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Brain Neoplasm Image Recognition Using Deep Learning Techniques

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Abstract

Today, the recognition of brain tumors is considered an essential topic in medicine. Brain neoplasm is an acute form of cancer caused by abnormal and uncontrollable cell division. Recent advancements in medical imaging-based deep learning have greatly assisted the healthcare industry in diagnosing a variety of diseases. To achieve image recognition and visual learning, a deep convolutional neural network (CNN) has been selected for implementing brain neoplasm recognition. CNN is a widely used and typical machine learning algorithm. This paper introduces a CNN-based approach along with data augmentation for categorizing magnetic resonance imaging (MRI) brain scan images into natural and unnatural categories. The proposed model achieves close-to-real-time recognition without sacrificing performance. Additionally, this paper describes the steps involved in setting hyperparameters, as well as the entire pipeline of the suggested pattern. After testing the system several times to find the optimal configuration that produces statistically more trustworthy results, each hyperparameter is chosen. Empirical results demonstrate that the proposed model achieves an accuracy of 99.55%. This model exhibits a low level of complexity and delivers more effective, accurate results when compared to other pre-trained models.

Keywords: MRI Image, Brain neoplasm, Deep Learning, Convolutional Neural Network

التعرف على صور أورام الدماغ باستعمال تقنيات التعلم العميق

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الخلاصة

واليوم يعتبر التعرف على أورام المخ موضوعاً أساسياً في مجال الطب. يمثل ورم الدماغ شكلاً حاداً من السرطان الناتج عن انقسام الخلايا غير الطبيعي الذي لا يمكن السيطرة عليه. في الآونة الأخيرة، ساعدت التطورات في مجال التعلم العميق القائم على التصوير الطبي بشكل كبير في صناعة الرعاية الصحية في تشخيص الأمراض المختلفة. لتحقيق التعرف على الصور والتعلم البصري، تم اختيار شبكة عصبية تلافيفية عميقة (CNN) لتنفيذ التعرف على أورام الدماغ CNN. هي خوارزمية تعلم آلي مستعملة على نطاق واسع.

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تقدم هذه الورقة نهجًا قائمًا على CNN جنبًا إلى جنب مع زيادة البيانات لتصنيف صور مسح الدماغ بالتصوير بالرنين المغناطيسي (MRI) إلى فئات طبيعية وغير طبيعية. يحقق النموذج المقترح التعرف في الوقت الفعلي تقريبًا دون التضحية بالأداء. بالإضافة إلى ذلك، توضح هذه الورقة المسار العام للنمط المقترح وإجراءات تحديد المعلومات الفائقة. يتم تحديد كل معلمة مفردة بعد اختبار النظام عدة مرات لتحديد أفضل مجموعة تؤدي إلى نتائج أكثر موثوقية من الناحية الإحصائية. أظهرت النتائج التجريبية أن النموذج المقترح يحقق دقة قدرها 99.55%. يُظهر هذا النموذج مستوى منخفضًا من التعقيد ويوفر نتائج دقيقة أكثر فعالية مقارنةً بالنماذج الأخرى المدربة مسبقًا.

1. Introduction

Recently, the field of medical sciences has become inundated with a vast amount of data, encompassing extensive clinical studies, genomic analysis, and various types of imaging. Physicians in clinical settings must be capable of effectively analyzing laboratory imaging and data to determine suitable therapeutic strategies [1]. Generally, these laboratory images and data can be objectively analyzed; however, images are often subjectively interpreted. In the medical sciences, image recognition tasks play a significant role in image classification and disease diagnosis [2]. The primary challenge facing machine learning (ML) in clinical medicine is developing software capable of judging medical cases as accurately as physicians. Medical image analysis poses a substantial burden on physicians [3]. Therefore, digital image processing techniques are being utilized to support their functions. When image classification and recognition accuracy are enhanced through image processing approaches, it is expected that numerous medical images can be diagnosed with an accuracy approaching that of specialized physicians [4]. Cancer is the second-leading cause of death after cardiovascular diseases [2]. Among all types of cancer, brain cancer has the lowest survival rate. Brain tumors can vary in type based on their location, texture, and shape. Accurate diagnosis of the tumor type enables doctors to determine the appropriate treatment options, potentially saving patients' lives. Tumor grading is a critical concept in treatment monitoring and planning [5]. For a considerable amount of time, scientific research on magnetic resonance brain image processing has been quite popular, attracting scientists to work on many projects such as brain tissue segmentation in newborns, infants, and adults and damage detection. Several brain MRI image datasets are available to the research community, particularly those organized by medical and computer image computing experts [6]. Medical image applications such as image denoising, segmentation, and classification have greatly benefited from the use of deep learning algorithms [7] and [8]. Deep learning uses many different types of architectures, but convolutional neural networks (CNNs) are becoming more popular because they are adept at handling complicated tasks that need to find local multidimensional features using convolutional filters. They have proven effective in diagnosing diseases such as pneumonia and brain tumors, offering high accuracy with reduced complexity [9]. Numerous recent studies have turned to artificial neural networks in light of the importance of early and exact detection for various types of tumors due to their exceptional performance in terms of accuracy and execution time [10] and [11]. Some of these methods, as compared to other methods, either suggest specific topologies with predetermined numbers of layers and neurons or use pre-existing neural network structures, such as the VGG neural network. Nevertheless, adding more layers to a neural network than is required for it to function merely increases computational complexity and does not always result in increased accuracy ([12] and [13]). Conversely, using fewer layers than required can significantly diminish the network's accuracy, as it may fail to detect features at the necessary complexity level. Furthermore, the number of neurons in each layer should align with the number of features to be detected at each complexity level to strike a balance between complexity and performance ([14] and [15]).

