



## Automatic Brain Tumor Detection and Classification using Modified DenseNet201

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### Abstract

The brain is the most significant organ in the body since it is responsible for controlling all of the other organs. A tumor is an abnormal development of cells that results from the unregulated division of cells. This results in the formation of the tumor. There are three different sorts of tumors namely glioma, meningioma and pituitary. In a variety of fields, including medical imaging, DL-based algorithms have demonstrated exceptionally high levels of performance. In this article, an automated method for the identification and categorization of brain tumors by using DenseNet201 deep learning model. The conventional DenseNet201 model is modified by adding dropout layer to remove extra connections and make the model optimal. A DenseNet is a specific kind of deep learning model that makes use of dense connections between layers. These connections are made using Dense Blocks, which include connecting all layers directly with each other and ensuring that their feature-map sizes are the same. The proposed model obtained an accuracy of 97.45% which is better than the existing models.

**Keywords:** Brain tumor, MRI images, glioma, meningioma, pituitary, DenseNet201

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### I. Introduction

In today's modern environment, the integration of information technology and machine learning into medical practice has become increasingly significant. The study of artificial intelligence, often known as ai, is a subfield of computer science that focuses on the creation of machines that are capable of self-directed learning without the need for human input in order to better equip themselves to solve problems on their own. Because tumour cells exhibit extremely unpredictable behaviour that is too

complicated to be regulated by traditional medicine, the application of this science finds great importance in the development of therapies for brain tumours.

The human brain is one of the most essential organs in the body since it assists with decision making and governs the whole performance of the body's other organs. It is basically the command-and-control centre of the central nervous system and is accountable for the execution of the daily actions, both voluntary and involuntary, that take place



within the human body. The tumour is a fibrous mesh of undesired tissue development that is occurring inside of our brain and is expanding in an unrestricted manner. A proper knowledge of brain tumours and the stages they progress through is a necessary step in the process of both preventing the sickness and treating it after it has shown itself. Magnetic resonance imaging, also known as MRI, is frequently utilised by radiologists in the diagnosis and evaluation of brain tumours.

When human brain tissue becomes infected with tumour cells, there is an increased risk of death from a variety of catastrophic conditions. In the absence of insightful answers, the prognosis for patients with brain tumours is exceedingly poor, and there is a possibility that they may pass away. During the early stages, the brain is the location where the tumour first begins to form, and it is from there that it may subsequently spread gradually to other parts of the body. It is possible for humans to create machines that behave like living beings and are capable of learning from experience and applying that learning to cater to the emerging issues that are caused by the accumulation of tumour cells in the brain [1]. This will allow humans to deal with issues of such a complex nature. In this context, the use of convolutional neural networks has had a significant influence on the fields of artificial intelligence (AI) and digital image processing (CNN) [2].

In light of the gravity of the situation, there is an urgent need for a technique that relies entirely on automated processes to identify brain tumours. The manual procedure of assessing several

scans produced in a clinic is a labor-intensive, time-consuming approach that is insufficient for fully comprehending how various cancers behave. It is necessary to develop more accurate computer-based methods of tumour detection and identification in order to fully comprehend and effectively address this intricate issue. In recent years, a number of different efforts have been made to examine various machine learning approaches with the purpose of digitizing this process. Recently, there has been a resurgence of interest in the use of deep learning techniques for more precise and reliable identification of tumor cells [3].

This paper presents a deep learning-based brain MRI image classification for tumor stage detection. Section I presented the introduction to the problem. Section II discusses the literature analysis. Section III presents the proposed model. Section IV presents experimental analysis followed by results and discussion.

## II. Literature

Mahmoud Khaled Abd-Ellah et al [4], This article provides an in-depth examination of both standard machine learning approaches as well as emerging deep learning techniques for the detection of brain tumours. This review study analyses the important successes that are represented in the performance assessment metrics of the used algorithms in each of the three diagnosis procedures.

