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Multiclass Classification of Brain MRI using Deep Learning Algorithm

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Abstract: *A brain tumor is one of the deadliest, most frequent, and most aggressive diseases. As a result, early detection and treatment of these illnesses are critical in averting mortality. In this procedure, MRI images are utilized to identify brain abnormalities. Manually identifying brain tumors is time-consuming and may result in a human mistake. As a result, precise analysis in a short period is essential. This approach includes an automated brain tumor classification system that employs a highly accurate Convolutional Neural Network (CNN) to categorize brain MRIs into normal and malignant categories. The brain is first segmented using a thresholding approach, then morphologically operated on. The classification strategy for glioma and meningioma classification using CNN and Vgg19 is presented in another approach.*

Keywords: MRI, Brain tumor, vgg16, vgg19, machine learning

I. INTRODUCTION

One of science's unresolved mysteries is the human brain. Its intricacy has confused and confounded scientists to this day. There are an equal amount of nonneuronal cells as there are neurons in them. Brian manages our fluid balance, blood pressure, pulse rate, body temperature, and mobility. Our emotions, fight-or-flight response, memory, cognition, motor learning, and learning, remembering, and communication processes are all controlled by it [1].The brain comprises a network of nerve cells that develop, create new synapses, and eventually die. However, aberrant and uncontrolled nerve cell proliferation can lead to tumor formation. Additionally, aberrant activity in other body organs, such as the lungs, breasts, and skin, can result in brain tumors. Brain tumors are one of the most frequent cancer-related causes of death globally. The Central Brain Tumor Registry of the United States' most recent statistics show that primary malignant brain and another central nervous system (CNS) tumors caused 81,246 fatalities between 2013 and 2017.Primary malignant brain tumors and other CNS cancers had a 36% survival rate after diagnosis; this percentage was lowest in those over 40 (90.2%) and most significant in children under 14 (97.3%). [2]. There are typically 16,249 fatalities per year on average.

Abnormal tumors in or on the brain are known as brain tumors. Uncontrolled cell proliferation, a breakdown of the normalcell death process, or both can cause tumor formation. Primary and secondary brain cancers exist. Primary tumors are made up of cells compared to those present in the organ or tissue that gave rise to them. Brain cells form the basis of an initial brain tumor. Tumors that are malignant spread quickly and might harm adjacent tissues. Almost always, "malignancy" or "malignant" refers to cancer.

Secondary tumors are made up of cells that have spread from one section of the body to another. Secondary brain tumors are cancer cells that have spread to the brain from somewhere else in the body [3].

A brain tumor is an abnormal growth of cells in the brain. Primary, secondary, and metastatic tumors are the three types of brain tumors, often known as lesions. The brain tumor begins in the tissues of the brain and its surroundings. Primary and secondary brain tumors exist. According to the malignancy status, the initial tumor can be classed as benign or malignant.Secondary brain cancer startsinone body part and spreads over another. American Association of Neurological Surgeons (AANS) has divided histological findings under the microscope into Grade I - Grade IV depending on their malignancy or benignity[4].

The purpose of this study is to classify brain MRI into malignant and benign groups, as well as glioma and meningioma. The brain MRI is first pre-processed to eliminate the skull region, a procedure known as skull stripping. This study presents two ways. The categorization technique of normal and abnormal brain MRI is presented in the first approach. In contrast, the second technique categorizes brain MRI into glioma and meningioma.

II. LITERATURE SURVEY

This study recommends pre-processing, feature extraction, feature reduction, and classification, as recommended by S. Ajikumar and Dr. A. Jayachandran [5]. In the first phase, the wiener filter minimizes noise and prepares the image for feature extraction. The image is partitioned into meaningful areas using the seeded region growing segmentation in the second step. The wavelet coefficients from the segmented image are extracted in the third stage using discrete wavelet transformation (DWT). The wavelet coefficients' dimensionality is reduced using PCA in the next step. The AdaBoost classifier divides the experimental images into normal and pathological categories during the classification step. The sensitivity, specificity, and accuracy of our suggested approach are examined.

