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Classification of Brain Tumor Using Deep Neural Network

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ABSTRACT: A brain tumour is the turbulent growth of abnormal brain tissue that can impair normal brain function. To analyse the tumours and choose a course of therapy based on their classes, it is essential to categorise brain tumours. In some cases, a proper diagnosis can save a patient's life. Even if there are many brain tumour segmentation and classification algorithms, it is still difficult to use multiclass classification and improving tumour segmentation approaches because brain tumour characteristics are complicated. However, MRI is frequently employed because it produces images of a higher quality and because it uses no ionising radiation. A fresh approach for classifying MRI images using deep neural networks has been suggested as a solution to this issue. A subset of machine learning called deep learning (DL) has lately displayed impressive performance, particularly in classification and segmentation issues. This research suggests a ResNet101-based approach for identifying the species of locust. The suggested solution makes use of ResNet101 as a feature extraction network, Transfer learning to enhance the pre-trained model, and data augmentation methods to avoid the network overfitting. A study done to assess the suggested ResNet101 model's accuracy reveals that it is capable of accurately classifying several species of locust.

I.INTRODUCTION

With an increase in the desire for automated, trustworthy, quick, and efficient diagnosis that can give insight to the image better than human eyes, the discipline of medical imaging is gaining prominence. A tumour is an abnormal growth of cells within the human body. Because the brain is such a fragile organ of the human body that it is treatable, brain tumours are an extremely serious and life-threatening condition. Brain tumours, however, can be either benign or malignant, which means they can be cancerous or not. The identification of a brain tumour is crucial, and treatment options vary depending on the kind, location, size, and stage of the tumor's development. If left untreated, brain tumours can cause a number of different disorders. The most crucial step in treating a tumour is its analysis. Analysis of benign and malignant tumours heavily relies on detection. The failure to treat tumours in their early stages is a significant factor in the rise in the number of cancer patients globally.

1.1 HUMAN BRAIN

Human brain is the first and foremost controller that controls the sympathetic and para-sympathetic activities. Brain is the seat of intelligence, initiator of body development and movement, and controller of behaviour. Human brain is the most complex organ which consists of more than 100 billion nerve cells which communicates through synapses. Neurons are the nerve cells which carry information from one organ to another organ of body. The human brain is the centre of control of the nervous system. Numerous neurotransmitters serve as the route via which different neurons can communicate. the channel of communication connecting the dendrites of the subsequent nerve cell to the synapses of the preceding nerve cell. The human brain is in charge of controlling muscular action, regulating internal temperature, and being aware of our surroundings. Our brain generates every original idea, sentiment, and strategy. The brain serves as the world's most complex bio-computing system's central processing unit (CPU) and is responsible for ideas, feelings, wisdom, communication, and the coordination of muscle actions from sense organs including pain, taste, sight, hearing, and touch.

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1.1.1 HUMAN BRAIN ANATOMY

The human brain weighs an average of 1.3–1.4 kg and is made up of neurons, blood vessels, and glial cells. The occipital lobe, frontal lobe, parietal lobe, and temporal lobe are the four lobes that make up the human brain. The greatest portion of the brain, the cerebrum, contains the cerebral cortex. As indicated in Figure 1, the basal ganglia, cerebellum, skull, and spinal cord are the other major brain coordinating centres.

