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Abstract

Despite significant advances in medical technology, classifying brain tumors remains extremely challenging. Recent times have seen the development of automated techniques for early brain tumor detection that are a substitute for the traditional manual process, which consumes a lot of time and is error-prone. Various classification algorithms have been designed to enhance the accuracy of the classification of brain tumors. The goal of this study is to offer a comprehensive survey of state-of-the-art techniques and their performance. In this study, the Convolutional Neural Network (CNN), a popular deep learning architecture, is used to generate multi-classification of brain tumors for early detection. The analysis used a large, publicly available dataset containing MRI scans. 8,582 training images and 1,705 test images were included in the Kaggle dataset. The CNN model can differentiate between four different forms of brain tumors: glioma, meningioma, pituitary, and no tumor. The various methods used for comparison are EfficientNet B7, ResNet50, MobileNet V3(small), VGG-19, and DenseNet 121. The ResNet50 approach yields superior classification outcomes for MRI images for the given input dataset.

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Contents

0.1	INTR	ODUCTION	5
	0.1.1	Motivation	6
	0.1.2	Objectives	6
	0.1.3	Literature Survey	6
0.2	PROF	POSED SYSTEM	8
	0.2.1	Understanding the data	8
	0.2.2	Dataset Description	8
	0.2.3	Visualization of the Data	9
	0.2.4	Data Preprossessing	9
	0.2.5	Data Augmentation	.1
0.3	Imple	mentation	.1
0.4	Exper	rimental Setup	.7
0.5	Result	ts and Discussion	.8
0.6	Refe	erences	8

List of Figures

1	Human Brain	8
2	Testing set of four classes	9
3	Training set of four classes	9
4	Glioma Tumor	9
5	Pituitary Tumor	10
6	Meningioma Tumor	10
7	No Tumor	10
8	Augmented images of the original image of the human brain	11
9	Train and validation accuracy vs number of epochs of EfficientNet B7 architecture	12
10	Train and validation loss vs number of epochs of Efficient Net B7 architecture	12
11	Train and validation accuracy vs number of epochs of VGG 19 architecture $$	13
12	Train and validation loss vs number of epochs of VGG 19 architecture	13
13	Train and validation accuracy vs number of epochs of ResNet 50 architecture $$.	14
14	Train and validation loss vs number of epochs of ResNet 50 architecture	14
15	Train and validation accuracy vs number of epochs of MobileNet V3(small) architecture	15
16	Train and validation loss vs number of epochs of MobileNet V3(small) architecture	15
17	Train and validation accuracy vs number of epochs of DenseNet 121 architecture	16
18	Train and validation loss vs number of epochs of DenseNet 121 architecture	17

0.1 INTRODUCTION

Brain tumors can be defined as an abnormal growth of a mass of tissues where the growth of the cells is uncontrollable and the count keeps multiplying. This happens because the cells reproduce way too much or do not die when they are supposed to. It is also known as an intracranial tumor, which means internal to the skull. Brain tumors are classified into two types: primary and metastatic. Tumors that are caused by cells or tissues within the environment of the brain and its surroundings are called primary brain tumors[8]. Metastatic tumors are the ones that spring up elsewhere in the human body and then, through the blood, move up to the brain.[21] These tumors are usually believed to be cancerous or malignant. Such tumors have a 25 percent chance of causing cancer in the patient. Benign Do not infiltrate; remain in your primary location. Do not spread to local structures. grow very slowly. have distinct borders. not very problematic. But if the required attention is not paid, it can cause serious consequences over time. Malignant tumors invade other sites and spread proliferation in the surrounding area. grow at an abrupt and unmanageable rate[6]. Tumors are cancerous. spread through the lymphatic system or blood. High medical attention is needed right from the start.

Meningioma, pituitary, and glioma are the three most common types of tumors in adults. While meningioma and pituitary fall under the benign class, glioma comes under the malignant family[13]. Meningioma Tumors originating on the meninges that envelop the brain and spinal cord membranes within the skull these are the most common types to form in humans. They have extremely slow growth, which accounts for growth over years, making it difficult to identify symptoms. Females are more prone to this tumor[4]. The pituitary is a small organ in the brain situated around the nose. Its main functionality is to secrete hormones. The growth of a tumor in this gland or organ is known as a pituitary tumor. Usually, symptoms are not observed. Discovered by processes like MRI scans intentionally.Non-cancerous tumors that do not spread. This may force the gland to change the hormones it produces, leading to additional medical complications [(]thirteen). Glioma is one of the most common types of tumors occurring in the brain (33% of all brain tumors are gliomas). They are formed in the glial cells that surround the neurons in the brain. Men are more prone to this tumor. Occurs mostly in adults. But can occur at any age[15].