The suggested work by Carlos Arizmendi, Alfredo Vellido, and coworkers [6] address this challenge in binary classification, for which MRS signal pre-processing is a crucial step in data analysis. The MRS data is pre-processed with a combination of the Discrete Wavelet Transform (DWT) and energy criteria for signal reconstruction. The data is then classified using features using Bayesian Neural Networks, and feature selection is performed.Using Bayesian neural networks, this method assesses a multi-center global database of single-voxel proton MRS (SV-H-MRS) linked to brain tumor illnesses.

Salim Lahmiri et al. [7] proposed a brain MRI classification system based on DWT and machine learning algorithms like KNN, LVQ, and PNN. The following step is to create an ensemble classifier system in which prior machines serve as basis classifiers and support vector machines (SVM) aggregate judgments. The new method achieves more effective rates of proper categorization than the prior strategy. The results show that, as is commonly assumed, the wavelet transform's horizontal and vertical sub-bands can extract features from the LL sub-band effectively and efficiently, concluding that the Wavelet transforms horizontal and vertical sub-bands can extract features from the LL sub-band effectively and efficiently.

Deji Lu et al. [8] suggest using non-negative and local non-negative matrix factorization (NMF, LNMF) to extract traits from metabolite profiles. The traits gathered by NMF and LNMF are utilized for training classifiers using SVM and linear discriminant analysis (LDA). The unique approach could be able to extract essential data, producing a classifier with a high generalization rate. Experiments have shown that the new technique outperforms previous strategies. When utilizing LNMF+LDA, the suggested system obtains a maximum accuracy of 96%, and when using LNMF+SVM, it achieves a maximum accuracy of 94%.

The majority of the strategies employed distinctive feature extraction methods, according to the literature review. The individual characteristics cannot sufficiently describe the brain MRI categorization. Different feature extraction strategies are required to categorize brain MRI scans into malignant and benign robustly and glioma meningioma.

III. DEEP LEARNING ALGORITHMS USED FOR CLASSIFICATION

This approach uses CNN and Vgg16 algorithms to classify brain MRI. This section presents a detailed explanation of the CNN and Vgg16 algorithms.

3.1 Convolutional Neural Network (CNN)

CNN is a very effective algorithm for classification strategies. It is a feed-forward neural network including convolutional, pooling, flattening, and dense layers. The filter and kernels are used to process the image.

Before beginning the training process, it is necessary to learn the fundamentals of CNN, which are detailed below. CNNs are a type of Neural Network that is exceptionally effective at image recognition and categorizationCNNs, or large-layer feed-forward neural networks, are one type of large-layer feed-forward neural network.

A. Convolutional Layer (CL)

A Convolutional Network's core component is the CL. CL's primary goal is to extract characteristics from the data it receives. Convolution preserves the spatial relationship between pixels by learning information from the input image's small kernel. A group of learnable neurons is used to hide the input image.

$$G[m,n] = (f * h)[m,n] = \sum_j \sum_k h[j,k] f[m-j, n-k] \quad (1)$$

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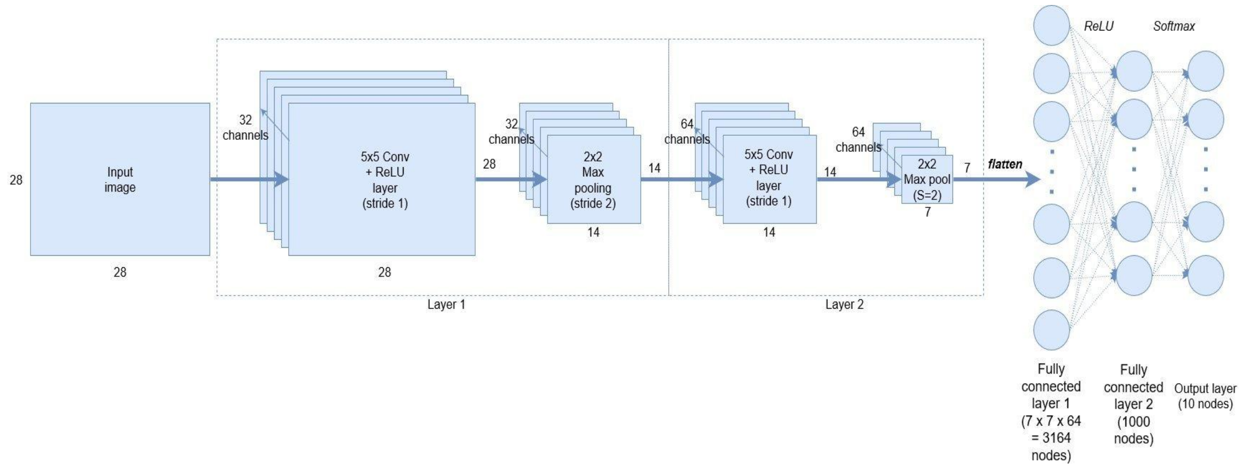

