CHAPTER 1

INTRODUCTION

Parkinson's Disease (PD) is a neurodegenerative disease more commonly observed in the elderly. Almost 1% of the world population suffer from PD of whom many cases present with complicated motor and cognitive issues. Over the course of the disease progression, cognitive and behavioral symptoms including a wide variety of personality changes, depressive disorders, memory dysfunction and emotion dysregulation may emerge. Moreover, movement symptoms get worse as the disease progresses. Dementia should be diagnosed at an early stage so that appropriate therapeutic interventions can be used to prevent cognitive deterioration.

In routine practice, clinicians diagnose PD based on the presenting symptoms including slowness, stiffness, tremor, and balance/coordination difficulties. Yet, such symptoms and their progression rate may differ case by case. Currently, there seems to be no specific blood test or biomarker to accurately diagnose PD or monitor underlying changes as the condition escalates.

Over the last three decades, MRI (magnetic resonance imaging) has been used as a tool to diagnose and differentiate various neurological diseases from suspected PD.

Researchers have found that changes in disease progression can be detected by brain MRI under a special protocol. Such neuroimaging modalities could be utilized in clinical trials, as an objective way to monitor the effectiveness of treatments.

With reference to the use of Convolutional Neural Networks (CNNs) in image processing, there appear to be new horizons to provide a comprehensive approach towards a wide variety of applications such as image recognition, segmentation, and retrieval. This new paradigm has created exceptional results over the recent years in terms of analyzing the content of images, speech and videos. Many studies have shown that the presenting state-of-the-art CNNs retains accuracies that surpass human-level performance.

Moreover, feature representation has been one of the most important factors in medical image processing. Deep learning methods such as CNN extracts and uses new and hidden features which would not be considered by traditional machine learning methods

CHAPTER 2

LITERATURE REVIEW

2.1 Machine Learning for the Diagnosis of Parkinson's Disease

Diagnosis of Parkinson's disease (PD) is commonly based on medical observations and assessment of clinical signs, including the characterization of a variety of motor symptoms. However, traditional diagnostic approaches may suffer from subjectivity as they rely on the evaluation of movements that are sometimes subtle to human eyes and therefore difficult to classify, leading to possible misclassification. In the meantime, early non-motor symptoms of PD may be mild and can be caused by many other conditions. Therefore, these symptoms are often overlooked, making diagnosis of PD at an early stage challenging. To address these difficulties and to refine the diagnosis and assessment procedures of PD, machine learning methods have been implemented for the classification of PD and healthy controls or patients with similar clinical presentations (e.g., movement disorders or other Parkinsonian syndromes). To provide a comprehensive overview of data modalities and machine learning methods that have been used in the diagnosis and differential diagnosis of PD, in this study, we conducted a literature review of studies published until February 14, 2020, using the PubMed and IEEE Xplore databases. A total of 209 studies were included, extracted for relevant information and presented in this review, with an investigation of their aims, sources of data, types of data, machine learning methods and associated outcomes. These studies demonstrate a high potential for adaptation of machine learning methods and novel biomarkers in clinical decision making, leading to increasingly systematic, informed diagnosis of PD.

2.2 Prediction of Parkinson's Disease using Machine Learning and Deep Transfer Learning from different Feature Sets

Precursors that appear diminutive hold a world of significance with regard to indicating and diagnosing premature stages of degenerative diseases, especially neurologically concerned ailments like Parkinson's disease (PD). PD usually shows symptoms like spasm in the limbs, jaw or head, rigidness of the limbs and trunk, sluggish movement, etc. and it is crucial to detect Parkinson Disease in early stages by keeping an eye out for these preliminary symptoms. In this paper, various datasets were researched, analyzed and run through certain algorithms to detect several symptoms. The Freezing of Gait dataset was used to predict if there were symptoms related to legs and trunk by analyzing the patient's gait, the Parkinson Clinical speech dataset to detect deviation in audio frequency and lastly the Parkinson Disease wave and spiral drawing dataset which can help find out impairment in writing due to a tremor in hand or arm. The detection of impairment in handwriting seems to be the most convenient method and Convolutional Neural Network using Transfer Learning is implemented on this image dataset.

2.3 Multi-modality machine learning predicting Parkinson’s disease

Personalized medicine promises individualized disease prediction and treatment. The convergence of machine learning (ML) and available multimodal data is key moving forward. We build upon previous work to deliver multimodal predictions of Parkinson’s disease (PD) risk and systematically develop a model using GenoML, an automated ML package, to make improved multi-omic predictions of PD, validated in an external cohort. We investigated top features, constructed hypothesis-free disease-relevant networks, and investigated drug–gene interactions. We performed automated ML on multimodal data from the Parkinson’s progression marker initiative (PPMI). After selecting the best performing algorithm, all PPMI data was used to tune the selected model. The model was validated in the Parkinson’s Disease Biomarker Program (PDBP) dataset. Our initial model showed an area under the curve (AUC) of 89.72% for the diagnosis of PD. The tuned model was then tested for validation on external data (PDBP, AUC 85.03%). Optimizing thresholds for classification increased the diagnosis prediction accuracy and other metrics. Finally, networks were built to identify gene communities specific to PD. Combining data modalities outperforms the single biomarker paradigm. UPSIT and PRS contributed most to the predictive power of the model, but the accuracy of these are supplemented by many smaller effect transcripts and risk SNPs. Our model is best suited to identifying large groups of individuals to monitor within a health registry or biobank to prioritize for further testing.

2.4 Prediction of Parkinson’s Disease using Machine Learning Techniques on Speech dataset

In the present decade of accelerated advances in Medical Sciences, most studies fail to lay focus on ageing diseases. These are diseases that display their symptoms at a much advanced stage and makes a complete recovery almost improbable. Parkinson’s disease (PD) is the second most commonly diagnosed neurodegenerative disorder of the brain. One could argue, that it is almost incurable and inflicts a lot of pain on the patients. All these make it quite clear that there is an oncoming need for efficient, dependable and expandable diagnosis of Parkinson’s disease. A dilemma of this intensity requires the automating of the diagnosis to lead accurate and reliable results. It has been observed that most PD Patients demonstrate some sort of impairment in speech or speech dysphonia, which makes speech measurements and indicators one of the most important aspects in prediction of PD. The aim of this work is to compare various machine learning models in the successful prediction of the severity of Parkinson’s disease and develop an effective and accurate model in order to help diagnose the disease accurately at an earlier stage which could in turn help the doctors to assist in the cure and recovery of PD Patients. For the aforementioned purpose we plan on using the Parkinson’s Tele monitoring dataset which was acquired from the UCIML repository.

2.5 Parkinson's Disease Prediction Using Machine Learning Approaches

Valued Radial Basis Function network (FCRBF), Meta-Cognitive Fully Complex-Valued Radial Basis Function network (Mc-FCRBF) and Extreme Learning Machine (ELM) for the prediction of Parkinson's disease. With the help of Unified Parkinson's Disease Rating Scale (UPDRS), the severity of the Parkinson's disease is predicted and for untreated patients, the UPDRS scale spans the range (0-176). The FC-RBF network uses a fully complex valued activation function . The performance of the complex RBF network depends on the number of neurons and initialization of network parameters. The implementation of the self-regulatory learning mechanism in the FC-RBF network results in Mc-FCRBF network. It has two components: a cognitive component and a meta-cognitive component. The meta-cognitive component decides how to learn, what to learn and when to learn based on the knowledge acquired by the FC-RBF network. Extreme learning mechanism uses sigmoid activation function and it works with fast speed. In ELM network, the real valued inputs and targets are applied to the network. The result indicates that the Mc-FCRBF network has good prediction accuracy than ELM and FC-RBF network.