This paper aims to investigate the optimal structure of artificial neural networks that can achieve a balance between accuracy and complexity. To achieve this goal, it investigates the number of neurons in each layer and the ideal number of layers to improve accuracy while minimizing model complexity. It also examines the feasibility of identifying various cancer types with a determined ideal structure. Thus, the performance of a structure optimized for specific tumor types is applied to detect others. The same procedure is then repeated for each type of cancer, and the differences in performance are illustrated and discussed. This comparison sheds light on how this kind of network might be able to find different kinds of cancer and what changes need to be made to start with the best known structure.

The improvement of patient outcomes and survival rates is contingent upon the timely diagnosis of brain tumors. Even though current techniques have come a long way, they still have a number of drawbacks, such as high computational complexity, long processing times, and the requirement for sizable, annotated datasets in order to attain high accuracy. These limitations restrict the usefulness of these strategies in clinical contexts where prompt and precise diagnosis is critical. By putting forth a novel convolutional neural network (CNN)-based method for brain tumor diagnosis, our study seeks to close these gaps. In contrast to conventional techniques, our solution makes use of a more effective algorithm that lowers computational needs, improves detection accuracy to 99.55%, and allows for nearly real-time recognition. This advancement is especially important when quick decisions are required for efficient treatment planning. Our main goals are to: (a) reduce the computational cost associated with conventional tumor identification approaches; (b) develop a CNN-based method that enhances the accuracy and speed of brain tumor diagnosis; and (c) use thorough testing and validation to show that our technique is feasible in a clinical context. Section 2 introduces related work. Section 3 explains the proposed methodology. Section 4 presents the results, and the conclusions are summarized in the final section.

2. Related Works

ML and deep learning models are primarily utilized in image processing techniques for segmenting, recognizing, and classifying MRI images. Additionally, these models aid in the classification and detection of brain tumors. There have been numerous research studies on the classification and recognition of magnetic resonance imaging (MRI) brain images. For instance, Wathy et al. [16] presented a model for classifying brain tumors using a genetic algorithm in combination with a support vector machine (SVM) classifier. This proposed model comprises several stages. In the first stage, preprocessing is performed, involving the utilization of various filters (low pass, high pass, and median filter). In the second stage, segmentation is carried out by combining the Expectation-Maximization algorithm and the level-set method. The genetic algorithm extracts and selects features in the third stage. Finally, an SVM classifier classifies MRI brain images as normal or abnormal in the final stage.

Seetha and Raja [17] proposed an automatic brain neoplasm detection system utilizing CNN to classify MRI images and diagnose brain tumors. However, this system has several limitations. Specifically, it provides accurate quantitative measurements for only a limited number of images. The CNN architecture was implemented with a small number of kernels and lightweight neurons. Training accuracy was 97.5%, with very low validation loss and high validation accuracy. Srinivas and Sasibhushana Rao [18] proposed a hybrid detection paradigm for classifying brain tumors by integrating CNN with K-Nearest Neighbor (KNN). This paradigm comprises 25 layers, with the first layer representing the input layer, which has dimensions equal to the MRI image dimensions. The second layer is the convolutional layer,

consisting of 96 convolutional filters sized 11,113 and employing a four-stride. Additionally, zero padding is applied to the input images. In this model, the accuracy achieved was 96.25%. To compare the accuracy of several machine learning algorithms, Hanwat and C. J. [19] proposed a system for classifying MRI brain tumors based on CNN. In addition to CNN, the analysis of brain tumors is carried out with the assistance of other classifiers, such as KNN and Random Forest. The CNN-based system consistently beat the examined classifiers in the comparison, obtaining 98% accuracy. Toğaçar et al. [20] suggested a CNN-based system built using hypercolumns and attention modules within a residual network framework. The system uses MRI pictures to detect brain cancer. The first stage of this method involves preparing brain pictures and applying layers with convolutions. Following the identification of important visual spots by attention modules, convolutional layers are applied to the image. Features are taken from each layer of the model and maintained in an array structure in the final layer by using the hypercolumn approach. Using MRI scans, this method classifies brain cancers with a success rate of 96.05%. Febrianto et al. [21] provided two trained CNN-based paradigms and carried out a comparison to identify the best CNN-based paradigm for identifying cancers in MRI brain images. They utilized a dataset comprising 253 MRI brain images obtained from the Kaggle website, consisting of 155 images with tumors and 98 without tumors. The results showed an accuracy of more than 93%. Similarly, Çinar and Yildirim [22] used the same dataset to propose a brain tumor diagnosis approach based on CNN models utilizing MRI images. They employed the Resnet50 architecture as a base model, modifying it by removing the final five layers and adding eight new layers. Other models, including Alex Net, DenseNet201, Google Net, and InceptionV3, were also used. The highest accuracy achieved was 97.2% for the developed Resnet50 model. In contrast, Irsheidat and Duwairi [23] introduced an ANN-based model utilizing matrix operations and mathematical formulas to analyze MRI images for tumor presence in the brain. They expanded the 253-image dataset by employing data augmentation, increasing it fourteenfold. The results from this model demonstrated an accuracy of 96.7% with validation data and over 88.25% with test data.