Figure 1: Architecture of CNN

B. ReLU Layer

ReLU stands for rectified Linear units in a non-linear process. All non-positive feature map values are replaced with zero in a pixel-by-pixel way. To understand how the ReLU works, we'll assume the neuron input is x, and the rectifier is given.

$$f(x) = \max(0, x) \qquad (2)$$

C. Pooling Layer

The pooling layer keeps the most relevant information while reducing the complexity of each activation map. A sequence of non-overlapping rectangles is created from the supplied images. A non-linear technique, such as average or maximum, is used to down sample each region. This layer, frequently placed between CLs, improves generalization and convergence speed while also being resistant to translation and distortion.

D. Flatten Layer

As the name implies, the 2D pooled feature map in this layer is converted into one column array.

E. Fully Connected Layer

So, you're going to snap images immediately. Examine each of the 24x24 windows. Apply 6000 different traits to it. Examine the image to find if it's a face or not. The image non-face region comprises the majority of the image. Instead, focus on regions where you could see a face. This allows us to spend more time checking probable areas.

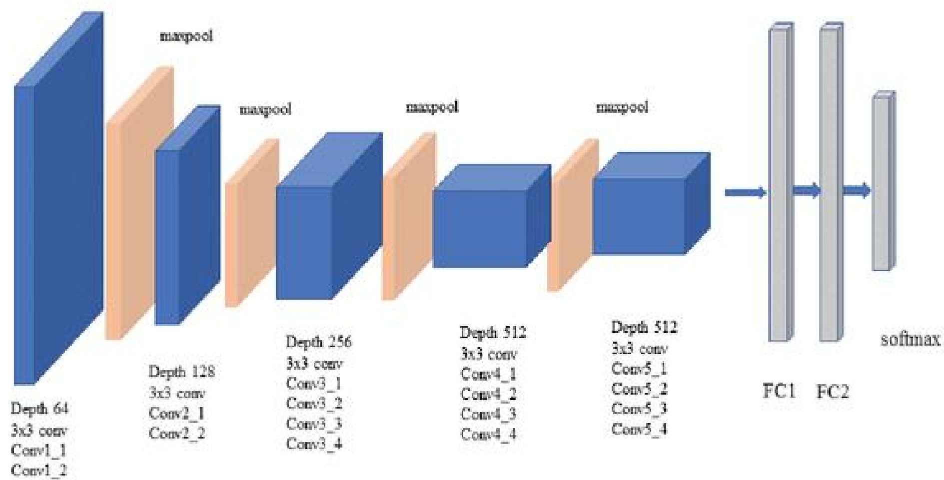

Figure 2: Architecture of Vgg19

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F. Vgg19

The 19 layers that makeup Vgg19 are divided into 16 convolutional layers, 3 fully connected layers, 5 max-pooling layers, and 1 softmax layer. In VGG19, there are 19.6 billion FLOPs. The millions of pictures in ImageNet were used to train CNN VGG-19. VGG, to put it simply, is a deep CNN used to classify images.