2.6 Early Prediction Of Parkinson disease using Machine Learning and deep learning Approaches

Parkinson disease(PD), the second most common neurological disorder that causes significant disability, reduces the quality of life and has no cure. Nerve cells in this part of the brain are responsible for producing a chemical called dopamine. Dopamine acts as a message between the parts of the brain and nervous system that help control and co-ordinate body movements. As dopamine generally neurons in the parts begin to experience difficulty in speaking, writing, walking or completing other simple task.Approximately,90% affected people with Parkinson have speech disorders. The average age of onset is about 70years,andthe incidence rises significantly with advancing age. However, a small percent of people with PD have “early-onset” disease that begins before the age of 50.More than 10 million people worldwide are living with PD. No cure for PD exists today, but research is ongoing and medications or surgery can often provide substantial improvement with motor symptoms. Parkinson disease is one of the most serious diseases. Hence diagnosing it at an earlier stage could help prevent or reduce the effects.

The machine learning classification algorithms are used to predict if a person has Parkinson disease or not, comparing different machine learning algorithm such as logistic regression, decision tree, k-nearest neighbour as well as some “Ensemble” learning techniques where we attempt to improve the accuracy by combining several models. The machine learning model can be implemented to significantly improve diagnosis method of Parkinson disease

CHAPTER – 3
SYSTEM SPECIFICATION

3.1.HARDWARE SPECIFICATION

PROCESSOR	:	Minimum 2.2GHz
HARD DRIVE	:	4 GB
RAM	:	256 MB
MONITOR	:	15’’ Color Monitor
KEYBOARD	:	104 Keys Standard Keyboard
MOUSE	:	Standard 3 Button Mouse
O.SYSTEM	:	Windows 7/8/10/11

3.2.SOFTWARE SPECIFICATION

TOOL	:	MATLAB
FRAMEWORK	:	MATLAB

CHAPTER 4
METHODOLOGY

4.1 Existing System

It is important to predict clinical tasks for health base systems. Recently, a wide range of speech signal processing algorithms (dysponia measures) aiming to predict PD symptom severity usingspeech signals have been introduced. There have been several studies reported focusing on the diagnosis of Parkinson disease. It present an assessment of measures for the identity of PD subjects from healthy by detecting dysphonia. They diagnosed 23 PD and 8 healthy people and their dataset recorded vowels and used a Support Vector Machine (SVM) for classification and achieved classification accuracy 91.4 %

4.2 Drawbacks:

1. SVM: It does not execute very well when the data set has more sound i.e. target classes are overlapping. In cases where the number of properties for each data point outstrips the number of training data specimens, the support vector machine will underperform.
2. Less Accuracy

4.3 Proposed Methodology

The proposed methodology towards predicting the severity of PD was based on deep learning. At first, the PD patients' MRI data were collected and data are subsequently underwent pre-processing. In the next step, deep neural networks were designed with an input layer, hidden layers and an output layer.

FLOW CHART

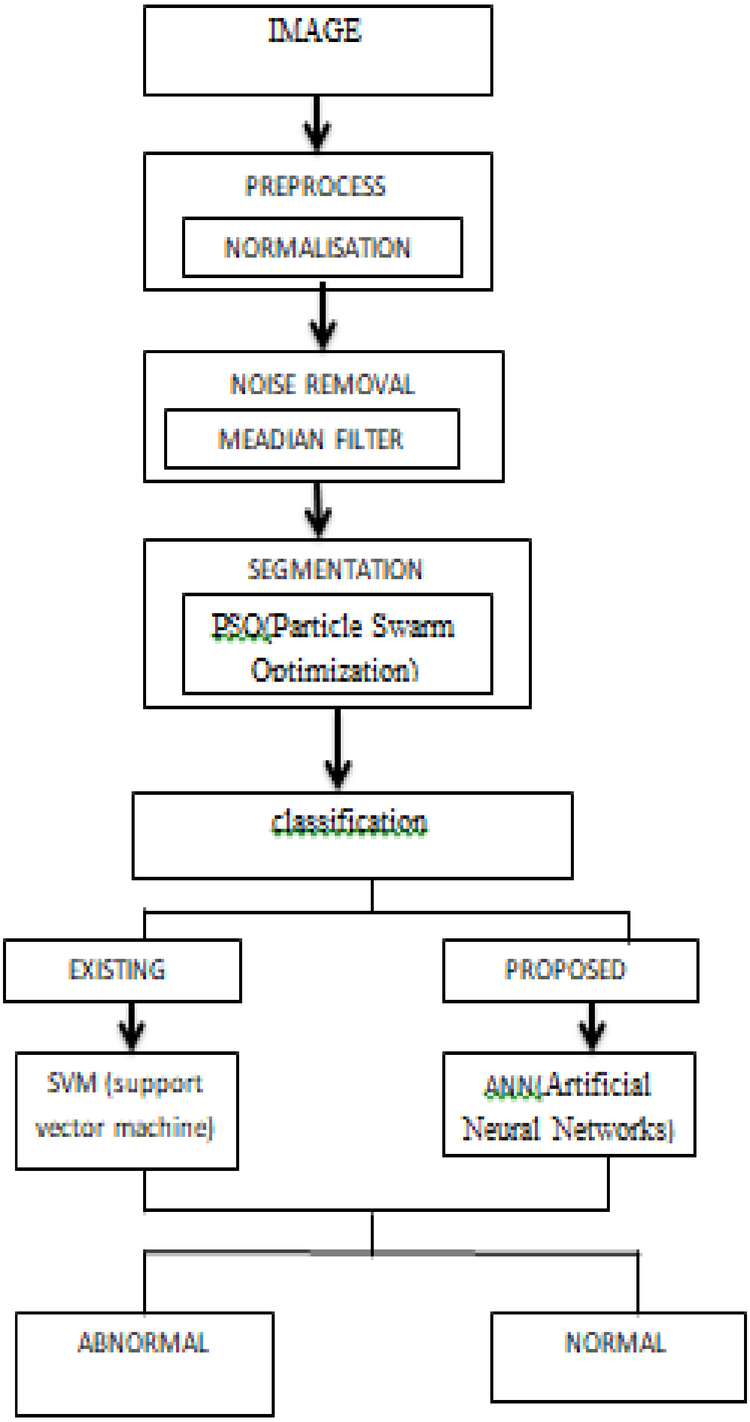


IMAGE
PREPROCESS
NORMALISATION
NOISE REMOVAL
MEADIAN FILTER
SEGMENTATION
PSO(Particle Swarm Optimization)
classification
EXISTING
PROPOSED
SVM (support vector machine)
ANN(Artificial Neural Networks)
ABNORMAL
NORMAL

4.4 MODULES

4.4.1 IMAGE ACQUISITION

Image Acquisition is a process of getting an input image for the process of automatic detection of normal and abnormal using Digital Image Processing.

4.4.2PRE PROCESSING

Pre-processing is a common name for operations with images at the lowest level of abstraction both input and output are intensity images. The aim of pre-.processing is an improvement of the image data that suppresses unwanted distortions or enhances some image features important for further processing.