Anjali Wadhwa et al [5], a comprehensive literature evaluation of contemporary techniques for segmenting brain tumours from brain MRI images is presented and discussed here. It encompasses a



performance and quantitative analysis of the most recent and cutting-edge methodologies. In this article, numerous techniques for picture segmentation are discussed, along with the latest contributions made by a variety of scholars. In this section, an attempt is made to provide additional dimensions for readers to investigate the subject matter that is being discussed.

Raheleh Hashemzahi et al [6], Utilize magnetic resonance imaging (MRI) data in order to train our newly developed hybrid paradigm, which is comprised of a neural autoregressive distribution estimation (NADE) and a convolutional neural network (CNN). After that, we put our model through its paces by analysing 3064 T1-weighted contrast-enhanced pictures of three distinct forms of brain tumours.

Fatih Özyurt et al [7], offers a hybrid approach that makes use of both neuroscience and convolutional neural networks (NS-CNN). The objective is to determine if a tumour region that has been segmented from an image of the brain is benign or malignant. In the initial step of the process, MRI images were segmented by employing a method known as neutrosophic set – expert maximum fuzzy-sure entropy (NS-EMFSE). CNN was used to acquire the features of the segmented brain pictures that were used in the classification stage, and SVM and KNN classifiers were used to do the classification. The experimental assessment was conducted out based on a 5-fold cross-validation on 80 cases of benign tumours and 80 cases of malignant tumours.

Ahmet Çinar et al [8], the MRI pictures were used in an attempt to make a diagnosis of the brain tumour. During the diagnostic procedure, CNN models, which are an example of deep learning networks, are utilised. The foundation of the network is the Resnet50 architecture, which is one of the CNN models. The Resnet50 model has had its final five layers stripped away, and eight more layers have been added.

B. Devkota et al [9], Mathematical Morphological Reconstruction is used in this study to offer a computer-aided detection strategy for diagnosing brain tumours in their early stages (MMR). After the image has been pre-processed to eliminate artefacts and noise, it is segmented to locate regions of interest that are likely to contain tumours. In order to determine the nature of the brain tumour depicted in the segmented picture and determine whether it is benign or malignant, a vast number of textural and statistical characteristics are extracted from the image.

Javeria Amin et al [10], Using magnetic resonance imaging, a proposed strategy is presented for the segmentation and classification of the brain tumour (MRI). For the purpose of tumour segmentation, an architecture based on Deep Neural Networks (DNN) is utilised. In the model that has been proposed, there are a total of 07 layers that are utilised for classification. These layers include 03 convolutional layers, 03 ReLU layers, and 1 softmax layer. After the input MR image has been segmented into several patches, the value of the patch's centre pixel is what is sent to the DNN. DNN will do



segmentation and assign labels based on the pixels that are in the centre.

C. Narmatha et al [11], An method for the segmentation and classification of medical images using a mix of fuzzy and brain-storm optimization approaches has been suggested. This algorithm is known as the fuzzy brain-storm optimization algorithm. The brain-storm optimization method focuses on the centres of the clusters and gives them the most importance; yet, it is possible that this method, like other swarm algorithms, will result in local optima.

Javaria Amin et al [12], The input slices are de-noised and improved with the use of a Weiner filter that utilises a variety of wavelet bands. Clustering based on the potential field (PF) allows for the discovery of subsets of tumour pixels. Additionally, in order to separate the tumour location in the Fluid Attenuated Inversion Recovery (Flair) and T2 MRI scans, a global threshold as well as several mathematical morphological techniques are utilised. Local Binary Pattern (LBP) and Gabor Wavelet Transform (GWT) characteristics are combined for the purpose of producing an accurate categorization.

Manorama Sharma et al [13], In medical imaging, diseased tissues may be separated from normal tissues with the use of a technique called image segmentation. The proposed study demonstrates a hybrid approach to the process of information retrieval from MRI scans of the brain. This body of work in research proposes an effective method that makes use of K-means and artificial neural networks (KMANN). Feature

extraction made possible with the use of a GLCM (Grey Level co-occurrence matrix). In order to identify brain tumours, a Fuzzy Inference System is developed through the utilisation of extracted features, which is then followed by thresholding, morphological operator, and Watershed segmentation.

