DEEP LEARNING BASED ALGORITHM FOR PARKINSON IMAGES

Major Project Report

Submitted in Partial Fulfillment of the Requirements for the Degree of

BACHELOR OF TECHNOLOGY

IN

INFORMATION TECHNOLOGY

By

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CERTIFICATE

This is to certify that the Major Project Report entitled "Deep learning based algorithm for parkinson images" submitted by Mr. Patel Takshkumar Kalpeshbhai (17BIT079) towards the partial fulfillment of the requirements for the award of degree in Bachelor of Technology in the field of Information Technology of Nirma University is the record of work carried out by him under our supervision and guidance. The work submitted has in our opinion reached a level required for being accepted for examination. The results embodied in this major project work to the best of our knowledge have notbeen submitted to any other University or Institution for the award of any degree or diploma.

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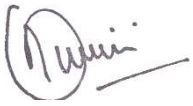

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I, Patel Takshkumar Kalpeshbhai, Roll No.17BIT079, give undertaking that the Major Project entitled “Deep learning based algorithm for parkinson images” submitted by me, towards the partial fulfillment of the requirements for the degree of Bachelor of Technology in Information Technology of Nirma University, Ahmedabad, is the original work carried out by me and I give assurance that no attempt of plagiarism has been made. I understand that in the event of any similarity found subsequently with any other published work or any project report elsewhere; it will result in severe disciplinary action.

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Secondly, I would like to thank my friends and my family for giving me strength and support.

ABSTRACT

Parkinson Disease(PD) is one of the most common neurodegenerative disease nowadays. It affects people of the age of above 60 years. It is caused by a dopamine deficit in the brain. Due to dopamine deficit neurons in the brain can not communicate with each other smoothly. A perfect cure for this disease is not found yet. This is still a research topic. In this project, T1 weighted MRI images are used to classify Parkinson disease and healthy control. The proposed method in this report is based on the classification of White matter(WM) and Gray matter(GM) using 3D CNN [4]. First, the segmentation of WM and GM was completed using Matlab tool SPM12 [2]. After that normalization was performed also using SPM12 [2]. After that data is ready for classification. Gender is also one criterion in Parkinson disease detection because women are less prone to Parkinson disease according to medical research [1]. So data was also separated into two sets. One for women and one for men. The project consists of four deep 3D CNN models. 1) for WM in women 2) for GM in women 3) for WM in men 4) for GM in men.

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NOMENCLATURE/ABBREVIATIONS

1. PD – Parkinson Disease
2. PPMI – Parkinson's Progression Markers Initiative
3. HC – Healthy Control
4. NC – Normal Controls
5. GM – Gray matter
6. WM – White matter
7. MRI – Magnetic Resonance Imaging
8. DTI – Diffusion Tensor Imaging
9. CSF – Cerebrospinal Fluid
10. ROI – Region of Interest
11. CNN – Convolutional Neural Network
12. SPM – Statistical Parametric Mapping
13. SPECT – Single-photon emission computerized tomography

CONTENTS

Chapter 1

Introduction

Parkinson Disease is a neurodegenerative disorder which affected 6.2 Million peoples globally. It is caused by dopamine deficit in the substantia nigra portion of the brain. Dopamine is a biological chemical which is generated in substantia nigra part of the brain and used for communication of neuron in the whole brain. If it is not generated in proper quantity then healthy communication between neurons is hampered. And symptoms of Parkinson disease include impaired gait, stooped posture, vocal disability, tremors, etc.

There is no perfect cure for Parkinson disease is available. And if 70-80 percent of neurons of the brain got damaged due to PD then it hard to save the patient. So it still research topic for early detection of Parkinson disease.

Deep learning is a trending technology in the medical field nowadays. Image classification techniques of deep learning is useful for the classification of Parkinson disease and healthy control using brain MRI. 3D CNN is the most suitable technique to classify 3D MRI [4].

The brain has three portions. 1)White matter 2) Gray matter 3) cerebrospinal fluid. If dopamine generation is hampered then the density of WM and GM decreases. And 3D CNN can classify the less density WM or GM MRI as Parkinson disease. So the segmentation and separation of GM and WM are required from whole brain MRI for that. I used SPM12 toolbox available in Matlab for the segmentation of WM and GM. After the segmentation normalization of WM and GM was also completed using SPM12. After that created a 3D CNN model for the classification of WM and GM.

According to medical research, women are less prone to Parkinson disease compared to men. Hence I separated the dataset into two sets based on gender [1].

Chapter 2

Objective

White matter and Gray matter are two major parts of the brain. Dopamine deficit causes density changes in both white matter and gray matter. So by checking voxel by voxel in gray matter and white matter Parkinson disease can be detected. For this purpose, a 3D convolutional neural network can be useful [4],[6].

There are different regions of interest in males and females for dopamine deficit in the brain. In men, basal ganglia, brainstem, fourth ventricle, lateral ventricle, and cerebellum are most affected. And in women, the occipital lobe, thalamus, basal ganglia, a small part of the cerebellum, and frontal lobe are most affected. So the classification of Parkinson disease based on gender may give better results[1].

Chapter 3

Literature Survey

3.1 Parkinson's Disease Detection Using Ensemble Architecture from MR Images [2]:

In this paper, the PPMI dataset is used. And for preprocessing of MRI images SPM12 toolbox available in Matlab was used.

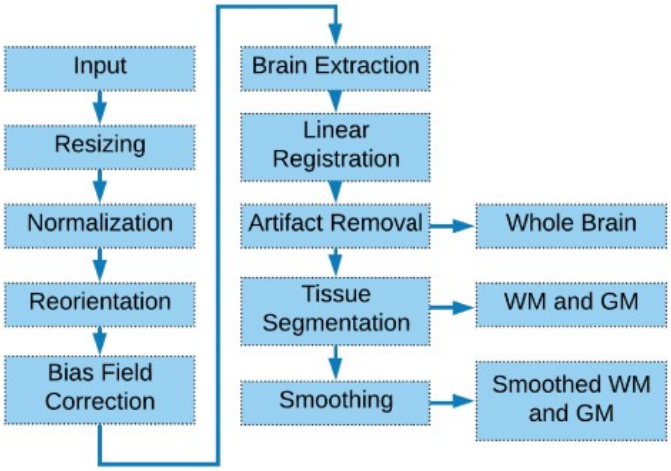

Figure 1. preprocessing pipeline

After the preprocessing steps they created three different datasets: Whole brain, segmented white matter and gray matter, smoothed white matter and gray matter.

For Parkinson detection, they created two ensemble models.

