

A Transfer Learning Approach with MobileNetV2 for Parkinson's Disease Detection using Hand-Drawings

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Abstract—Parkinson's disease is a condition that affects common human movements because of the brain's failing neurons. The primary cause of this disease is a deficiency of dopamine in the brain, which can also cause changes in blood pressure, eating difficulties, and disrupted sleep. For patients to receive proper treatment and to improve their health, it is essential to detect Parkinson's disease at an early stage, as there is currently no cure for the disease. To address this, our research focuses on using spiral and wave hand-drawings as a means of early detection. We developed a modified MobileNetV2 approach with deep learning to accurately predict Parkinson's disease using these drawings. Our approach achieved a high accuracy of 97.70%, with a low error rate of 2.30%, while using fewer parameters than other models. Our findings suggest that using hand-drawings as a diagnostic tool can greatly improve the accuracy of Parkinson's disease diagnosis.

Index Terms—Deep Learning, Modified MobileNetV2, Parkinson's Disease Detection, Transfer Learning.

I. INTRODUCTION

Parkinson's disease is a neurological disorder that affects movement and usually it is combined with a physical assessment, neurology tests, and medical records helps to make the diagnosis. Parkinson's disease individuals of more severe symptoms draw spirals at a slower pace with lesser pressure upon that pen [1]. Like an average starting age between 40 to 70 and just a maximum beginning age between 50 to 60, Parkinson's disease is the second-largest cause of neurodegenerative disease. It has increased in frequency worldwide between 1990 and 2016 [2]. Stationary stiffness, tonicity, delayed movements, poor balance, and many other functional impairment are common clinical signs of Parkinson's disease [3]. Despite the reality that neuropathological research has shown that a variety of non-motor symptoms, including digestive, smell, temperament, sleeping, and mental behaviour, can come before Parkinson's disease remain throughout the duration of its disease. Non-motor symptoms frequently lack consistency, which makes detecting early Parkinson's disease challenging. A few of the features for Parkinson's disease is shaking when at resting [4].

A neurological examination, diagnostic tests like a magnetic resonance imaging (MRI) or computed tomography (CT) scan,

and blood tests to check out all the other related diseases that could be causing similar symptoms. In some cases, a doctor may also prescribe medication to observe how the patient responds, which can help confirm a Parkinson's diagnosis [5].

The disease has five distinct stages and is progressive. Parkinson's disease cannot be diagnosed with a specific, conclusive test, but a doctor or neurologist may use various methods to evaluate symptoms, such as tremors, stiffness, slowness of movement, and balance problems.

Phase 1: Minor symptoms, such as trembling and problems moving just on one part of the body, which normally will not affect everyday living.

Phase 2: This condition worsens, having stiffness as well as trembling increasingly affecting two sides of the human body. Everyday activities get difficult.

Phase 3: Imbalance and unsteadiness, involving regular and frequent falls.

Phase 4: Painful and constricting symptoms. This same patient cannot live alone and requires assistance to complete everyday tasks.

Phase 5: It is extremely difficult to stand or walk. Very importantly wheelchair-bound, because the patient can possibly have delusions.

This research's main contribution is stated as follows:

- i. A new architecture for the proposed model has been created by incorporating 5 additional layers into the standard MobileNetV2 (MNV2) model, resulting in Modified MobileNetV2 (MMNV2) model.
- ii. Our suggested method is developed for classification and detection of healthy and Parkinson's disease.
- iii. A novel design has been created to increase the accuracy of detecting Parkinson's disease, which is achieved by utilizing fewer parameters.

In this study, the designed MMNV2 model is a modified version of the MNV2 model [6]. Our MMNV2 model uses significantly less parameters and achieves high accuracy compared to the standard MNV2 model [7].

The main goal of this study is to use the MMNV2 model to identify differences between Parkinson's disease patients and healthy people. Detailed further information is provided in the following sections. The relevant work is described in Section II. The advantages of using MMNV2 over the original MNV2 model design is discussed in Section III. Section IV explains about dataset and data augmentation technique implemented in this work. Section V explains healthy and Parkinson's disease detection by utilizing the MMNV2. In Section VI description is included the efficiency of the model's performance by using confusion matrix and several other parameters. Further, the healthy and Parkinson's disease detection accuracy and results were discussed. Finally, the paper's conclusion is presented in Section VII.