MRI [7]scans generate elaborated images. They use magnetic fields over traditional methods using X-rays. Radio waves are passed through a very strong magnet to the body, where protons react and high-definition images are created that include tissues, cells, etc[10]. One of the main reasons MRI scans are preferred to CT scans is that the former is much more effective at exposing the subtle differences between the tissues and cells than the latter. Our contributions are summarized as follows: a) This paper takes advantage of a deep learning algorithm to perform automatic classification of MRI brain images. b) The current methodology intends to measure the performance of various deep learning models. c) The outline of this paper includes a comparison of five popular deep learning models (DenseNet, VGG19, MobileNet V3 Small, EfficientNet B7, and RestNet 50)[9] in terms of accuracy.

The rest of the work is split as follows: Section I is the introduction section. Section II sheds light on the literature review done, while Section III explains the system architectures and methodology with a detailed description of each part. Section IV describes the experimental setup used for the work. Results and conclusions can be found in Section V. Section VI explains the future scope of this work and how it can be carried forward. The final section, Section VII, concludes this paper by providing acknowledgements to our guides.

0.1.1 Motivation

Detecting and classifying brain tumors manually can be error-prone, so we propose this system of detecting and classifying the brain tumor by the means of machine learning (ML) and deep learning (DL) architectures. The motive of this system is to prevent incorrect classification of the tumor, which may lead to improper results. The system is very helpful for the doctors to classify the type of brain tumor based on Magnetic Resonance Imaging (MRI) and go ahead with the treatment. Therefore, this proposed system will be one of the best methods to detect and classify the brain tumor,, which can be further improved by various techniques.

0.1.2 Objectives

- To replace the manual classification system to computational method with Deep Learning (DL) architectures.
- To classify whether given image is affected with brain tumor or it belongs to 'Notumor' class.
- Later classifying to which class it belongs to among the three (3) classes used i.e.. Pituitary, Glioma and Meningioma.

0.1.3 Literature Survey

Author: Emrah Irmak et.al. proposed .[4] The main aim of the work is to propose three different neural networking models. Publicly available datasets have been chosen for the implementation of the same. The authors have combined four different datasets into one for the purpose of execution. They add up to 428090 images. The authors initially did well-planned research and identified the two main features occurring in a convolutional neutral network[1], which are feature extraction and image classification. They further discovered the five layers responsible for the same, namely the input layer, the convolution layer, the pooling layer, the fully connected layer, and the classification layer. As described above, the authors propose three different models. The first is the simplest of all, simply detecting the presence of a tumor in the input data. [twentythree] This model contains three weighted layers. Since it is a binary classification indicating either the presence or absence of the tumor, the output layer will contain two neurons. The second model aids in classifying the given tumor image input into five different tumor classes, namely normal, glioma, meningioma, pituitary, and metastatic. This model contains twenty five weighted layers[2]. The third helps classify the given tumor image input into three different tumor classes, namely grades II, III, and IV. This model contains sixteen weighted layers. Since the output has to lie in one of the three classes, the output layer will contain three neurons. The authors imply that reducing these computational costs and achieving more successful results relies heavily on the use of powerful hardware and hyperparameter optimization of established networks [sixteen]. In this article, Brain tumor detection is achieved with a high accuracy of 99.33 %. Furthermore, 92.66% accuracy is obtained in classifying brain MR into glioma, meningioma, pituitary, normal brain, and metastases. [fourteen] Finally, glioma brain tumors are classified into grades II, III, and IV with 98.14 % accuracy. The proposed CNN

model is trained and tested using a sufficiently large number of medical images. The results obtained with the proposed CNN model, as well as the comparison with prior art methods, demonstrate the effectiveness of the CNN model built with the proposed optimization framework.

