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Detection of Brain Tumor

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Abstract- **A study conducted by the "New England Journal of Medicine" for brain tumor revealed that more than half the cases diagnosed were delayed for a year or longer. This low percentage of correct diagnosis by physical practitioners was astonishing with an average pre-diagnostic symptomatic interval (PSI) being 60 days with a parental delay of 14 days and a doctor's delay of 30 days. This meant, there existed a delay of almost 104 days in the diagnosis. Among the diagnosed brain tumors only 33% of them were diagnosed by the end of the 1st month after the onset of first signs and symptoms. Physical segmentation of the MRIs by a radiologist is often a monotonous and prolonged process. A viable solution is a Deep Learning aided brain tumor detection and segmentation from brain MRIs. The detection of brain tumor from the magnetic resonance images is an extremely important process for deciding the right therapy at the right time.**

Keywords- **Magnetic Resonance Images, Deep Learning, Convolution neural networks, data augmentation, data generators, Data pre-processing, Image Normalization.**

I. INTRODUCTION

A tumor can develop in any part of the body and hamper the normal working of the body's functions; however, a tumor in the brain can be fatal. It is found that tumors present in the brain account for the most common cause of deaths related to cancer in children and people up to the age of 40 years. This along with the fact that 67% of brain tumors were diagnosed only after the first month of the onset of their symptoms makes it of paramount importance that once diagnosed; the tumor is correctly detected so the best course of treatment can be deployed.

There has been an exponential increase in the use of technology in medical sciences which has been a great boon to the healthcare sector. With this in mind, the most common method of diagnosis for brain tumors is via the use of MRI scans as they serve as a non-invasive method for medical imaging.

The traditional method of physical segmentation of medical images by radiologists is not only a monotonous and prolonged process but also presents a lot of scope for error. It normally takes an average of 24-48 hours for the MRI scans to be interpreted by a radiologist. Automating this process of detection will not only help in availing the results faster but will also increase the accuracy of detection of brain tumors.

So, in this project we are developing a model that will detect the presence or absence of a brain tumor in the MRI scans which are going to be given as the input. Since detection forms the basis of classification, the work done in this project can be further used for developing a model that will classify the brain tumor that was detected.

II. BRAIN TUMOR DETECTION USING CONVOLUTIONAL NEURAL NETWORKS

1. Problem Statement:

Brain tumors are one among the most dangerous illnesses in which early detection and accurate detection is of utmost importance. Now most identification and diagnosis methods rely on decision of medical specialists like neuro specialists, and radiologists for image observation and evaluation and because of this, the occurrence of human error is possible and it is also time consuming.

2. Methodology:

In order to build a CNN model for brain tumor detection, an appropriate dataset is required. In this project, we chose to use Brain MRI images for brain tumor detection dataset from Kaggle (Chakrabarthy, 2020).

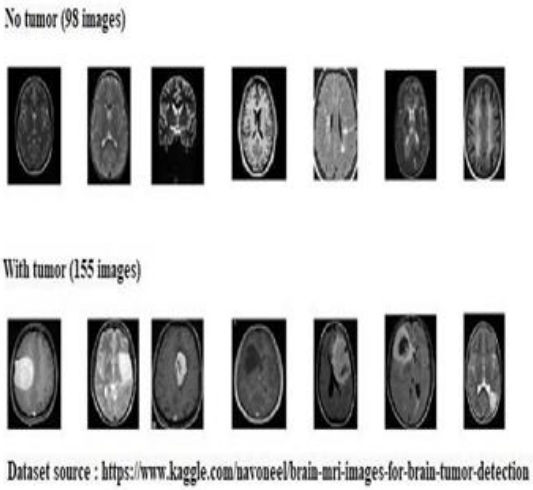

Fig 1. Some images in the dataset.

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The dataset consists of 2 folders: The "yes" folder which consists of brain MRI scan images which have tumors in them. There are 155 images in this folder. The other folder is the "no" folder which consists of brain MRI scan images which do not have any tumors in them. There are 98 images in this folder. So, around 61% (155 images) of the dataset consists of positive images and around 39% (98 images) of the dataset consists of negative images. Fig.1 shows some images from the dataset.

3. Data Pre-Processing:

- First data generators were set up to read pictures in the source folders, convert them to tensors, and feed them (with their labels) to our network.
- Data augmentation was applied to the images. Data augmentation maybe a deep learning pre-processing strategy that allows practitioners increase the range of knowledge available for training models (Habib et al., 2020).
- Unfortunately, we did not have sufficient images in the dataset to develop the neural network and augmenting the data was very useful in solving the data imbalance issue.
- For augmentation, the following operations were applied: rotation_range, width_shift_range, height_shift_range, shear_range, zoom_range, horizontal_flip and vertical_flip.
- Images were resized to (240, 240, and 3) so that all the images have a similar shape and size to give it as an input to the neural network.
- Normalization was done to scale pixel values to the range 0-1. All the operations can be done in Keras via the keras. Pre processing image. Image Data Generator class.