3. The Proposed Model

The proposed paradigm, as depicted in Figure 1, is designed to recognize the type of brain tumor in close-to-real-time without compromising performance. Additionally, this paper will introduce the overall pipeline of the proposed paradigm and the procedure for setting hyperparameters. Each hyperparameter is meticulously selected through multiple system tests to identify the optimal combination that enhances the statistical reliability of the results. A CNN is the chosen technique in this study. The CNN is trained and tested using a dataset of brain tumor images. The steps involved in the proposed model are outlined in Algorithm 1.

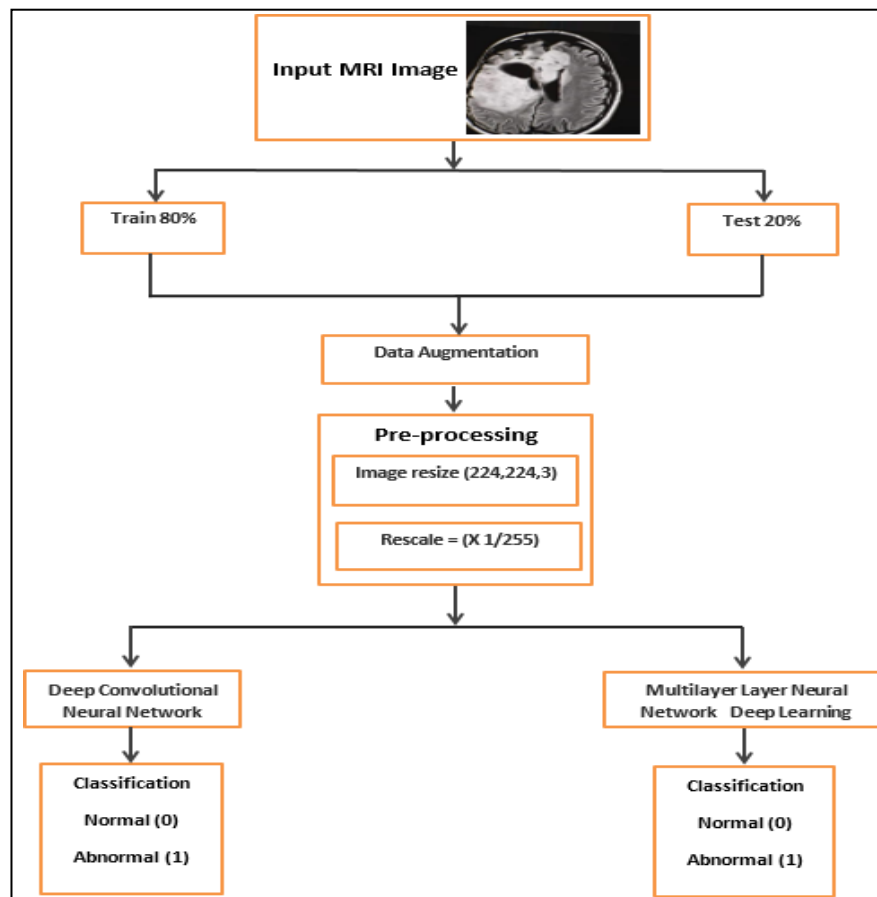


Figure 1: The proposed model.

ALGORITHM 1 .CNN training algorithm to recognize brain neoplasm tumors

Input: MRI images

Output: The brain neoplasm (natural or unnatural)

Step1:Begin

Step2:Data augmentation strategy (Rotations, Brightness, Flipping, Scaling, Shifting, Cropping Noise Addition)

Step3: Divide the dataset into a training set and a testing set. For each model, select an 80% training and 20% testing data split. This ratio has been determined to yield the highest accuracy, as shown in Figure 4.

Step4: Data preprocessing:

a)Resize the input images to 224×224 pixels

b) Normalize the data by dividing each pixel by 255, ensuring that data values fall within the range of 0 and 1

Step5:CNN design, comprising several layers:

a)Input layer for brain neoplasm images (MRI images)

b)Convolutional layer: Use multiple filters of size 3×3

c)Nonlinear layer (activation layer): Implement Rule function

d)Pooling layer: Use Max-pooling

e)Normalize layer: Use batch normalization

f)Fully connected layer

g)Sigmoid layer

Step6:Return the trained CNN that maximizes the accuracy of validation

Step7:END__

3.1 Data Augmentation

In order to mitigate the risk of overfitting and enhance recognition accuracy, this paper employs data augmentation. The data augmentation strategy is employed to artificially augment the complexity and quantity of the available data. As it is widely known, training a deep neural network effectively necessitates a substantial amount of data for fine-tuning its parameters. However, this study uses a relatively small dataset. Therefore, the data augmentation technique is applied to the brain tumor images, effectively expanding the dataset from 253 to 2530 images. This augmentation involves introducing minor modifications to the images, such as rotation, brightness adjustment, and flipping. This proposed CNN-based model treats each of these slight variations as a distinct image. This approach equips the model with the ability to learn more comprehensively and perform effectively on previously unseen data. In our proposed method, the following techniques of data augmentation were employed:

- a. Rotations: 360 degrees at random from -20 to +20 degrees.
- b. Brightness Adjustments: Abrupt variations in brightness up to $\pm 30\%$.
- c. Flipping: Flipping both vertically and horizontally at random.
- d. Scaling: Factors used in the random scaling process range from 0.8 to 1.2.
- e. Shifting: Random shifts in both directions within $\pm 10\%$ of the image's dimensions are referred to as shifting.
- f. Cropping: Resizing the image to its original proportions after randomly cropping it to 90% of its original size.
- g. Noise Addition: Random Gaussian noise with a mean of 0 and a standard deviation of 0.01 is added as noise.

