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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 Dense Net 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*

I. INTRODUCTION

Integrating information technology and machine learning into medical practice has become increasingly significant in today's modern environment. The study of artificial intelligence, often known as AI, is a subfield of computer science that focuses on creating machines capable of self-directed learning without the need for human input to equip themselves better to solve problems on their own. Because tumor cells exhibit extremely unpredictable behavior that is too complicated to be regulated by traditional medicine, the application of this science finds great importance in developing therapies for brain tumors [1-3].

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 the command-and control center of the central nervous system. It is accountable for the execution of the daily actions, both voluntary and involuntary, that take place within the human body. The tumor is a fibrous mesh of undesired tissue development inside our brain and expands unrestrictedly. A proper knowledge of brain tumors and the stages they progress through is a necessary step in preventing the sickness and treating it after it has shown itself. Magnetic resonance imaging, also known as MRI, is frequently utilized by radiologists to diagnose and evaluate brain tumors [4-5].

When human brain tissue becomes infected with tumor 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 tumors is exceedingly poor, and there is a possibility that they may pass away. During the early stages, the brain is the location where the tumor first begins to form, and it is from there that it may subsequently spread gradually to other parts of the body. Humans can create machines that behave like living beings, learn from experience, and apply that learning to cater to the emerging issues caused by the accumulation of tumor cells in the brain [6]. This will allow humans to deal with matters 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) [7-8].

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 tumors. 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. Developing more accurate computer-based tumor detection and identification methods is necessary to understand and effectively address this intricate issue fully. In recent years, several efforts have been made to examine various machine learning approaches to digitize this process. Recently, there has been a resurgence of interest in using deep learning techniques for more precise and reliable identification of tumor cells [9-11]. 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**

This article [12] provides an in-depth examination of both standard machine learning approaches and emerging deep learning techniques for detecting brain tumors. This review study analyses the critical successes in the performance assessment metrics of the algorithms used in the three diagnosis procedures. A comprehensive literature evaluation of contemporary techniques for segmenting brain tumors from 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 various scholars. In this section, an attempt is made to provide additional dimensions for readers to investigate the subject matter that is being discussed [13-14].

The author [15-16] 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 analyzing 3064 T1-weighted contrast-enhanced pictures of three distinct forms of brain tumors. The author offers a hybrid approach that makes use of both neuroscience and convolutional neural networks (NS-CNN). The objective is to determine if a tumor region that has been segmented from an image of the brain is benign or malignant [15]. In the initial step of the process, MRI images were segmented by employing a method known as Neutroscophic 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 tumors and 80 cases of malignant tumors [16-17].

The MRI pictures were used in an attempt to make a diagnosis of the brain tumor. CNN models, an example of deep learning networks, are utilized during the diagnostic procedure. The foundation of the network is the Resnet50 architecture, which is one of the CNN models. The Resnet50 model has stripped its final five layers away, and eight more layers have been added [18]. Mathematical Morphological Reconstruction is used in this study to offer a computer-aided detection strategy for diagnosing brain tumors 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 likely to contain tumors. Many textural and statistical characteristics are extracted from the image to determine the nature of the brain tumor depicted in the segmented picture and whether it is benign or malignant [19-20].

The author presents [21-22] Using magnetic resonance imaging, a proposed strategy is presented for segmenting and classifying the brain tumor (MRI). An architecture based on Deep Neural Networks (DNN) is utilized for tumor segmentation. In the proposed model, a total of 07 layers is utilized 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 center pixel is sent to the DNN. DNN will segment and assign labels based on the pixels in the center. A method for segmenting and classifying medical images using a mix of fuzzy and brainstorm optimization approaches has been suggested. This algorithm is known as the fuzzy brainstorm optimization algorithm. The brainstorm optimization method focuses on the centers 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 [23-25].