In another study, Auhtor name: Ramdas Vankdothu et.al. proposed [14] The current work plans on implementing a neural network called RCNN (Recurrent Convolutional Neural Network). The authors considered achieving the goal of higher accuracy with fewer complexities as a goal. They further modularized the task into 1) preprocessing (adaptive filtering algorithms), and 2) clustering algorithms for segmentation. 3) Feature extraction using GLCM 4) classification by RCNN. In preprocessing, eliminating noise to focus more on achieving efficient results was the goal, for which an adaptive filter was used. The process of identifying the right segmentation becomes important because each technique offers something distinct from the others, and the user must determine which technique will assist him with his problem.[fourteen] One of such techniques identified here is K-means clustering, as it not only helps classify images among multiple output classes but also aids in improving the edging in the images. Improved k-means clustering is employed as it helps further with feature extraction. Feature extraction is used to reduce the number of materials expected to describe huge amounts of data.[15] In feature extraction from images, many intensity levels of an image are provided as input to feature extraction. Output can consist of high-level data such as variance, shape, mean, and color. In imaging applications, the GLCM method is one of the leading methods. [1] GLCM is the most commonly used feature extraction technique for MRI images due to its high efficiency. Texture analysis can aid in tumor identification and grade determination. Accuracy, sensitivity, and specificity were the evaluation parameters[13]. The work is concluded by the authors, who provide some light on how the proposed model had better accuracy than other algorithms like back propagation and U-Net, which achieved accuracies of 88.83 % and 90.86 %, respectively. The RCNN model proposed achieved an accuracy of 95.17%.

Author: Nivea Kesav and M.G. Jibukum proposed [5] Here, the authors have mainly focused on offering a method for analyzing brain tumors and attempting to reduce the execution time of a traditional RCNN architecture using a low-complexity framework. The MRI images are taken from two publicly available datasets from Figshare and Kaggle. There are three types of brain tumors: gliomas, meningiomas, and pituitary tumors. Under the proposed model, they have first classified the tumor pictures from MRI data using Two Channel CNN, and then they have transmitted them to an object detection system using RCNN, where they swap out the RCNN's feature extraction layer with Two Channel CNN because it had performed better in their preliminary trials.[12] Initially, the authors tested and proved that the two-channel CNN could classify Meningioma and pituitary tumor images. Now, while they are extending their research to detect the location of the tumor. Execution time and parameter count are the key attractiveness parameters. [6] Similar to their past research, the execution time of their suggested solution in this categorization scenario is as low as 64.5s with a total of just 1,008,226 parameters. This is as a result of the architecture's low complexity, which enables it to function successfully on systems with fewer specifications. This can also assist in decreasing the system's overall time consumption, allowing for effective real-time processing. In order to assess the performance, they contrasted their suggested model with the various existing architectures, including RCNN and Alexnet[3], VGG16, VGG19, Googlenet, and Resnet. Their suggested RCNN, which substitutes a two-channel CNN for the feature extraction layer CNN in the detection stage, executes in 277.174 seconds. Consequently, combining both of these operations only requires 341.674 seconds. Two-channel RCNN has a relatively simple structure with only 1,008,269,296 trainable parameters in total. [11]Comparing the validation accuracies of the architectures used, they have achieved 100% accuracy for AlexNet, VGG-16, and GoogleNet, while VGG-19 has obtained an accuracy of 90.63% and ResNet has 71.88% of accuracy. They have mentioned the pixel-wise segmentation of the tumor areas in their future work.

Original Image

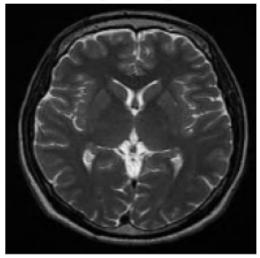


Figure 1: Human Brain

0.2 PROPOSED SYSTEM

0.2.1 Understanding the data

Here, we have used a publicly available dataset from kaggle known as "MRI images for brain tumor classification." The dataset contains 10.2k images in total, with each training and testing set containing four classes. The number of images in training of 'NOTUMOR' class is 1990. The number of images in training of 'Glioma' class is 2147. The number of images in training of 'Pituitary' class is 2294. The number of images in training of 'Meningioma' class is 2161. The number of images in testing of 'OTUMOR class is 510. The number of images in testing of 'Glioma class is 400. The number of images in testing of 'Pituitary' class is 374. The number of images in testing of 'Meningioma' class is 421.

0.2.2 Dataset Description

The dataset used here is a publicly available dataset of "brain tumor classification" from the Kaggle website. The dataset consists of a training and testing set in which there are four different classes, namely "glioma," "pituitary," "meningioma", and "tumor." There are a total of 8,592 images in the training set and 1,705 images in the testing set. The train test split ratio is 85:15.