ConvNet Configuration					
A	A-LRN	B	C	D	E
11 weight layers	11 weight layers	13 weight layers	16 weight layers	16 weight layers	19 weight layers
input (224 × 224 RGB image)					
conv3-64	conv3-64 **LRN**	conv3-64 **conv3-64**	conv3-64 conv3-64	conv3-64 conv3-64	conv3-64 conv3-64
maxpool					
conv3-128	conv3-128	conv3-128 **conv3-128**	conv3-128 conv3-128	conv3-128 conv3-128	conv3-128 conv3-128
maxpool					
conv3-256 conv3-256	conv3-256 conv3-256	conv3-256 conv3-256	conv3-256 conv3-256 **conv1-256**	conv3-256 conv3-256 **conv3-256**	conv3-256 conv3-256 conv3-256 **conv3-256**
maxpool					
conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512 **conv1-512**	conv3-512 conv3-512 **conv3-512**	conv3-512 conv3-512 conv3-512 **conv3-512**
maxpool					
conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512	conv3-512 conv3-512 **conv1-512**	conv3-512 conv3-512 **conv3-512**	conv3-512 conv3-512 conv3-512 **conv3-512**
maxpool					
FC-4096					
FC-4096					
FC-1000					
soft-max					

Figure 3: The actual configuration of the networks and the ReLu layers are not shown for brevity.

Layers in the VGG19 model are: The 19-layer network can classify images into 1000 different categories, such as keyboards, mice, pencils, and other animals. As a result, the network has amassed a diverse set of rich feature representations for variousimages.

- Input: 224x224 RGB images
- Pre-processing: determined the mean RGB value for each pixel over the training set.
- Kernel size for convolution: 3X3 with stride 1
- The image's spatial resolution was preserved by using spatial padding.
- Max pooling: kernel size 2X2 pixel windows with sride 2.
- Rectified Linear Unit(ReLu):used to increase the non-linearity and improve computation time
- It created three ultimately linked layers, the first of which were 4096 bytes each, followed by a 1000-channel layer for ILSVRC classification in 1000 ways and a SoftMax function.

IV. MODI CHARACTER RECOGNITION SYSTEMS

Detecting brain tumors with an MRI is challenging because of the intricacy and diversity of malignancies. This method uses a convolutional neural network to evaluate the brain MRI as normal or abnormal after identifying the tumor using a thresholding technique.

4.1 Dataset

The clinical database of brain MRI is used in this method. There are both normal and aberrant MR images in the database. Table I shows the complete database distribution for normal and abnormal. The database consists of raw images that have been pre-processed and segmentation and augmentation methods after separating training and testing data.

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Table 1: Database Distribution Normal Abnormal Classification

Table Head	Database Distribution		
	Total Images	Training Images	Testing Images
Normal	273	212	61
Abnormal	194	163	31

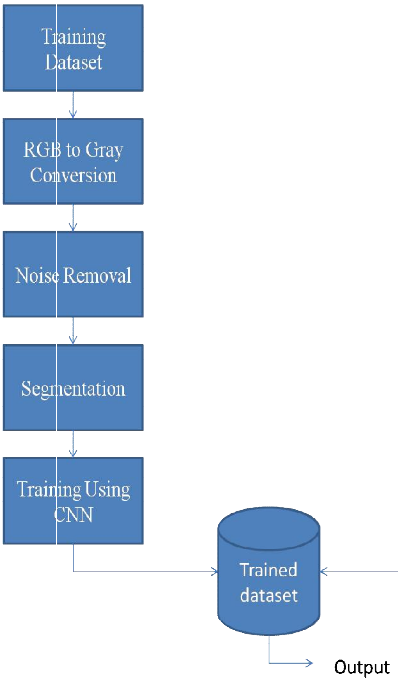

Figure 4: Flow diagram of the proposed system

Kaggle provided the dataset for the second approach, Glioma, Meningioma, and No Tumor Classification. The distribution of the dataset for Glioma, Meningioma, and no tumor categorization is shown in Table II.

Table 2: Database Distribution Glioma, Meningioma, and No Tumor Classification

	Database Distribution		
	Total Images	Training Images	Testing Images
Glioma	370	250	120
Meningioma	370	250	120
No tumor	3112	2862	250

4.2 Pre-processing

The patient data text is included in the raw, noisy database images. The images are initially in RGB color format. Grayscale is created by converting RGB color to the weighted average. Rician and salt and pepper noise have the most significant impact on medical imaging. In salt and pepper noise, the median filter is adequate. Low contrast is another issue with medical images. The power-law transformation can help low-contrast images. It is expressed mathematically as.

$$S = Cr^{\gamma} \qquad (3)$$

4.3 MRI Segmentation and Tumor Identification

To separate the brain from the skull, segmentation is essential. This technique segments the brain using thresholding.

$$f_{g(x,y)} = \begin{cases} 1 & I(x,y) > T \\ 0 & \text{else} \end{cases} \qquad (4)$$

The pixel's grayscale value is I(x,y), while the binary image is f g(x,y).