3.1.1 Model for whole brain:

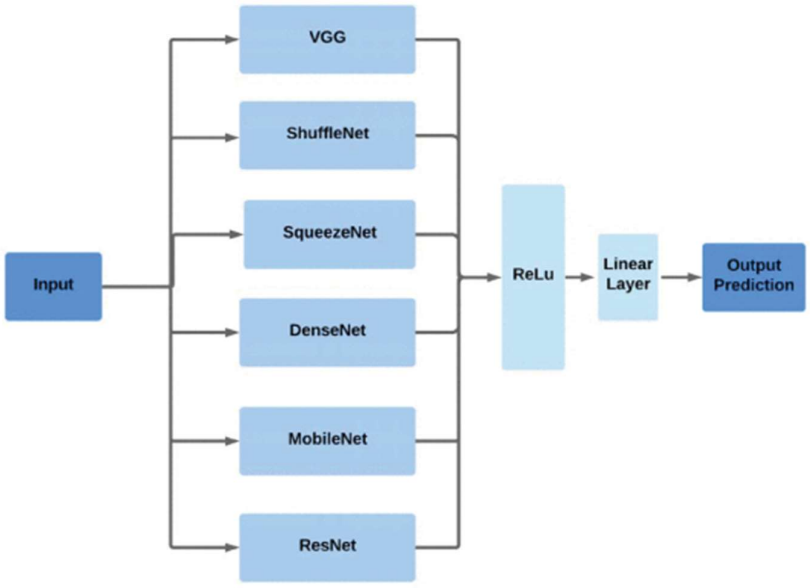

Figure 2. Ensemble architecture for whole brain architecture

3.1.2 Model for extracted WM and GM:

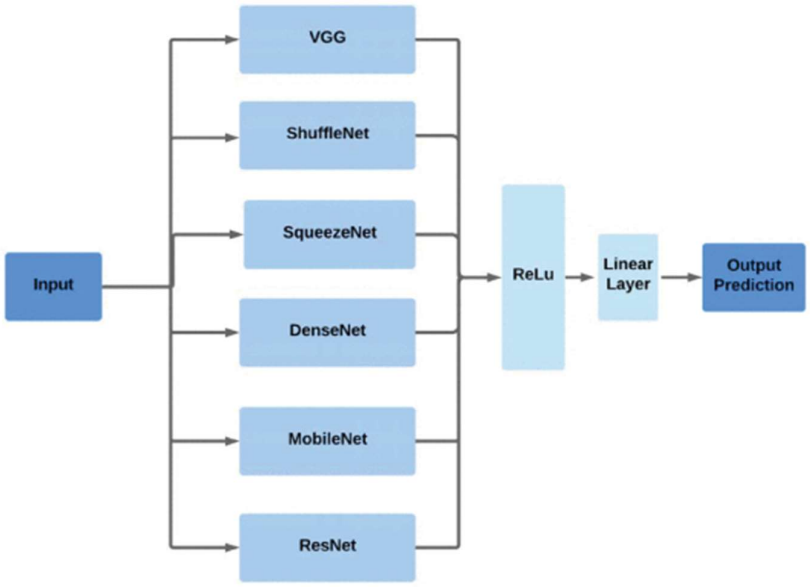

Figure 3. Ensemble architecture for Extracted GM and WM Scans

Here all 3D CNN is available in PyTorch. Are Relu activation function is used for faster execution.

Using the whole-brain ensemble model they got average accuracy of 0.7617 ± 0.0041. using extracted GM and WM ensemble model they got average accuracy

of 0.9366 ± 0.0170. using smoothed GM and WM ensemble model they got an even more average accuracy of 0.9470±0.0083.

3.2 Classification of PPMI MRI scans with voxel-based morphometry and machine learning to assist in the diagnosis of Parkinson's disease [1]:

In this research paper, they used the PPMI dataset. Methodology is divided into 5 steps.

3.2.1 detection of region of interest:

for ROI detection whole-brain MRI was segmented in white matter(WM), gray matter(GM) and cerebrospinal fluid(CSF). And WM and CSF were discarded.

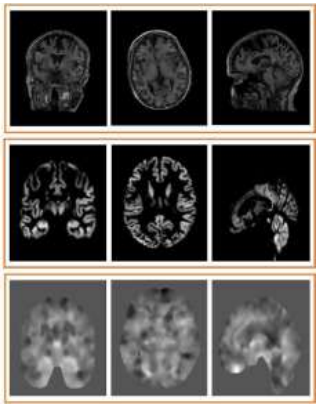

Figure 4. whole brain MRI(first row), segmented grey matter(second row) and t-map(third row)

t-map is used for the detection of the region of interest.

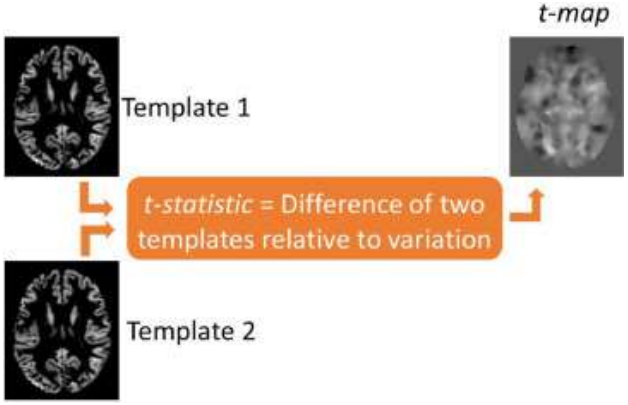

Figure 5. generation of t-map

t-map was created by comparing concentrations of GM with PD and GM with healthy control voxel by voxel. The region which has the significant difference in concentration comparing with healthy control is registered as ROI.

3.2.2 Feature extraction:

A feature like a number voxel in each ROI, the distance between two ROIs, the angle between two ROIs, etc were extracted by some mathematical techniques.

3.2.3 Feature selection:

Feature extracted from each ROI were thousands in number. so there was a need for dimensionality reduction. PCA is used for that. But after performing PCA there were still a significant number of features remained. So subset selection method was used, selects a subset of all feature which provide batter results.

3.2.4 Classification:

Various machine learning algorithms K nearest neighbours, support vector machine, multi-layer perceptron, random forest, naïve Bayes classifier, and a logistic classifier were used for classification.
The following table shows the results.

	Classifier	Population	Accuracy
1.5-T MRI Scan	Naive Bayes	Male	0.9901
	Logistic	Female	0.9677
3.0-T MRI Scan	SVM	Male	09556
	Logistic	Female	0.9328

Table 1. results of classification (Literature survey)

3.3 Refining diagnosis of Parkinson's disease with deep learning-based interpretation of dopamine transporter imaging [3]:

In this paper, they used SPECT images from the PPMI dataset. Because dopamine deficit can be accessed using DTI imaging such as SPECT. So they developed deep learning-based SPECT interpretation model called PD Net.

