Multiclass Brain Tumor Classification from MRI Images using Pre-Trained CNN Model

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ABSTRACT

A brain tumor is an accumulation of malignant cells that results from unrestrained cell division. Tumors can result in crucial effects if they are not promptly and accurately recognized. Misdiagnosis can result in ineffective therapy, which decreases the patient's survival rate. The standard procedure for determining the presence of brain tumors and the type of tumors is magnetic resonance imaging (MRI). But as technology advances, it gets harder to comprehend huge amounts of data generated in an acceptable time. However, building a deep learning model from the start requires collecting enormous amounts of labeled data, which is a costly, time-consuming operation. A method to solve these issues is transfer learning of a deep learning model that has already been trained on the ImageNet dataset. In this research, the classification of brain tumors using several pre-trained deep learning models, i.e., different variations of ResNet, VGG, and DenseNet models, are being trained on a brain tumor dataset and compared. According to experiments, the ResNet50 model with a fine-tuned and transfer learning approach has achieved the highest training accuracy of 99%, validation accuracy of 96%, and test accuracy of 80%.

INTRODUCTION

Brain tumor is a significant reason for the growth in deaths for both children and adults. Brain tissue is made up of tissue that grows abnormally in the presence of normal growth-restraining processes. According to the tumors' origin, size prototype, and malignancy, diverse brain tumors can be divided into two main categories. Primary brain tumors are malignancies that start in brain tissue, such as the brain's outer layer or cells. When primary tumors from another body part first infect the brain, it results in an inferior or metastatic brain tumor. The bulk of studies conducted in developed nations shows that during the past 30 years, more people have suffered brain tumors and passed away as a result—possibly as many as 300. The computationally effective method produces outcomes comparable to or better than advanced methods while operating orders of magnitude faster.

The basic idea behind our challenge is to identify a tumor and quantify it from a specific MRI scan of brain imaging, then estimate the tumor's area utilizing fully automated processes and symmetry study. In recent years, a significant amount of research in the domain of medical imaging has been concentrated on brain tumor detection. Although automatic tumor prediction is unquestionably advantageous, it is not yet a common clinical approach; as a result, automatic brain tumor prediction is still a hotly debated research topic. The fundamental challenges in automatic tumor detection are connected to the fact that brain tumors frequently alter other neighboring anatomical landmarks and are exceedingly diverse in color, shape, position, and texture.

An advanced medical imaging method called magnetic resonance imaging (MRI) creates comprehensive scanned images of the inside organs and other body parts. Brain tumor treatments frequently involve MRI imaging. The development of the human brain is examined using these high-fidelity images to look for anomalies. There are numerous classification methods available now for MR images. MRI allows for the simple diagnosis of anomalies in the brain due to its high resolution. Generally, radiologists have examined and evaluated MR images. This paper tries to replace the manual procedure with machine learning approaches to diagnose a patient. Convolutional neural networks (CNNs) that have been some pre-trained models are what we suggested using to identify and classify brain tumors. A method to solve these issues is transfer learning of a deep learning model that has already been trained. It applies information from a neural network that has already been trained to a related model when training data is lacking or when workload reduction is desired.

This work describes an organized method for predicting brain tumors to remove tumor tissues from MR images. Classifying voxels based on their tissue type, which includes Grey Matter, Cerebrospinal Fluid, White Matter, and

occasionally diseased tissues like a tumor, is a well-known classification challenge in MRI. Brain tumors are divided into different categories according to the tissue types, the tumor's location, whether it is malignant or benign, and other factors. Brain tumors that have origins in the brain and are referred to as primary tumors carry the names of the cellular processes from which they were formed. They may not spread to new locations or assault nearby tissues, making them benign (not malignant). Growing brain tumors that have affected other body organs and become secondary or metastatic have their start in tumor cells. Most often, melanomas in the skin or tumors in the lumpy breast or kidney are the origin of cancers that spread to the brain and cause secondary brain tumors. The core objective of this research work was to create an architecture framework for the dependable and accurate detection of a broad class of brain tumors in MR images.

RELATED WORK

Cheng et al. projected a methodology for tumor region augmentation and partitioning to enhance the performance of the classifier of brain malignancies. They collected several features, such as an intensity histogram, a grey-level co-occurrence matrix, and a bag-of-words (BOW), to assess the effectiveness of their model (GLCM). A support vector machine (SVM) technique was utilized to organize attributes in a widely accessible Figshare dataset consisting of 3064 MRI scan images and got an accuracy of 91.28% [1].

Tahir et al. created a model to categorize brain cancers [2] based on MRI data. To increase the effectiveness of the classification process, the model generated 2D-DWT by using the attributes of Daubechies wavelets. An SVM is employed to guarantee classification accuracy; on a dataset source containing 3064 MRI scans from Figshare, the model has an accuracy of 86%. Ismael et al. [3] integrated a neural-based methodology for classifying brain tumors on the Figshare dataset. These statistical variables were combined, which increased the classifier's performance to 91.9%.