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Using the thresholding procedure, the tumor component is discovered. The colored MRI image is first transformed to grayscale using the weighted average approach. Through the use of median filtering and thresholding, the grayscale picture is converted to binary. The binary image is subjected to morphological filters like erosion and dilation to produce smoother edges. The tumor identification process employs the contour technique. The most noticeable object is selected as a tumor after counting the number of binary elements using the contour technique.

4.4 Brain MRIclassification into Normal and Abnormal

The clinical data divides brain MRI into normal and abnormal groups. Table I includes information on the dataset. The dataset is divided 80:20 between training and testing. This technique splits brain MRI into normal and abnormal groups using the CNN algorithm.

4.5 Brain MRI Classification into Glioma and Meningioma

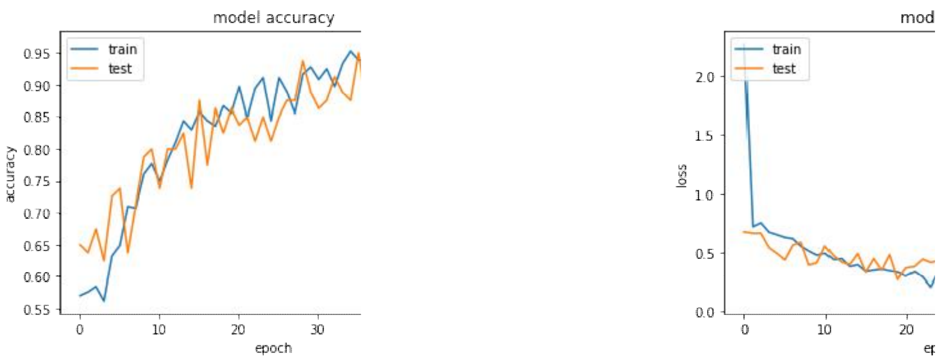
The clinical information is utilized to classify brain MRI into normal and pathological categories. Table II contains the dataset's specifics. The dataset is split into 80:20 training andtesting. This categorization approach divides brain MRI images into three categories: glioma, meningioma, and no tumor.

V. RESULTS

The system is written in Python and uses the Keras package. The Google Colab cloud platform is used for the training. The suggested system's findings are given through qualitative and quantitative analysis. Two categorization methodologies are offered in this approach: normal and abnormal brain MRI, as well as glioma, meningioma, and no tumor.

5.1 Analysis of Brain MRI Classification into Normal and Abnormal

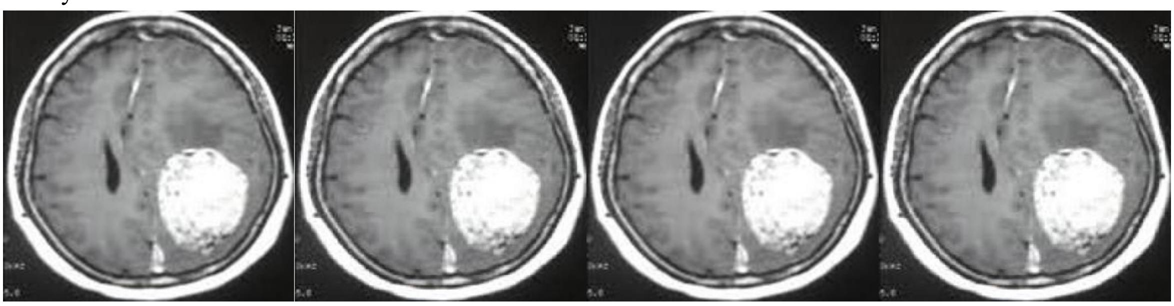
The suggested approach divides brain MRI into normal and pathological categories using the CNN algorithm. Fig.5 shows the CNN training progress for brain MRI categorization into normal and abnormal.



(a) (b)

Fig.5. Performance of CNN for classification of brain MRI into normal and abnormal (a) Accuracy (b) Loss

The result of the brain tumor detection on the abnormal and normal images is shown in Fig.6.2 and Fig.6.3, respectively.