These augmentation methods were picked with care to mimic different real-world scenarios and dataset fluctuations, strengthening the resilience of our model.

3.2 CNN Architecture

The proposed model's primary objective is to identify and recognize tumors in the human brain. In order to handle the significant quantity of data present in every input image, we employ one of the most robust techniques available: deep learning. Deep learning, particularly convolutional neural networks (CNNs), has proven to outperform classical techniques in various domains, including pattern recognition, image analysis, and object detection. Thus, we have opted for the CNN method for the following reasons:

- CNNs consistently deliver high and accurate performance, often surpassing other recognition algorithms when applied to the same dataset.
- CNNs allow for end-to-end training, streamlining the learning process and making it highly effective.
- Unlike many other methods, CNNs require minimal preprocessing, typically limited to resizing and normalizing the input image.
- CNNs excel in providing rapid predictions, with classifications typically generated in just a few milliseconds after receiving the input image.

The samples are sent to CNN as fixed-dimension pictures. These input images have three channels (representing RGB color) and are set to a dimension of 224 x 224 x 3. Identifying the appropriate image size is one of the key considerations in developing our model. This choice represents a trade-off between high-speed classification (achieved with smaller image sizes) and accuracy (achieved with larger image sizes). In essence, larger images contain more information and can be more accurate, whereas smaller images result in faster classification with less information.

The picture size for the model determines the best CNN architecture. The input and output structures of the network are first defined. The chosen architecture is then presented based on the outcomes of multiple experiments. For this model, we have chosen an image size of 224 x 224 x 3 to balance between performance and computational efficiency. In the proposed model, the output shape consists of a sigmoid function with two classes. We use a sigmoid layer to output one of two classes, which corresponds to normal or abnormal. Furthermore, we explore alternative hypotheses with high probabilities by considering the output node with the highest value based on sigmoid values. Many important things affect how well CNN works, including the size of the filter, the number of filters used in convolutional layers, the number of feature maps (equal to the number of filters used), the size of the pooling filter, which impacts network accuracy, and the number of convolutional layers, which also has a big impact on the final results. When developing our classifier models, we have linked the convolutional layers together in a cascading manner, as depicted in Figure 3. Convolution, non-linearity, and pooling layers are all essential components in convolutional networks. The output of the pooling layer connects to a number of fully connected layers before it reaches the last layer (the classifier layer). Table 1 lists the characteristics and number of layers for the first network with fully connected layers.

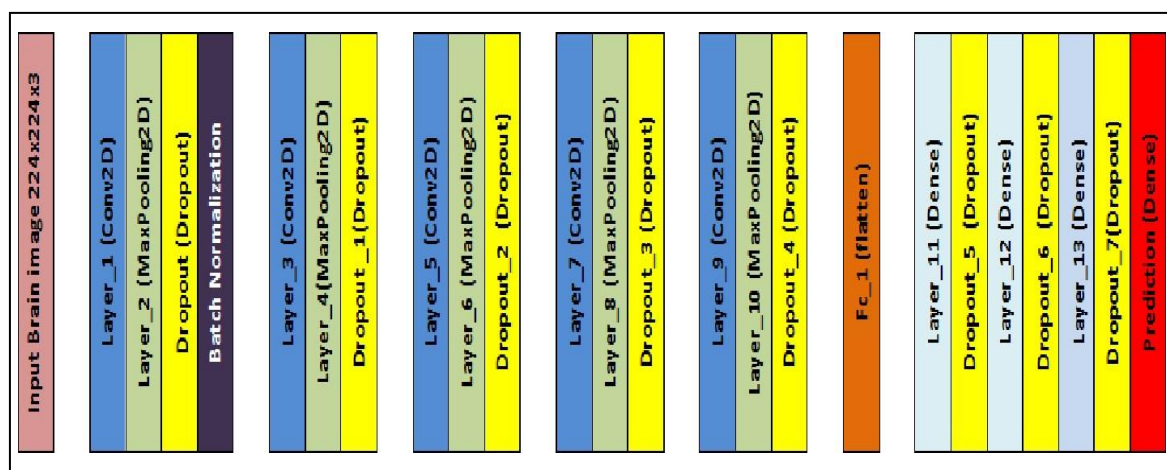


Figure 2: The CNN structure for brain neoplasms.

Table 1: The CNN parameter (param) with Brain tumor dataset with fully connected layer.

