (PCA) [27] to identify the salient features. These features were then inputted into a Support Vector Machine (SVM) classifier for categorization. The study resulted in an accuracy rate of over 90% for differentiating between PD patients and controls.

An AlexNet CNN architecture used by Sivaranjini et al. [28] attained 88.9% accuracy. Shah et al. [29] demonstrated the efficiency of their proposed Convolutional Neural Network (CNN) model for categorizing Parkinson's disease (PD) in the Parkinson's Progression Markers Initiative (PPMI) MRI data. Their model produced 96% accuracy. Another work by Shinde et al. [30] has achieved an 85% accuracy to catch Parkinson's disease from Neuromelanin sensitive MRI using a CN network. Rana et al. [31] presented a Computer-Aided Diagnosis (CAD) technique that utilizes T1-weighted MRI and focuses on specific regions of interest (ROI) to distinguish between Parkinson's disease (PD) patients and healthy individuals. Their model achieved 86.67% accuracy. A few past methods suggested so far are highlighted in Table 1.

TABLE 1: A COMPARATIVE ANALYSIS OF PRIOR APPROACHES. [13]

Ref.	Data	Method	Size	Accuracy
[13]	SPECT	CNN models+ FRLF	654	98.45%
[19]	PPMI-MRI(T1-weighted)	3D CNN	406	95.29%
[20]	PPMI-SPECT	ANN	200	94%
[21]	Custom-rsf MRI	SVM	133	86.96%
[23]	PPMI-MRI	SVM	543	93%
[25]	PPMI-MRI+DTI	Sparse feature selection	208	78.37%
[26]	PPMI-MRI(T1-weighted)	PCA followed by SVM	84	>90%
[28]	PPMI-MRI	AlexNet	-	88.9%
[29]	PPMI-MRI(T2-weighted)	CNN	500	96%
[30]	Custom-NMS-MRI	CNN	100	85%
[31]	Custom-MRI(T1-weighted)	ROI based diagnosis	60	86.67%

III. DATA SOURCE

A. Data Collection

The magnetic resonance imaging dataset we used is taken from Kaggle in png format. The dataset consisted of two directories as 3_class and 4_class. Both the directories had two sub-directories- the train directory and the test directory. We took the data from the 3_class directory. Each sub-directory in 3_class was consisting 3 folders AD (Alzheimer's Disease), PD (Parkinson's Disease), and CONTROL (Healthy Patients). We removed the directory of AD to only work on Parkinson's data. The training directory has the data of 3916 patients and the test directory has 723 data samples, each of size 176x208 [8]. The data is grayscale imagery data. Data details are described in Table 2.

TABLE 2: DATA DETAILS

Category	PD	Control	Total
Train	906	3010	3916
Test	61	662	723

B. Data Preprocessing

All the MR images were in png format. All the images were resized to 150x150 resolution to fit the DL model and we performed normalization to re-scale them in values between 0 to 1. We used Image Data Generator to generate the images for the model in a single batch equal to the number of images in respective directories. For each directory, we separated the data generators into image data and label data then resized the array to a size of Nx1. The next step is followed by the splitting of data into training data, testing data, and validation data as shown in Table 2. Fig. 2 shows a selection of sample

images from the dataset, depicting individuals with Parkinson's disease, and Fig. 3 for a healthy being.

TABLE 3: SPLIT DATA DETAILS

Training Samples	Testing samples	Validation Samples
2748	776	392

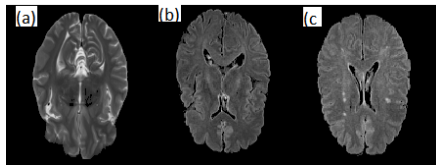


Fig. 2. Sample images for a person with PD (a) non-symmetrical basal ganglia (b) WM lesions in ganglia and caudate (c) lesions around ganglia and in ventricular [8]

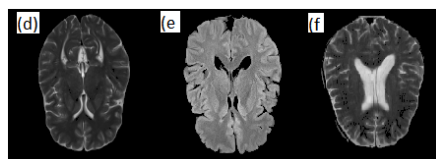


Fig. 3. sample images for a healthy being [8]

IV. PROPOSED METHODOLOGY

The proposed technique uses T1-weighted, T2-weighted and FLAIR MRI reports of earlier diagnosed patients with PD and healthy controls for training and optimizing deep learning models. The models are trained using a large dataset of MR images and are optimized to accurately predict the dopamine status, nigral changes, present of white matter lesions around basal ganglia for suspected PD patients.

Fig. 4 Describes the complete process flow of the proposed methodology that is divided into four steps to detect the Parkinson's disease. MRI scan image from Kaggle data to give input to the model and preprocessing of data is discussed in section **Error! Reference source not found.** 2D convolutional neural network and result and evaluation is going to be discussed in the following section.