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

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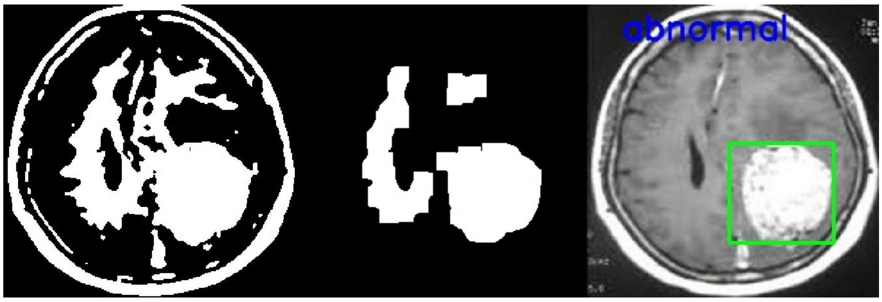
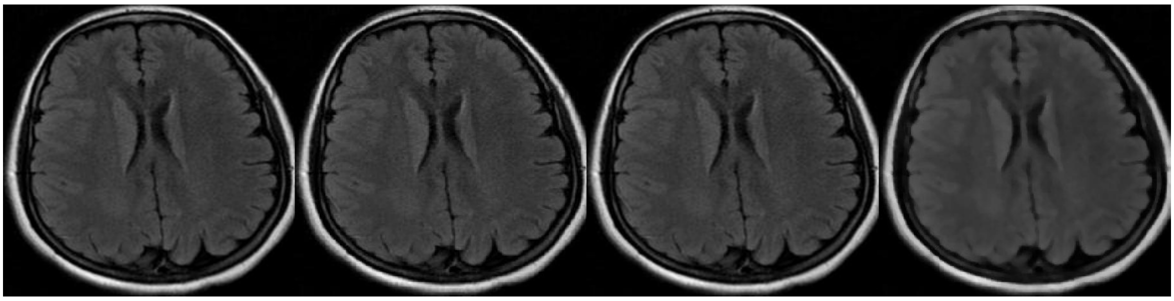
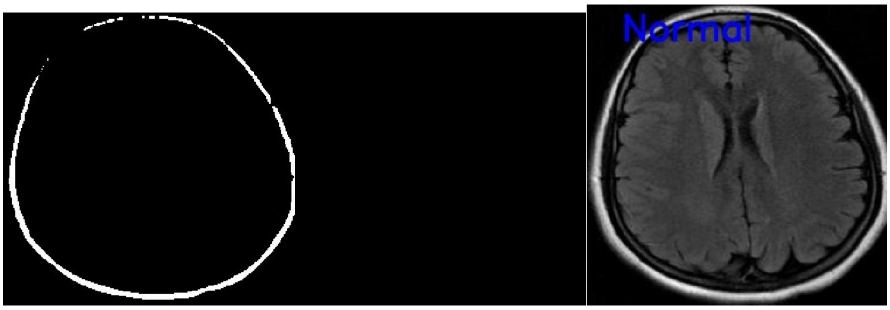


(e) (f) (g)

Figure 6: Flowchart of the system (a) Input abnormal Brain MR image (b) Resized image (c) grayscale image (d) filtered image (e) Segmented image (f) image after the morphological operation (g) Output



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

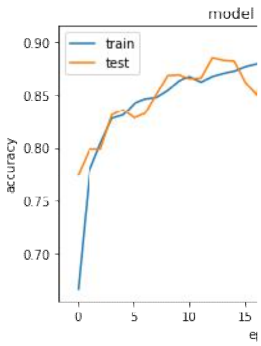


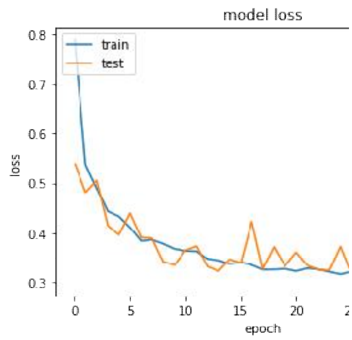
(e) (f) (g)

Figure 7: Flowchart of the system (a) Input normal Brain MR image (b) Resized image (c) grayscale image (d) filtered image (e) Segmented image (f) image after the morphological operation (g) Output

5.2 Analysis of brain MRI classification into Glioma, Meningioma, and No tumor

The second method categorizes brain MRI data into glioma, meningioma, and no tumor categories using the CNN and VGG19 algorithm. Figure 8 displays the CNN algorithm's performance for this categorization technique.