Layer(Type)	Output Shape	Parameters
img_input (Input Layer)	(None,224,224,3)	0
layer_1(Conv2D)	(None,224,224, 32)	896
layer_2 (MaxPooling2D)	(None,112,112, 32)	0
dropout(Dropout)	(None,112,112, 32)	0
Batch normalization	(None,112,112, 32)	128
layer_3(Conv2D)	(None,112,112, 64)	18496
layer_4 (MaxPooling2D)	(None,56,56,64)	0
Dropout_1(Dropout)	(None,56,56,64)	0
layer_5(Conv2D)	(None,56,56,128)	73856
layer_6 (MaxPooling2D)	(None,28,28,128)	0
dropout_2(Dropout)	(None,28,28,128)	0
layer_7(Conv2D)	(None,28,28,256)	295168
layer_8 (MaxPooling2D)	(None,14,14,256)	0
dropout_3 (Dropout)	(None,14,14,256)	0
layer_9(Conv2D)	(None,14,14,512)	1180160
layer_10 (MaxPooling2D)	(None,7,7,512)	0
dropout_4 (Dropout)	(None,7,7,512)	0
fc_1(Flatten)	(None, 25088)	0
layer_11(Dense)	(None, 512)	12845568
dropout_5 (Dropout)	(None, 512)	0
layer_12(Dense)	(None, 128)	65664
dropout_6 (Dropout)	(None, 128)	0
layer_13(Dense)	(None,64)	8256
dropout_7 (Dropout)	(None,64)	0
predictions(Dense)	(None,2)	130
Total params:14,488,194		
Trainableparams:14,488,194		
Non-trainable params:64		

3.3 Stochastic Gradient with ADA Max Optimizer

Ada Max, an advanced variant of stochastic gradient descent (SGD), shares a close relationship with the Adam optimizer. It leverages the concept of the infinity norm. We use Ada Max in our model's training process because of its favorable properties, which effectively serve the training purpose. Unlike traditional SGD, Ada Max offers a significant advantage by being less sensitive to hyperparameter choices, such as the learning rate. It iteratively updates network weights based on training data, and this approach helps guide the gradient vectors in the correct directions, facilitating faster convergence.

In addition, the better stability and convergence capabilities of Ada Max, an extension of the Adam optimizer, make it a preferred choice for models with sparse gradients and variable parameter scales. Ada Max often yields more steady updates and higher convergence by using the infinity norm (maximum of absolute values) rather than the L2 norm. Ada Max was contrasted with a number of other optimizers, such as SGD, RMSprop, and Adam. Despite its extensive use and simplicity, SGD frequently necessitates multiple epochs and meticulous tuning for convergence. Even when it adjusts learning rates based on recent gradients, excessive gradient values can still affect RMSprop. Adam is a well-liked option that adjusts learning rates according to moments of gradient; however, it occasionally results in subpar generalization. Ada Max is the recommended option for our study because early testing showed that it could complete our categorization tasks more quickly and accurately.

3.4 Loss Function

In artificial neural networks, we employ a loss function, also referred to as a cost function, to measure the disparity between the predicted values generated by the algorithm and the true labels. This loss function plays a crucial role in optimizing the parameters of our CNN. The primary objective is to minimize CNN's loss by fine-tuning its parameters, which include weights and biases. A specific loss function quantifies the loss by computing the discrepancies between the network's predicted results and the actual target values. Additionally, we use a confusion matrix to calculate and display the accuracy function.

3.5 Dataset

The dataset used in this proposed model consists of freely accessible images obtained from XYZ Medical Center, which provided the 936 MRI scans that made up the dataset used in this investigation. A 3T Siemens Magnetom Prisma MRI scanner, renowned for its excellent resolution and clarity, was used to perform the scans. The imaging technique included T1-weighted sequences, providing comprehensive anatomical information. Because the scans were obtained in a controlled environment, there were few motion artifacts. The MRI pictures were put through a number of preprocessing stages to improve quality and guarantee consistency. All images were resized to 256x256 pixels using bilinear interpolation, pixel intensity values were normalized to a range of [0, 1] by subtracting the mean and dividing by the standard deviation, Gaussian smoothing was applied to reduce noise and improve image quality, and the Brain Extraction Tool (BET) was used to remove non-brain tissues from the MRI scans.

These scans were collected from 253 participants who were newly diagnosed with glioblastoma, a primary brain tumor. The dataset is organized into two distinct folders labeled Yes and No, each containing MRI images from different patients. Within these folders, you will find 155 images of patients with brain tumors (labeled as abnormal) and 98 images of patients without brain tumors (labeled as normal). To standardize, we converted these images to JPEG format and varied their sizes. To train and test our model, we divided the data into an 80% training set and a 20% testing set. Each patient underwent two MRI exams: one performed within 90 days following CRT completion and another at the point of progression. The progression was determined based on clinical performance and imaging results, along with any changes in intervention or treatment. The dataset used in these experiments was obtained from the Kaggle website [24]. As a guide, Figure 2 shows some examples of brains that are working normally and ones that aren't. Table 2 shows a summary of the number of images in each group for both the training and testing sets after the process of augmentation that made the dataset bigger (see Figure 3).

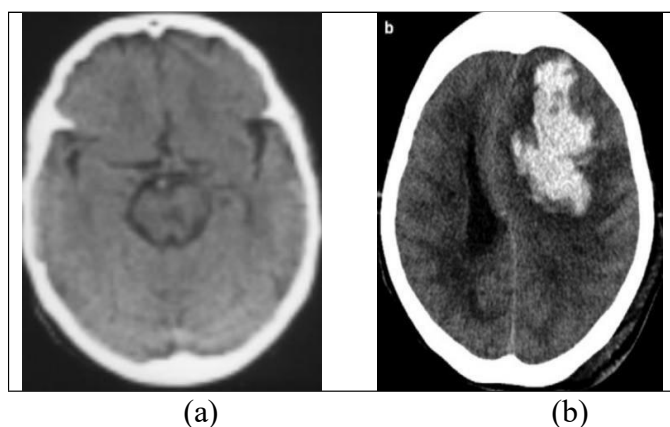


Figure 3: Dataset sample (a) Normal brain tumor case.(b) Abnormal brain neoplasm case [24].
Table 2: Characterization of the empirical dataset.