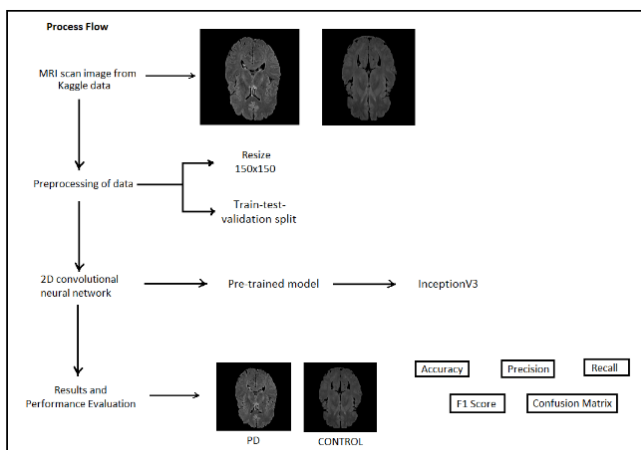


Fig. 4. Complete workflow of the proposed study

A. Convolutional Neural Network Architecture

In CNN architecture, there are three layers [32] has to be built for feature learning. Those layers are convolutional layer that is the interior most building block of the network followed

by max pooling layer for dimension reduction of feature maps and the fully-connected layer at the end is used for classification. The follow up of CNN architecture has been shown in Fig. 5.

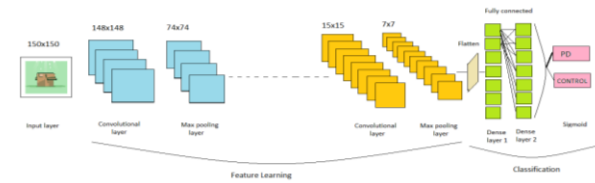


Fig. 5. Follow up structure of CNN layers

In this study, we used FLAIR and T1 and T2 weighted MRI samples to train a 2D convolutional neural network (CNN) for determining Parkinson's disease. With the exception of the input layer, the built-in CNN network architecture depicted in Fig. 6 contains a total of 12 layers. Four 2D convolutional layers make up the model's feature representation of the input images. If any pixels protrude outside of the window, valid padding has been applied to cover them all or to remove the black border. The ReLU activation function supports each layer, and the max-pooling layer is used to down-sample the feature maps. A flattened layer is then built to transmit the feature maps to a fully linked layer after the feature learning is finished. One neuron and the sigmoid activation function are used to further feed the dense layer's output to the output dense layer, which produces a

single output that can be either a PD or a control.