The author presents [26-28] input slices that are de-noised and improved using a Weiner filter that utilizes a variety of wavelet bands. Clustering based on the potential field (PF) allows for discovering subsets of tumor pixels. Additionally, to separate the tumor location in the Fluid Attenuated Inversion Recovery (Flair) and T2 MRI scans, a global threshold and several mathematical morphological techniques are utilisedutilized. Local Binary Pattern (LBP) and Gabor Wavelet Transform (GWT) characteristics are combined to categorize accurately [29]. In medical imaging, image segmentation may separate diseased tissues from normal tissues. The proposed study demonstrates a hybrid approach to information retrieval from brain MRI scans. This body of research suggests an effective method that uses K-means and artificial neural networks (KMANN). Feature extraction was made possible with a GLCM (Grey Level co-occurrence matrix). To identify brain tumors, a Fuzzy Inference System is developed by utilizing extracted features, which include thresholding, a morphological operator, and Watershed segmentation [30].

Centered efforts on noise reduction methods, the extraction of gray-level co-occurrence matrix (GLCM) features, and DWT-based brain tumor 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 recognize the location of tumors in MRI scans of the brain [31].

Proposed Model

The Densely Connected Convolutional Network, commonly known as Dense Net, was developed to overcome a fundamental challenge encountered in deep neural networks namely, the vanishing gradient problem. As the depth of a neural network increases, its theoretical ability to learn complex patterns improves. However, in practice, this added depth often results in performance degradation. This occurs because, in standard network architectures, the gradient signals used to update the network's weights become increasingly weaker as they are propagated backward through the layers. As a result, the early layers receive minimal updates during training, which hampers the overall learning process and reduces model accuracy. Dense Net tackles this issue by establishing direct connections between every layer and all of its preceding layers. Unlike traditional networks, where each layer only communicates with the one immediately following it, Dense Net enables each layer to both receive input from and send output to multiple layers. This configuration facilitates stronger gradient flow and richer feature propagation, effectively maintaining important information throughout the network. By ensuring efficient information sharing and reusing learned features, Dense Net not only alleviates the vanishing gradient problem but also reduces model complexity. It delivers high performance and accuracy with significantly fewer parameters than conventional deep architectures, making it a highly effective design for deep learning applications.

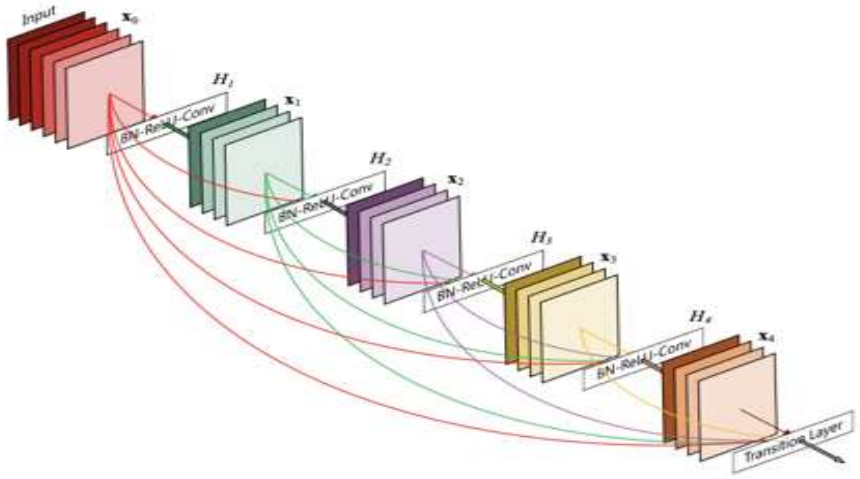


Figure 1: Dense Net Structure

In the Dense Net architecture, a composite functional operation is employed wherein the output of one layer directly serves as the input to each subsequent layer. This composite operation encompasses several essential components, including convolutional layers, pooling operations, batch normalisation, and non-linear activation functions [33]. Due to the direct connectivity pattern between all layers, the total number of connections in the network can be calculated as L(L+1)/2, where *L* represents the total number of layers. Dense Net is available in multiple configurations, such as DenseNet-121, DenseNet-160, and DenseNet-201, where the numerical suffix indicates the total number of layers within the model. For instance, in DenseNet-121, the calculation is as follows [34].