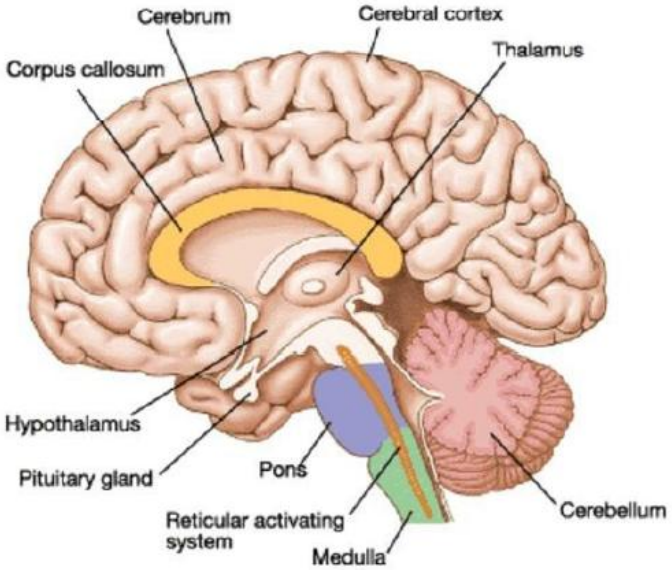

Figure 1: Human Brain Anatomy

1.1.2 BRAIN TUMOR

A brain tumour is the uncomfortable growth of a damaged or abnormal cell in the brain. Increased intracranial pressure from a brain tumour affects the cerebrospinal fluid (CSF), grey and white matter (GM), and white matter (WM) regions of the skull. The severity of a tumour depends on the size, nature, and location of the tumour and can impact any portion of the brain. Like the body's regular aged cells, tumour cells proliferate uncontrollably and don't expire. The creation of cysts and the accumulation of cells both contribute to the tumor's continued growth. There are two types of brain tumours: benign and malignant.

1.2. BENIGN TUMOR

Invasion of nearby tissues by benign tumour cells is rare. Other bodily parts are not affected by them spreading. Benign tumours, however, can irritate the brain's delicate structures and result in life-threatening medical issues. Fortunately, benign tumours are easily treatable and seldom recur.

1.2.1 MALIGNANT TUMOR

Cancerous cells infect nearby healthy tissues to form malignant tumours, which then spread to other parts of the brain or spine. This kind of tumour spreads quickly and is more deadly than benign tumours. Due of cell penetration close, the edge cannot be seen properly. It expands quickly and begins to devour the surrounding, healthy brain tissue.

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Several variables affect how a brain tumour grows and develops: • Size and origin location.
• Biological characteristic and type of tissue affected.
• Spread of tumor within brain or spinal cord.
• Primary and secondary tumor

1.2.2 MENINGIOMA TUMOR

The cells of the membrane that covers the brain and spinal cord are where meningiomas grow. Approximately 15% of all intracranial tumours are meningiomas, commonly known as meningeal tumours. The majority of these tumours are benign, or slow-growing and non-cancerous. Surgery is often used to remove meningiomas. Some meningiomas might not require immediate care and could go unnoticed for years. Because content may be readily deleted without the right permission. The deletion of nodes that are referring to specific pieces of data in the virtual machine is completely necessary for data elimination.

II.LITERATURE REVIEW

2.1 CLASSIFICATION USING DEEP LEARNING NEURAL NETWORKS FOR BRAIN TUMORS.

A dataset of 66 brain MRIs was classified into four classifications in [1] using a Deep Neural Network classifier, one of the Deep Learning architectures, including normal, glioblastoma, sarcoma, and metastatic bronchogenic carcinoma tumours. The discrete wavelet transform (DWT), a potent feature extraction method, principle components analysis (PCA), and the classifier were integrated, and the performance was evaluated as being pretty good across all performance parameters.

2.2 MRI IMAGE CLASSIFICATION USING ADABOOST FOR BRAIN TUMOR TYPE

Using the Adaboost machine learning algorithm, the author of suggested an efficient automatic classification approach for brain MRI in [2]. Three components make up the proposed system: pre-processing, feature extraction, and classification. The noise in the raw data has been eliminated using pre-processing, which also applies a median filter, thresholding segmentation, and a grayscale conversion of the RGB image. 22 features were recovered from an MRI utilising the GLCM approach for feature extraction. Adaboost is a classification-boosting approach. With 89.90% accuracy, it can detect benign or malignant tumours as well as normal brain tissue.

2.3 CLASSIFICATION OF TUMORS AND IT STAGES IN BRAIN MRI USING SUPPORT VECTORMACHINE AND ARTIFICIAL NEURAL NETWORK

Using an artificial neural network (ANN), a new technique is presented in [3] that includes steps including picture pre-processing, segmentation, feature extraction, SVM classification, and tumour stage classification. Three contrast enhancement approaches are used in the pre-processing stage: adjusted, adaptive threshold, and histogram imaging using the weiner2 and median2 filters. The TKFCM method, which combines K-means and Fuzzy c-means with minor modifications, is used for segmentation. Features are extracted in two different orders. Property-based statistical characteristics are produced for both first and second order regions. SVM will then classify the MRI of the brain as either normal or tumorous. ANN classifier is used to categorise the stage of brain tumour. 39 pictures, including 3 normal, 9 benign, 17 malignant I, 6 malignant II, 3 malignant II, and 1 malignant IV stage tumour brain MRI images, were utilised to collect the data for each MRI image of a normal brain, malignant tumour, and benign tumour.