II. RELATED WORK

Two separate convolutional neural networks (CNNs) methodologies were developed to detect the drawing patterns of the spiral as well as wave designs [8]. A machine learning (ML) approach is developed for automated diagnosis of Parkinson's disease. To evaluate all unprocessed signals of several sensors in a device connected to a pen and extract relevant details, like shakes as well as hand movement, to clinically diagnose the patient [9]. CNN and hyper-sinh were utilized to help in earlier Parkinson's disease identification by differentiating pathophysiological patterns to maximize the classification performance of input features retrieved from spiral diagrams [10]. Deep convolutional neural network (DCNN) such as ConvNet is created, using four convolutional layers along with two fully connected (FC) layers to identify spiral drawing's of Parkinson's disease during an initial stage. These convolution layers and also pooling layers inside a ConvNet helps to extract and evaluate a given image's features [11].

CNN's deep learning approach combined random forest (RF), k-nearest neighbor (KNN) and support vector machine (SVM), in order to automatically detect sinusoidal and spiral handwriting pattern movement in individuals with Parkinson's disease [12]. SVM, RF, AdaBoost, and XGBoost four classifiers mechanism has been developed for investigating various kinematic parameters acquired out of handwritten spirals for Parkinson's disease detection [13]. A machine learning approach designed that includes the use of techniques like KNN, RF, SVM, Naive Bayes, and multi-layer perceptron. These help in the performance of several classifiers that utilize speech utterances, kinematic, and pen-based features to identify Parkinson's disease [14]. CNN and long-short-term memories (LSTM) combinedly designed, and used as a hybrid model of ML and deep learning (DL). These techniques are utilized for prediction, for improving Parkinson's disease diagnosis and severity measurement [15]. Gaussian Naive Bayes technique is designed and applied for Parkinson's disease identification based using handwritten drawings, to prevent bias in the built model [16]. A CNN methodology is created for detection from drawing activities of Parkinson's disease to be discovered early. The most effective categorization approach for various kinds of drawings, including

spiral, curve, and wave data collected from both patients and healthy individuals [17]. A continuous convolution network (CC-Net) approach was developed for minimizing a pooling layer for extracting a variety of features from hand-drawn images indicating Parkinson's disease as well as improving image data preservation [18].

A statistical test along with the SVM classifier model is combined utilizing online handwriting signals for digital analysis to find Parkinson's disease, a novel non-invasive and economical technique has been developed. Secondly, two graphical representations of such variability rate were created from the dynamic handwriting signals, which have been utilized to assess the variation level of handwritten signals [19]. A deep learning-based model on different diagnostic approaches is designed to identify Parkinson's disease and to solve associated diagnostic problems [20]. A prototype machine-learning strategy is used to monitor the disease by logistic regression and an SVM classifier on different evaluations of static and dynamic drawings. Using a logical approach on time-series data obtained through a spiral drawing assessment, experiment based on digital tablets upon Parkinson's and healthy humans [21].

Dynamic handwriting evaluation has been created as a highly effective model, based on collecting data on materials, tasks, feature extraction, noninvasive, and inexpensive tools to accurately diagnose Parkinson's disease. In order to assist Parkinson's disease, the analysis of data among the most important research undertaken in the area of digital handwriting analysis is the final stage [22]. A CNN algorithm is developed through an improved performance for kinematics with 40% of the cross fold. With images and signals collected through a smart pen as well as a tablet, Parkinson's disease can often be detected in its beginning phases [23]. The fast Fourier transform (FFT) of recording frames is utilized by the signal methodology, together with a CNN for modeling. The hand-crafted method makes use of statistics computed through temporal signals processes, an RF classifier is utilized to identify Parkinson's disease [24]. DL technique with application of a genetic algorithm and the KNN approach, designed to pick the best features of Parkinson's disease early identification [25].