A deep neural-based model for brain tumor classification technique was suggested by Paul et al. [4]. This technique improved classification accuracy by a convolutional neural network (CNN). The model attained 5k-fold cross-validation accuracy on the Figshare brain tumor imaging collection was 90.26% accuracy. The model demonstrated that reducing the dimension of a picture can enhance training effectiveness and help physicians treat patients. Afshar et al. [5] constructed a Capsule Network to classify brain cancers using the datset of Figshare accurately. The proposed system improves classification performance by using the interrelations between cancer and areas covered around it, a limitation of prior CNN-based models [4,9,10]. While including extra data like tumor-associated tissues, the method increases classification accuracy. The accuracy of this model is higher than that of its rivals [3,9,10], with segmentation at 86.56% and without segmentation at 72.13%.

In addition, Afshar et al. suggested a revised version of CapsNet for classifying brain tumors that addresses CNN's shortcomings [6]. Their model takes less training data than CNN and is robust to input alterations like rotation and affine transformation. This model surpassed its rivals with an accuracy rate of 90.89% on Figshare images. Similar efforts to improve classification results were made by Zhou et al. [7]. The technique used automated recurrent neural area segmentation to classify and retrieve features from axial slices in images. The model's remarkable 92.13% accuracy on Figshare MRI images demonstrates its value. A CNN-based approach for diagnosing brain tumors was suggested by Pashaei et al. [8]. This technique uses a CNN-based model to retrieve attributes from the Figshare MRI images before classifying them with a KELM network. The experimental findings demonstrate that when compared to other traditional machine learning approaches like radial basis function neural network (RBFNN), Support Vector Machines (SVM), and k-nearest-neighbors (KNN), where the coupled method of CNN and KELM produces a good accuracy, 93.68%.

Anaraki et al. [11] offered a different study examining how genetic algorithms can improve CNN's ability to classify brain tumors accurately. They updated the CNN design with the aid of a genetic algorithm to improve the efficiency of their work. Using the Figshare dataset, they got the best accuracy of 94.2%. Additionally, Ayadi et al. [12] introduced a deep CNN with numerous layers to diagnose brain tumors and improve tumor classification efficiency. The effectiveness of the proposed approach was evaluated using three datasets: Radiopaedia, Figshare, and the collection of molecular brain neoplasia data (REMBRANDT). Their model performed admirably and required much less preprocessing than earlier methods.

Sheikh Basheera et al. [13] described a technique for categorizing brain malignancies that involve extracting the tumor's segmentation from scanned images of brain tumors and then retrieving the segmented area using a pre-trained neural model with a stochastic gradient descent approach. Muhammad Sajjad et al. [14] suggested a method for classifying multi-grade cancers by leveraging a pre-trained VGG-19 CNN Model to fine-tune the results of the data augmentation methodology applied to MRI images.

According to Carlo, Ricciardi, et al. [15], Pituitary Adenoma tumor MRIs can be categorized using multinomial k-nearest neighbor and logistic regression algorithms. The method had an AUC curve of 98.4%, a multinomial logistic regression accuracy of 83%, and a k-nearest neighbor accuracy of 92%. By adopting the CNN model - Alex-Net, which demonstrated 91% accuracy. Sunanda Das et al. [16] trained a classification ConvNet model to identify different kinds of brain tumors and accomplished an accuracy score of 94.39% with an average precision score of 93.33%.

Romeo, Valeria, et al. [17] proposed a machine learning technique to forecast nodal status and tumor grades from CT scans of early brain tumor lesions, and they achieved the most remarkable accuracy of 92.9% using Naive Bayes (NB) and k-nearest neighbor (KNN). Khwaldeh, Saed, et al. [18] offered a framework for categorizing normal and tumor

brain MRI scan images, with a grading method for separating brain-diseased MRI scans into low-level and high-level grades. The study [19] developed a unique CNN architecture for classifying brain tumors. The three classes of brain tumors were identified containing enhanced MRI images using a T1-weighted database. When used with record-wise cross-validation, this approach of a 10-k fold cross-validation set has an accuracy rate of 92.50%.

METHODOLOGY

In this section, the methodology's detail is discussed with deep learning concepts.

Dataset

In this paper, the suggested approach experiments were carried out on the Kaggle dataset. Both training and testing categories were created for this dataset. A training set of 2870 different MRI scan images and a testing set of 394 were used to expand the descriptive analysis. Data preprocessing operations like brain stripping were also given. Four classes are used in the process of performance computation: meningioma tumor, glioma tumor, no-tumor, and pituitary tumor. The proposed methodology uses a public access dataset that is accessible at (https://www.kaggle.com/navoneel/brain-mri-images-for-brain-tumor-detection/) and is titled 'MRI Brain Tumor Classification, see Figure 1 for sample images of considered dataset.

