



4 Way Classification of Brain Tumor Using Shallow Convolution Neural Network.

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4 Way Classification of Brain Tumor Using Shallow Convolution Neural Network.

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Abstract: - The range of Central Nervous System (CNS) tumors in India is from 5 to 10 per 100000 of the population on average that is increasing as the time passes. The medical services in India are still out of reach for many people. However, the author has the view that the advancement in the field of deep learning, machine learning and artificial intelligence can be utilised to solve this issue. In this paper, we are trying to identify three types of brain tumor namely meningioma, glioma, and pituitary while separating the no tumor category. Here we are using MRI scan images. These images are of jpeg form, pre-processed taken from kaggle database. The accuracy of our model in identifying the above mentioned four classes is 90.16%. Similarly, the precision for Glioma, meningioma, pituitary and no tumor are 81.48%, 78.94%, 94.73% and 97.36 % respectively.

Keyword: - *Brain tumor, Machine learning, Deep Learning, Artificial Intelligence, Central Nervous System. CT(Computed Tomography), MRI(Magnetic Resonance Imaging).*

I. Introduction

The unintentional and abnormal rise of cells in cluster paves way for brain tumor which later affects the functioning of the normal brain. The symptoms of brain tumor are commonly as increasing severity of headaches, weakness in hand operations and legs, loss of balancing ability while walking, fits or seizures, memory loss, sudden mood change etc. The best way to combat this is to detect the brain tumor at an earliest possible stage. This early detection then helps in early start of treatment. In various studies, it is found that life saving rate of patients of brain tumor can be increased significantly by early detection and early start of treatment.

The diagnosis or detection of brain tumor is done using two methods. One is CT(Computed Tomography) scan and MRI (Magnetic Resonance Imaging) scan. The CT(Computed Tomography) is done using x-rays, strong magnets or radioactive materials to generate pictures of brain and spinal cord. MRI (Magnetic Resonance Imaging) is a scan that utilises the strong magnetic fields and radio waves to produce images with great details of the inside of the brain. An MRI scanner is often very large tube sized that has strong magnets and the patients lie inside the tube when the scan is done.

After these CT scan and MRI scan, the radiologist will examine the images to identify the brain tumor growth. This process involves a lot of time and money. There is also the chance of error due to the low pixel density or presence of noise.

This process of identification of brain tumor can be speeded up using machine learning or deep learning models. We already know that CNN (convolution neural network) is already used for image classification. In this work, we have used CNN (Convolution Neural Network) to identify images. Here we are categorising the classification in four classes namely meningioma, glioma, pituitary and no tumor.

II. Recent Work

The detection of brain tumor has been devised by multiple approaches using machine learning. This includes time consuming manual process also. Due to the achievements in deep learning, remarkable progress has been achieved in recent times. This process (classification using deep learning) has also reduced the cost of identification very low.

In 2018 Seetha et al. [1] used FCM (Fuzzy C-Means) algorithm for image segmentation. B. Shrinivas et al. [2] used K-means to show that it is better than FCM (Fuzzy C-Means).

In 2019 Krishna Pathak et al. [3] used CNN (convolution neural network) for binary classification. Here, the two classes were brain tumor detected or not. If the result is detected than images were segmented incorporation watershed algorithm. The accuracy was 98 % achieved.

In 2020 MRI (Magnetic Resonance imaging) images are used by Zeineldin et al. [4] and automatic brain segmentation was achieved using deep neural network. Tommooy Hossain et al. [5] designed two models using FCM (Fuzzy C-Means) and SVM (Support Vector Machine) classifier. Auto encoder is used by Raut et al. [6] to generate new images and later perform segmentation using K-means algorithm.

III. Methods

A. **Dataset** :- This dataset is taken form kaggle database DOI 10.34740/kaggle/dsv/2645886 [7]. This dataset consist of two types of dataset which are as following :

Figshare:- Figshare is a database that allows the researchers ability to upload, download, share, cite and discover all types of research outputs and stores the data for long term.