III. PROPOSED MODEL ARCHITECTURE

MobileNetV1 (MNV1) and MobileNetV2 (MNV2) are two different versions of a popular deep-learning architecture designed for efficient image classification on mobile and embedded devices. Both MNV1 and MNV2 are utilized for transfer learning due to their lightweight architecture and high accuracy on various computer vision applications. In transfer learning, MNV1 and MNV2 can be used as feature extractors, where the pre-trained weights are frozen, and a new classifier is trained on top of the extracted features. MNV1 was the first version of the MobileNet architecture and consists of depthwise separable convolutional layers that reduce the number of parameters while maintaining high accuracy. It has been widely used for image classification, object detection, and semantic segmentation tasks. In contrast, MNV2 builds upon

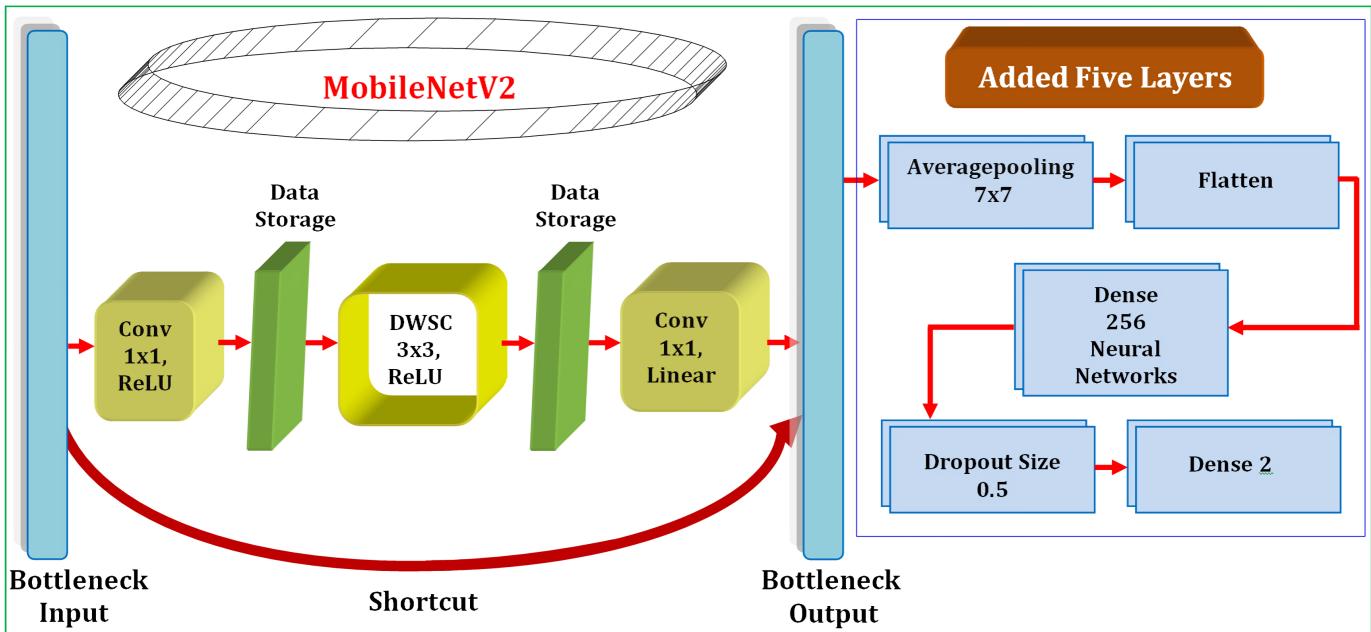


Fig. 1: MMNV2 Model Architecture

the original MobileNetV1 design and incorporates several enhancements, including the following:

Linear Bottleneck: This block consists of a 1×1 pointwise convolution, a depthwise convolution, and another 1×1 pointwise convolution. The first pointwise convolution reduces the number of input channels, while the last pointwise convolution increases the number of output channels. The depthwise convolution performs the main computation, and the linear bottleneck reduces the number of parameters and computational costs.

Inverted Residual Block: The inverted residual block is different from the traditional residual block used in other designs in that it increases the number of channels before decreasing them, which is how it obtained its name. Using additional nonlinearities while maintaining reduced computing costs allows MobileNetV2 to perform better despite using the same model size.