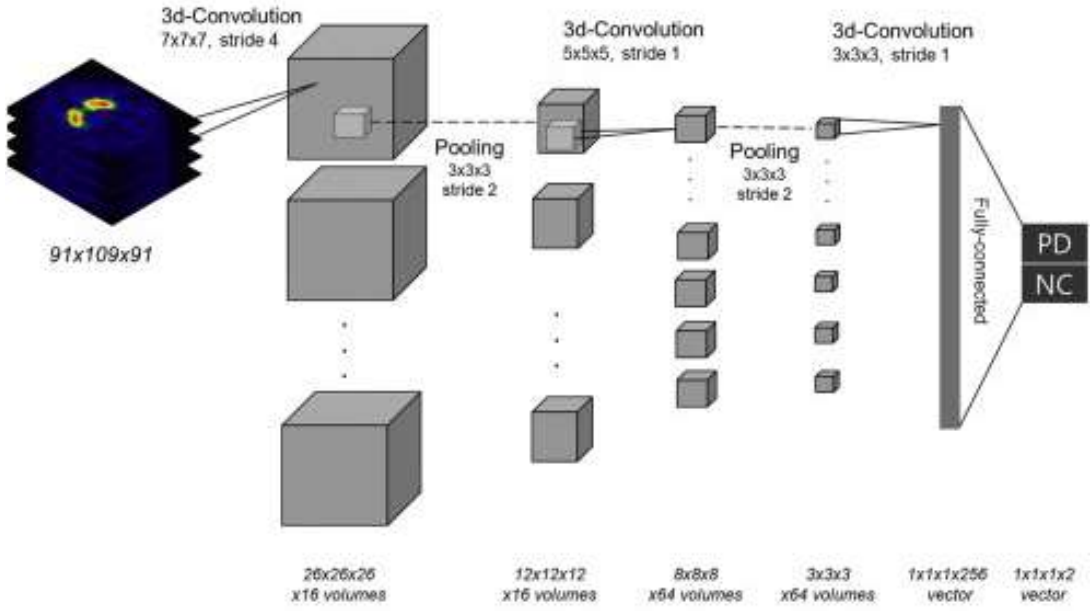

Figure 6. PD Net.

In this PD Net 3D convolution layer, 3D max-pooling layer and 3D fully connected dense layer was used.

For the test set, they achieved 96% accuracy.

Chapter 4

Dataset Selection

I explored PPMI and Brats dataset. And found out that brats dataset can only be useful for brain tumor segmentation. And the other side PPMI is a large collection of DTI, MRI and SPECT images for Parkinson disease as well as healthy controls. So We selected the PPMI dataset for this project.

MRI images are suitable to classify structural changes like density degradation using 3D CNN. So selected MRI images for this project [18].

In MRI three types of sequences are available in PPMI.

1. T1 weighted
2. T2 weighted
3. Proton density

T1 and T2 weighted MRI both can be used to identify brain atrophy and tissue loss. But T2 weighted MRI has more limitations compared to T1 weighted MRI. Like T2 weighted MRI overestimates cortical atrophy [5]. So I selected T1 weighted MRI for this project.

Chapter 5

Dataset Description

In PPMI dataset magnetic resonance imaging(MRI), Diffusion tensor imaging(DTI), single-photon emission computerized tomography (SPECT) are available for Parkinson disease as well as Healthy control.

For MRI there are different sequences like T1 weighted, T2 weighted and proton density(PD) are available.

MRI images are available in the format of .nii for pre-processed images and in .dicom format for original images.

Apart from that additional information like gender, age, arm swing data, gait data, etc are also available.

There are various research group data are available. But for this project only two research group data are useful. PD corresponding to Parkinson disease and Control corresponding to healthy control.

For this project, T1-weighted MRI images were selected [8]. Because it is used for the evaluation of brain atrophy and tissue losses. if the intensity of the signal between neurons is changed then this causes structural changes in the basal ganglia part of the brain. Which can be detected by T1 Weighted MRI images. T2 weighted MRI also has these advantages but it has a limitation of overestimation of cortical atrophy of the brain[5].

I worked with pre-processed images directly. Following is a table corresponding to a number of the object selected from PPMI.

Gender/Class	PD	Control
Male	100	94
Female	80	41

Table 2. Data Collection

Chapter 6

Proposed Methodology

6.1 Segmentation in White matter and Gray matter:

For this SPM12 toolbox from Matlab was used. SPM12 is a GUI-based toolbox that is widely used for brain image pre-processing. It is easy to use and gives efficient results [2], [11].

6.1.1 SPM12 workflow steps:

1. Resizing: all input images are resized in the same dimension.
2. Reorientation: all input images are rotated in the same orientation.
3. Brain Extraction: removes skull, fat, and other background volumes which do not provide useful information for prediction.
4. Segmentation: segmentation of GM and WM from the whole brain.
5. Normalization: all MRIs collected from the different machines so they can have intensity variations so normalization is needed to remove those variations.

6.1.2 Original 3D MRI:

The following figure shows pre-processed MRI scan image directly available in PPMI dataset.

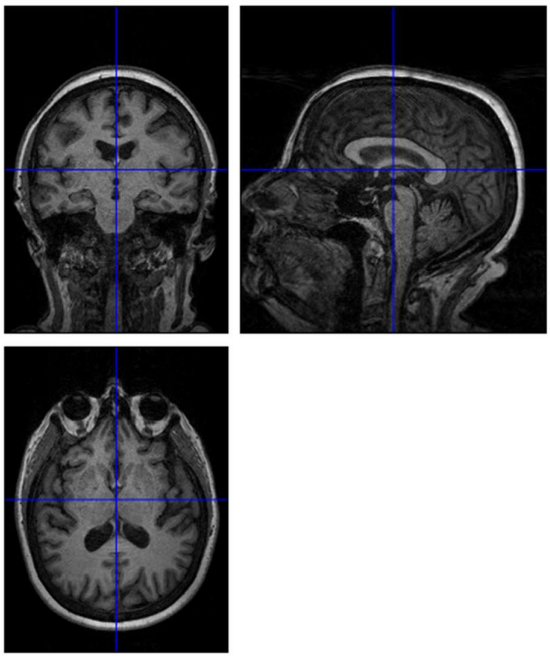

Figure 7. Whole brain MRI (coronal view - top left, sagittal view - top right, axial view - bottom left)

The following figure shows 100 slices of pre-processed 3D MRI available in the PPMI dataset in axial view.