2.4 EFFICIENT DETECTION OF BRAIN TUMOR FROM MRIS USING K-MEANS SEGMENTATION AND NORMALIZED HISTOGRAM

A unique approach that uses K-means segmentation and normalisation of the histogram is presented in [4]. The supplied image is first pre-processed to get rid of any undesirable signals or noise. The MRI pictures are de-noised using filters such the Median filter, Adaptive filter, Averaging filter, Un-sharp masking filter, and Gaussian filter. The pre-processed image's histogram is normalised, and MRI classification is carried out. [4] describes a unique approach that uses K-means

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segmentation and normalisation of the histogram. To eliminate any undesirable signals or noise from the input picture, preprocessing is done first. In order to reduce noise in MRI pictures, filters such the Gaussian filter, Median filter, Adaptive filter, Averaging filter, and Un-sharp masking filter are utilised. The pre-processed image's histogram is normalised, and the MRI is classified. To remove the tumour from the MRI, the image is then segmented using the K-means method. In order to give precise prediction and classification, the MRIs are efficiently classified using the NB Classifier and SVM. Accuracy is 87.23% using the SVM Classifier and Naive Bayes. The suggested approach has numerous drawbacks, including the inability to determine the exact or correct boundaries of the tumour zone.

2.5 TUMOR DETECTION IN BRAIN USING GENETIC ALGORITHM

In [5], DWT is used to de-noise a brain MRI picture by thresholding the wavelet coefficient. It uses a genetic algorithm to find tumour pixels. The optimum information extraction strategy using the chosen criterion is then determined using a genetic algorithm. The current method incorporates k-Means clustering techniques into genetic algorithms to direct this final evolutionary algorithm's search for the best or worst possible data split. Based on ground truth, our technique was able to accurately segment 82 to 97 percent of tumour pixels. This work's shortcoming is the high computational cost and significant storage requirements of the wavelet transform.

2.6 INTELLIGENT BRAIN TUMOR LESION CLASSIFICATION AND IDENTIFICATION FROM MRI IMAGES USING K-NN TECHNIQUE

The proposed methodology in [6] includes techniques like the histogram, resampling, K-NN algorithm, and distance matrix. The first thing a histogram provides is the overall distribution of pixels with the specified value in a given picture. Image resized to 629 x 839 for suitable geometric representation after resampling. brain tumour classification and detection utilising k-NN, which is based on k's training. Manhattan metric has been used in this study to apply and determine the classifier's distance. Utilising Lab View, the algorithm has been put into practise. On 48 photos, the algorithm has been tested. The overall identification rate is around 85%.

2.7 BRAIN TUMOR DETECTION USING SEGMENTATION BASED OBJECT LABELING ALGORITHM

The author of [7] presented a segmentation-based object labelling algorithm for brain tumour detection. By employing the K-means algorithm and the Object labelling algorithm, this technique removes the tumour. Additionally, morphological operations and median filtering are performed as pre-processing procedures for the goal of tumour identification. It has been shown that the experimental findings of the suggested strategy produce superior outcomes than those of other approaches.

2.8 MRI BRAIN IMAGE RETRIEVAL USING MULTI-SUPPORT VECTOR MACHINE CLASSIFIER

The approach described in [8] was created using a multi-support vector machine classifier. The picture has undergone median filter pre-processing. For feature extraction, the Grey Level Co-occurrence Matrix is employed. Three different types of images are classified using the Multi-Support Vector Machine (M-SVM) classifier. Multiple picture queries perform better on the system than a single image query.

2.9 ROBUST ALGORITHM FOR BRAIN MAGNETIC RESONANCE IMAGE CLASSIFICATION BASED ON GARCH VARIA NCES SERIES

[9] describes a strategy for categorising MRI results as either normal or indicative of one of seven distinct disorders. The brain MRI two-level 2D DWT coefficients are calculated. GARCH is used to model the estimated coefficients of detail sub-bands. Principal component analysis (PCA) and linear discriminant analysis (LDA) are used to extract the right features and eliminate duplication from the primary feature vector following feature vector normalisation. Finally, to identify the kind of illness or normal picture, the collected features are individually put to the K-nearest neighbour (KNN) and support vector machine (SVM) classifiers.