4.4.3 NOISE REMOVAL USING MEDIAN FILTER

The median filter is a nonlinear digital filtering technique, often used to remove noise from an image or signal. Such noise reduction is a typical pre-processing step to improve the results of later processing (for example, edge detection on an image). Median filtering is very widely used in digital image processing because, under certain conditions, it preserves edges while removing noise (but see discussion below), also having applications in signal processing. The main idea of the median filter is to run through the signal entry by entry, replacing each entry with the median of neighboring entries.

4.4.3SEGMENTATION

In computer vision, image segmentation is the process of partitioning a digital image into multiple segments (sets of pixels, also known as super-pixels). The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze. Image segmentation is typically used to locate objects and boundaries (lines, curves, etc.) in images. More precisely, image segmentation is the process of assigning a label to every pixel in an image such that pixels with the same label share certain characteristics.

4.4.5 FUZZY WITH PSO

The proposed method, named FPSOFCM (Fuzzy Particle Swarm Optimization for FCM) uses the FPSO algorithm to get the initial cluster centers of FCM according to a new fitness function which combines fuzzy cluster validity indices. Image segmentation is an important task in image processing and computer vision applications.

4.4.6. FUZZY C-MEANS ALGORITHM

FCM algorithm and cluster validity indices The FCM algorithm assigns pixels to each category by using fuzzy memberships.

1. Particle swarm optimization (PSO)

The PSO is a population-based stochastic method inspired by bird flocking and fish schooling to find optimal or near-optimal solutions. It was first introduced in 1995 by social-psychologist Eberhart and electrical engineer Kennedy . In very short time the PSO has made the great progress and has been used in many fields of engineering optimization.

2. Standard PSO algorithm

The PSO algorithm starts with a population of particles. Each particle i consists of potential solutions called positions X, and velocities V and maintains the following information

xi, the current position of the particle.

vi, the current velocity of the particle.

yi, the personal best position of the particle (pbest); the best position visited so far by the particle.

y , the global best position of the swarm (gbest); the best position visited so far by the entire swarm.

In each iteration t, the performance of each particle i is measured using a predefined fitness function f. The personal best position (pbest) is obtained as follows

3 Fuzzy particle swarm optimization for fuzzy clustering

The FPSO algorithm was initially proposed by Pang et al to solve Traveling Salesman Problem (TSP).

In FPSO algorithm, X the position of particle, represents the fuzzy memberships of pixels In which uij is the membership function of the i-th pixel to the j-th cluster with constraints stated in Eq. 2. Therefore, the position matrix of each particle is similar to the fuzzy matrix U276 M. Semchedine, A. Moussaoui in FCM algorithm. Also, the velocity of each particle is stated using a matrix V with the size Nrows and c columns.

4.5. PROPOSED METHOD

In order to overcome the problem of random initialization of FCM, we propose a FCM segmentation algorithm based on FPSO. Firstly, the FPSO algorithm is used to minimize a new fitness function given in Eq.17 to get the initial cluster centers. Then, these centers are used as the initial seed of the FCM. We shall use the notation presented in table

Algorithm description In the proposed algorithm FPSOFCM, first, p particles are initialized. Each of particle positions represents a matrix U containing the membership function uij of the i-th pixel to the j-th cluster. In each of iterations, particles are displaced in the problem space with minimizing the fitness function parameterized by _ and _ parameters. In order to restrict the particles from moving too far beyond the search space, a technique called velocity clamping [37] is
used to limit the maximum velocity of each particle to the range[□vmax;+vmax]. After convergence of FPSO, the cluster centers Z corresponding to gbest solution which have been found by particles so far is considered as the input of FCM algorithm. Then, FCM is applied to segment the original image.

Algorithm 2 : FPSOFCM

1: input: original image

2: Fix the parameters.

3: Create a swarm with p particles: initialize randomly X and V

4: Initialize randomly cluster centers Z (c _ p matrix)

5: best-global-fitness

7: for t 1 to itermax do

8: Calculate the cluster centers Z for each particle

9: Calculate the fitness value Fitness of each particle

10: Update the best global fitness best-global-fitness

11: Calculate pbest and gbest

12: Update the velocity matrix V for each particle

13: Limit the velocity to the range [□vmax;+vmax]

14: Update the position matrix X

15: Normalize the position matrix

16: if

best-global-fitnesss(t) □ best-global-fitnesss(t□1)

< " then

17: break

18: end if

19: end for

20: FCM

21: Initialize cluster centers

22: for t 1 to itermax do

23: Update the membership function

24: Update the cluster centers

25: Compute the objective function

26: if

J(t)□J(t+1)

< " then

27: break

28: end if

29: end for

30: return U the membership degrees of each pixel to c clusters

31: Defuzzyfication of the partition matrix U

32: output: segmented image

4.6 FEATURE EXTRACTION

In machine learning, pattern recognition and in image processing, feature extraction starts from an initial set of measured data and builds derived values (features) intended to be informative and non-redundant, facilitating the subsequent learning and generalization steps, and in some cases leading to better human interpretations. Feature extraction is related to dimensionality reduction.

4.7 STATISTICAL FEATURES MEAN

For a data set, the arithmetic mean, also called the mathematical expectation or average, is the central value of a discrete set of numbers: specifically, the sum of the values divided by the number of values. The arithmetic mean of a set of numbers x_1, x_2, ..., x_n is typically denoted by, pronounced "*x* bar".

Standard Deviation

In statistics, the **standard deviation** (**SD**, also represented by the lower case Greek letter sigma **σ** or the Latin letter s) is a measure that is used to quantify the amount of variation or dispersion of a set of data values.[1] A low standard deviation indicates that the data points tend to be close to the mean (also called the expected value) of the set, while a high standard deviation indicates that the data points are spread out over a wider range of values.

4.8 VARIANCE

In probability theory and statistics, **variance** is the expectation of the squared deviation of a random variablefrom its mean. Informally, it measures how far a set of (random) numbers are spread out from their average value. Variance has a central role in statistics, where some ideas that use it include descriptive statistics,statistical inference, hypothesis testing, goodness of fit, and Monte Carlo sampling. Variance is an important tool in the sciences, where statistical analysis of data is common. The variance is the square of the standard deviation, the second central moment of a distribution, and the covariance of the random variable with itself.

4.9 GLCM FEATURE

The Gray Level Co-occurrence Matrix[1] (GLCM) and associated texture feature calculations are image analysis techniques. Given an image composed of pixels each with an intensity (a specific gray level), the GLCM is a tabulation of how often different combinations of gray levels co-occur in an image or image section. Texture feature calculations use the contents of the GLCM to give a measure of the variation in intensity (a.k.a. image texture) at the pixel of interest.

Echoview offers a GLCM Texture Feature operator that produces a virtual variable which represents a specified texture calculation on a single beam echogram.