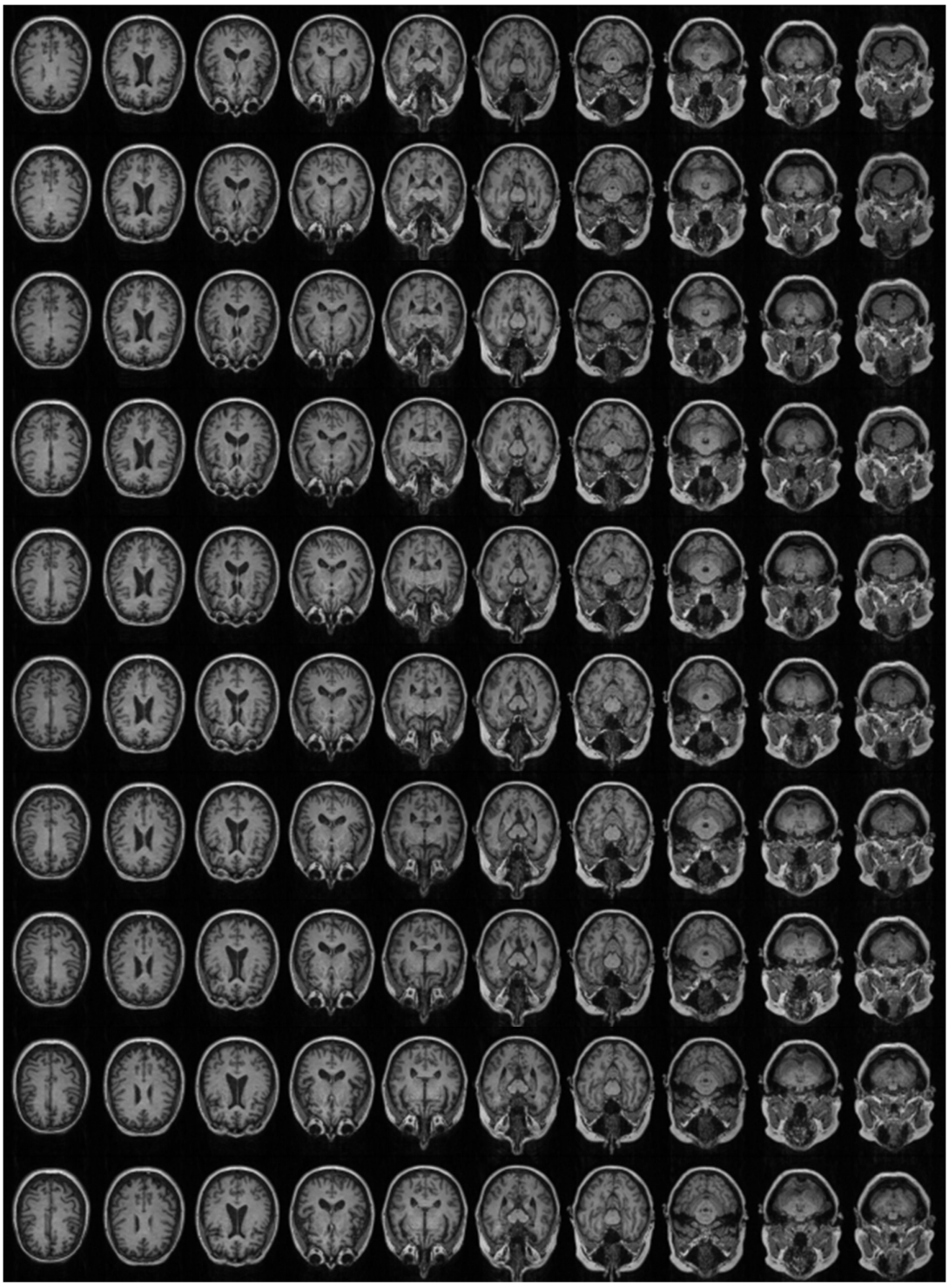

Figure 8. Axial view of 3D MRI of brain

6.1.3 Results of SPM12:

The following figure shows the result of separated grey and white matter after voxel by voxel 3D segmentation of MRI. But it needs to be normalized because MRI scans in PPMI were collected from different machines. They should be normalized in the same range to remove high and low-intensity variations.

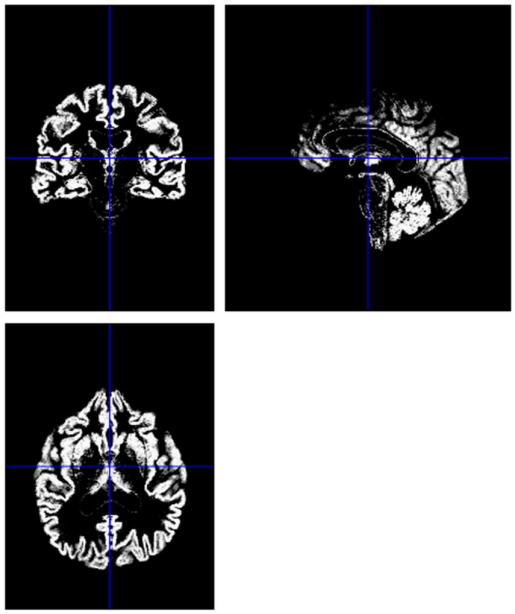

Figure 9. Gray matter (coronal view - top left, sagittal view - top right, axial view - bottom left)

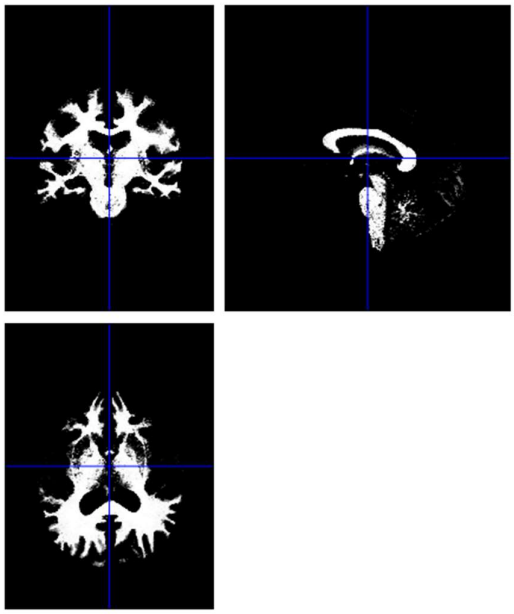

Figure 10. White matter (coronal view - top left, sagittal view - top right, axial view - bottom left)

6.1.4 After Normalization:

The following figure shows segmented grey and white matter After removing intensity variations using spm12.

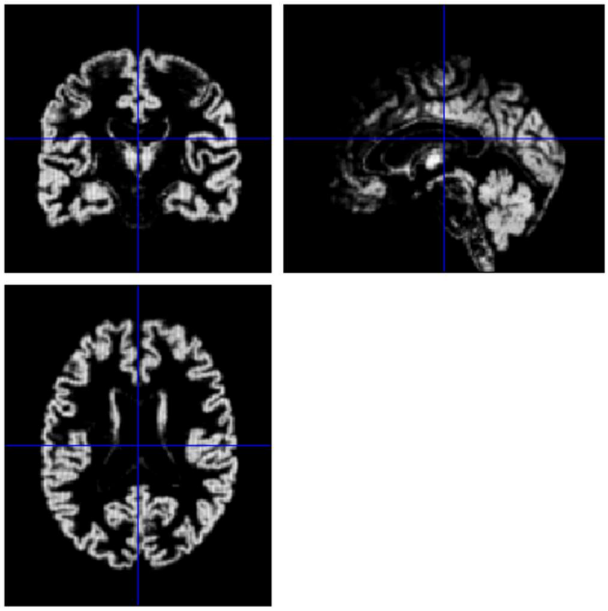

Figure 11. Normalized Gray matter (coronal view - top left, sagittal view - top right, axial view - bottom left)