Additional layers have been incorporated into the pretrained architecture of the MobileNetV2 model [7], as illustrated in Fig. 1. These five layers were utilized for the purpose of transfer learning. This improved structure includes a 7×7 average pooling layer, followed by flattening, a layer containing a dense of 128 neural networks, a dropout size of 0.5, and ultimately dense_1 of 2.

IV. DATASET

K Scott Mader is the creator of a dataset of images that are related to healthy and Parkinson's disease, and this dataset can be found on Kaggle [26]. The collection of data consists of a total images of 204 that belong to two different classes. It was collected by 55 people, including 28 healthy individuals and 27 patients with Parkinson's disease. However, due to the limited availability of data, the dataset wasn't enough to

train the model for better classification. This lack of data is a widespread issue in deep learning applications, which can severely restrict the performance of the model. In order to overcome this difficulty, the training dataset's size has been artificially increased through the use of data augmentation.

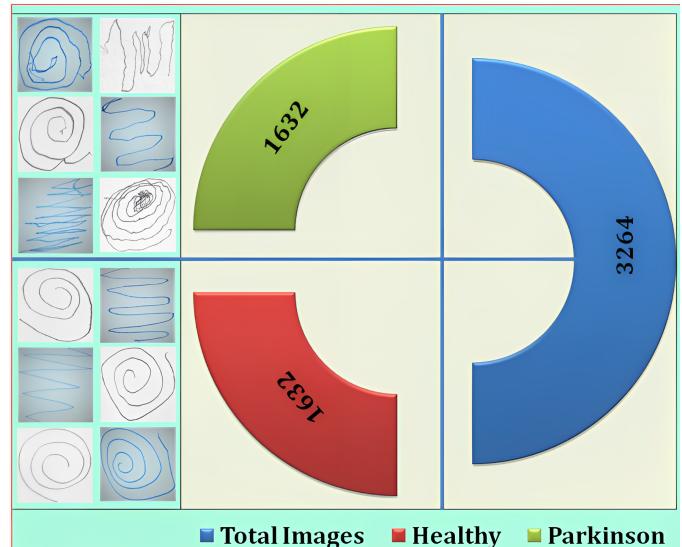


Fig. 2: Data Visualization

Data augmentation includes random translations, scaling, reversals, rotations, and other operations that preserve the label of the original image. In this work, the data is augmented by rotating 90° , 180° , 270° , flipping by 180° vertically, and then all converted to colour images in this work. Original images of 204 related to healthy and Parkinson's disease is increased to 3264 images and utilized for evaluating

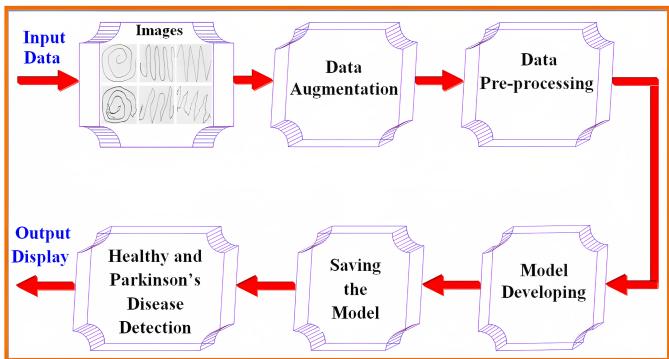


Fig. 3: Block Diagram

performance of suggested MMNV2 approach. Complete augmented data of our work is available in the Kaggle <https://www.kaggle.com/datasets/banilkumar20phd7071/handwritten-parkinsons-disease-augmented-data>. Our entire dataset is split to 2611 images, which consists 80% of the training data, as well as 653 images, which consists 20% of the testing data for classification. The suggested research work has 3264 images in total, as indicated in Fig. 2.

V. PROPOSED METHODOLOGY

Our MMNV2 approach was used in this study for identifying between cases of Parkinson's disease and those involving healthy people. To improve classification accuracy, significantly fewer model parameters are used in the assessment process. The suggested methodology's sequential process diagram is shown in Fig. 3.