The virtual variable is created in the following way (using the settings on the GLCM Texture page of the Variable properties dialog box identified in **bold**):

1. Quantize the image data. Each sample on the echogram is treated as a single image pixel and the value of the sample is the intensity of that pixel. These intensities are then further quantized into a specified number of discrete gray levels as specified under **Quantization**.
2. Create the GLCM. It will be a square matrix *N* x *N* in size where *N* is the **Number of levels** specified under **Quantization**. The matrix is created as follows:
    a. Let *s* be the sample under consideration for the calculation.
    b. Let *W* be the set of samples surrounding sample *s* which fall within a window centered upon sample s of the size specified under **Window Size**.
    c. Considering only the samples in the set *W*, define each element *i*,*j* of the GLCM as the number of times two samples of intensities *i* and *j* occur in specified **Spatial relationship** (where *i* and *j* are intensities between 0 and **Number of levels**-1)The sum of

all the elements *i*, *j* of the GLCM will be the total number of times the specified spatial relationship occurs in *W*.

d. Make the GLCM symmetric:

  i. Make a transposed copy of the GLCM

  ii. Add this copy to the GLCM itself

  This produces a symmetric matrix in which the relationship *i* to *j* is indistinguishable for the relationship *j* to *i* (for any two intensities *i* and *j*). As a consequence the sum of all the elements *i*, *j* of the GLCM will now be twice the total number of times the specified spatial relationship occurs in *W* (once where the sample with intensity *i* is the reference sample and once where the sample with intensity *j* is the reference sample), and for any given *i*, the sum of all the elements *i*, *j* with the given *i* will be the total number of times a sample of intensity *i* appears in the specified spatial relationship with another sample.

e..Normalize the GLCM:

  i. Divide each element by the sum of all elements

  The elements of the GLCM may now be considered probabilities of finding the relationship *i*, *j* (or *j*, *i*) in *W*.

Calculate the selected **Feature**. This calculation uses only the values in the GLCM. See:

- Energy
- Entropy
- Contrast
- Homogeneity
- Correlation
- Shade
- Prominence

The sample *s* in the resulting virtual variable is replaced by the value of this calculated feature.

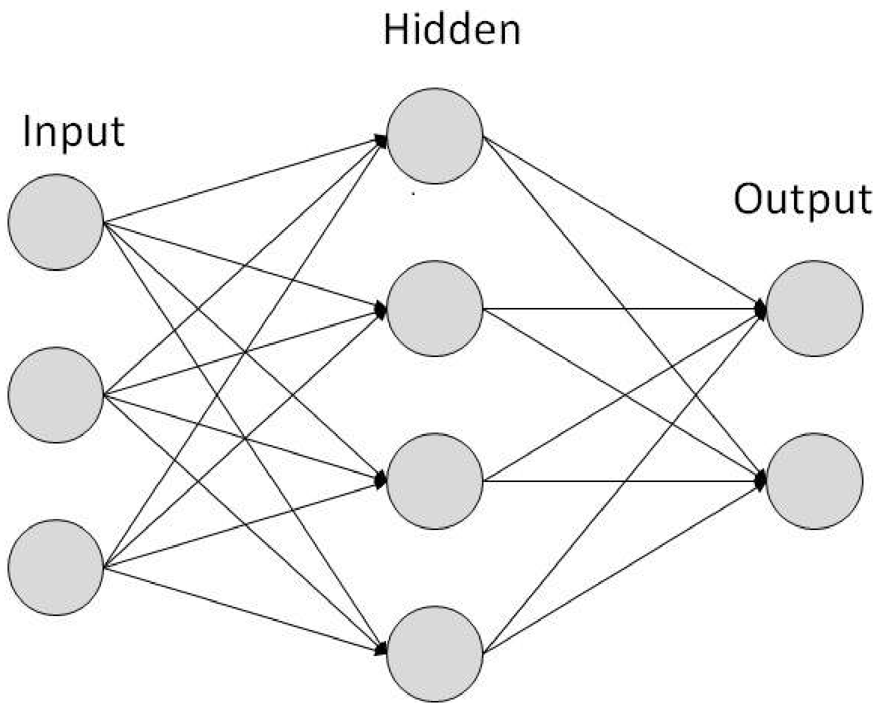
4.10 CLASSIFICATION USING ANN

Image classification analyzes the numerical properties of various image features and organizes data into categories. Classification algorithms typically employ two phases of processing: *training* and *testing*. In the initial training phase, characteristic properties of typical image features are isolated and, based on these, a unique description of each classification category, *i.e. training class*, is created. In the subsequent testing phase, these feature-space partitions are used to classify image features.

4.11 Artificial Neural Network Classifier:

Artificial neural networks (**ANN**) or **connectionist systems** are computing systems inspired by the biological neural networks that constitute animal brains.[1] The neural network itself is not an algorithm, but rather a framework for many different machine learning algorithms to work together and process complex data inputs.[2] Such systems "learn" to perform tasks by considering examples, generally without being programmed with any task-specific rules. For example, in image recognition, they might learn to identify images that contain cats by analyzing example images that have been manually labeled as "cat" or "no cat" and using the results to identify cats in other images. They do this without any prior knowledge about cats, for example, that they have fur, tails, whiskers and cat-like faces. Instead, they automatically generate identifying characteristics from the learning material that they process.

Each link is associated with **weight.** ANNs are capable of learning, which takes place by altering weight values. The following illustration shows a simple ANN −



SOFTWARE USED

MATLAB

MATLAB (*matrix laboratory*) is a multi-paradigm numerical computing environment and proprietary programming languagedeveloped by MathWorks. MATLAB allows matrix manipulations, plotting of functions and data, implementation ofalgorithms, creation of user interfaces, and interfacing with programs written in other languages, including C, C++, C#, Java,Fortran and Python.

Although MATLAB is intended primarily for numerical computing, an optional toolbox uses the MuPAD symbolic engine, allowing access to symbolic computing abilities. An additional package, Simulink, adds graphical multi-domain simulation and model-based design for dynamic and embedded systems.

As of 2018, MATLAB has more than 3 million users worldwide. MATLAB users come from various backgrounds ofengineering, science, and economics.

Sturctures

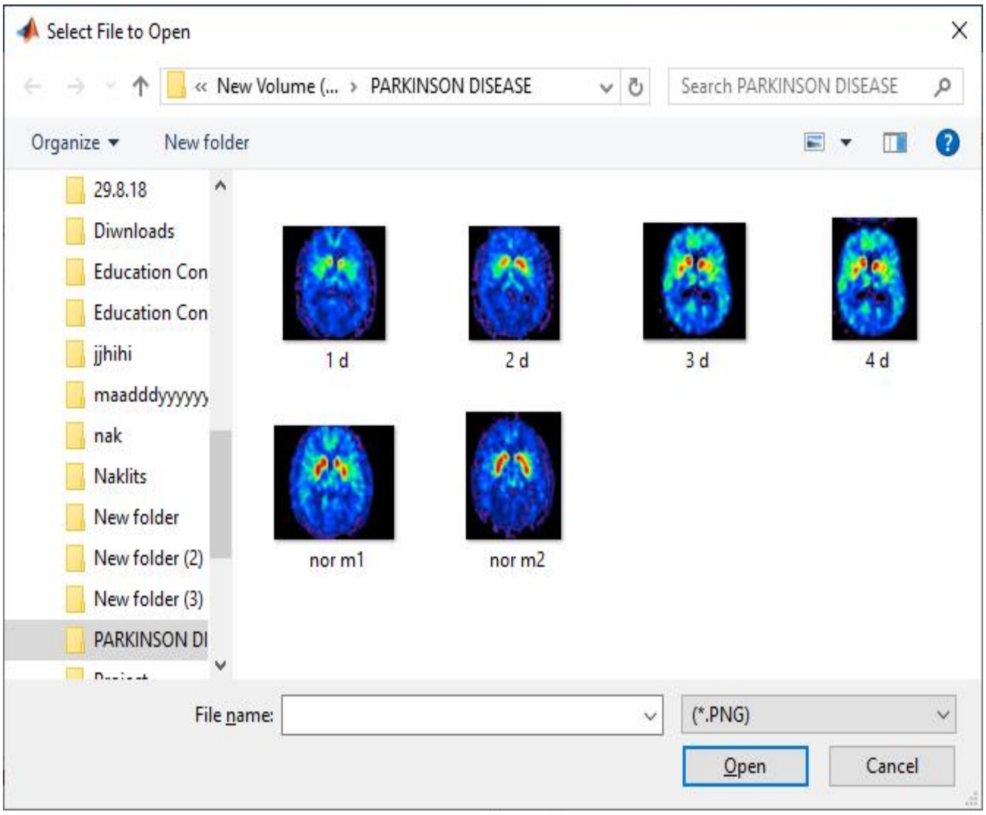
MATLAB has structure data types. Since all variables in MATLAB are arrays, a more adequate name is "structure array", where each element of the array has the same field names. In addition, MATLAB supports dynamic field names (field look-ups by name, field manipulations, etc.). Unfortunately, MATLAB JIT does not support MATLAB structures, therefore just a simple bundling of various variables into a structure will come at a cost.