N. Varuna Shree et al [14], centred efforts on noise reduction methods, the extraction of gray-level co-occurrence matrix (GLCM) features, and DWT-based brain tumour region growing segmentation in order to simplify the process and boost its effectiveness. After this step, morphological filtering was performed, which cleans out any noise that may have been created as a result of segmentation. The probabilistic neural network classifier was put through its paces during training and testing to determine how well it could recognise the location of tumours in MRI scans of the brain.

M. Mohammed Thaha et al [15], Enhanced Convolutional Neural Networks (ECNN) is a method that has been developed for automated segmentation. This method optimises the loss function using the BAT algorithm. The fundamental objective of this study is to offer an optimization-based approach to the segmentation of MRIs. A deep architecture can be designed since small kernels allow for it. It has a beneficial effect with regard to overfitting provided that the network is given the lighter weights to use. During the pre-processing stage, methods for skull stripping and picture enhancement are utilised.



### III. Proposed Model

DenseNet was designed expressly with the intention of reversing the reduction in accuracy that high-level neural networks experience as a result of the diminishing

gradient. In more layman's words, the information is lost before it reaches its destination because the trip from the input layer to the output layer is so much longer than the distance between the two layers.

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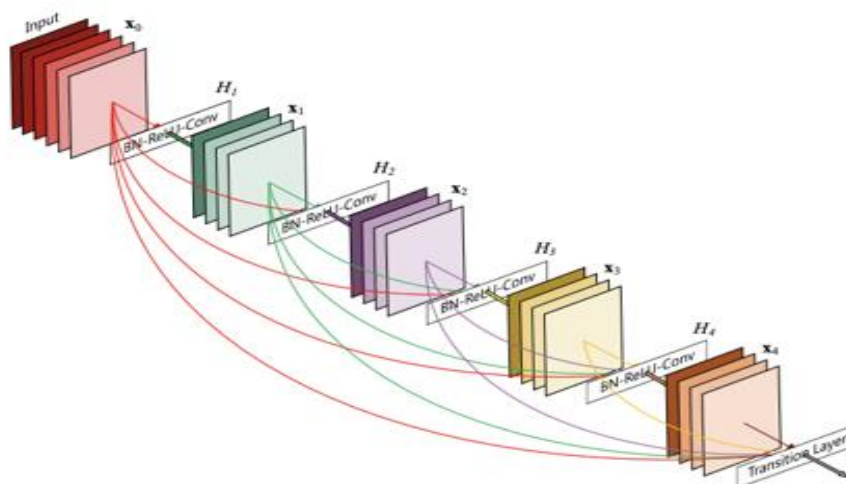


Figure 1: DenseNet Structure

Through the utilisation of composite function operation, an output from the layer below functions as an input for the layer above it. The convolution layer, the pooling layer, the batch normalisation, and the non-linear activation layer are the constituent parts of this composite procedure.

Because of these links, the network has an absolute maximum of  $L(L+1)/2$  direct connections. The number of levels in the architecture is denoted by the letter  $L$ .

The DenseNet has several variants, such as DenseNet-121, DenseNet-160, DenseNet-201, etc. The digits represent the number of layers that are present in the neural

network. The following is a computation of the number 121:

$$\text{DenseNet 121: } 5 + (6 + 12 + 24 + 16) * 2 = 121$$

5- Convolution and pooling layer

3- Transition layers (6,12,24)

1-Classification layer

2-Dense block (1x1 and 3x3 conv)

#### Convolution Layer

The straightforward operation of applying a filter to an input, which then yields an activation, is an example of a convolution. A feature map is a map of activations that indicates the positions and strength of a recognised feature in an input such as an image. This map is the result of repeatedly



applying the same filter to an input, and its name comes from the term "feature." The ability of convolutional neural networks to automatically learn a large number of filters in parallel that are specific to a training dataset while adhering to the constraints of a particular predictive modelling problem, such as image classification, is the innovation that these networks bring to the table. The end product is a set of highly specialised characteristics that can be found anywhere on the input photos.