Dense Net 121: 5+(6+12+24+16) *2=121

The model includes five initial convolution and pooling layers, three transition layers separating dense blocks, and one final classification layer. Each dense block comprises two convolutional operations, typically a 1×1 followed by a 3×3 convolution, accounting for the multiplicative factor of 2.

Convolution Layer

Convolutional neural networks (CNNs) rely on the fundamental operation of convolution, where a filter (or kernel) is applied to the input data to generate an activation. By sliding this filter across the entire input, a set of activations is produced, forming what is known as a feature map. This map pinpoints the locations and intensity of features detected within the input, effectively capturing spatial information about the learned patterns. The term feature map reflects its purpose: to illustrate the existence and strength of specific features throughout the input space. A significant advantage of CNNs is their ability to learn various filters during the training process automatically. Each of these filters becomes specialised in identifying distinct characteristics. What makes CNNs particularly powerful is their ability to learn many filters simultaneously, each adapted to different aspects of the training data and modelling goal. This results in a rich set of feature representations capable of recognising important patterns regardless of their location within the input, which is crucial in tasks like image classification [35].

Pooling Layer

The fact that the output feature maps are sensitive to the placement of the features in the input is one issue that arises with these maps. One strategy for dealing with this sensitivity is to decrease the sample size of the feature maps [36]. This makes the resultant down-sampled feature maps more resistant to changes in the feature's location in the picture. This is called "local translation invariance" in the technical jargon. Pooling layers offer a method for down-sampling feature maps by summarising 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 and its maximum level of activation.

Transition Layer

In Dense Net, all of the feature maps are joined together instead of summing the residual as done in Res Net. Combining feature maps of various scales would be impossible in practice (although some resizing may work). As a result, the feature maps of each layer have the exact dimensions inside each thick block. CNN, on the other hand, cannot function without the use of down sampling [37]. Transition layers between two thick blocks ensure this duty. The following components make up a transition layer:

- Batch Normalization
- 1x1 Convolution
- Average pooling

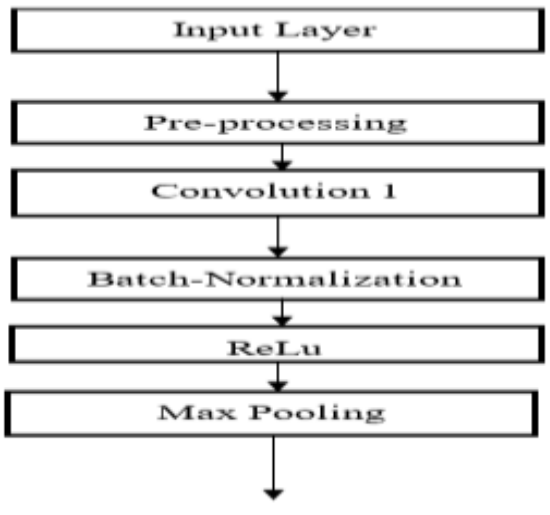
Classification Layer

A classification layer is responsible for computing the cross-entropy loss for classification and weighted classification tasks that involve incompatible classes. The output size of the layer before this one is used to infer the number of existing courses.