Figure 2: Testing set of four classes

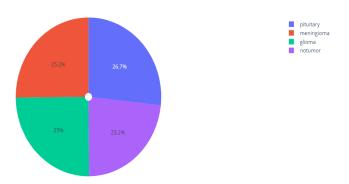


Figure 3: Training set of four classes

0.2.3 Visualization of the Data

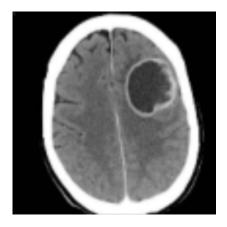


Figure 4: Glioma Tumor

0.2.4 Data Preprossessing

We begin by importing MRI images of the brain as input data. Many of the machine learning applications face the problem of data scarcity, due to which there is incorrect output and inefficient predictions on the dataset. To overcome this issue, we use a method to increase the

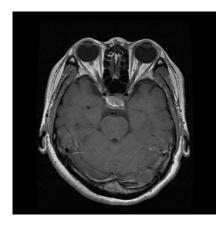


Figure 5: Pituitary Tumor

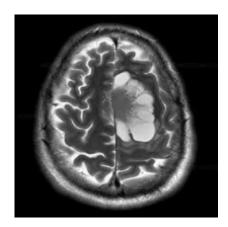


Figure 6: Meningioma Tumor

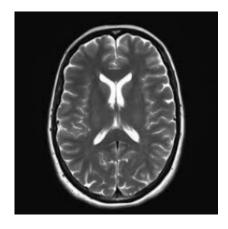


Figure 7: No Tumor

data known as "data augmentation". It focuses on taking current images as input and give the corresponding resultant as output images.

0.2.5 Data Augmentation

The variety of data supplied during training heavily influences the accuracy of predictions. Also, the amount of data also affects the predictions. In order to fulfill the needs, augmentation can be employed. We augmented our data with a width and height range of 0.05, a rotation range of 7, and a zoom range of 0.1 to increase the number of MRI images for our training model.

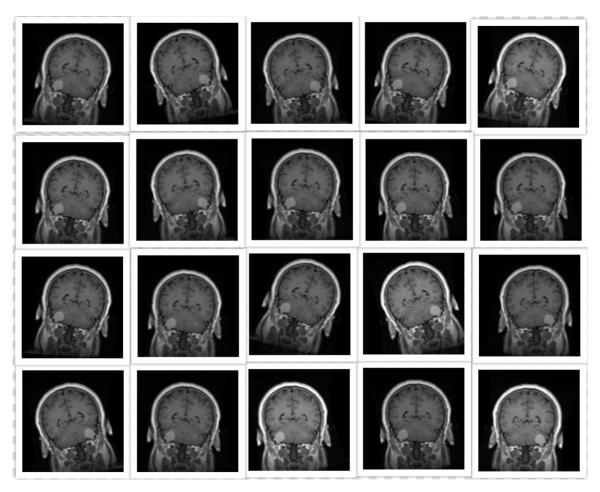


Figure 8: Augmented images of the original image of the human brain

0.3 Implementation

Model 1: Efficient Net B7

With a predetermined set of scaling coefficients, the Efficient Net B7 model equally scales the network's depth, width, and resolution. This model is used to train the dataset to detect tumors and classify them according to their type. The default input size of EfficientNet B7 is 224x224x3. There are 813 layers in EfficientNet B7. EfficientNet B7 has secured 84.4% accuracy in the state-of-art Convolutional Models by using very few parameters on ImageNet dataset.

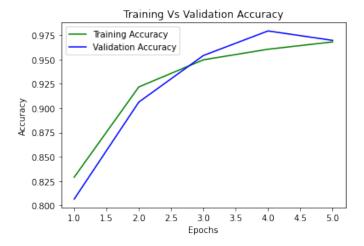


Figure 9: Train and validation accuracy vs number of epochs of EfficientNet B7 architecture

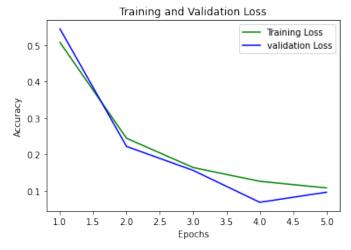


Figure 10: Train and validation loss vs number of epochs of EfficientNet B7 architecture