Functions

When creating a MATLAB function, the name of the file should match the name of the first function in the file. Valid function names begin with an alphabetic character, and can contain letters, numbers, or underscores. Functions are often case sensitive

4.RESULT AND ANALYSIS

SCREENSHOT



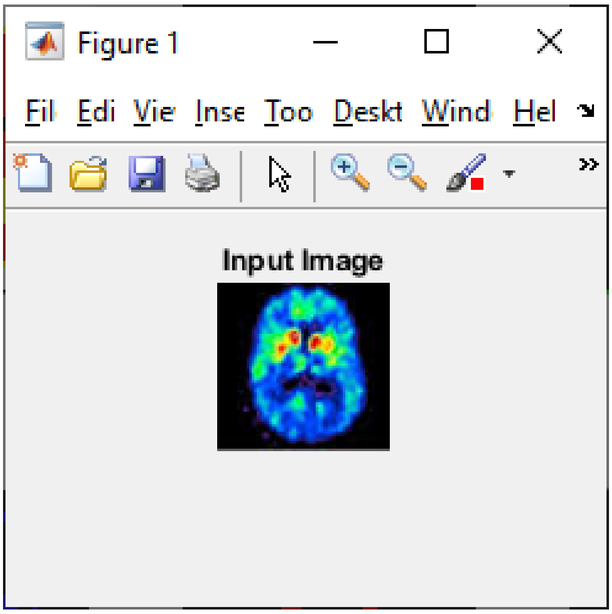


Figure 1
Fil Edi Vie Inse Too Deskt Wind Hel
Input Image

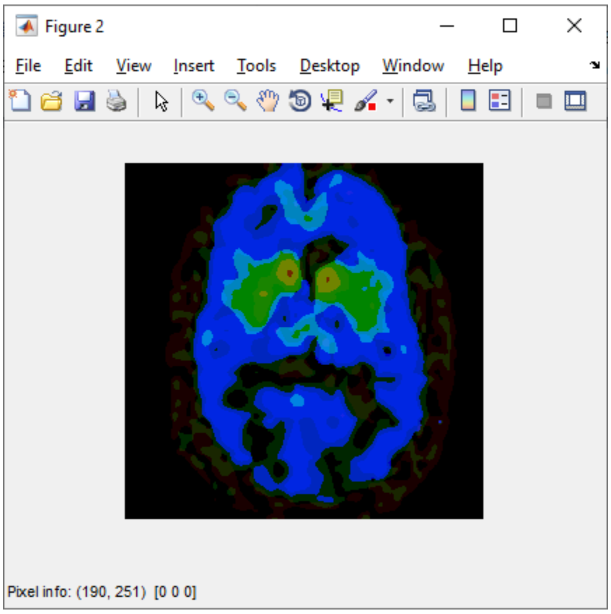


Figure 2
File Edit View Insert Tools Desktop Window Help
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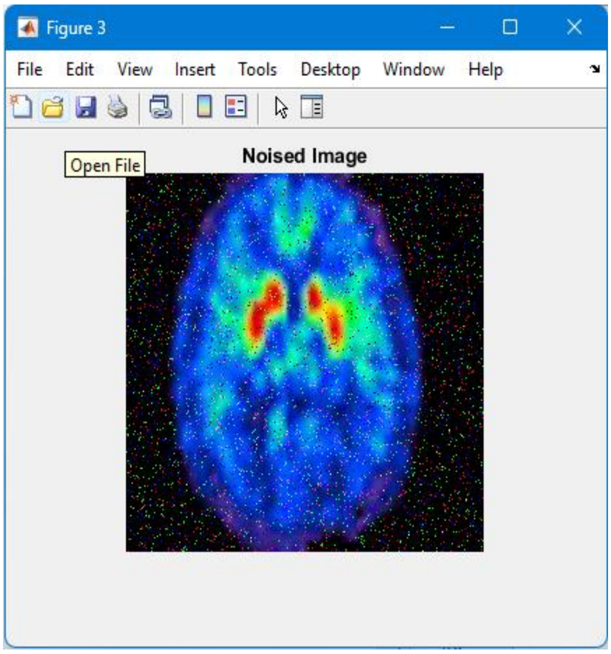