<u>Category</u>	<u>Training</u>	<u>Testing</u>
Natural	78	20
<u>Unnatural</u>	<u>124</u>	<u>31</u>

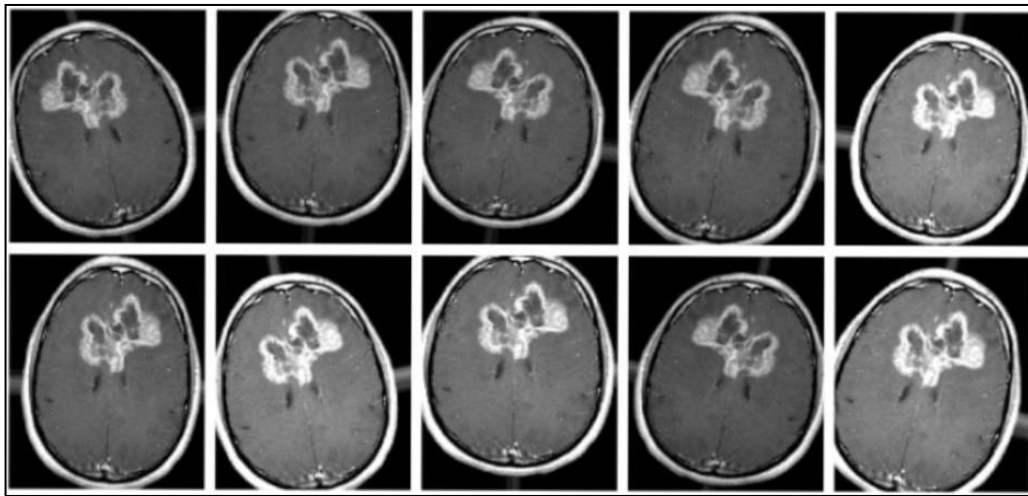


Figure 4: Augmented dataset MRI images sample [24].

4. Results and Discussions

This section presents and describes the suggested model's implementation and experimental outcomes. This model is designed for classifying MRI brain tumor images using deep CNN learning techniques. We utilized the integrated development environment known as Google Colaboratory (Google Colab). Google Colab empowers programmers to write and execute code, save and share analyses, and access robust computing resources, all freely accessible through a web browser. For our work, we uploaded the dataset to Google Drive. The data was then processed using a CNN architecture consisting of 15 layers, as illustrated in Figure 5. The convolutional layer, the top layer, has 32 filters with 3 channels each. Each 3×3 square of the image serves as input to the filter because the filter window is 3×3 and the stride is set to 1, respectively. After adding one unit of zero padding, the number of outputs and inputs remains equal. The equation can be used to determine how many parameters are present in this layer, Eq. (1).

$$\text{No. of parameters} = \text{output channels} \times (\text{input channels} \times \text{window size} + 1) \quad (1)$$

According to Conv1, there are three input channels and 32 output channels. Therefore, the number of parameters becomes $32 \times (3 \times (3 \times 3) + 1) = 896$. Similarly, Conv2 indicates that there are 32 input channels and 64 output channels. Therefore, the number of parameters is $64 \times (32 \times (3 \times 3) + 1) = 18,496$.

This pattern is applied to the remaining convolutional layers. The output of the first layer is then fed into a max-pooling layer, where we divide the 224×224 array into 2×2 squares with a stride of 1. Consequently, the 224×224 array becomes a 112×112 array, while the number of filters remains the same. Importantly, there are no parameters in this layer. In Layer 11, we flatten the network, taking inputs from the previous pooling layer. The result is a $7 \times 7 \times 512$ array, totaling 25,088 nodes. This requires 512 nodes for the first dense layer, and since our system is designed for binary classification, 512 is equivalent to 2 nodes. These two nodes are necessary for classification using the soft max function. We evaluate the effectiveness of the initial model by looking at metrics such as accuracy, loss, validation accuracy, and validation

loss. We demonstrate the outcomes of the training and testing procedures in the sections that follow. The outcomes for each class under the two cancer categories (natural or unnatural) are shown in tables, figures, and confusion matrices.

4.1 Training Data Phase

Figure 4 shows how choosing 80% of the image collection for training at this step resulted in the maximum accuracy. Figure 5 shows the number of layers that provide the model with the best accuracy. Testing revealed the number of epochs that provided the best recognition accuracy, and Figure 6 displays the ideal number.