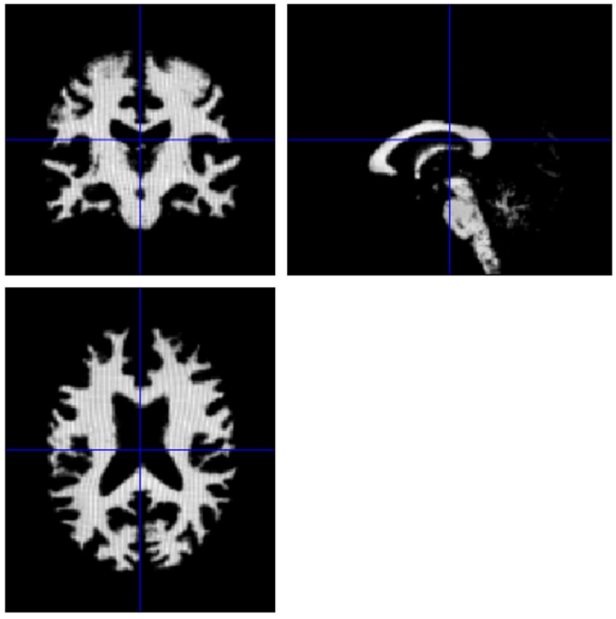

Figure 12. Normalized White matter (coronal view - top left, sagittal view - top right, axial view - bottom left)

The following figure shows 100 slices of the grey matter of the brain in axial view. It is plotted using nibabel and matplotlib libraries of python.

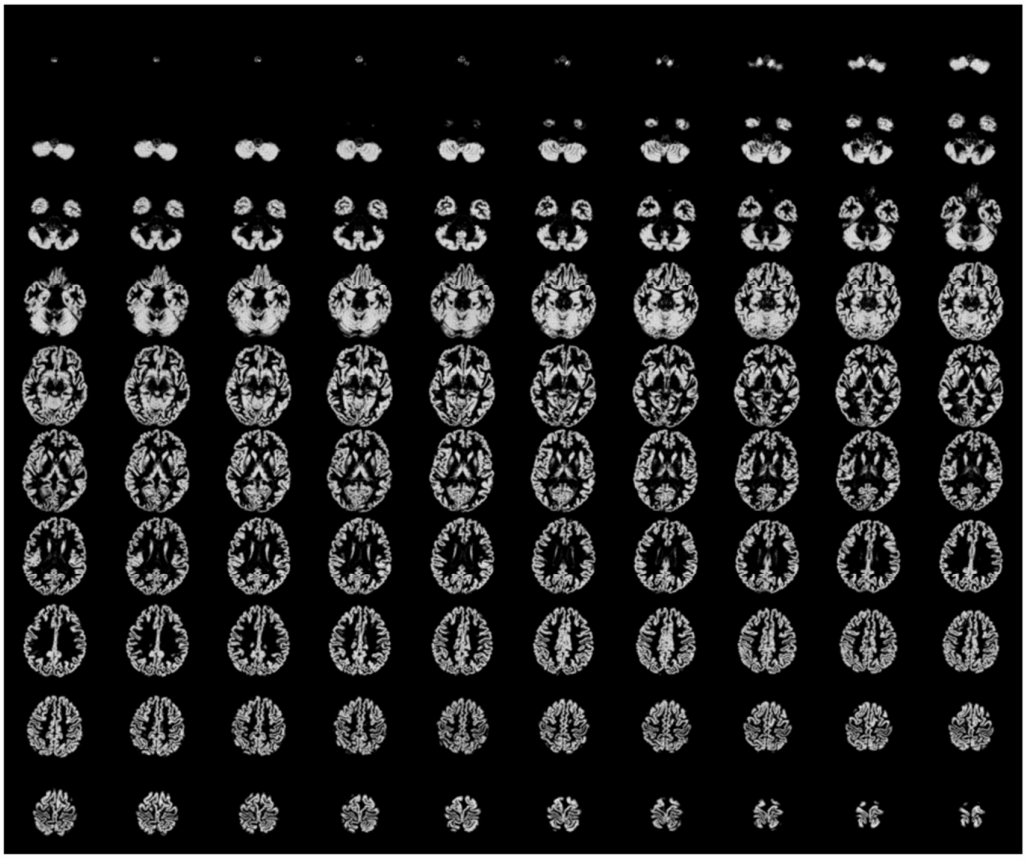

Figure 13. Axial view of grey matter of brain

The following figure shows 100 slices of the white matter of the brain in axial view using nibabel and matplotlib libraries of python.