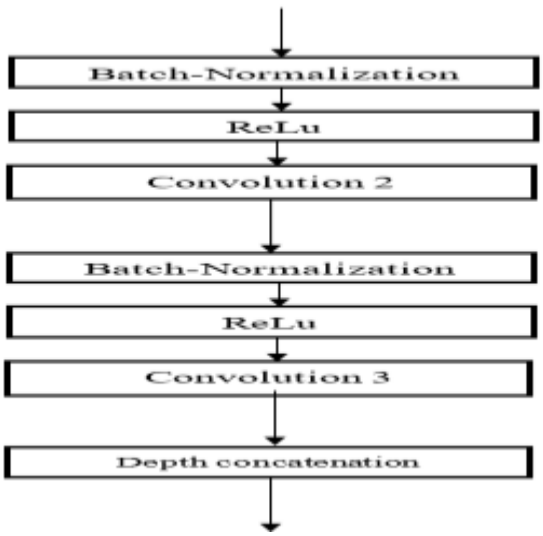
Dense block

In convolutional neural networks, a Dense Block is a module responsible for directly connecting all of the layers (with feature-map sizes that are the same) with each other. It was at first suggested that it be incorporated into the Dense Net design. The suggested Dense Net model has a layered design, as seen in Figure 2. The strata may be broken down into three distinct groups. The components that make up the first layer set are the input layer, the pre-processing layer, the convolution layer 1, the batch normalisation layer, the ReLu layer, and the max-pooling layer, as seen in Figure 3a. The batch normalisation layer, the ReLu layer, the convolution layers 2 and 3, the depth concatenation layer, and the other layers that comprise layer set-2 are all convolution layers. Figure 3b illustrates this point further. Multiple iterations of Batch Normalisation, 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 prevent overfitting by setting input units to 0 in a random manner with a predetermined frequency at each step during training period, which sets input units to 0.

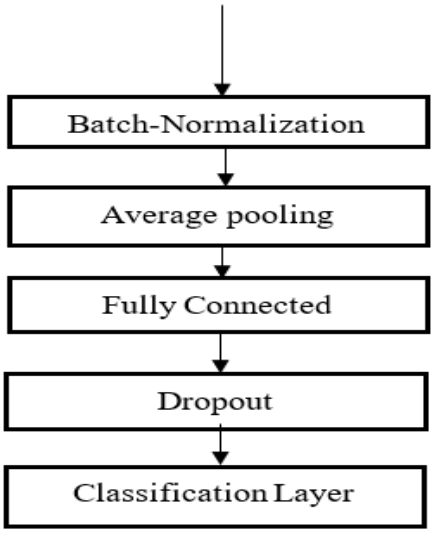


(a) Layer set 1



(b) Layer set 2

(a) (b)



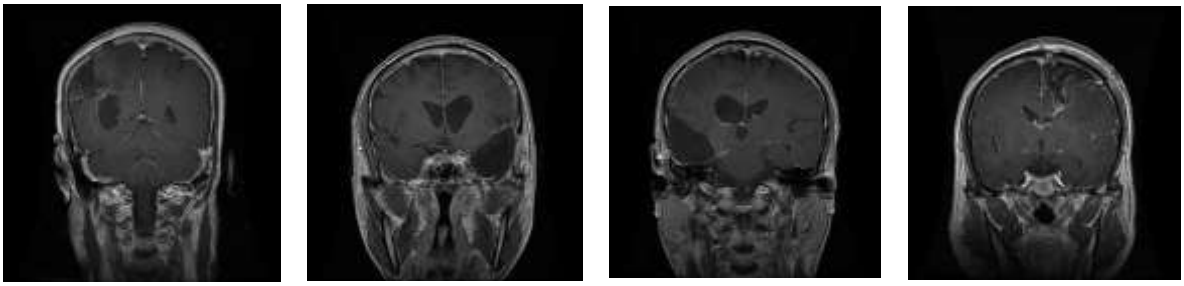
(c) Layer Set 3

Figure 2: Layer set

Layer set 3, which is seen in Figure 2c, is the culmination of the Batch normalisation 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 after a SoftMax layer follows it, followed by the classification output layer.