Kaggle:- Kaggle is a database that allows users to explore the available dataset, modify them according to the need and also perform graphics intensive computation for their research work.

This dataset consists of 7022 images of human brain MRI (Magnetic Resonance Imaging) images which are of JPEG type. A total of 22% images are reserved for model testing and the rest approximately 78% are for model training. These images are further classified into four category:

- Glioma: - An image for representation of glioma type tumor is shown below in fig 1. Here we have 826 jpeg images of Glioma tumor.

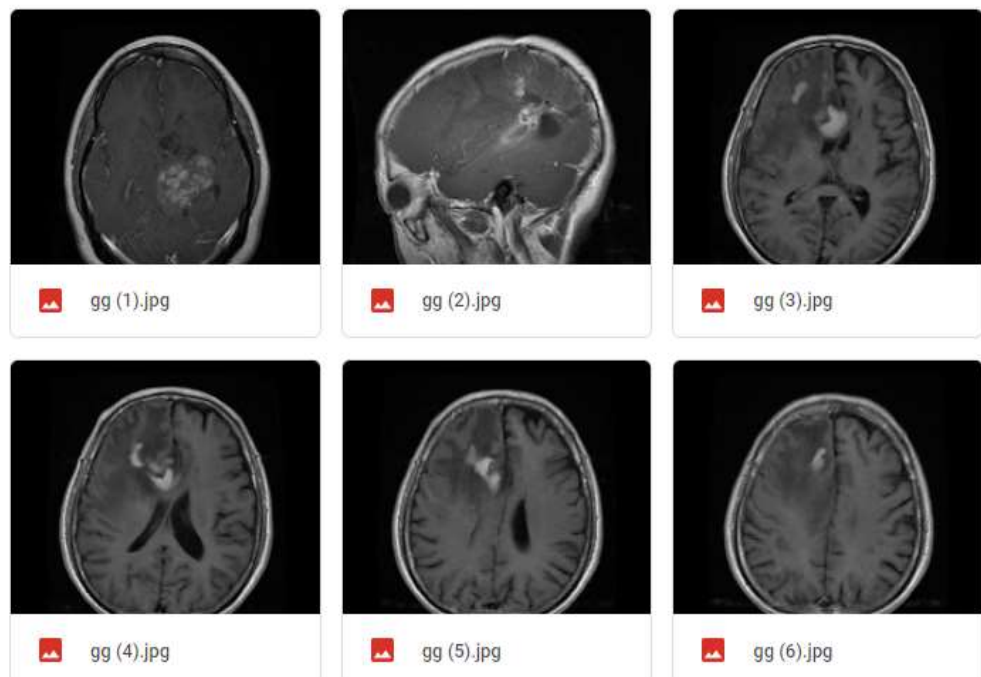


Fig 1. Glioma Tumor Image

- Pituitary: - An image for representation of pituitary type tumor is shown below in fig 2. Here we have 827 jpeg images of pituitary tumor.