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2.10 AN EFFICIENT BRAIN TUMOR DETECTION METHODOLOGY USING K- MEANS CLUSTERING ALGORITHM

The author of [10] offers an effective technique for automatically segmenting brain tumours in order to retrieve tumour tissues from MR images. For greater performance, segmentation is done in this approach utilising the K-means clustering algorithm. When compared to other clustering techniques, this improves the tumour borders more and is quite quick.

III. PROPOSED METHODOLOGY

3.1. INTRODUCTION

Meningioma, glioma, and pituitary tumour are the three forms of brain tumours that are to be classified using a Deep Neural Network architecture using T1-weighted contrast-enhanced magnetic resonance imaging. An important benefit of this strategy is that classification using a DNN classifier may efficiently lower computing costs and enhance recognition performance. This technique aids in the early tumour detection.

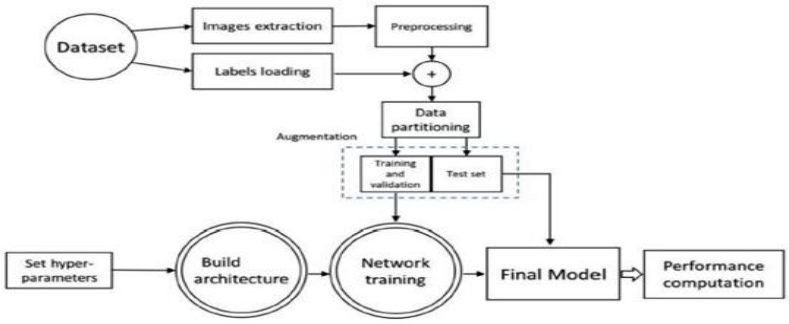

Figure 2: Architecture Diagram

The suggested method's architecture is depicted in Figure 2, where the system begins by loading and extracting pictures and labels from raw dataset files before performing pre-processing and augmentation approaches immediately after dividing the dataset into training, validation, and test sets. Following the introduction of the suggested method's structure, the hyper-parameter setup, regularisation strategies, and optimisation algorithm are discussed. Finally, computations for network training and performance are shown.

3.2. MODULE DESCRIPTION

MODULE 1: DATASET COLLECTION
MODULE 2: IMAGE PRE-PROCESSING & DATA AUGMENTATION
MODULE 3: CLASSIFICATION

3.3. MODULE 1: DATASET COLLECTION

Dataset consists of,

- Different types of tumor images like,
    - Meningioma -Tumor images
    - Glioma -Tumor images.
    - Pituitary- Tumor images

Downloaded from [11].

The dataset was obtained between 2005 and 2010 from Nanfang Hospital and General Hospital at Tianjing Medical University in China. It was then released online in many iterations starting in 2015 and ending with its most recent release in 2017. The meningioma (708 slices), the glioma (1426 slices), and the pituitary tumour (930 slices) are the three types of brain tumours included in this brain tumour dataset, which includes 3064 T1-weighted contrast-enhanced images from 233 patients. Due to the repository's file size restriction, we divided the entire dataset into 4 subsets, putting them in 4.zip files, each of which had 766 slices. Depending on their types and grades, brain tumours can vary in size, location, and

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form. Axial, coronal, and sagittal images are all included in the dataset. Three planes—sagittal (1025 photos), axial (994 images), and coronal (1045 images)—were used to collect all the images from 233 patients. Figure 3. displays instances of several distinct tumour kinds on a variety of planes. The tumours have a red border to identify them.