Figure 3
File Edit View Insert Tools Desktop Window Help
Open File
Noised Image

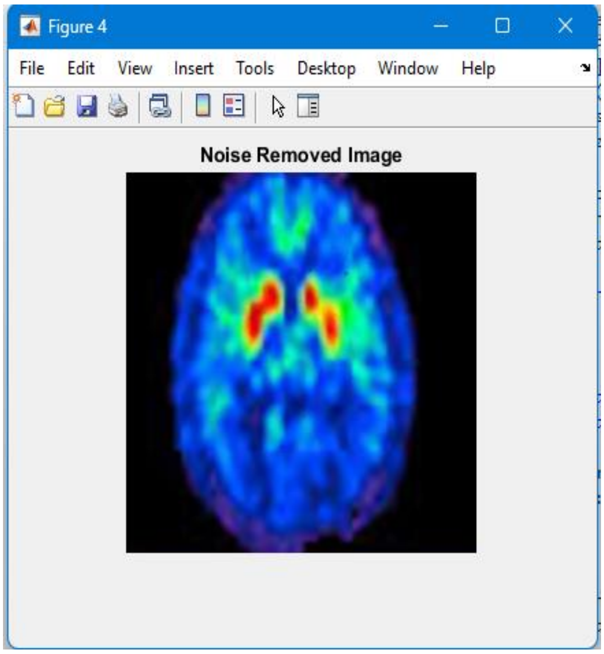


Figure 4
File Edit View Insert Tools Desktop Window Help
Noise Removed Image

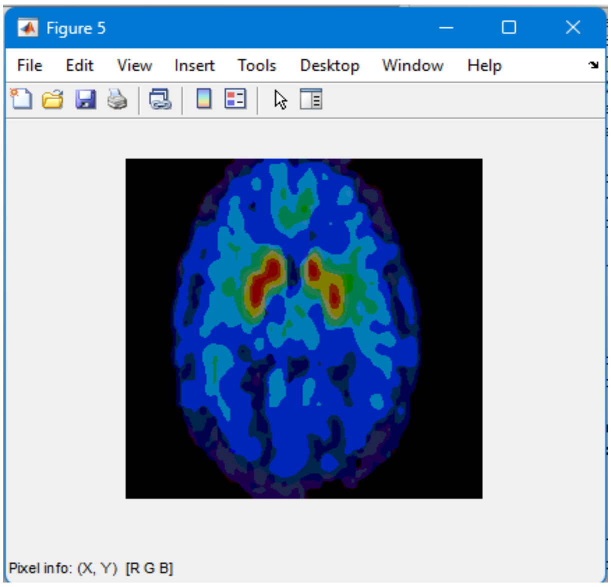
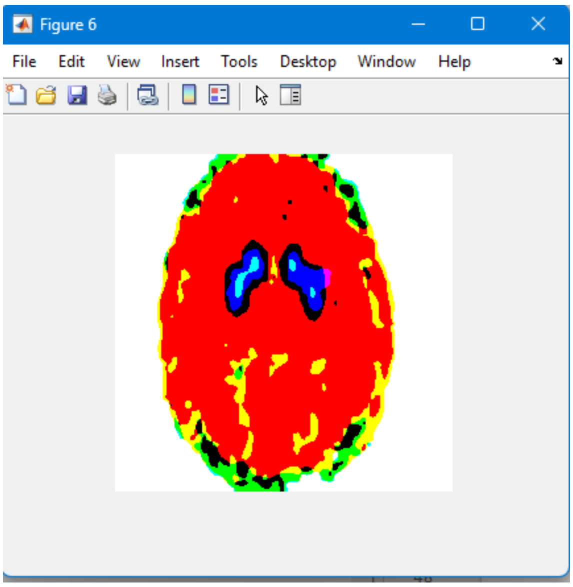


Figure 5
File Edit View Insert Tools Desktop Window Help
Pixel info: (X, Y) [R G B]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File Edit View Insert Tools Desktop Window Help

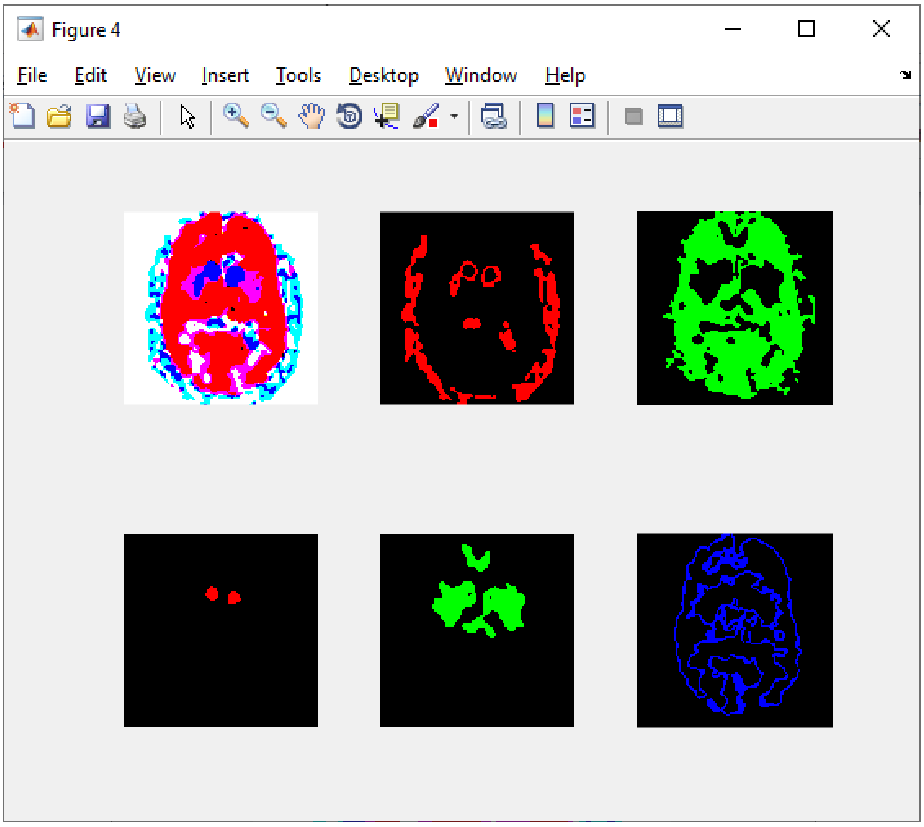
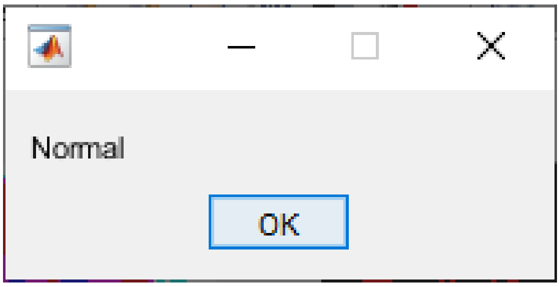