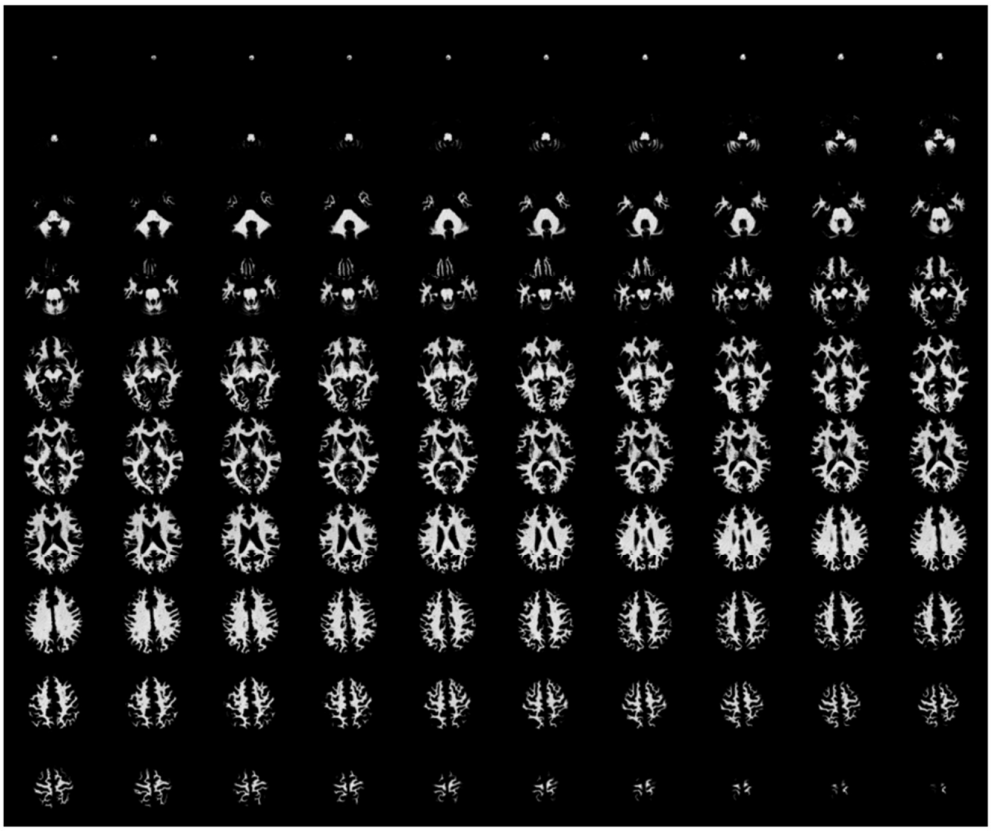

Figure 14. Axial view of white matter of brain

6.2 3D CNN Architecture

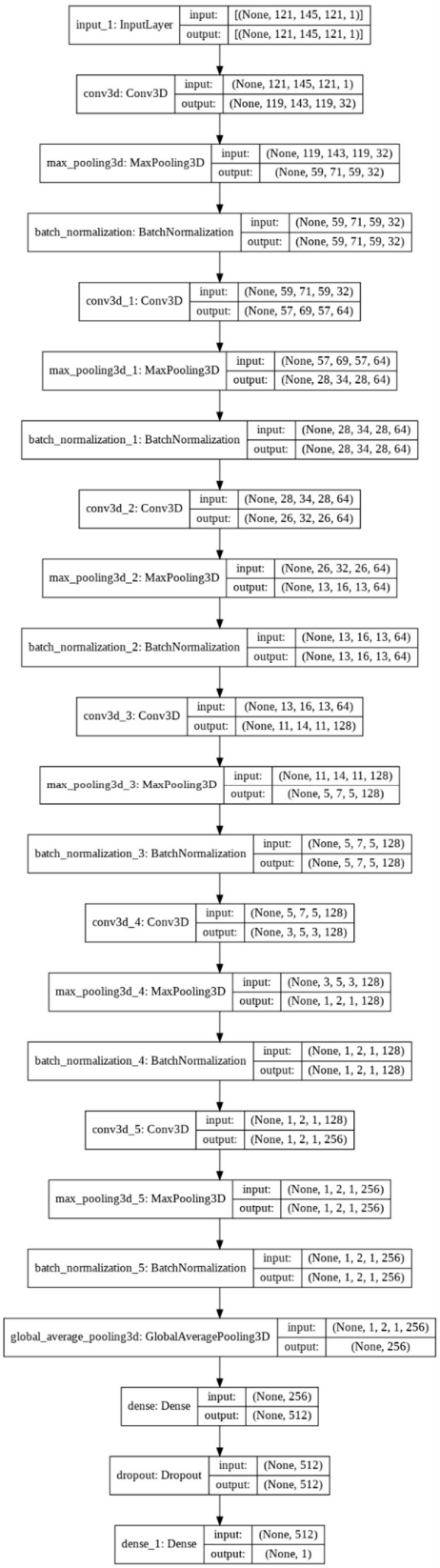

Figure 15. Model Architecture

Coding of the model

```
def get_model(width=121, height=145, depth=121):

    inputs = keras.Input((width, height, depth, 1))

    x = layers.Conv3D(filters=32, kernel_size=3, activation="relu")(inputs)
    x = layers.MaxPool3D(pool_size=2)(x)
    x = layers.BatchNormalization()(x)

    x = layers.Conv3D(filters=64, kernel_size=3, activation="relu")(x)
    x = layers.MaxPool3D(pool_size=2)(x)
    x = layers.BatchNormalization()(x)

    x = layers.Conv3D(filters=64, kernel_size=3, activation="relu")(x)
    x = layers.MaxPool3D(pool_size=2)(x)
    x = layers.BatchNormalization()(x)

    x = layers.Conv3D(filters=128, kernel_size=3, activation="relu")(x)
    x = layers.MaxPool3D(pool_size=2)(x)
    x = layers.BatchNormalization()(x)

    x = layers.Conv3D(filters=128, kernel_size=3, activation="relu")(x)
    x = layers.MaxPool3D(pool_size=2)(x)
    x = layers.BatchNormalization()(x)

    x = layers.Conv3D(filters=256, kernel_size=1, activation="relu")(x)
    x = layers.MaxPool3D(pool_size=1)(x)
    x = layers.BatchNormalization()(x)

    x = layers.GlobalAveragePooling3D()(x)
    x = layers.Dense(units=512, activation="relu")(x)
    x = layers.Dropout(0.6)(x)

    outputs = layers.Dense(units=1, activation="sigmoid")(x)
    # Define the model.
    model = keras.Model(inputs, outputs, name="3dcnn")
    return model
```

Figure 16. Coding of 3D CNN (Keras)

Keras library was used to create a 3D CNN model. Input passed in 3D convolution layer followed by 3D max-pooling and batch normalization layer. And this pattern continues for filter sizes 32, 64,128, and 256. After that global average pooling layer was applied to reduce the number of the parameter followed by a 3D fully connected dense layer of 512 units. In all those layers rectified linear unit (ReLU) activation function was used. Here dropout 0.6 used to overcome model overfitting. after that 3D fully connected dense layer of unit 1 with sigmoid activation function was used as an output later [7], [12].

6.2.1 Input size:

height-145, width-121, depth-121

6.2.2 3D Convolutional Layer:

used because inputs have 3 dimension.

6.2.3 ReLU activation function:

used for faster execution.

6.2.4 Kernel size: 3

6.2.5 3D Max Pooling Layer:

In this layer pool size is 2, which means it halves the size of each dimension in a 3D image.

6.2.6 Batch Normalization Layer:

It applies a transformation that makes the mean output close to 0.

6.2.7 3D Global Average Pooling Layer:

It is used to avoid overfitting by reducing parameters in the model. The work of this layer is also the same as the max-pooling layer. But it performs an extreme level of dimensionality reduction.

6.2.8 3D Dense Layer:

It is most commonly used in various models. It is a regular deeply connected neural network layer.

6.2.9 Dropout:

It is used to avoid overfitting. Here 0.6 dropout used means 60% neurons retained during training.

6.2.10 Sigmoid activation Function:

It is used in the output layer because in binary classification problems it is widely used.

6.3 Model Training

Coding of Model training

```
[ ] initial_learning_rate = 0.0001
    lr_schedule = keras.optimizers.schedules.ExponentialDecay(
        initial_learning_rate, decay_steps=100000, decay_rate=0.96, staircase=True
    )
    model.compile(
        loss="binary_crossentropy",
        optimizer=keras.optimizers.Adam(learning_rate=lr_schedule),
        metrics=["acc"],
    )

    # Define callbacks.
    checkpoint_cb = keras.callbacks.ModelCheckpoint(
        "/content/drive/MyDrive/PPMI/WM_women.h5", save_best_only=True
    )
    early_stopping_cb = keras.callbacks.EarlyStopping(monitor="val_acc", patience=15)

    # Train the model, doing validation at the end of each epoch
    epochs = 100
    model.fit(
        train_dataset,
        validation_data=validation_dataset,
        epochs=epochs,
        shuffle=True,
        verbose=2,
        callbacks=[checkpoint_cb, early_stopping_cb],
    )
```

Figure 17. Coding of Model training

Here model.compile() function uses binary cross-entropy loss function because it is binary classification problem. It used Adam optimizer which takes the learning rate schedule as an argument. And Here initial learning rate of 0.0001 was passed into the Exponential decay function to reduce the learning rate exponentially while training. Model checkpoint callback is used to save the best model only. An early stopping callback was used to stop training early to avoid overfitting. model.fit() function takes training dataset, validation dataset, number of epochs, callbacks as arguments to train a model [7].