Model 2: VGG 19

VGG 19 is an acronym for Visual Geometry Group. It has a input size of 224x224x3, with 19 layers. It has convolution layer with 3x3 filter size, with stride and padding of size one. In the MaxPooling layer we use filter of 2x2 size and stride of size two. We use the pooling method to reduce the height and width of the brain tumor images. At the end we have convolution of size 7x7x512. VGG-19 has three more fully connected layers than VGG-16 (16 convolution layers, 3 fully connected layers, 5 MaxPool layers, and 1 SoftMax layer)

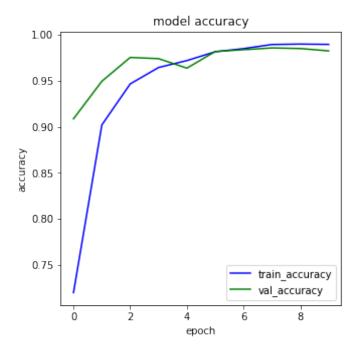


Figure 11: Train and validation accuracy vs number of epochs of VGG 19 architecture

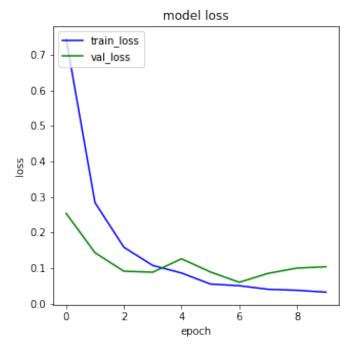


Figure 12: Train and validation loss vs number of epochs of VGG 19 architecture

Model 3: ResNet 50

ResNet 50 introduces the residual method which is a stack of layers set in such a way that the output of one layer is added to another layer in the block, this is also called the "skip connection", which means it skips the in-between layers and processes the next layer. It has

a default input size of 224x224x3. ResNet consists of 48 convolutional layers, one MaxPool layer, and one average pool layer, a convolution of a 7x7 kernel with 64 additional kernels and a two-sized stride. A stride of two sizes with a maximum pooling layer. There are nine more layers: 3x3, with 64 kernel convolutions, 1x1 with 64 kernels, and a third, with 1x1, with 256 kernels. These three layers are repeated three times.

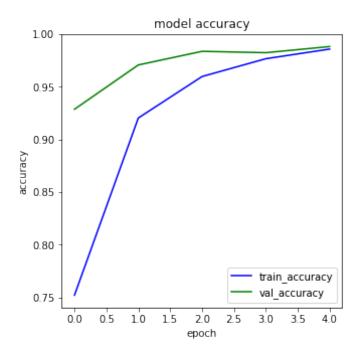


Figure 13: Train and validation accuracy vs number of epochs of ResNet 50 architecture

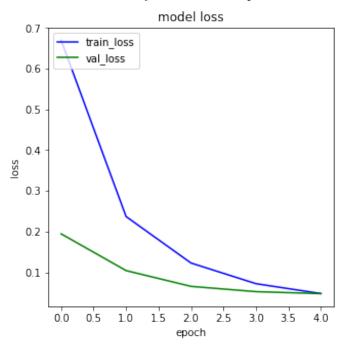


Figure 14: Train and validation loss vs number of epochs of ResNet 50 architecture

Model 4: MobileNet-V3

MobileNet-V3 consists of 53 deep layers. The default input size of MobileNet V3 is greater than 32x32. It provides high classification accuracy. It consists of convolutional 2D layer, pooling layer of stride size one and it makes use of bottle-neck layer (squeeze and excitation block).

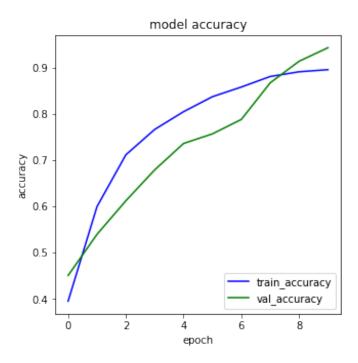


Figure 15: Train and validation accuracy vs number of epochs of MobileNet V3(small) architecture

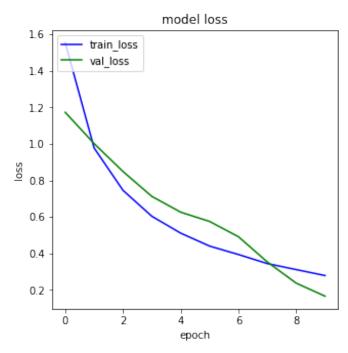


Figure 16: Train and validation loss vs number of epochs of MobileNet V3(small) architecture

Model 5: DenseNet 121

DenseNet-121 is a convolutional neural network where each layer is connected to all other layers in the network. It has 120 convolutional layers, 4 average pooling layers, and 1 fully connected layer. DenseNet results in more compact models. Contrary to Resnets, it concatenates the features rather than combining them by summation. The default input size for this model is $224 \times 224 \times 3$ with a batch size of one. The input size is downsampled to $7 \times 7 \times 512$ at the end of the network. It consists of 3 Dense blocks inside the architecture for feature concatenation and convolution(1x1) + average pooling(2x2) layer outside to down sample the network.