Figure 4
File Edit View Insert Tools Desktop Window Help


Normal
OK

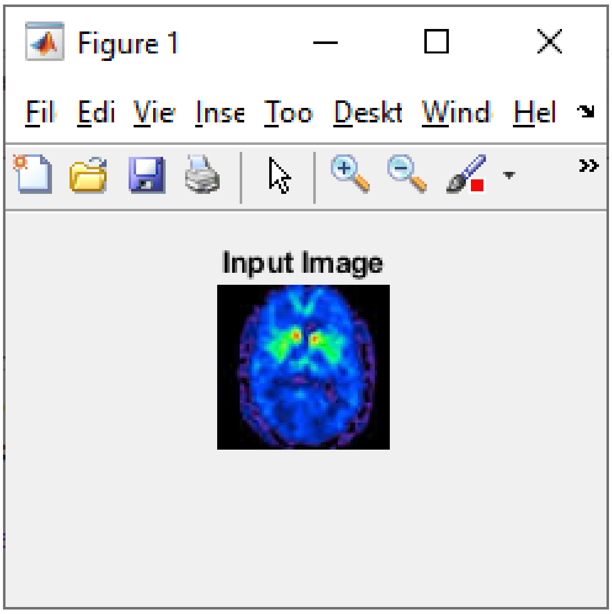


Figure 1
Fil Edi Vie Inse Too Deskt Wind Hel
Input Image

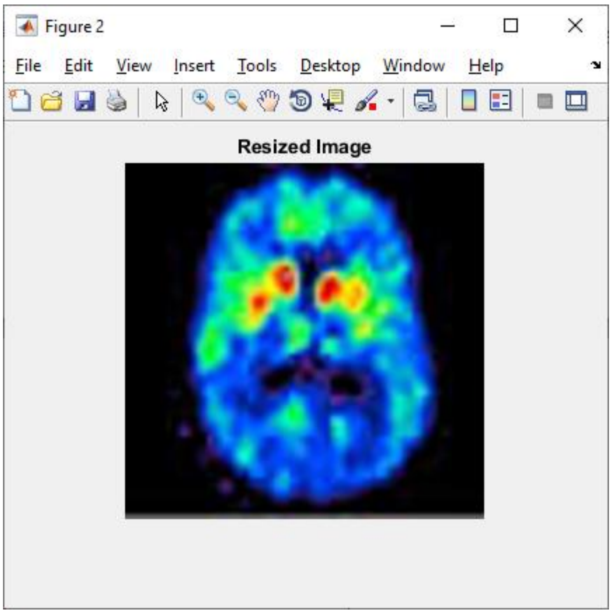


Figure 2
File Edit View Insert Tools Desktop Window Help
Resized Image

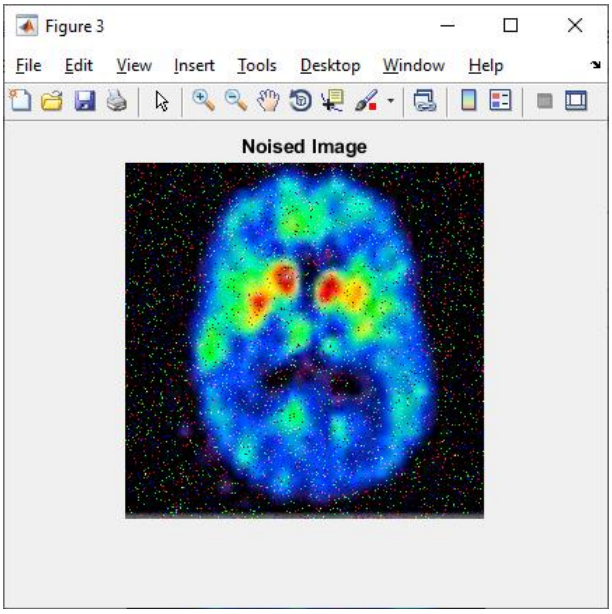


Figure 3
File Edit View Insert Tools Desktop Window Help
Noised Image

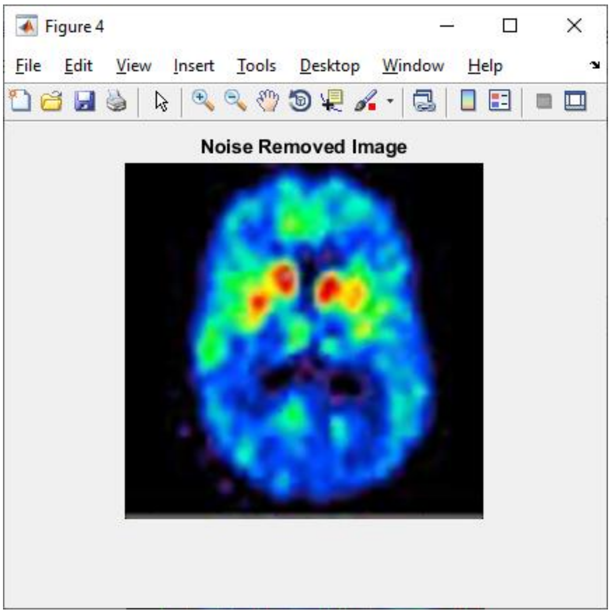


Figure 4
File Edit View Insert Tools Desktop Window Help
Noise Removed Image

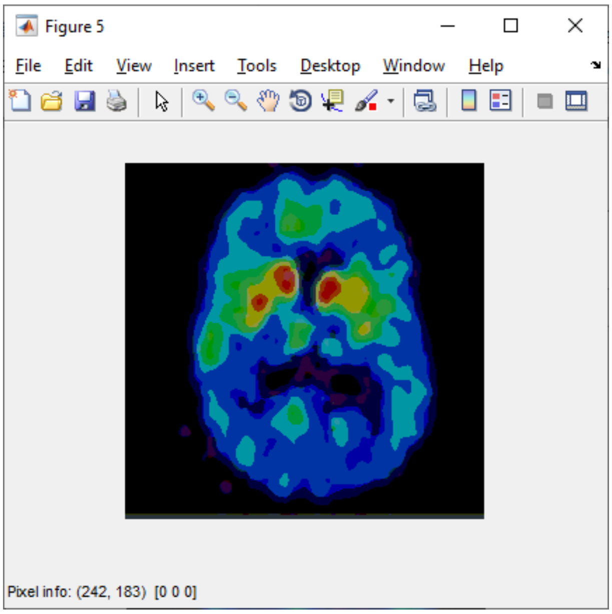


Figure 5
File Edit View Insert Tools Desktop Window Help
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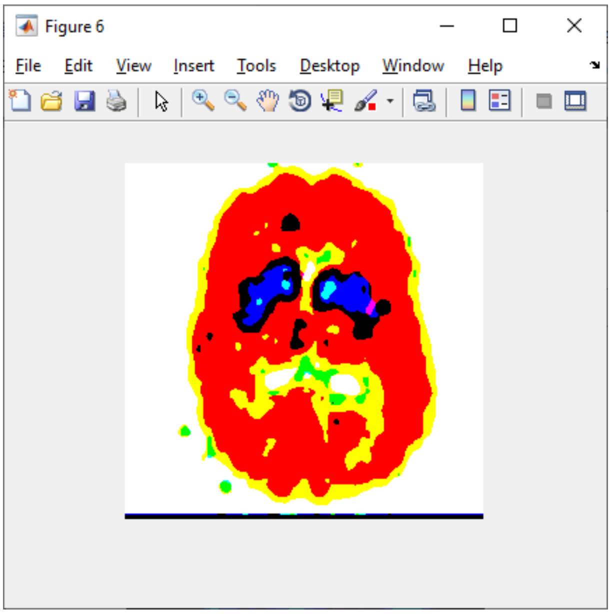


Figure 6
File Edit View Insert Tools Desktop Window Help

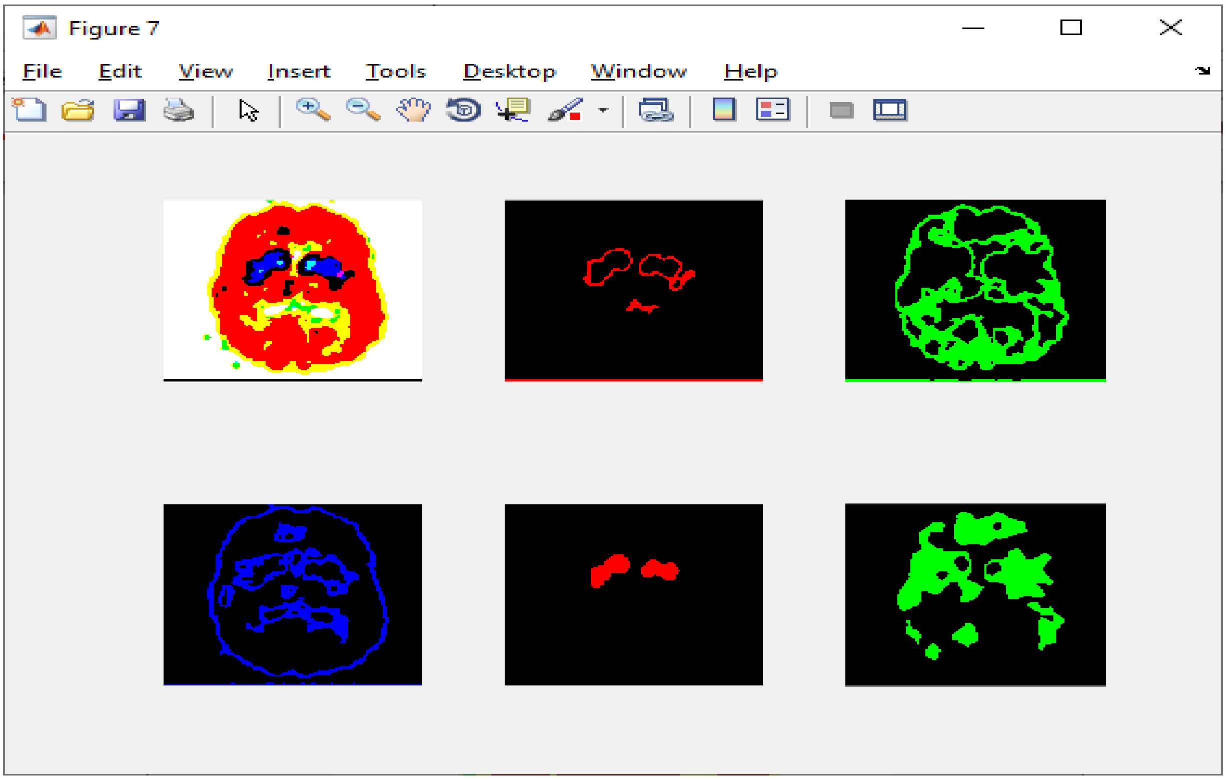
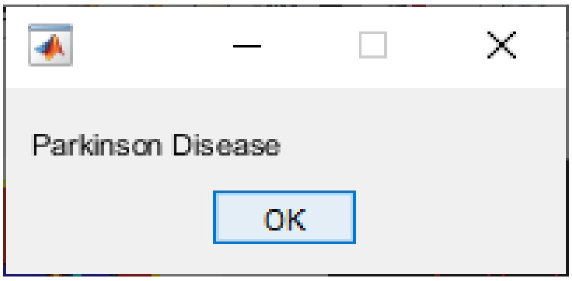