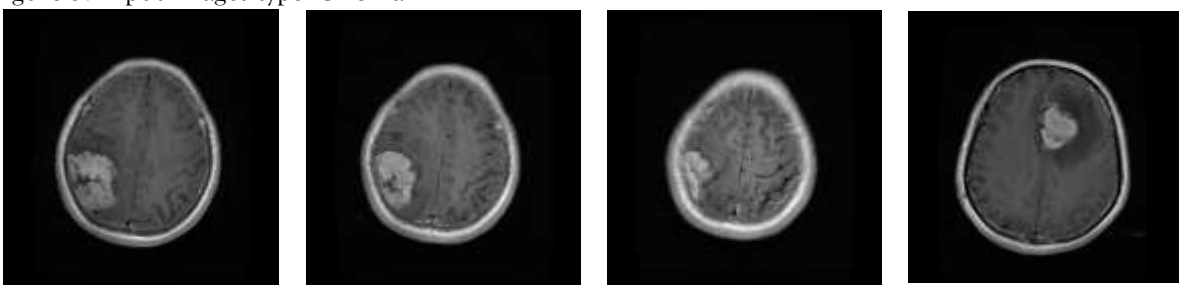
IV EXPERIMENTAL RESULTS

This section presents the experimental analysis carried out to evaluate the proposed model. The dataset contains 7022 human brain MRI images classified into glioma, meningioma, pituitary and normal MRI. Seventy per cent of the images are used for training, and 30 per cent of the total images are used for testing. Figures 3, 4, 5 and 6 show the input images of categories Glioma, meningioma, pituitary and normal MRI.



(a) (b) (c) (d)

Figure 3: Input images type- Glioma



(a) (b) (c) (d)

Figure 4: Input images type- meningioma

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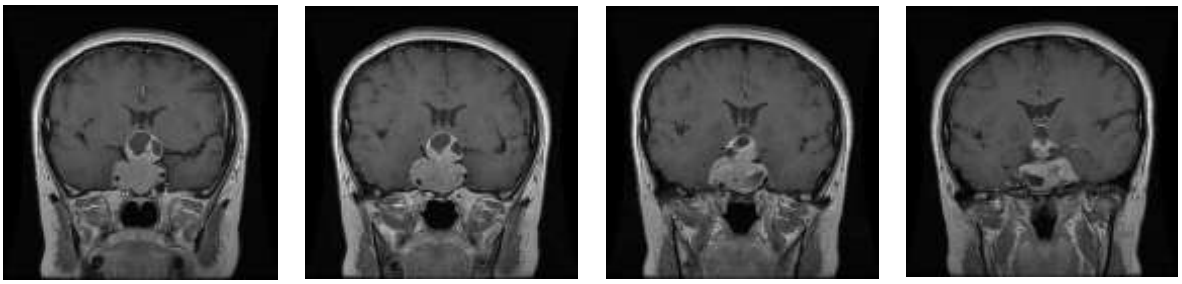
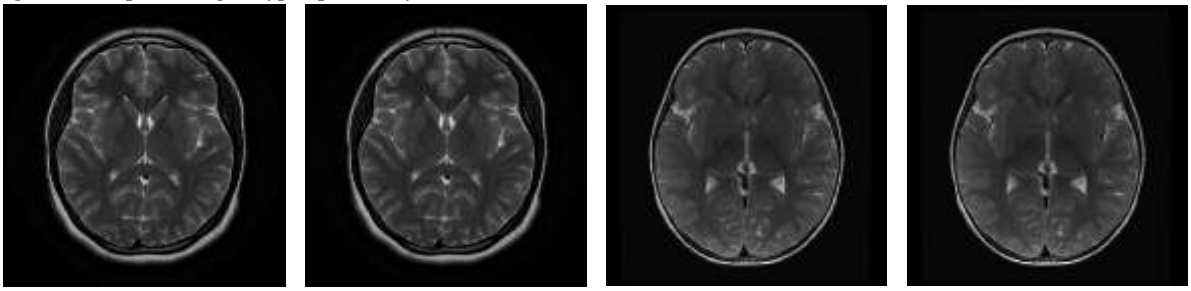