6.3.1 Split dataset :

the dataset was divided into three portions.

- **Training:** 60%
- **Validation:** 20%
- **Testing:** 20%

Here validation set is used to evaluate the model at the end of each epoch.

6.3.2 Initial Learning rate: 0.0001

6.3.3 Learning Rate:

during the training of the model, it is often recommended that to reduce the learning rate along with training progresses.

So exponential decay function (available in Keras optimizers) is used to reduce the learning rate during training progress [7].

6.3.4 Loss Function:

there are a lot of loss functions available but this is a binary classification problem, so the Binary cross-entropy loss function is used.

It computes cross-entropy loss between true labels and predicted labels.

6.3.5 Adam Optimizer:

when the model is in the training phase our aim should be to reduce loss, optimize predictions as much as possible.

Adam stands for adaptive moment estimation. Based on the current learning rate it will change the weight of the model to minimize the loss.

Apart from that it is computationally efficient and required less memory. And it is suited for problems where data is in high dimension and the parameter of the model is also high [7].

6.3.6 Callbacks:

6.3.6.1 Model Checkpoint callback:

Used with model.fit() function during training to save weight in some intervals. So weights are loaded in the model later to continue the training smoothly from the state saved.

6.3.6.2 Early Stopping callback:

Default epochs to train model is 100. But this callback checks loss at the end of each epoch and whenever it finds out that loss is no longer decreasing it stops the training.

6.4 Python Libraries Used

6.4.1 os

It is used to interact with the file system to read input and store output.

6.4.2 Numpy

It is used to work with multidimensional arrays and fast execution of high-dimensional data.

6.4.3 TensorFlow

It is the most important library that was used to create a deep learning model directly.

6.4.4 Keras

It is supporting a library of TensorFlow which is used to implement deep learning models as fast and easily possible. It has direct APIs for convolution layer, max-pooling layer, dropout, etc.

6.4.5 nibabel

It is used to get read and write access to .nii 3D files of the brain.

6.4.6 matplotlib

It is used to plot results in the form of graphs.

Chapter 7

Results

	Training accuracy	Validation accuracy	Testing accuracy
GM male	0.7512	0.4615	0.6842
WM male	0.7110	0.5128	0.4737
GM female	0.8139	0.6667	0.6667
WM female	0.6438	0.6667	0.6667

Table 3. Results of Proposed Methodology

Here default epochs are set to100, but I used an early stopping callback which checks validation accuracy at the end of each epoch with patience 15. This means after 15 epochs if validation accuracy no longer increases then it will stop the training of the model.

7.1 Grey matter of male

Epochs completed achieving above accuracy: 45

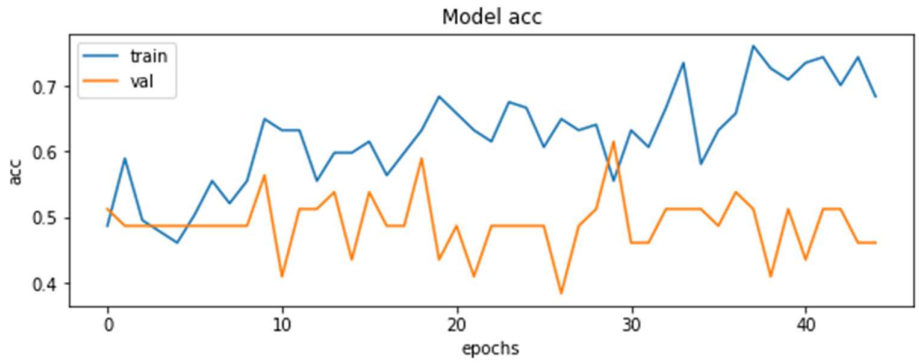

Figure 18. accuracy (grey matter of male)

Training accuracy: 0.7512

Validation accuracy: 0.4615

Testing accuracy: 0.6842

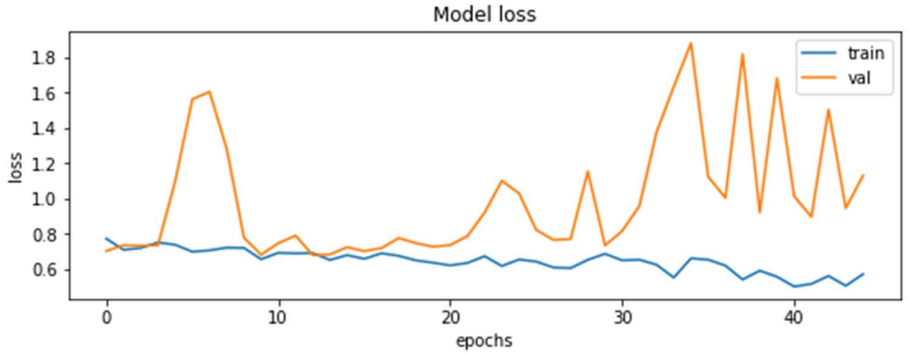

Figure 19. loss (grey matter of male)

Training Loss: 0.4937

Validation Loss: 1.1294

Testing Loss: 0.6843

7.2 White matter of male

Epochs completed achieving above accuracy: 36

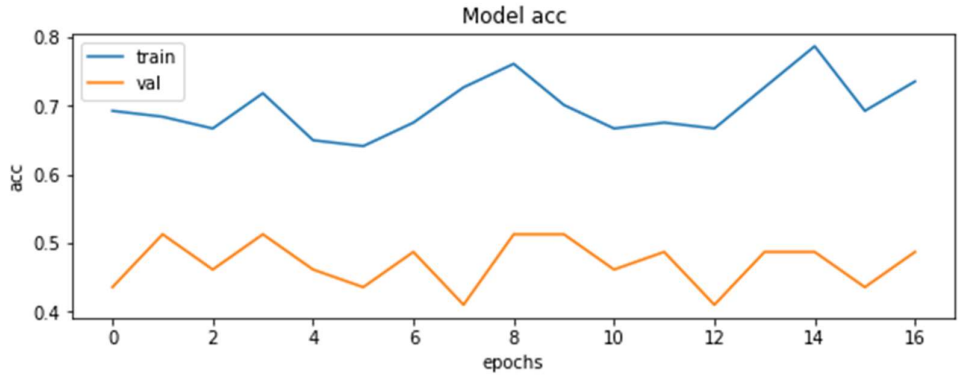

Figure 20. accuracy (white matter of male)