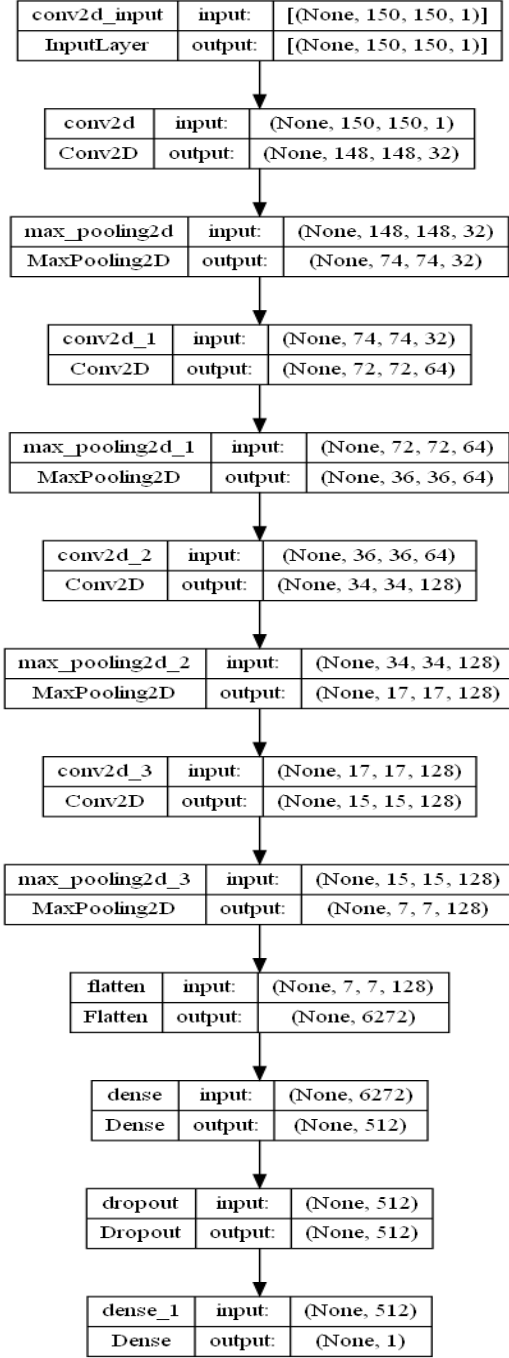


Fig. 6. 2D convolutional neural network architecture

B. InceptionV3

InceptionV3 [17] is a technique of ImageNet Large Scale Visual Recognition Challenge [33] used for transfer learning [34]. It is an optimized genre of the original Inception V1 model that features several improvements, including deeper network architecture, higher efficiency, reduced computational cost, and the use of additional classifiers for regularization. The model has been improved by the use of auxiliary classifiers, factoring into smaller convolutions, spatial factorization into asymmetric convolutions, along with efficient grid size reduction.. With 42 layers, Inception networks have a more efficient use of computation resources than its predecessors [35] as they have fewer parameters and require less memory and other resources, which allows them

to achieve better accuracy. Fig.7 depicts the InceptionV3 model's architecture..

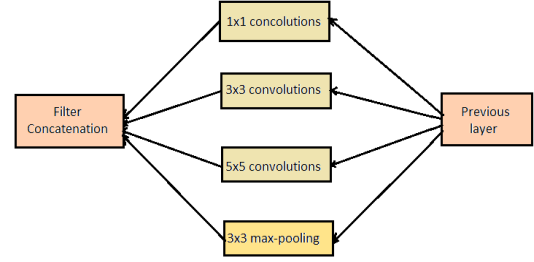


Fig. 7. Architecture of InceptionV3 model

C. Optimization and Model Fitting

An optimizer is basically an algorithm that is used in the training of dataset for parameters adjustment (weights and biases) to minimize the loss function [36]. Optimizing the training process in deep learning models is crucial. The optimizer function's hyperparameters control this process and aim to minimize validation and testing errors. To achieve this, hyperparameters outside the main model must be tuned to produce optimal internal parameters (weights and biases). However, the challenge lies in selecting hyperparameters in a model-specific manner to increase the model's generalizability on unseen data. Therefore, we have used Root Mean Square propagation (RMSProp) optimizer in our model.

RMSProp is an extension of the RProp (Resilient Propagation) and unpublished algorithm [37]. RProp requires the computation of the gradient for the entire dataset at each iteration, which can be computationally expensive. RMSProp addresses these issues by controlling the influence of past gradients on the learning rate, which is used to normalize the gradient during the update. In this algorithm, the gradient gets divided by the moving average square root of the squared gradient, which helps to keep the learning rate robust and stable regardless of the scale of the gradients [36].

Previously, we used Stochastic Gradient Descent (SGD) [38] optimizer and Adam optimizer through which we got the accuracy rate of 78.6% and 89.48% respectively. However, by using RMSProp optimizer with learning rate of 0.001, accuracy was increased by 20.5% which was 95%. Till date, the usage of RMSProp is extremely less than others which is 0.0003 in proportion of studies [39]. Therefore, the main motivation behind RMSprop is that the number of function evaluations required to reach the local minima is decreased by the algorithm and the optimization process is improved to achieve a balance between the fitness of RPPROP and the competency of mini-batch updates.

$$v(w, t) := \gamma v(w, t - 1) + (1 - \gamma)(\nabla Q_i(w))^2 \quad (1)$$

In (1), gamma is the neglecting factor, and weights are updated by the below formula in (2)

$$w := w - \frac{\eta}{\sqrt{v(w, t)}} \nabla Q_i(w) \quad (2)$$

where $\sqrt{v(w, t)}$ is the moving average of squared gradients, $\nabla Q_i(w)$ is a gradient of the cost function with respect to the weight w , η is the learning rate, and γ is the moving average parameter

Another very crucial part is loss functions in deep learning models. These models estimate the difference between the

forecast value (\hat{y}) and the real value (y) using the mean squared error estimation and help to increase the model's accuracy by reducing the loss. The output of a loss function is a non-negative value calculated by using below (3).

$$MSE = \frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{n} \quad (3)$$

The categorization in this study is for two categories: PD and control, hence a binary cross-entropy loss function was applied. Each prediction and the actual value are compared to get a loss score in the binary cross-entropy loss. The loss score is a logarithmic measure that punishes the projected likelihood. This indicates that while smaller variations between the predicted and true value result in a smaller penalty, larger disparities result in a larger penalty [46].

V. RESULT

The built model demonstrated satisfactory outcomes in the classification of Parkinson's disease from MR images, with an average recall and precision of 1.00 and 0.95 respectively, and an accuracy score of 0.95. We observed that the highest accuracy is attained by using the RMSProp optimizer which is 95% in the evaluation of test data. Table 4 shows the classification report of the preferred optimized model.