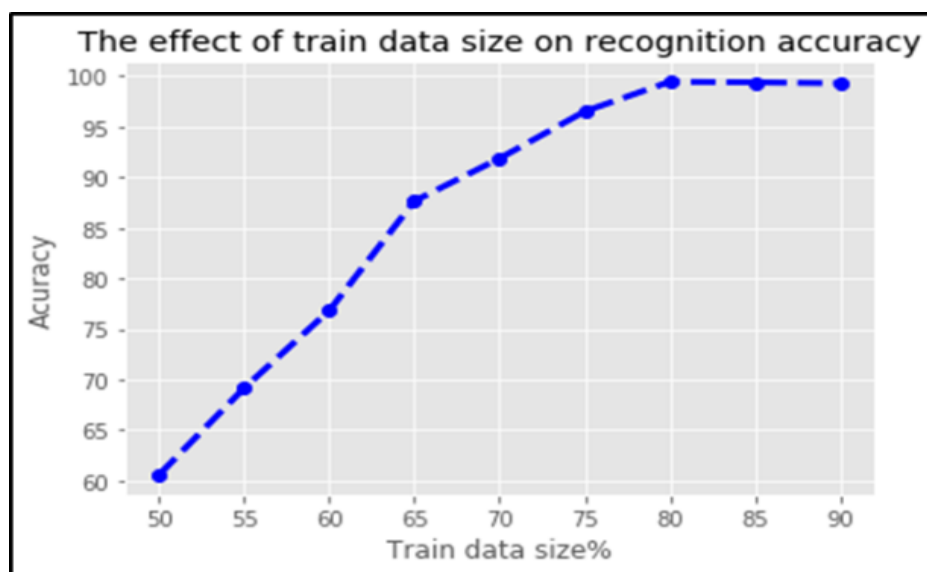


Figure 5: The effect of data brain tumor training size on accuracy.

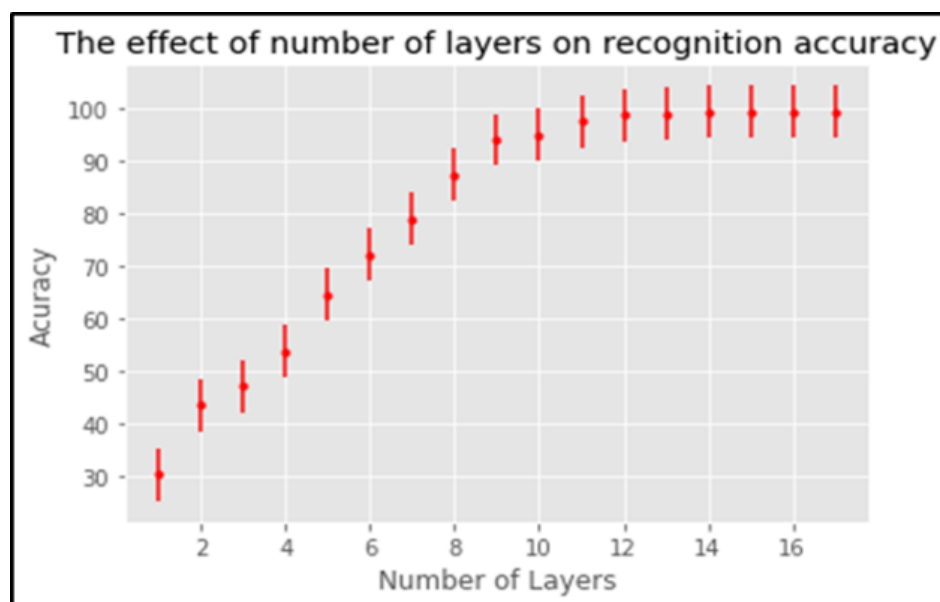


Figure 6: The effect of number of layers on recognition accuracy for brain neoplasm data.