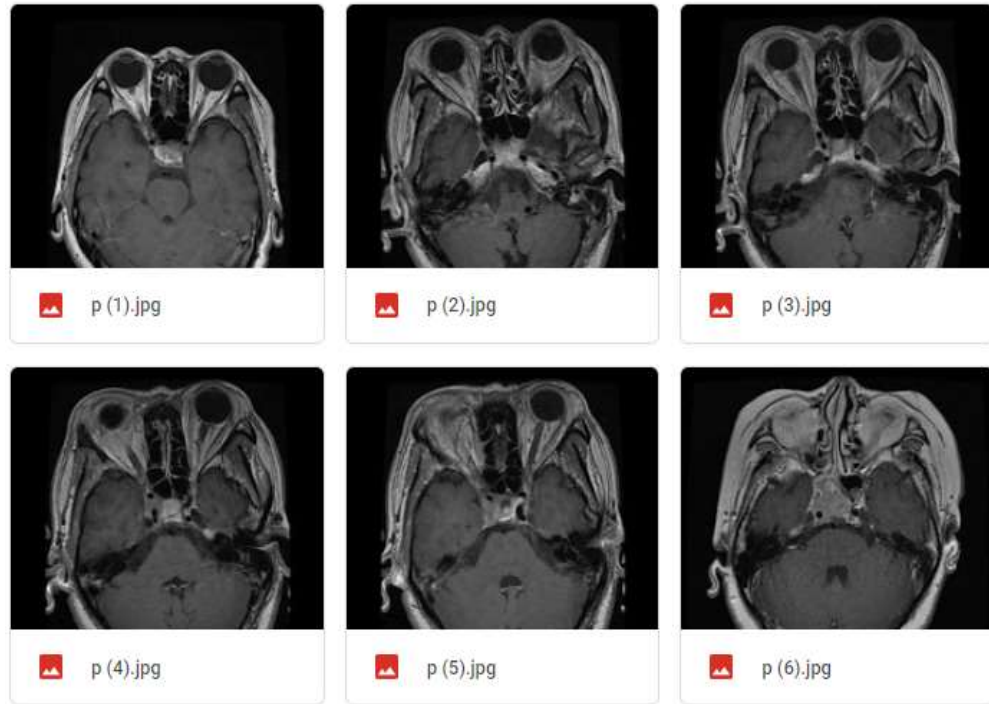


Fig 2. Pituitary Tumor Image

- Meningioma: - An image for representation of glioma type tumor is shown below in fig3. Here we have 822 jpeg images of meningioma tumor.

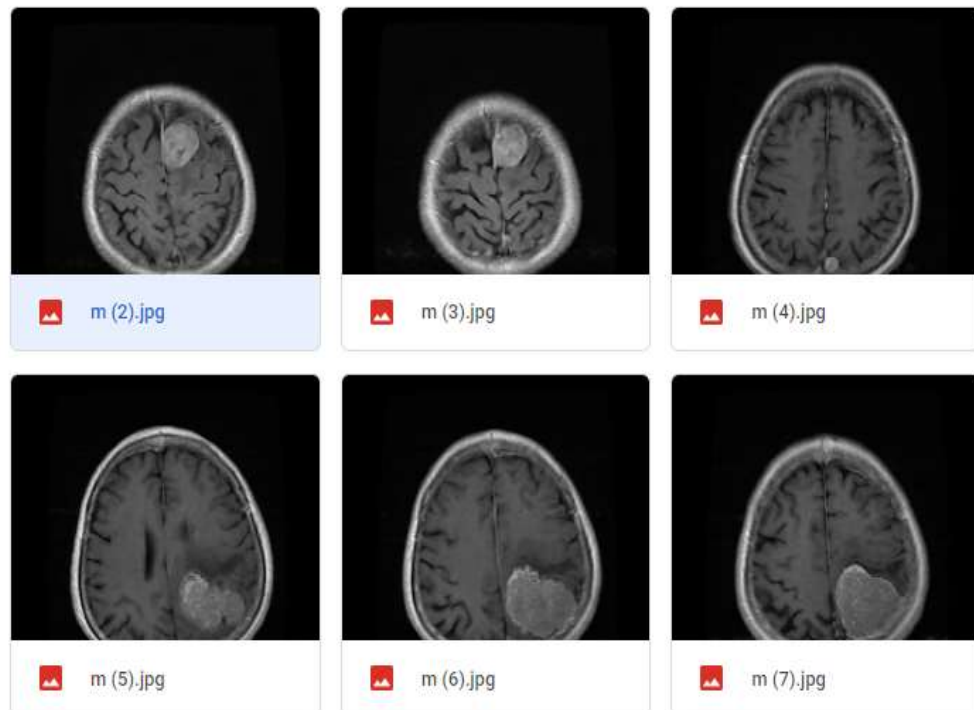


Fig 3. Meningioma Tumor Image

- No Tumor: - An image for representation of no tumor is shown below in fig 4. Here we have 395 images of no tumor.