(a) (b) (c) (d)

Figure 5: Input images type- pituitary



(a) (b) (c) (d)

Figure 6: Input images type- normal MRI

Figures 7 and 8 depict the model's performance during the training phase regarding loss and accuracy, respectively. In Figure 7, the training and validation loss curves show how the model's error decreases over successive epochs. A gradual decline in both losses indicates that the model is learning effectively, while a small gap between the two suggests good generalisation. In Figure 8, the training and validation accuracy curves represent the model's ability to classify data correctly. A steady increase in both curves, with minimal divergence, reflects consistent improvement and stable learning. These plots help assess whether the model is underfitting, overfitting, or achieving optimal performance.

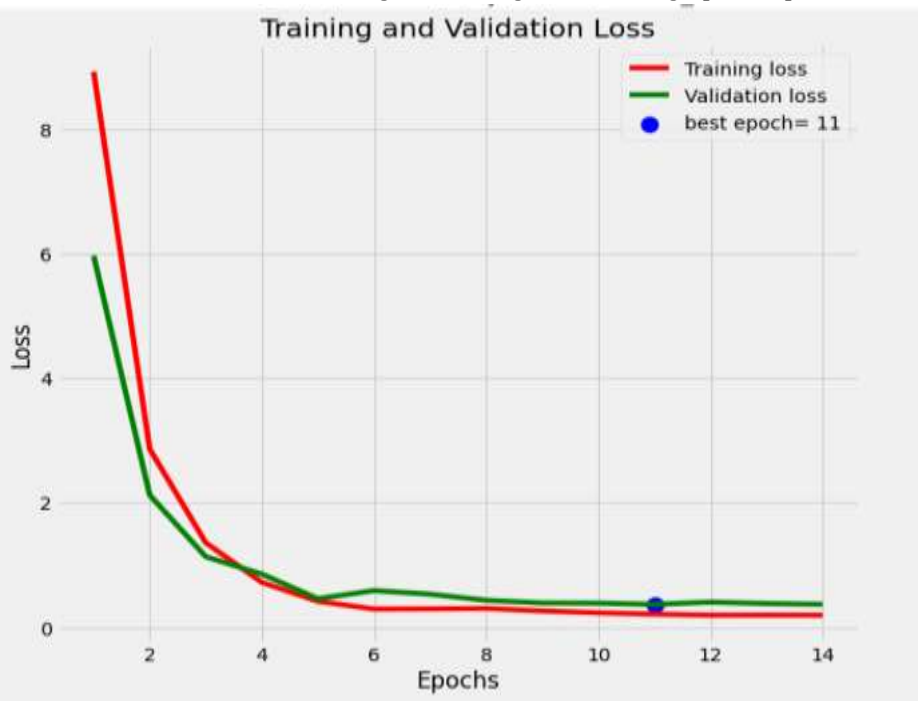


Figure 7: Training and Validation loss

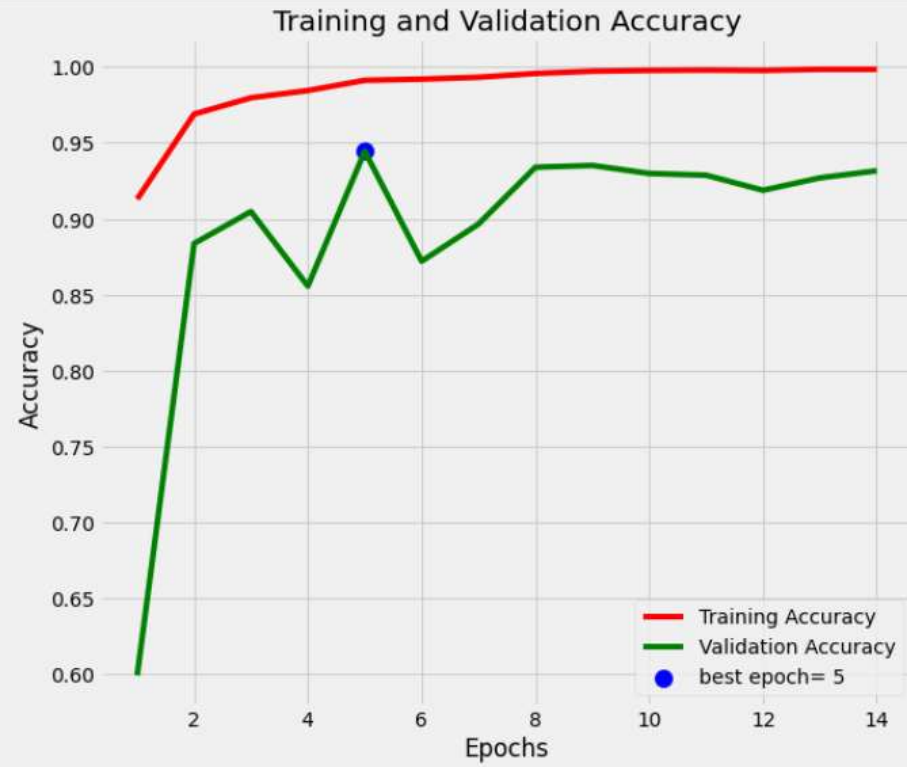


Figure 8: Graph of Training and ValidationAccuracy

Table 1 presents the key validation metrics achieved by the proposed model, highlighting its robust performance in classification tasks. The model attained a validation loss of 0.252, indicating a low error rate during prediction on unseen data. The accuracy reached 97.45%, demonstrating the overall effectiveness of the model in correctly classifying the majority of instances. Additionally, the precision was recorded at 97.41%, which reflects the model's ability to minimise false positives and deliver highly reliable optimistic predictions. The sensitivity (recall) stood at 96.97%, signifying the model's strong capability to identify actual positive cases correctly. Meanwhile, the specificity was 98.41%, indicating excellent performance in correctly recognising negative cases and minimising false negatives. These results confirm that the proposed model maintains a well-balanced trade-off between true favourable and accurate negative rates, making it highly reliable for practical deployment.

Table 1: Validation parameters

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