### **Pooling Layer**

The fact that the output feature maps are sensitive to the placement of the features in the input is one of the issues that arises with these maps. One strategy for dealing with this sensitivity is to decrease the sample size of the feature maps. This has the effect of making the resultant down sampled feature maps more resistant to changes in the location of the feature in the picture. This is referred to as "local translation invariance" in the technical jargon. Pooling layers offer a method for down sampling feature maps by providing a summary of the presence of features in different regions of the feature map. Average pooling and max pooling are two prominent types of pooling algorithms. These approaches summarise the existence of a feature by determining its average level of activation as well as its maximum level of activation.

### **Transition Layer**

In DenseNet, all of the feature maps are joined together, as opposed to summing the residual as it is done in ResNet. Combining feature maps of various scales would be impossible to do in practise

(although some resizing may work). As a result, the feature maps of each layer have the same dimensions inside each thick block. CNN, on the other hand, cannot function without the use of downsampling. This duty is ensured by the presence of transition layers between two thick blocks.

The following components make up a transition layer:

- Batch Normalization
- 1x1 Convolution
- Average pooling

### **Classification Layer**

A classification layer is responsible for computing the cross-entropy loss for classification and weighted classification tasks that involve classes that are incompatible with one another. The output size of the layer before this one is used to make an inference about the number of classes that exist.

### **Dense block**

In convolutional neural networks, a Dense Block is a type of module that is responsible for directly connecting all of the layers (with feature-map sizes that are the same) with each other. It was at first suggested to be incorporated into the DenseNet design. In order to maintain the feed-forward character of the structure, each layer takes extra inputs from all of the levels that came before it and then passes on its own feature maps to all of the layers that come after it. The suggested DenseNet model has a layered design, which is seen in Figure 2. The strata may be broken down into three distinct groups. The Input layer, the pre-processing layer, the convolution layer 1,





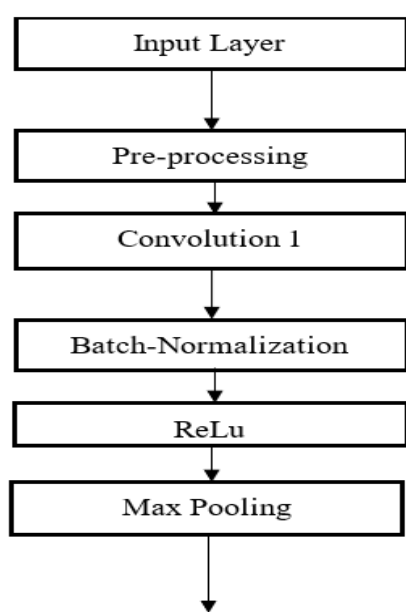
the batch normalization layer, the ReLu layer, and the max-pooling layer are the components that make up the first layer set that is seen in figure 3a. The batch normalization layer, the ReLu layer, the convolution layers 2 and 3, the depth concatenation layer, and the other layers that make up layer set-2 are all convolution layers. Figure 3b illustrates this point further. Multiple iterations of Batch Normalization, ReLu, and convolution layers make up the network,

and depth concatenation is performed at predetermined intervals throughout the structure. In the layer responsible for depth concatenation, the inputs from the two sets are combined into one.

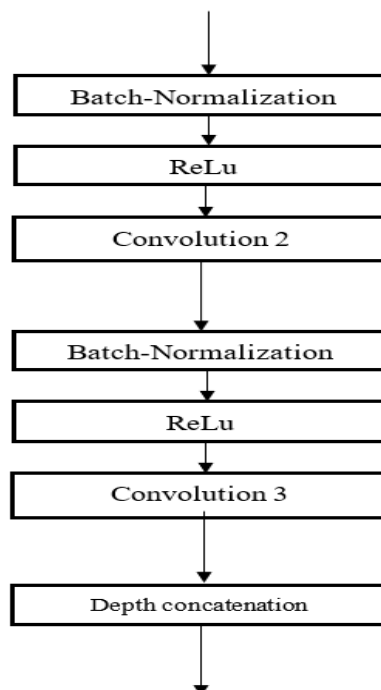
### Dropout Layer

The Dropout layer helps preventing overfitting by setting input units to 0 in a random manner with a predetermined frequency at each step during training period, sets input units to 0.