Fig2 shows the diagrammatic representation of the data pre-processing details.

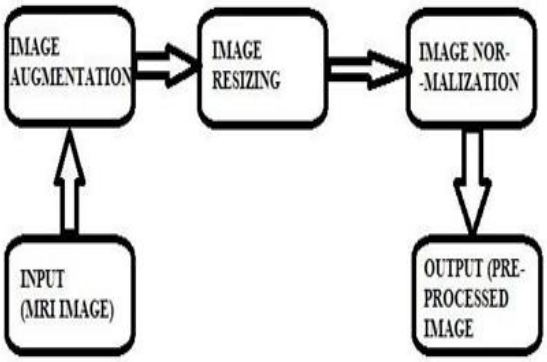

Fig 2. Pre-processing details.

Fig 3 Shows images before and after data augmentation.

4. Data Split:

- A split_data function was defined which takes in the training, testing and source dataset paths and spilts the dataset according to the given split size.
- 80% of the dataset was used for training the model and 20% was used for testing. So, the split size was given as 0.8.

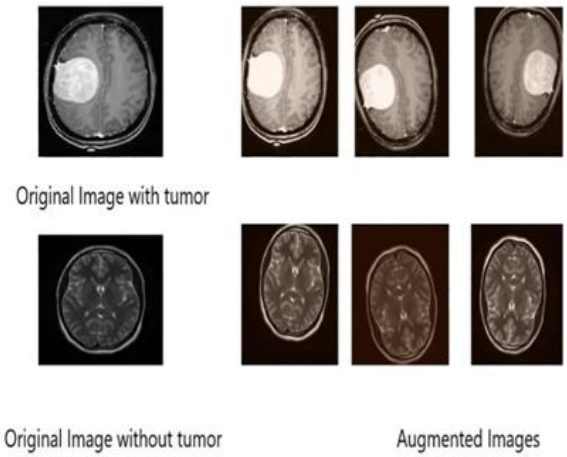

Fig 3. Images before and after augmentation.

5. Details of the model:

- The sequential model was used to make the CNN. Two convolutional layers have been used with 32 and 64 filters respectively.
- Two max pooling layers was used with f=4 and s=4.

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 239, 239, 32)	416
max_pooling2d (MaxPooling2D)	(None, 59, 59, 32)	0
dropout (Dropout)	(None, 59, 59, 32)	0
conv2d_1 (Conv2D)	(None, 58, 58, 64)	8256
max_pooling2d_1 (MaxPooling2	(None, 14, 14, 64)	0
dropout_1 (Dropout)	(None, 14, 14, 64)	0
flatten (Flatten)	(None, 12544)	0
dense (Dense)	(None, 128)	1605760
dense_1 (Dense)	(None, 1)	129

Total params: 1,614,561
Trainable params: 1,614,561
Non-trainable params: 0

Fig 4. Summary of the model.

- Three ReLu activation layers.
- A Flatten layer was used so that we could flatten the 3-dimensional matrix into a one-dimensional vector.

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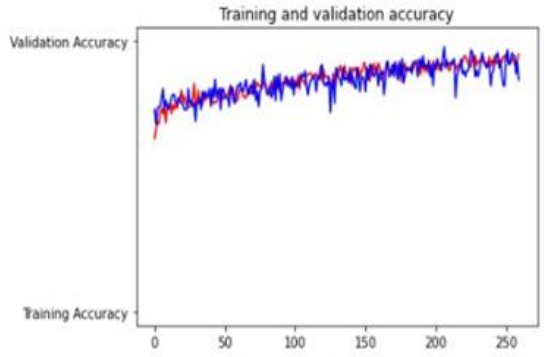
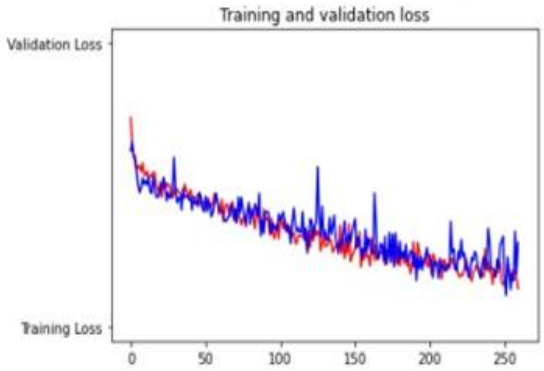
- A Dense fully connected layer was utilized with one neuron with a sigmoid activation function. Fig.4 shows the details of the model that were obtained using model.summary () function.

6. Training the model:
The model after bring trained for 239 epochs has the loss and accuracy plots as shown in Fig 5:



(a)



(b)

Fig 5. Accuracy and loss plots.

Since a callback class was utilized to stop the training of the model any further as soon as an accuracy of 95% was reached, it can be seen that the model has achieved the best accuracy in the last epoch.