(a) (b)

Fig.8. Performance of CNN for classification of brain MRI into Glioma, Meningioma, and No tumor (a) Accuracy (b) Loss

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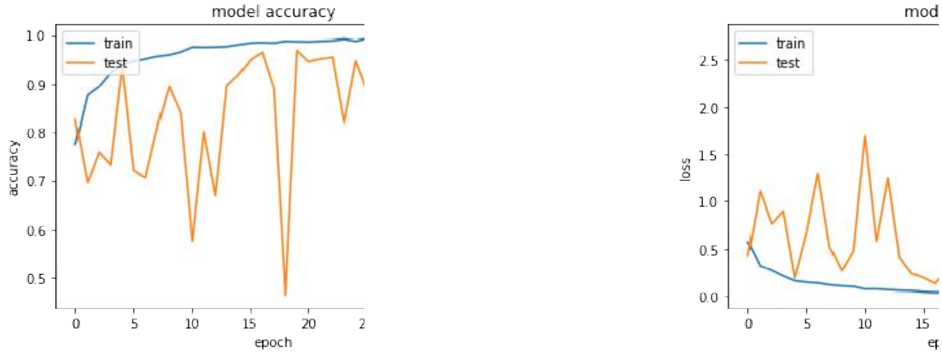
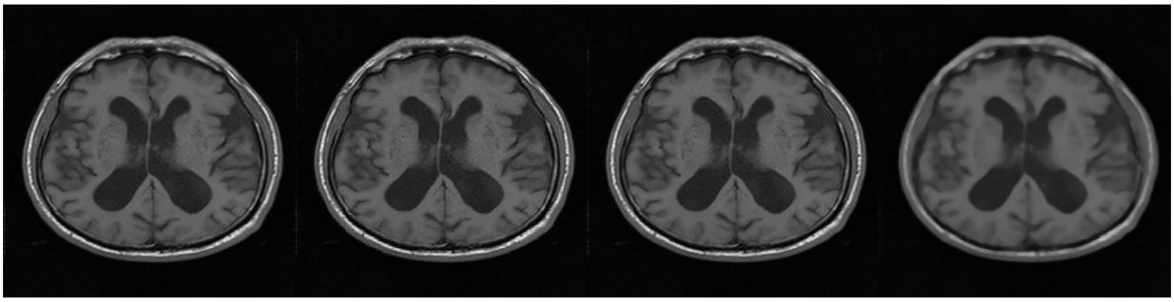
The performance of the Vgg19 algorithm for this classification strategy is shown in Fig. 9.



(a) (b)

Fig.9. Performance of Vgg19 for classification of brain MRI into Glioma, Meningioma, and No tumor (a) Accuracy (b) Loss

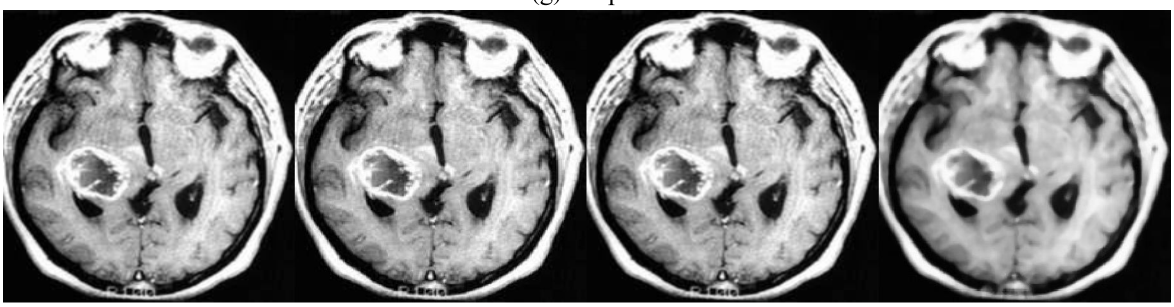
The result of the vgg19 for brain MRI classification into glioma, meningioma and no tumor is shown in Fig.10, Fig.11, and Fig.12, respectively.