Training accuracy: 0.7110

Validation accuracy: 0.5128

Testing accuracy: 0.4737

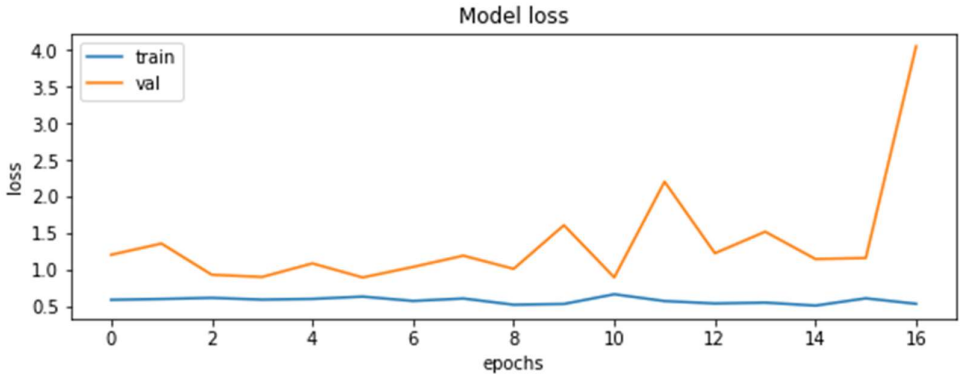

Figure 21. loss (white matter of male)

Training Loss: 0.5788

Validation Loss: 1.2320

Testing Loss: 3.9117

7.3 Grey matter of female

Epochs completed achieving above accuracy: 16

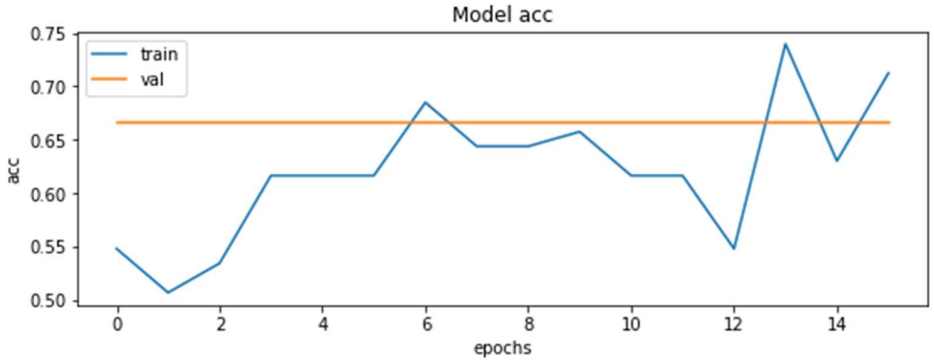

Figure 22. accuracy (grey matter of female)

Training accuracy: 0.8139

Validation accuracy: 0.6667

Testing accuracy: 0.6667

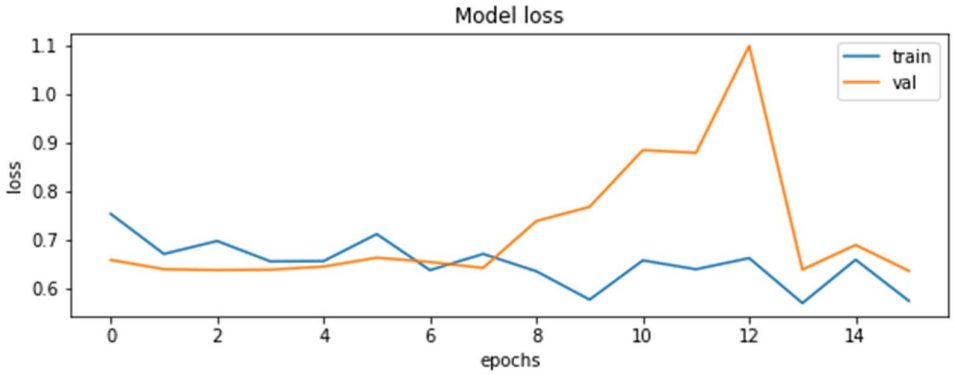

Figure 23. loss (grey matter of female)

Training Loss: 0.5263

Validation Loss: 0.6355

Testing Loss: 0.6743

7.4 White matter of female

Epochs completed achieving above accuracy: 35

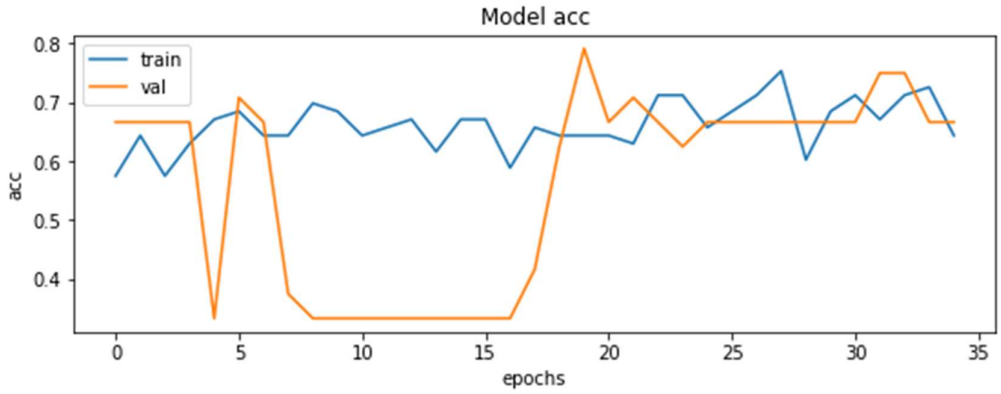

Figure 24. accuracy (white matter of female)

Training accuracy: 0.6438

Validation accuracy: 0.6667

Testing accuracy: 0.6667

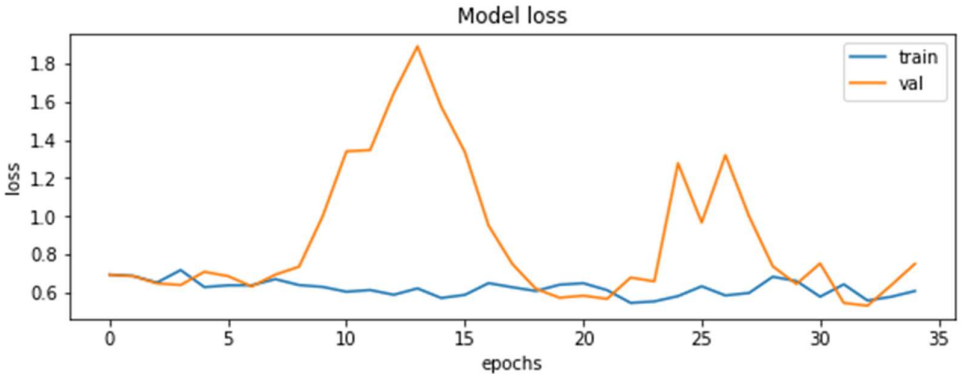

Figure 25. loss (white matter of female)

Training Loss: 0.6072

Validation Loss: 0.7496

Testing Loss: 0.7197

Conclusion

Based on results achieved in this project it can be concluded that a model based on the grey matter of the brain gives high accuracy in both males as well as females. This means it is easy for 3D CNN to classify grey matter of Parkinson patient and healthy person because there is a significant decrease in the density of grey matter of the brain due to Parkinson disease. So it is concluded that grey matter is more affected than white matter due to Parkinson disease.

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