7. Results:
After training the model for epochs, the results were:

- Accuracy – 0.95
- Loss – 0.16
- Validation accuracy – 0.89
- Validation loss – 0.24

III. SCOPE FOR FUTURE STUDY

An end to end trained CNNs approach has been preferred for the analysis of medical images in the last couple of years but the extensively varying results upon an increase in the size of the dataset is a point of concern. The model hyper-parameter optimization aspect also affects the performance of the network by a great deal. Unfortunately, there have been no clear techniques or methods to assess the best set of hyper-parameters for empirical exercises. Some researchers have also experimented with the Bayesian methods for hyper- parameters' optimization but in this domain of brain image analysis, these techniques have not yet been implemented. (Castano et al., 2019)

The lack of the availability for larger training datasets is a challenging obstacle for deep learning techniques as the increase in the size dataset has often led to the varying of the desired results. The introduction of the structured report labels in the analysis of brain tumors is required to turn out to be a lot simpler later on. It is anticipated that the utilization of a text free and a structured report for training a network may increase quickly. The labelling of tumorized images is not only time-consuming but it also requires a high level of expertise which is a challenge in the analysis of brain tumors.

The training of systems based on the deep learning algorithms that perform the segmentation of tumors, generally in a 3-dimensional network, and it needs slice-by-slice annotations (Nadeem et al., 2020) which are a difficult as well as a tedious undertaking.

The efficient learning of deep learning methods from a limited amount of image data is also a major limitation of deep learning algorithms, as that would result in the variation of the output with an increase in the size of the dataset. Another issue identified with the dataset is the class imbalance. One such example is the data augmentation technique which is used to generate newer lesions for the brain tumor by the process of scaling and rotation and hence may cause class-imbalance. (Nalepa et al., 2019)

IV.CONCLUSIONS

In this project, our main objective was to develop a model to detect the presence of brain tumor from Magnetic Resonance Images via a deep learning model. This would aid in quicker and a more efficient detection of brain tumor. The model was trained for a dataset which consisted of a folder with brain tumor scans containing 149 images and another folder with healthy brain scans containing 92 images. The model was tested for a dataset which consisted of a folder with brain tumor scans containing 56 images and another folder with healthy brain scans containing 34 images.

The datasets were preprocessed by generating "patches" of our data which were sub-volumes of the entire Magnetic Resonance Images. The generation of the patches was a necessary procedure as the network that could process the entire volume of the Magnetic Resonance Images would not fit in our current environment's GPU. Hence, we

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generated spatially consistent sub-volumes of our data which we would feed into our network. Since the large portions of the MRI were just brain tissues or black background without any tumor regions present on them, we wanted to make sure that we picked up only the "patches" that included at least some amount of tumor, hence we picked up "patches" with at-most 95% non-tumor regions so that at least 5% of the regions would consist of tumor regions. This was done by filtering the volumes based on the values present in the background labels. The filtering was by Gaussian filters since it was optimal in the flat parts of the image.

Following the preprocessing, we performed data augmentation, which expanded the scale of the training dataset by creating modified versions of the images in the dataset. This introduced variations in the data samples, improved the ability to fit the models (reduced overfitting) and generalized their learning to the new images. With the use of the transfer learning and the data augmentation techniques, we were able to achieve high accuracies of 95% on the training data and an accuracy of 89% on the validation data which was a significant improvement given that the initial model had an accuracy of only 80%.

For the purpose of augmentation, we had to create and configure our ImageDataGenerator, which we fit on our data. This would calculate the statistics to be performed on the transforms to our image data. This was done by calling the fit() function on the data generator and passing it to our dataset. The data generator being and iterator by itself, returned batches of image samples upon request. We then configured the batch size and prepared the data generator by calling the flow () function. When we replaced the fit () function with the fit_generator() function and passed it on the data generator with the desired length of the epochs, we could observe a significant improvement in the accuracy.

The images in the dataset were subjected to random shifts which were supported in the keras framework as width_shift_range and height_shift_range respectively. This was performed as the images in our dataset may not have been centered properly in the frame. By utilizing the random shift operations, we can handle off-center objects by artificially creating shifted versions of our training data.

1. Confusion Matrix:

N=TotalCases	Target Class Non- Tumor Output(0)	Target Class Tumor Output (1)
Non- Tumor Input (0)	3	0
TumorInput (1)	1	5

The confusion matrix describing the classification on our data for which the true values were known is given above. From the above table it can be inferred that there may occur two instances of our detection of brain tumor. The presence of the brain tumor and the absence of the brain tumor.

However, since our model is not 100% accurate, there may arise a certain amount of ambiguity. We conducted a total of 9 tests for our model, which demonstrated five cases which showed the presence of the tumor which was a true prediction (True Positive), three cases demonstrated the absence of the tumor which was also a true prediction (True Negative) and 1 case demonstrated the absence of the tumor which was a false reading as there was a presence of the tumor in that case (False Negative).

We came across no cases which demonstrated a false positive that is, showing a presence of the tumor in the absence of it. (False Positive).

The precision and the recall were found to be 1 and 0.83 respectively. The precision was 1 since there existed no false positives, that is, no tumor detected where there were no tumors present. The F1-score which is a weighted average of the precision and the recall was found to be 0.907.

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