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(a) Layer set 1



(b) Layer set 2



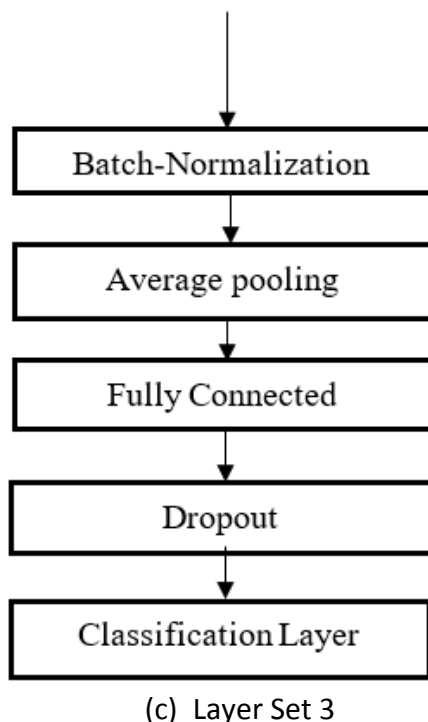


Figure 2: Layer set

Layer set 3, which is seen in figure 2c, is the culmination of the Batch normalization process and has 1920 channels. After this layer comes an average pooling layer with a size of 7x7, a stride of [7 7], and no padding. The fully connected layer that comes after it is followed by a softmax layer and then the classification output layer.

#### IV. Experimental Results

This section presents the experimental analysis carried out to evaluate the proposed model. The dataset contains 7022 images of human brain MRI images which are classified into 4 classes: glioma, meningioma, pituitary and normal MRI. 70 percentage of images are used for training and 30 percentage of the total images are used for testing. Figure 3, 4, 5 and 6 shows the input images of categories Glioma, meningioma, pituitary and normal MRI.