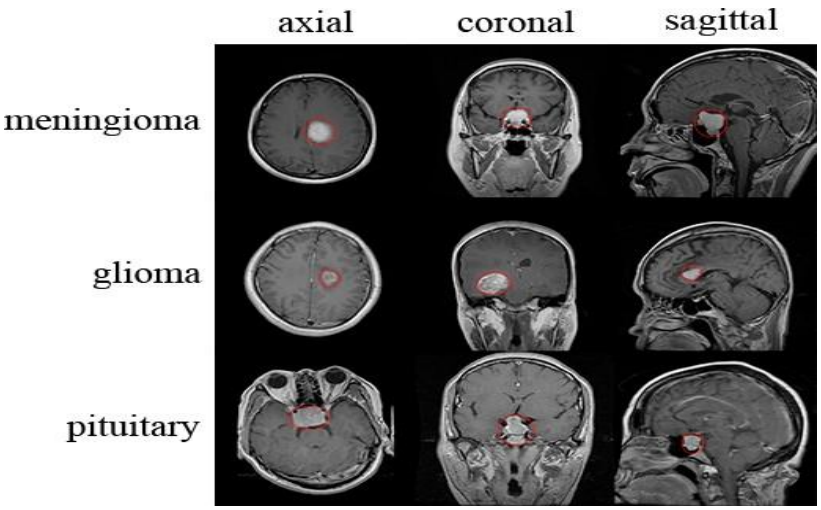

Figure 3: Representation of normalized magnetic resonance imaging (MRI) images showing different types of tumors in different planes. In the images, the tumor is marked with a red outline. The example is given for each tumor type in each of the planes.

TABLE 1. Number of slices for each brain tumor type (meningioma, glioma and pituitary) in dataset & number of patients.

Tumor Category	Number of Patients	Number of Slices
Meningioma	82	708
Glioma	91	1426
Pituitary	60	930
	233	**3064**

3.4 MODULE 2: IMAGE PRE-PROCESSING & DATA AUGMENTATION

A pre-processing phase is carried out before to feeding the photos into the suggested structure. The first step is to reduce the original picture from 512 x 512 x 1 pixels to 128 x 128 x 1 pixels in order to reduce dimensionality, simplify computations, and enable the network perform better in less time. To keep the system trained on unsorted data and prevent concentrating on a certain area of the whole dataset, data are then separated and then shuffled. Three pieces of data—training, validation, and test sets—each with a separate goal label are used to organise the data (68% for training and 32% for system test and validation).

3.5 MODULE 3: CLASSIFICATION

A Deep Neural Network was employed to classify tumours. As illustrated in Figure 4, the network design is composed of input, two major blocks, a classification block, and output. The convolutional layer in the first major block, Block A, produces an output picture that is twice as tiny as the input image. The dropout layer and the rectified linear unit

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(ReLU) activation layer come after the convolutional layer. The max pooling layer, which provides an output two times smaller than the input, is also included in this block. Only the convolution layer, which keeps the same output size as the layer's input size, distinguishes the second block, or Block B, from the first. The classification block comprises of two fully connected (FC) layers, the first of which reflects the output that has been flattened from the previous max pooling layer. The second FC layer's hidden unit count corresponds to the number of tumour class subtypes. The input layer, two Blocks A, two Blocks B, a classification block, and an output layer make up the entire network design.