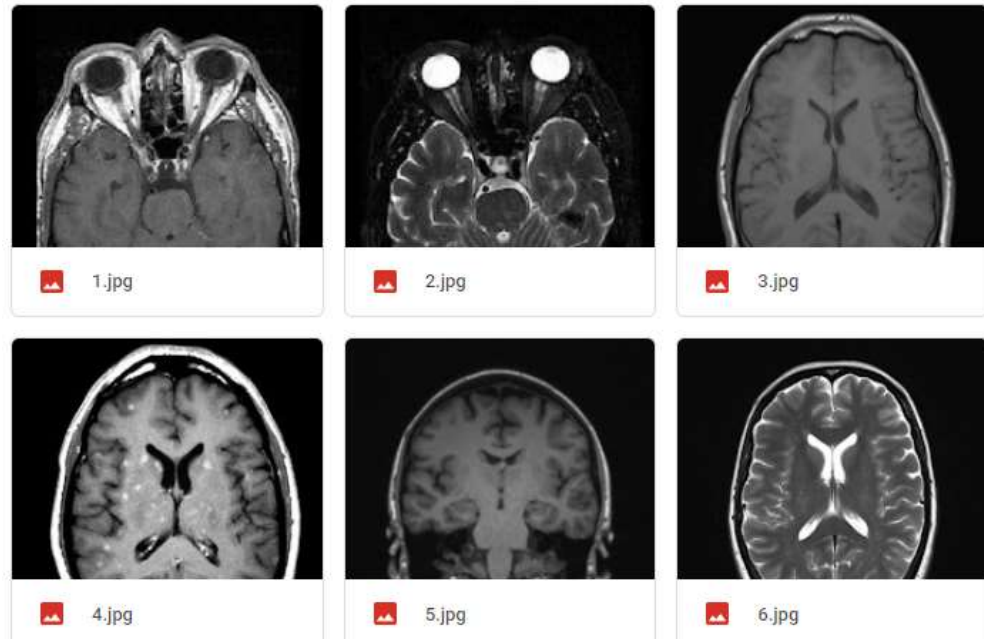


Fig 4. No Tumor Image

- B. **Pre Processing of Images** :- Images are pre-processed using OpenCV and Preprocessing.py. the images are obtained from the database after the images are already pre-processed from MRI (Magnetic Resonance Imaging) format and converted to jpeg format and later utilised by us in the Convolution Neural Network. An example is show below for representation in fig 5.

Original Image

Cropped Image

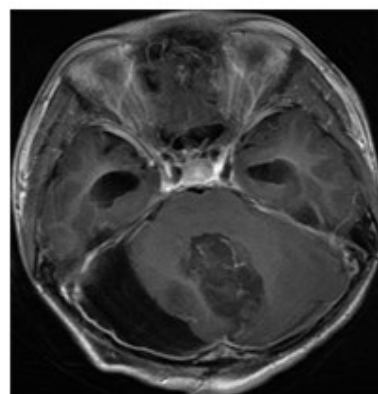
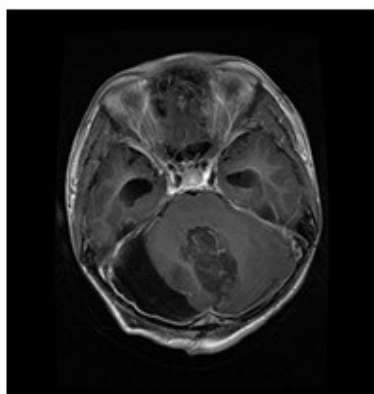


Fig 5. Processed Image of MRI scan

- C. **Basic System Requirement** :- For this Convolution Neural Network the following system requirements are needed which are shown in table 1