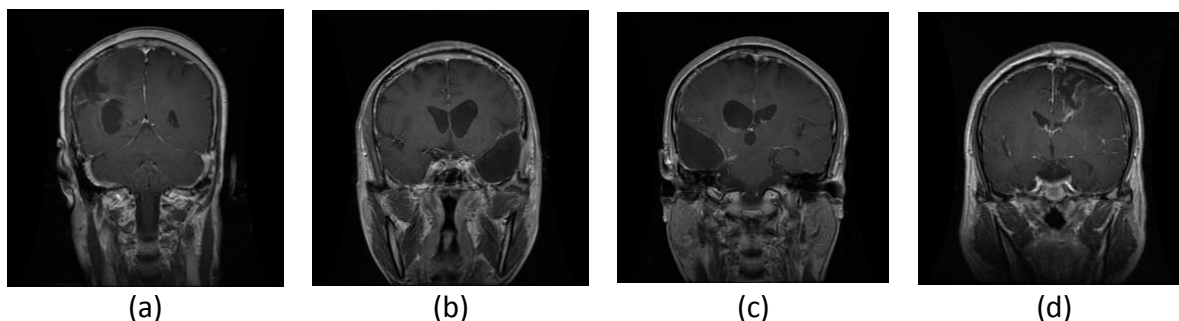


Figure 3: Input images type- Glioma



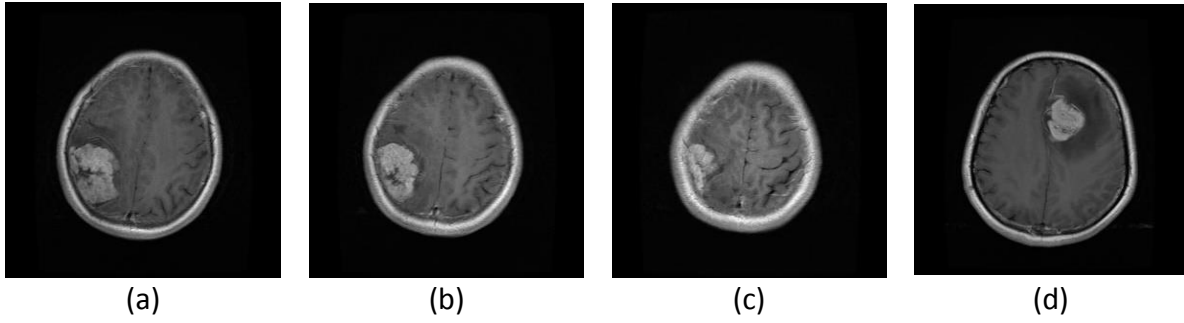


Figure 4: Input images type- meningioma

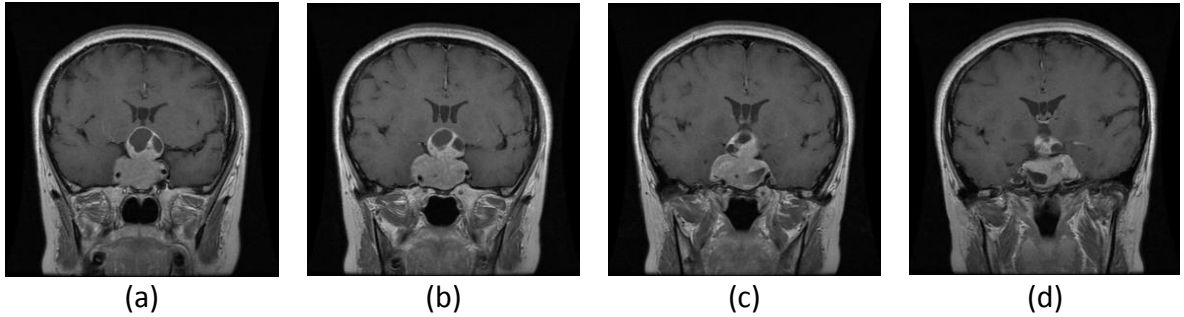


Figure 5: Input images type- pituitary

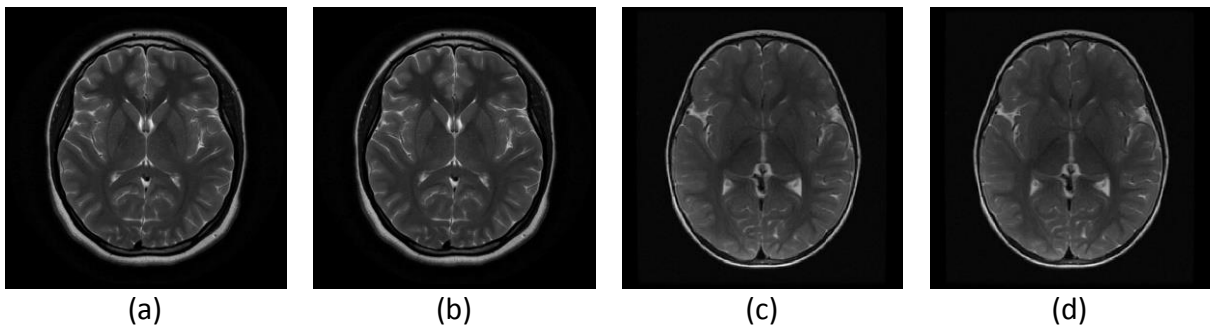
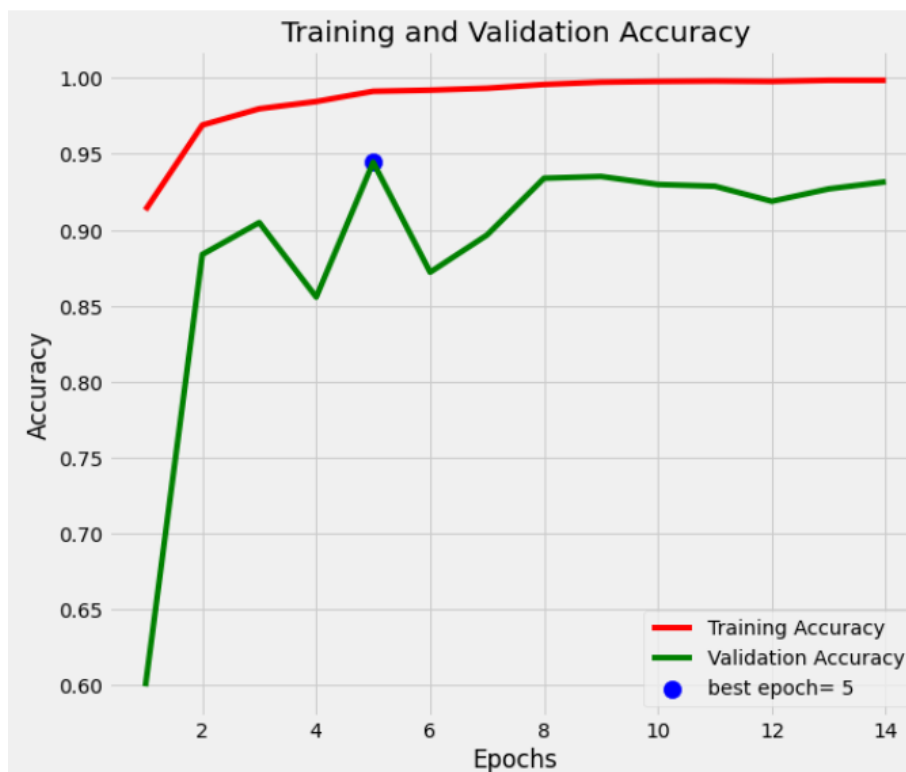