TABLE 4: CLASSIFICATION REPORT

	<i>Precision</i>	<i>Recall</i>	<i>F1-score</i>
<i>Control</i>	0.95	1.00	0.97
<i>PD</i>	1.00	0.44	0.61
<i>Accuracy</i>	-	-	0.95
<i>Macro Average</i>	0.98	0.72	0.79
<i>Weighted Average</i>	0.96	0.95	0.94

Variance in accuracy and the loss function while training the model can be seen in Fig. 8 which depicts that the accuracy is continuously increasing and the loss function is decreasing as well.

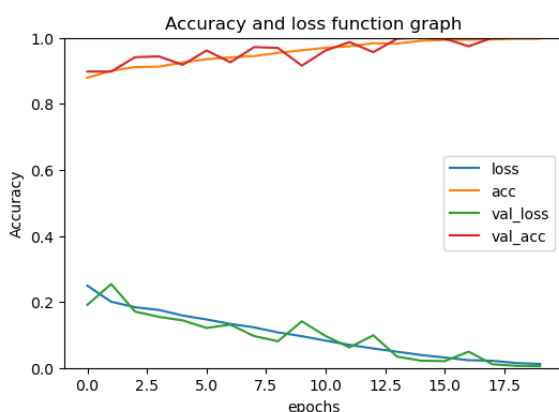
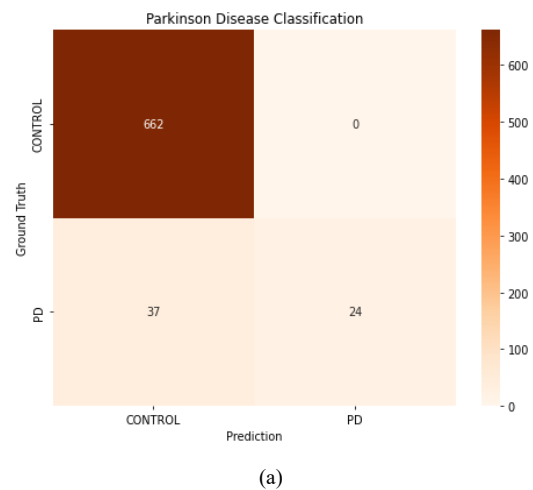


Fig. 8. Accuracy and loss function depiction

Fig. 9 represents the confusion matrix that was produced using the results obtained from the model.

Overall, the study highlights the results from deep learning models on a very large data set to detect Parkinson's disease

from T1, T2-weighted, and FLAIR MR images and the results from different optimizers on the same dataset.



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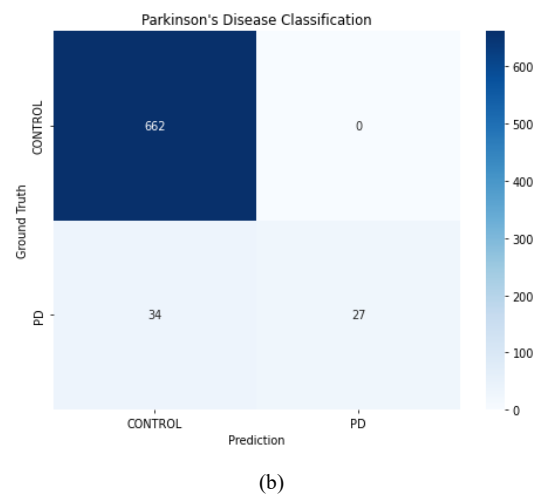


Fig. 9. Confusion matrix depicting the predicted results using 2D CNN (a) and inceptionV3 (b)

VI. CONCLUSION

This research study has presented an analysis on the potential and feasibility of monitoring the T1 and T2 weighted and FLAIR MRI scan analysis for detecting PD by observing 'silent strokes' areas around or in basal ganglia or the structural changes and presence of white matter lesions due to which neurological dopamine losses. Our focus was on classifying the MRI reports of PD patients in comparison of healthy patients. We used the InceptionV3 from transfer learning as pre-trained model to classify the image data objects. The trained model is then applied to predict the status of test images. If 'silent strokes' or structural changes are detected by the system, the suspected patients are classified into the PD category and are recommended to consult with a trained neurologist for further diagnosis. The system can be re-trained if necessary, using re-diagnosed reports.

In conclusion, early diagnosis seems a positive sign and gives confidence to fight against the disease. Practically, seemingly modest research steps for cure are required. Researchers have a vast area of opportunity for further investigation into the creation of novel architectures that can

effectively detect Parkinson's Disease using 3D CNN and RNN. After seeing the encouraging results, the focus of future work is on investigation of further study which will include examination of specific sub cortical structures and the refinement of more efficient detection architectures.

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