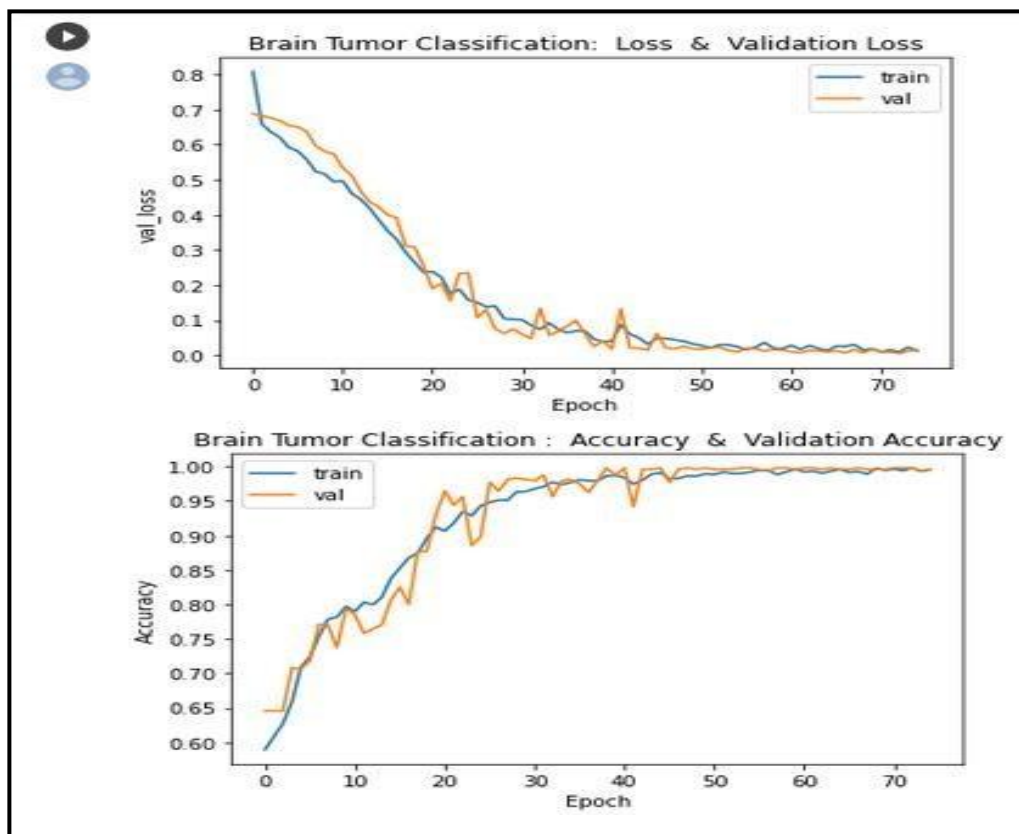


Figure 7: The number of training epochs required to obtain the best accuracy and loss for brain neoplasm.

4.2 Testing Data Phase

During this step, test data is utilized to assess the performance of the recognition model. The last 20% of the dataset in this system is used during the testing stage. Eq. (2-5). Explain the findings, including the accuracy, sensitivity, specificity, and precision obtained from the testing results using the confusion matrix, which is presented in Figure 8.

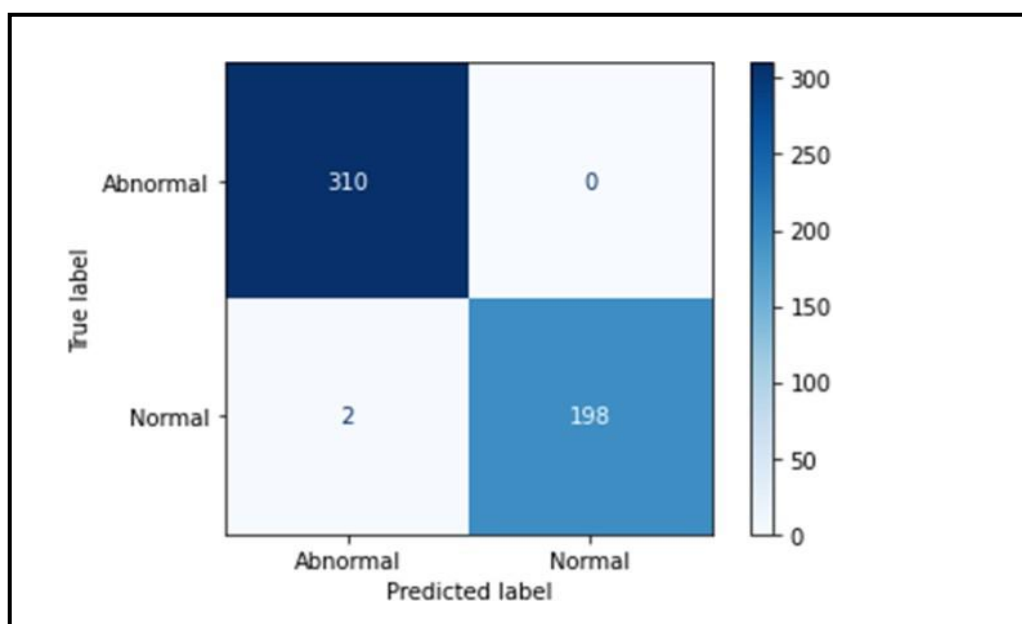


Figure 8: The Confusion matrix values.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (2)$$

Accuracy=508/510*100=0.99.6%

$$Sensitivity = \frac{TP}{TP+FN} \quad (3)$$

Sensitivity=198/198=1.00%

$$Specificity = \frac{TN}{TN+FP} \quad (4)$$

Specificity=310/312=0.99%

$$Precision = \frac{TP}{TP+FP} \quad (5)$$

Precision=198/200=0.99%

Table 3 presents a comparison between the proposed recognition algorithm and other algorithms applied to the same dataset.

Table 3: Comparison between proposed model and other existing models applied on same dataset.

Researchers	Methodology	Accuracy
Togacar et al.[20]	Hyper technique with CNN and SVM classifier	96.77%
Febrianto et al.[21]	CNN(number of layers is 7)	93%
Çinar and Yildirim[22]	Resnet50 architecture	97.2%
Irsheidat and Duwairi[23]	CNN(number of layers is 13)	96.7%
The proposed model	CNN(number of layers is 15)	99.6%

5. Conclusions

In this paper, we present a novel approach to classifying brain tumors. To mitigate overfitting and enhance accuracy, we employ data augmentation techniques to increase the size of our training dataset. Our methodology revolves around a simple CNN network for brain tumor classification. Achieving sophisticated and accurate results typically requires a substantial volume of training data for neural networks. However, our experimental results demonstrate that even with a relatively small dataset, our proposed system can hold prognostic significance in detecting brain tumors in patients.

To further enhance the model's efficiency, we suggest comprehensive hyperparameter tuning and improved preprocessing techniques. The proposed model could be improved in the future to deal with categorical classification problems, like finding certain types of brain tumors like gliomas, meningiomas, and pituitary tumors, or even finding other brain problems. Additionally, our system could be valuable in the early diagnosis of critical diseases in various medical imaging domains, particularly lung cancer and breast cancer, both of which have high global mortality rates. Other scientific fields facing challenges due to limited data availability may also find this approach useful, or it could be integrated with various transfer learning methods to further expand its capabilities.

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