Table 2 compares the proposed model against several well-established deep learning architectures regarding classification accuracy. Among the existing models, NAS Net Mobile achieved the lowest accuracy at 81.84%, reflecting its limited effectiveness for the given task. VGG19 performed better, reaching 90.99%, while Mobile Net and InceptionV3 demonstrated improved performance with accuracies of 93.59% and 95.95%, respectively. ResNet slightly outperformed these with an accuracy of

96.49%, closely followed by another variant of Mobile Net at 96.56%. Notably, the proposed model surpassed all baseline techniques, achieving the highest accuracy of 97.45%, indicating its superior feature extraction and classification capability within the given dataset. This performance underscores the model's effectiveness and robustness compared to existing state-of-the-art approaches.

Table 2: Comparative analysis

Method Name	**Accuracy**
NAS Net Mobile	0.81846
VGG19	0.90999
MobilenetV2	0.93593
InceptionV3	0.95957
ResNet50V2	0.96491
Mobile Net	0.96568
DenseNet201	0.97453

II. CONCLUSION

Manually analysing MRI scans for brain tumour diagnosis is often time-consuming and can lead to errors in identifying and classifying tumour types. This study introduces an automated method for brain tumour classification to reduce the burden on medical professionals and improve accuracy. The approach is based on the DenseNet201 architecture, which has been modified by adding a dropout layer to remove unnecessary connections and enhance efficiency. DenseNet201 is characterized by its dense connectivity, where each layer is directly connected to all subsequent layers within a thick block, ensuring consistent feature map sizes and efficient feature reuse. This structure allows the model to extract detailed and relevant features for accurate classification. The proposed method achieved an accuracy of 97.45%, demonstrating its effectiveness and improved performance compared to other existing techniques.

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