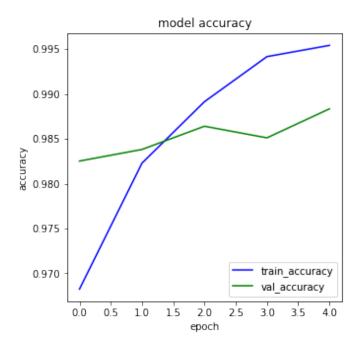


Figure 17: Train and validation accuracy vs number of epochs of DenseNet 121 architecture

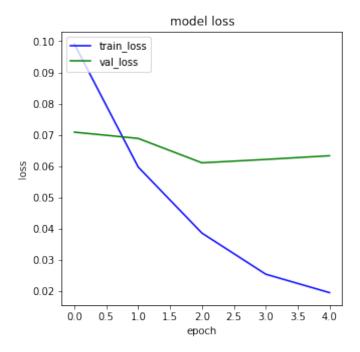


Figure 18: Train and validation loss vs number of epochs of DenseNet 121 architecture

Stimulated Model

We have used the optimization technique to reduce the risk of errors or loss of predictions. The optimizer used here is "Adam." Adam, which is a combination of Adagrad and RMSProp, works well with sparse gradients and in online settings. The activation function is used to indicate or decide whether the neuron should be activated or not. The activation functions used here are "Softmax" and "Elu." Softmax is best for multi-class classification because it assigns probabilities to each class. Basically, it converts the number vector to a probability vector. Another activation function used here is "Elu." "ELU" stands for "Exponential Linear Unit," and its main aim is to reduce the cost function and give more accurate results. For negative input values, "Elu" reduces them to zero.

0.4 Experimental Setup

The five deep learning models (DenseNEt, VGG-19, MobileNet, EfficientNet, and ResNet) are implemented on Google Colab, which is a hosted Jupyter notebook service that requires no setup to use, while providing free access to computing resources, including GPUs. Colab is an excellent choice because of the features it offers, such as running entirely on the cloud, requiring no setup, and supporting many popular machine learning libraries that can be easily loaded and used. allows multiple users to simultaneously work on the same notebook. Laptops with a specification of 8 gigabytes of RAM and Intel Core i5 or i7 CPUs with octa-core processors would be sufficient.

0.5 Results and Discussion

The experimental outcomes of the suggested systems are addressed above in the Table No.2. In order to diagnose a tumor and plan its treatment, it is crucial to classify it. This article focuses on a multiclass (4-class) classification to distinguish between the four forms of brain tumors—gliomas, meningiomas, pituitary tumors, and no tumor. The survey covers deep learning-based techniques like ResNet 50, VGG-19, DenseNet 121, EfficientNet B7 and MobileNet V3(small) which are compared in our survey. The highest accuracy among the 5 architectures is 98.64% which is achieved by ResNet50 and the least accuracy obtained is 75.79% by MobileNet V3(small). The accuracy of 96.95%, 97.73% and 98.38% is achieved by VGG-19, DenseNet 121, and EfficientNet B7 respectively, after being trained and assessed on 10,287 MRI images. As a result, ResNet50 outperforms all previous methods in comparable research on brain tumor classification.

Parameters	VGG-19	DenseNet121	MobileNetV3	EfficientNetB7	ResNet50
Accuracy	96.95%	97.73%	75.79%	98.38%	98.64%
Precision	0.97	0.98	0.76	0.98	0.99
Recall	0.97	0.98	0.76	0.98	0.99
F1 score	0.97	0.98	0.75	0.98	0.99
No. of parameters	20,055,408	7099248	973984	64251591	23710896
Trainable Parameters	20,055,408	7015600	961872	63940864	23657776
Untrainable Parameters	0	83648	12112	310727	53120

Table 1: Comparison of the five architectures

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