To create a design of MMNV2, we started with the regular MNV2 model from the imangenet [27] as the base model. We then made modifications to the pretrained architecture of the MNV2 model by adding five additional layers. Our proposed MMNV2 model was created using a deep neural network (DNN) structure in order to identify between healthy and Parkinson's disease detection. The neural network is provided nonlinearity by applying a rectified linear activation unit (ReLU) activating function after each convolution layer. The convolution layer turns positive for linear or identity values and equals zero for all negative values as a result of the ReLU function. The input data is downloaded, then saved in a folder that can be easily accessed in the following sequence. Pre-processing involves importing all of the images from a folder as inputs and afterwards reshaping them to be used with MMNV2.

In order to pre-process those images, data is loaded and then transferred and turned into an array. These images are converted into a numerical python (NumPy) library that is used to work with values and speeds up calculations. Just before patterns are further analyzed, the classes 0 and 1 integer values for this image data have been determined using a label binarizer (LB). The images are divided into sets for testing and training in a later stage. Using ImageNet as a foundation model, the pre-trained MNV2 architecture is imported. Our

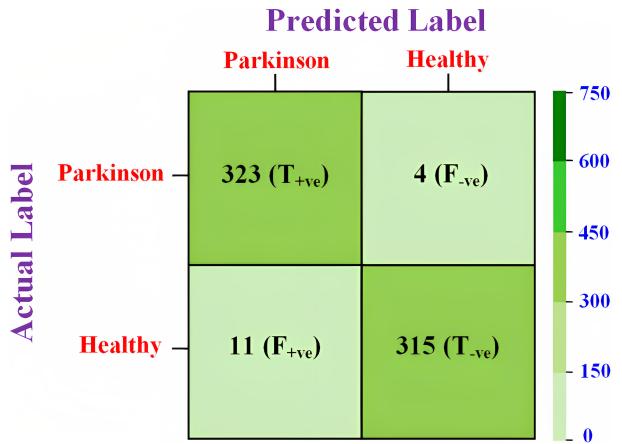


Fig. 4: MMNV2 confusion matrix

five layers for transfer learning were added after importing the transform method, as shown in Fig. 1. To add more layers, our approach involves creating an average pooling of 7×7 dimensions, flattening, utilizing dense neural networks consisting of 128, including a dropout of 0.5, and introducing a final layer named dense_1 of 2. The incorporation of these layers significantly increased the accuracy of MNV2. Creating an average value by means of the average pooling layer and also flattening into a single dimension. Dense layers utilizing activation functions like ReLU provide fully connected layers, where each output depends on each input. It is advantageous to include a dropout layer as well as two robust layers that provide binary classification to prevent overfitting. Multiple output neurons were present, thereby a softmax layer was utilized.

In order to avoid the loss of features that have been previously acquired, all primary layers were frozen. An additional set of trainable layers is constructed using the information obtained, and these layers are then utilized to identify possible features for identifying between healthy and Parkinson's disease detection. Once all weights have been saved, our design is then updated. With the help of this pre-trained technique, systems may benefit from bias weights while maintaining previously learned features without experiencing additional computational expenses. Our MMNV2 model is trained using 74 epochs, a learning rate of 0.001, and a batch size of 44. Afterward, an Adam optimizer is employed that calculates the gradient's initial and secondary moments to fine-tune the learning rate for all neural network weights. The DNN design utilized to analyze previously imported files in addition to importing the original MNV2 model that has been improved by adding parameters. Our model converts the test image's input data into a classification value using deep learning. Finally, the output results for the identification of both healthy and images with Parkinson's disease are shown in Fig. 7.

VI. RESULTS AND DISCUSSION

In machine learning, deep learning, and statistical analysis, a confusion matrix is a useful tool for evaluating the perfor-

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jupyter B.Anil Kumar(20PHD7071) - Parkinson Disease Detection Last Checkpoint: 5 minutes ago (autosaved)
File Edit View Insert Cell Kernel Widgets Help Trusted Python 3 [ipykernel] o
In [29]: predict_model.predict(X,batch_size=85)
predict_no.argmax(predict,axis=1)
print(classification_report(test_V.argmax(axis=1),predict,target_names=lb.classes_))