Table 1. Basic Requirements

Package Name	Version
Python	3.7.12
Tensorflow	2.6.0
Keras	2.6.0
Keras-Preprocessing	1.1.2
Matplotlib	3.0.2
OpenCV	4.1.2
Scikit-learn	0.22.2

- D. **Our work:** - We have designed our model based on Convolution Neural Network. Here we have used Conv2D, Maxpool2D, flatten, dense and dropout layers for our network. The image size is taken as 128*128. The kernel size has been reduced to 1*1 using dimension reduction feature. Total no of parameters used are 569412. A snapshot image of the model consisting its layers has shown in fig 6. For comparison we have also included results of two models namely Resnet50 and InceptionV3.
- Resnet50:- It is a 50 layer convolution neural network model is used for classification of images. It is also used for object detection. For this to work, the images were sized at 224*224. The meaning of Resnet is residual meaning feature detection.
 - InceptionV3:- It is a 22 layer model which was designed to make deep computational model less GPU extensive. We are using third version of InceptionV3. Here the image size is 299*299.
 - **Proposed Model:** - In the proposed model we are using 1 dropout model. The image size is 128*128 and the kernel size is 3. We are also using Conv2D, Maxpool2D in our layers. Total parameters considered in the model are 569412.

Layer (type)	Output Shape	Param #
input_2 (InputLayer)	[(None, 128, 128, 3)]	0
conv2d_9 (Conv2D)	(None, 126, 126, 32)	896
max_pooling2d_3 (MaxPooling 2D)	(None, 63, 63, 32)	0
conv2d_10 (Conv2D)	(None, 61, 61, 64)	18496
conv2d_11 (Conv2D)	(None, 29, 29, 128)	204928
max_pooling2d_4 (MaxPooling 2D)	(None, 14, 14, 128)	0
conv2d_16 (Conv2D)	(None, 7, 7, 128)	16512
conv2d_17 (Conv2D)	(None, 3, 3, 256)	295168
max_pooling2d_5 (MaxPooling 2D)	(None, 1, 1, 256)	0
flatten_1 (Flatten)	(None, 256)	0
dense_2 (Dense)	(None, 128)	32896
dropout_1 (Dropout)	(None, 128)	0
dense_3 (Dense)	(None, 4)	516
=====		
Total params: 569,412		
Trainable params: 569,412		
Non-trainable params: 0		

Fig 6. Architecture snapshot of the model

E. **Evaluation:** - In order to evaluate our model, we have used Accuracy, Recall and Precision. These terms are explained as following :-

$$\text{Accuracy} = \frac{\text{True Positive} + \text{True Negative}}{\text{True Positive} + \text{True Negative} + \text{False Positive} + \text{False Negative}}$$

$$\text{Recall} = \frac{\text{True Positive}}{\text{True Positive} + \text{False Negative}}$$

$$\text{Precision} = \frac{\text{True Positive}}{\text{False Positive} + \text{True Positive}}$$

F. **Result:** - Convolution Neural Network models based on machine learning has to perform successfully in classification of the given class. Here we are also comparing our model to to models namely InceptionV3, and Resnet50.

Table 2. Result of 4 Way Classifications

	Class	Precision	Recall	Accuracy
Resnet50	Pituitary	82.05	80.00	73.77
	Glioma	51.16	78.57	
	Meningioma	100.00	66.66	
	No Tumor	86.66	66.66	
InceptionV3	Pituitary	75.00	82.50	77.86
	Glioma	66.66	50.00	
	Meningioma	81.25	86.66	
	No Tumor	85.36	89.74	
Our model	Pituitary	91.89	85.00	85.24
	Glioma	67.74	75.00	
	Meningioma	85.71	80.00	
	No Tumor	92.50	94.87	