Figure 6: Input images type- normal MRI

Figure 7 shows the plot of training and validation loss. Figure 8 shows the training and validation accuracy.



Figure 7: Training and Validation loss



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Figure 8: Graph of Training and Validation Accuracy

Table 1: Validation parameters

Metric	Value
loss	0.25260
Accuracy	0.9745
Precision	0.9741
Sensitivity	0.9697
Specificity	0.9841

Table 1 shows the validation parameters of the proposed model. The loss obtained is 0.252, accuracy of 97.45%, precision of 97.41, sensitivity of 96.97 and specificity of 98.41 respectively.

Table 2: Comparative analysis

Method Name	Accuracy
NASNetMobile	0.81846
VGG19	0.90999
MobilenetV2	0.93593
InceptionV3	0.95957
ResNet50V2	0.96491
MobileNet	0.96568
DenseNet201	0.97453



Table 2 shows the comparative analysis of the proposed model with the existing techniques. NASNetMobile obtained an accuracy of 81.84%. VGG19 produced an accuracy of 90.99%. Mobilenet gained an accuracy of 93.59%. InceptionV3 produced an accuracy of 95.95%. ResNet obtained an accuracy of 96.49%. MobileNet produced an accuracy of 96.56%. The proposed model obtained an accuracy of 97.45%.

## V. Conclusion

The manual analysis of MRIs for the purpose of diagnosing tumors is a labor-intensive process that raises the risk of human error and may result in incorrect identification as well as categorization of the tumor type. Therefore, in order to automate the complicated medical processes, a deep learning framework has been developed for brain tumor classification in order to make it easier for medical professionals to make diagnoses. An automated approach for identifying and classifying different types of brain tumors is shown in this paper. The method makes use of the DenseNet201 deep learning model. By including a dropout layer in addition to the standard DenseNet201 model, it is possible to get rid of unnecessary connections and make the model more efficient. A deep learning DenseNetmodel is employed with a significant number of connections between its various levels. Dense Blocks are used to make these connections, which involves linking all of the layers directly with each other and making sure that the feature-map sizes of all of the layers are the same. The suggested model

was able to achieve an accuracy of 97.45%, making it superior to the models that were already in use.

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