Figure 7
File
Edit
View
Insert
Tools
Desktop
Window
Help


Parkinson Disease
OK

5.CONCLUSION

The model presented in this paper looked at the problem of detecting PD from a different angle than existing approaches. The results obtained are very much applicable to real life situations. These results are not the means to an end, rather many works lay ahead to build up this model to be actually implemented in real life situation. Building up usable software with this approach can assist physicians to detect Parkinson's disease with better accuracy than before. A model with more dataset can give an even more reliable accuracy. Training the ANN with more data can make it more efficient in classification. There is still some limitation to overcome. Not many images of prodromal stage could be found. In addition, in this preliminary work, we could not cross check with actual clinicians/specialist to compare our results and performance. Early diagnosis of Parkinson's disease is very important for the patient to reduce its impact. As earlier the detection can be done, the better chance a patient has of slowing down the loss of neurons. The diagnosis process requires taking into account the various features and symptoms of patient and all these data needs to be analyzed by experienced specialists. The prediction/classification model presented in this paper with the aid of artificial intelligence aims to make it easier for doctors to do precise diagnosis.

6.FUTURE ENHANCEMENT

(i) This model obtained reliable accuracy in terms of classification using only one feature extracted from the the images.

(ii) The sample size used was large enough and diverse

(iii) Using image processing and artificial neural network separately, makes application of this model easier in real world situations, i.e., this approach takes very less processing power and its accuracy is reliable. It can be inferred from this proposed model that, area analysis and use of a simple artificial neural network is useful in developing prediction models that can help a doctor reduce the long process of diagnosis of PD and eradicate any human error. Future scope will be concentrate on Other type of dataset and also increase the size of the data for giving all possibility of the disease to get more accurate result.

7.REFERENCES

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APPENDIX

CODING

```
clc
clear all
close all

%Image Acquisition
[aa bb]=uigetfile('.PNG');
I=imread([bb aa]);
figure,imshow(I);
title('Input Image');

%Pre processing
%Resizing of an Image
I1=imresize(I,[256 256]);
figure,imshow(I1);
title('Resized Image');

%Adding Noise
In=imnoise(I1,'salt & Pepper');
figure,imshow(In);
title('Noised Image');

%Noise Removal using Median Filter
J=In;
winsz=3;
[s1,s2]=size(J);
sz=min([s1 s2]);
p=(winsz-1)/2;
if (size(In,3)>1)

for mnpk=1:3
ipnoise=J(:,:,mnpk);
```

```
medop=padarray(ipnoise,[p p]);

for i=1+p:sz+p
for j=1+p:sz+p
submed=medop(i-p:i+p,j-p:j+p);
medop(i,j)=median(submed(1:9));
end
end

medop=medop(1+p:sz+p,1+p:sz+p);
op1(:,:,mnpk)=medop;
end

else
ipnoise=J;
medop=padarray(ipnoise,[p p]);

for i=1+p:sz+p
for j=1+p:sz+p
submed=medop(i-p:i+p,j-p:j+p);
medop(i,j)=median(submed(1:9));
end
end
medop=medop(1+p:sz+p,1+p:sz+p);
op1=medop;
end

figure,imshow(op1);
title('Noise Removed Image');

% Segmentation
level=3;
[Iout]=segm(I1,level);
figure,imshow(Iout);
```

```
impixelinfo

Ik1=zeros(size(Iout));
Ip=Iout;
jk=unique(Ip);
op=jk(1,:);
Ik1(Ip==op)=255;
Ik1(Ip~=op)=0;
Ik11=double(bwareaopen(Ik1,200));
figure,imshow(Ik11,[]);


Ik2=zeros(size(Iout));
op=jk(2,:);
Ik2(Ip==op)=255;
Ik2(Ip~=op)=0;
Ik22=double(bwareaopen(Ik2,200));
%figure,imshow(Ik22,[]);


Ik3=zeros(size(Iout));
op=jk(3,:);
Ik3(Ip==op)=255;
Ik3(Ip~=op)=0;
Ik33=double(bwareaopen(Ik3,200));
%figure,imshow(Ik33,[]);


Ik4=zeros(size(Iout));
op=jk(4,:);
Ik4(Ip==op)=255;
Ik4(Ip~=op)=0;
Ik44=double(bwareaopen(Ik4,200));
%figure,imshow(Ik44,[]);
```

```
Ik5=zeros(size(Iout));
op=jk(5,:);
Ik5(Ip==op)=255;
Ik5(Ip~=op)=0;
Ik55=double(bwareaopen(Ik5,200));
%figure,imshow(Ik55,[]);

Ik6=zeros(size(Iout));
op=jk(6,:);
Ik6(Ip==op)=255;
Ik6(Ip~=op)=0;
Ik66=double(bwareaopen(Ik6,200));


figure,
subplot(2,3,1),imshow(Ik11,[]);
subplot(2,3,2),imshow(Ik22,[]);
subplot(2,3,3),imshow(Ik33,[]);
subplot(2,3,4),imshow(Ik44,[]);
subplot(2,3,5),imshow(Ik55,[]);
subplot(2,3,6),imshow(Ik66,[]);


%Feature Extraction
%Statistical Feature
m=mean(mean(Ik11));
s=std(std(double(Ik11)));
v=var(var(double(Ik11)));
sk=skewness(skewness(double(Ik11)));
k=kurtosis(kurtosis(double(Ik11)));

Stat_Fea=mean(mean([m s v sk k]));
```

```
%Texture Feature
GLCM2 = graycomatrix(rgb2gray(Ik11),'NumLevels',8,'Offset',[0 1]);
stats = GLCM_Features(GLCM2);
con=stats.contr;
ene=stats.energ;
sos=stats.sosvh;
ent=stats.entro;
hom=stats.homop;
sav=stats.savgh;
Text_Fea=mean([con ene sos ent hom sav]);

%Shape Feature
Ib1=rgb2gray(Ik11);
t=graythresh(Ib1);
Ib=im2bw(Ib1,t);
ss=regionprops(Ib);
ar=ss.Area;
cent=ss.Centroid;
bb=ss.BoundingBox;
Shape_Fea=mean([ar cent bb]);

Fea=mean([Stat_Fea Text_Fea Shape_Fea])
Feat=Fea/100;
%save Fs6 Fea6

%Classification using ANN
load netan
y=round(abs(sim(netan,Feat)))
if y==1
msgbox('Parkinson Disease');
elseif y==2
msgbox('Normal')
end
```