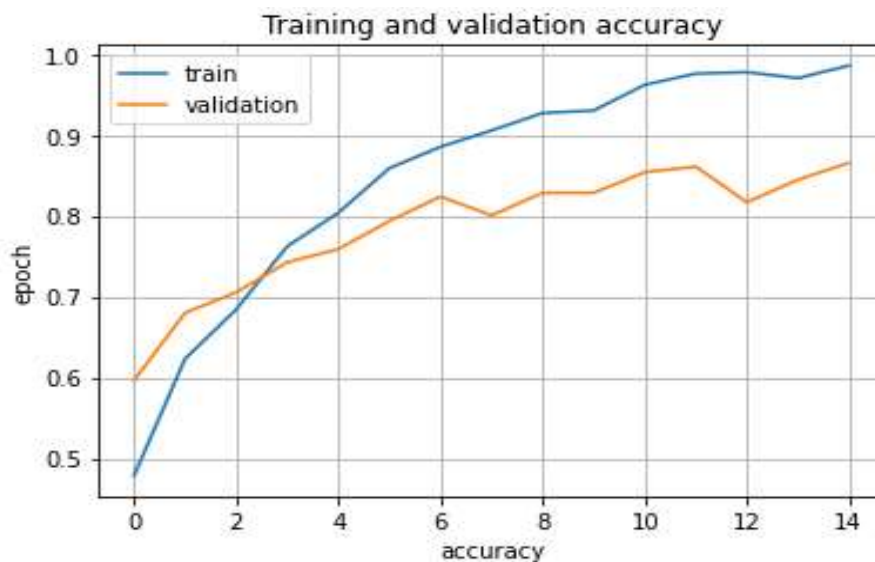


Fig 6. Training and Validation accuracy of the model

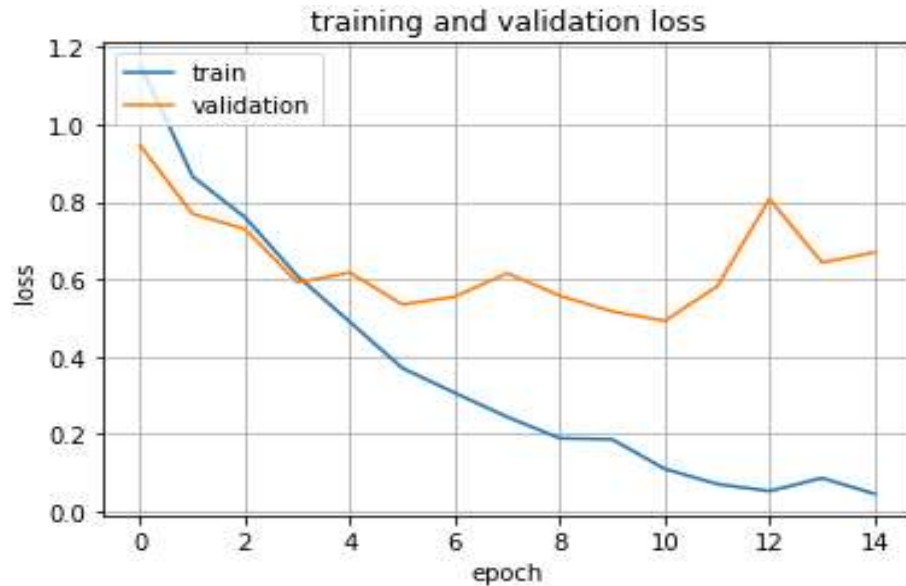


Fig 7. Training and Validation loss of the model

IV. Conclusion :-

In this work, we have designed a model to predict the four classes namely Glioma, Meningioma, Pituitary or No tumor from the jpeg image. For this model to train we have used images from kaggle database and the experiments were performed on Google Colab. The Keras models used for this work are Dense, Flatten, Conv2D, Maxpool2D, and Dropout. TensorFlow framework is used to build the model. The Epoch were set at 15 with callback for early stop. The size of the batch is 32.

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