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

(e) (f) (g)

The output of classification of brain MRI into glioma meningioma and normal (a) Input no tumor Brain MR image (b) Resized image (c) grayscale image (d) filtered image (e) Segmented image (f) image after the morphological operation (g) Output



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

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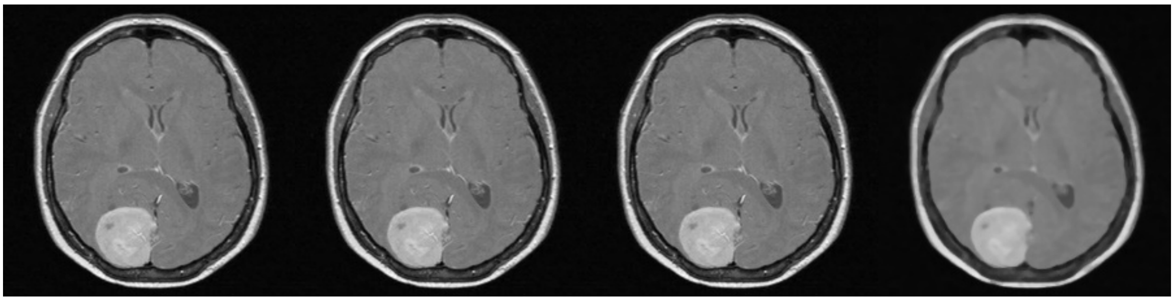
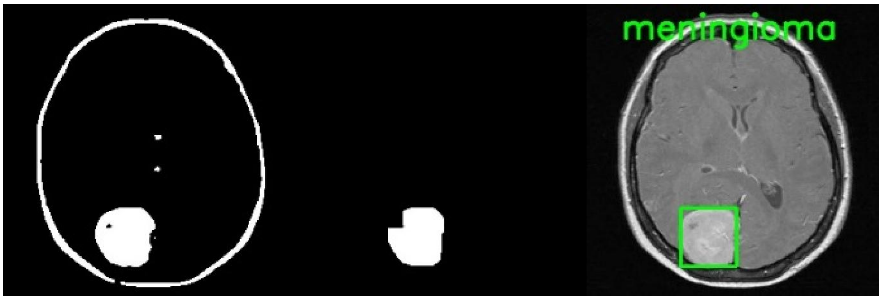
(e) (f) (g)

The output of classification of brain MRI into glioma meningioma and normal (a) Input Glioma Brain MR image (b) Resized image (c) grayscale image (d) filtered image (e) Segmented image (f) image after the morphological operation (g) Output



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



(e) (f) (g)

The output of classification of brain MRI into glioma meningioma and normal (a) Input Meningioma Brain MR image (b) Resized image (c) grayscale image (d) filtered image (e) Segmented image (f) image after the morphological operation (g) Output

The qualitative analysis of the proposed system shows promising results. For the first approach, i.e., analysis of brain MRI classification into normal and abnormal, the CNN performs better on unknown testing samples. In the second approach, i.e., analysis of brain MRI classification into Glioma, Meningioma, and No tumor, the Vgg19 outperforms the CNN algorithm on the dataset used

VI. CONCLUSION

The contribution of this research, a fully automated method for brain MRI classification from MR anatomical images, is summarized by the outcomes of this study, which demonstrate the effectiveness of the applied technique in distinguishing human brain images into normal and abnormal. This technique provides two ways to classify brain MRIs: first, into normal and abnormal, and second, into no tumor, glioma, and meningioma. The accuracy of the first technique, which used the CNN algorithm, was 0.8750 after 50 iterations. The accuracy of the second technique, which used the CNN and VGG19 algorithms, was 0.8967 and 0.9413, respectively.

In the future, this approach can be implemented for the further subclass of the brain cancer stages like low-grade glioma and high-grade glioma. The dataset samples. The limited dataset is one of the hurdles in implementing a real-time system, and hence in the future, the model needs to train on a more significant number of samples

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