15/15 [=====] - 8s 473ms/step - precision: recall: f1-score: support:
          Dataset/Healthy      0.97      0.97      0.97      327
          Dataset/Parkinson     0.97      0.97      0.97      326
accuracy                           0.97
macro avg       0.97      0.97      0.97      653
weighted avg    0.97      0.97      0.97      653

In [30]: predict=(predict>0.5)
predict=np.argmax(predict,test_X)
predict_no.argmax(predict,axis=1)
test_V.argmax(test_V,axis=1)
cnf=ConfusionMatrix(test_V,predict)
print(cnf)

21/21 [=====] - 8s 354ms/step
[[323  4]
 [ 11 315]]

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Fig. 5: Python code run on jupyter notebook of MMNV2

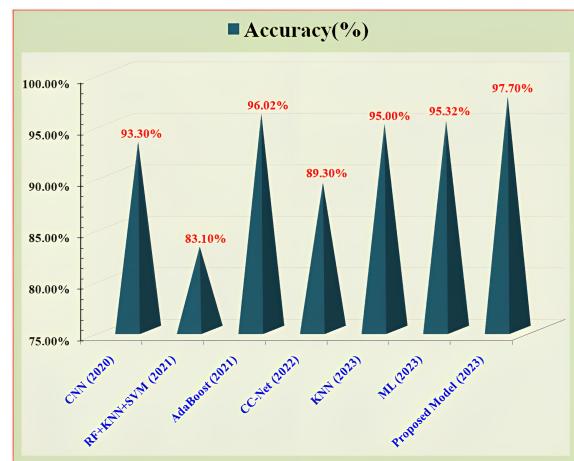
mance of a classification model [28]. The matrix shows the predicted and actual classes of a dataset, and the four possible outcomes are true positive (T_{+ve}), true negative (T_{-ve}), false positive (F_{+ve}), and false negative (F_{-ve}). The confusion matrices for the obtained values of suggested MMNV2 model are displayed in Fig. 4.

TABLE I: Accuracy and error rate of several models comparison

Sl.No.	Model Name	Year	Dataset	Accuracy (%)	Error rate (%)
1	CNN [8]	2020	204	93.30	6.70
2	RF+KNN+SVM [12]	2021	960	83.10	16.90
3	AdaBoost [13]	2021	80	96.02	3.98
4	CC-Net [18]	2022	166	89.30	10.70
5	KNN [25]	2023	119	95.00	5.00
6	ML [21]	2023	77	95.32	4.68
7	MMNV2	2023	3264	97.70	2.30

In a specific case for evaluating Parkinson's disease classification model, a true positive (T_{+ve}) occurs when both the actual and predicted classes are 'Parkinson's disease', and the value is 323. A true negative (T_{-ve}) occurs when both the actual and predicted classes are 'healthy,' and the value is 315. A false positive (F_{+ve}) occurs when the predicted class is 'Parkinson's disease', but the actual class is 'healthy', with a value of 11. Lastly, a false negative (F_{-ve}) occurs when the anticipated category is "healthy" yet the real category is "Parkinson's disease," with a value of 4. The cells within the matrix display the count of accurately or inaccurately classified instances for each class.

For evaluating the effectiveness of classification model using data in the confusion matrix, various metrics can be computed. Metrics such as f1-score, recall, precision, accuracy, and error rate are commonly used. While precision, recall, and f1-score are suitable for unbalanced datasets. In contrast, a balanced dataset is used in this study, which is why accuracy and error rate are employed to assess how well the suggested disease-classifying model performs. Equation (1) as well as (2) are used to compute accuracy and error rate, respectively. After dividing the total number of occurrences by the sum of true positive as well as true negative predictions, accuracy is determined. The sum of false positive and false negative



(a) Accuracy graph



(b) Error rate graph

Fig. 6: Comparison of graphs for several models

predictions is then divided by the total number of occurrences to determine the error rate.

$$\text{Accuracy} = \frac{T_{+ve} + T_{-ve}}{T_{+ve} + F_{+ve} + F_{-ve} + T_{-ve}} = 97.70\% \quad (1)$$

$$\text{Error rate} = \frac{F_{+ve} + F_{-ve}}{T_{+ve} + F_{+ve} + F_{-ve} + T_{-ve}} = 2.30\% \quad (2)$$

The utilization of the jupyter notebook platform of MMNV2 has facilitated the implementation of Python code. Where after the completion of training and testing of our suggested MMNV2, the achieved precision, recall, and f1-score values can be seen in Fig. 5.