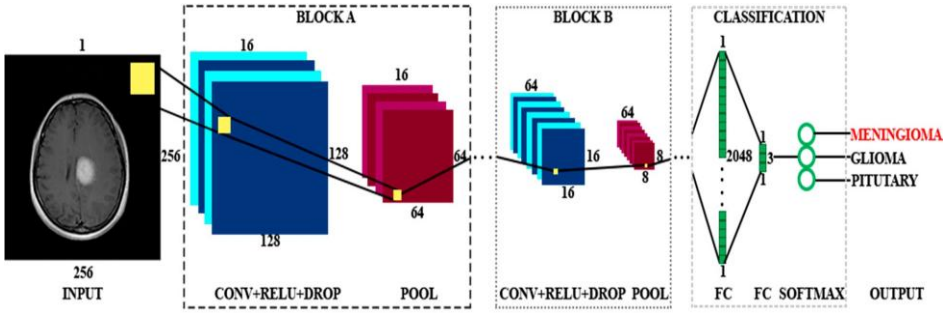

Figure 4. Schematic representation of Deep neural network (DNN) architecture

3.6. Training the Network

We used a k-fold cross-validation approach to assess the network performance. The dataset contained only.mat format files. The Deep Neural Network will go through several steps throughout the training phase. In FIGURE 4, the recommended DNN structure is displayed. Starting with the input layer, which includes the augumented pictures from the previous pre-processing stage, and proceeding through them as needed for features selection and downsampling, are layers like convolution, Rectified Linear Unit (ReLU), normalisation, and pooling. To evaluate the network performance, we applied a k-fold cross-validation technique. All of the files in the dataset were in.mat format. During the training phase, the Deep Neural Network will go through a lot of processes. The suggested DNN structure is shown in FIGURE 4. Layers such as convolution, Rectified Linear Unit (ReLU), normalisation, and pooling are included, starting with the input layer, which contains the augumented images from the previous pre-processing step, and moving through them as needed for features selection and downsampling. A dropout layer is employed to prevent over-fitting, followed by a fully connected layer, a softmax layer, and a classification layer to yield the predicted class. When a picture is entered during the convolution stage, a feature detector is applied to the image. A feature detector is a 3x3 square with randomly generated integers allocated to each square that range from 0 to 256. The feature detector is modified as the neural network is trained to recognise particular features that have an impact on an image's categorization. The value of the relevant squares in the input picture is multiplied by the feature detector. One square of the Feature Map will be filled with the total of all the products. When the entire picture has been processed, the feature detector will proceed by moving one pixel to the right and repeating the previous step. For quicker training, the data is compressed using the Feature Map. The researcher doesn't want rotation, squashing, flipping, or other events to cause the neural network to get "confused" when processing a picture. The researcher employs "Max Pooling" as a result. The feature map is checked at this step using a 2x2 square that is moved 2 pixels to the right each time. The Pooled Feature Map is turned into a column of integers during the flattening process. To enter the numbers into the neural network as inputs for the deep neural network, this is done.

The flattened Pooled Feature Maps' inputs are sent via a deep neural network (DNN) during the Full Connection process.The 'neurons' of a DNN process the inputs and evaluate the results to determine how they will affect the categorization outcome. The DNN chooses the weights for the inputs, which chooses which inputs and how much they influence the output. Over several training sessions, the weights fluctuate. The DNN is applied to the data, and the classification accuracy is checked. If not, the weights are adjusted, and the network's training is continued.

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3.7. Training and Validation accuracy and Loss for Fold -1

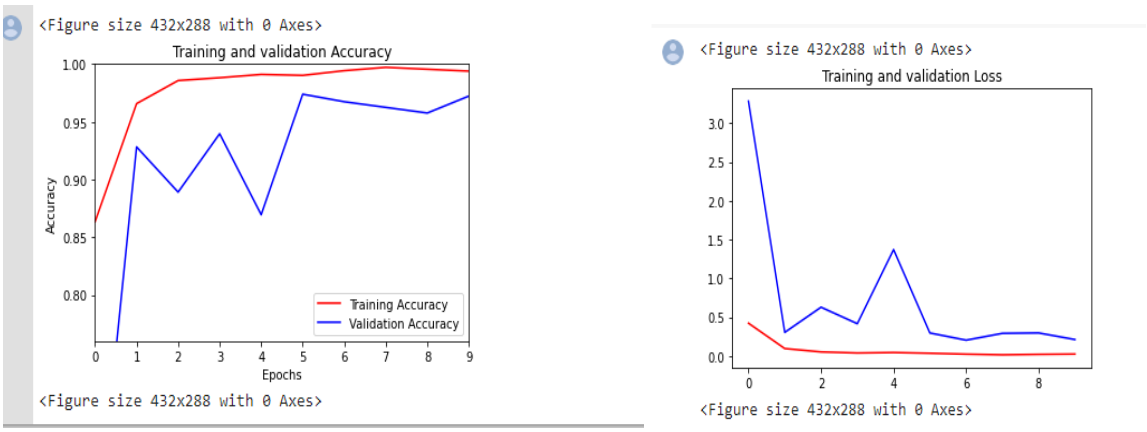

Figure 5. Training and Validation accuracy and Loss for Fold -1

Predicting the tumor type ---- Class 0 ----> Meningioma
Class 1 ----> Glioma
Class 2 ----> Pituitary tumor

Confusion matrix for three types of tumor

```
[[ 707    0    1]
 [   0 1426    0]
 [   0    0  930]]
```

IV.CONCLUSION AND FUTURE WORK

A method for classification of brain tumor MR images into three types (meningioma, glioma, and pituitary) using a deep neural network was proposed. The suggested network is built starting with an input layer that contains the pre-processed pictures and moving via convolution layers and their activation functions. It uses a fully connected layer, a softmax layer, and a classification layer to forecast the output, producing the predicted class in the process. Despite the fact that the dataset is not very large (because of the variety of imaging viewpoints), data augmentation really assisted in displaying better findings and so resolving this issue. With a precision of 98.7%, our suggested architecture has the maximum accuracy. Tumour categorization experiments have demonstrated the viability and efficacy of the suggested approach.

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