A total of six existing work results related to two classes, such as Parkinson's disease and healthy are compared with our proposed MMNV2. Our obtained results in terms of accuracy and the error rate of the utilized dataset of 3264 images are compared with previous works carried on the different datasets

and obtained results of CNN, RF+KNN+SVM, AdaBoost, CC-Net, KNN, ML is shown in Table I.

The Table I and Fig. 6(a) and Fig. 6(b) results demonstrate that our MMNV2 approach has a better performance compared to previous methods. According to study results, this paper shows that the proposed MMNV2 model can diagnose Parkinson's disease with more accuracy and utilizes less parameters and error rates than the existing models.

An illustration of the category results for healthy individuals is displayed in Fig. 7(a) to Fig. 7(f). Parkinson's disease is illustrated in Fig. 7(g) to Fig. 7(l).

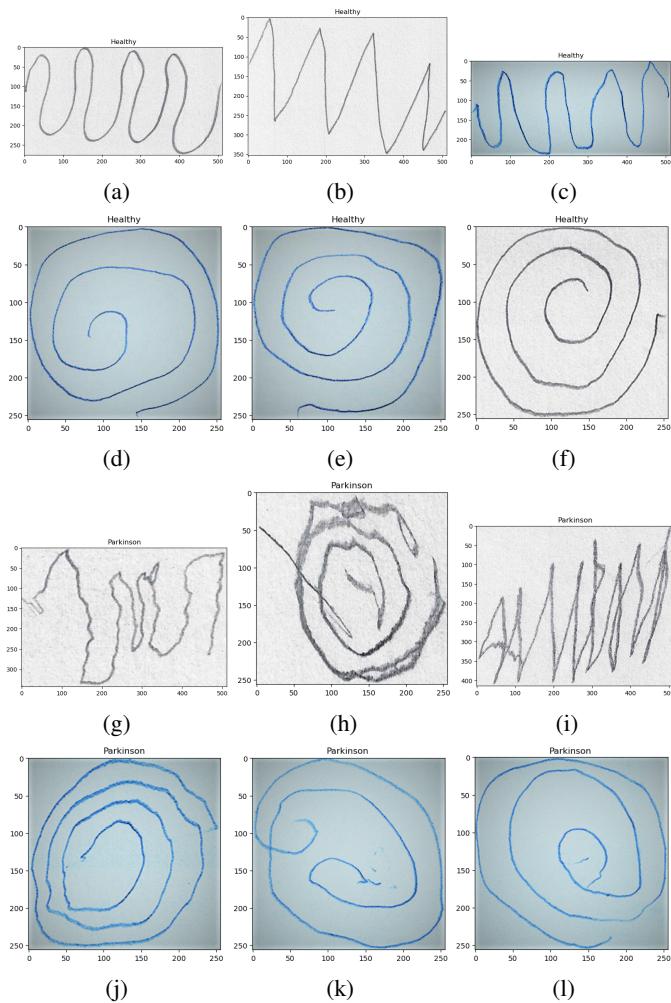


Fig. 7: Output result of Parkinson's disease detection

VII. CONCLUSION

The approach presented in this study has been implemented on a balanced dataset. The feature extraction was based on a transfer learning strategy that allowed for the classification and detection of hand-drawings of spiral and wave related to Parkinson's and healthy individuals on images. Research has also shown that creative activities, such as drawing, can have therapeutic benefits for people with Parkinson's disease. Art therapy can help alleviate symptoms such as depression

and anxiety, and it can also provide a sense of accomplishment and self-expression. In conclusion, while Parkinson's disease can make hand drawing more difficult, it does not have to prevent people from enjoying the benefits of artistic expression. Through adaptation, perseverance, and creativity, individuals with Parkinson's can continue to create beautiful and meaningful works of art. The MMNV2 approach in this paper has worked effectively, by a prediction accuracy with 97.70% and the error rate of 2.30%. Additionally, our model's effectiveness is assessed by utilizing its accuracy, error rate, and parameter use.

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