Transfer Learning

Transfer learning is training a baseline model on a source dataset in which the learned parameters are moved to another network that will be trained on a target dataset. It retains knowledge from a previous task with a sizable benchmark dataset and applies that information to a new model with smaller datasets. In several computer vision tasks, including object localization and image classification, this concept has been demonstrated to enhance the generalization capacities of deep neural networks. Using a pre-trained deep neural net to fine-tune the model rather than starting from scratch possibly enhances the model's accuracy. In this study, we examine the idea of utilizing the pre-trained models obtained from the enormous sample dataset and then transferring them to the particular job discovered from the objective dataset.

Pretrained CNN Models

Pre-trained models have already undergone training using various types of data with multi classes. Neural network models that have been pre-trained were developed using extensive benchmark datasets, such as ImageNet. Pre-trained models are also a significant contributor to the quick progress of computer vision research. These cutting-edge models can be used by other academics and professionals rather than having to start from scratch. The deep CNN architectures employed in this research are rarely used to catalog brain tumor MRI scan images. ResNet-50 has 26 million parameters and 50 layers of ResNet blocks. VGG-16 consists of 13 layers of convolutions and three layers of full-connected. Similar to

other networks, it utilized ReLU activation functions on hidden layers. Later a deeper version of VGG-19 was developed. Inception-V3, an updated version of Inception-v1 contains 48 deep layers and 24 million parameters. Xception consists of 71 layers containing 23 million parameters. Inception-V4 is an enhanced Stem module containing 43 million parameters and is said to have a significantly faster training rate because of residual connections.

A network trained on a problem comparable to the new dataset is deployed. No modifications or further training are performed to the pre-trained model; it is used to categorize new images with fine-tuning and transfer learning approach. We only have to download the network architecture together with its pre-trained weights, and then we execute the predictions on our latest dataset. When we remark that the aspect of our different problem is highly comparable to the domain on which the pre-trained network was trained, then indicate that the network is prepared for deployment.

Fine Tuning

Transfer learning is very effective when the domains are highly dissimilar. The correct feature maps must be extracted from the given dataset and adjusted to fit the target domain. The pre-trained model is used as a classifier, downloading the complete network without making changes and simply running predictions. Convolutional layers are frozen, and the pretrained model is used as a feature extractor while all its feature maps are transferred into another domain. Fine-tuning is defined as freezing some network layers used for feature extraction and simultaneously training the newly updated classifier layers d the non-frozen layers of the pre-trained model. After retraining the feature extraction layer, the higher-level feature representations are fine-tuned to make them more applicable to the new dataset. That is why this process is known as "fine-tuning." We have added two layers as dense layers of (256, 4) with "GlobalAvgPooling" and Dropout layers. We have only considered the last convolutional block of pertained models in this study, and all other layers are frozen.

Hyperparameter Tuning

Hyperparameters are controllable parameters that allow you to fine-tune the model training phase before training the model, which the ML engineer sets and then adjusts them. These factors affect how the model is trained and establish the network's structure. For instance, we can choose how many hidden layers and nodes there are in a neural network. Hyperparameters play a significant role in the model's performance by determining optimal hyperparameters. Usually, the process needs manual setting and is computationally costly. Our research covers batch size, number of hidden layers, learning rate, number of epochs, and other hyperparameters instances.

Batch Normalization

Inter-layer outputs are converted into a traditional format via batch normalization. Each data value is re-calibrated as a result of batch normalization using the variance and mean for a particular data batch. Batch normalization

makes DNN designs more stable and frequently speeds up convergence.
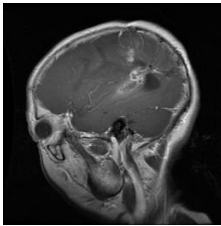
ReLU & SoftMax

Every convolution layer uses the ReLU function for a simple computation that returns the input value to its original form. If any negative input value is received, the function returns zero; nevertheless, if any positive input value (x) is received, the function returns the given value.
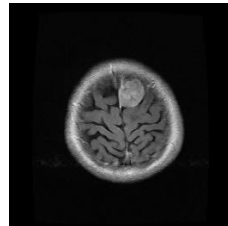
$$ReLU = \max(0, x) \qquad (1)$$

A generalization of the sigmoid function is the SoftMax function. It calculates classification likelihood when there are more than two classes, transforming the probability value into a range between 0 and 1. Predicting a single class out of numerous possibilities is a fairly standard use case in deep learning challenges. Here is the equation of the SoftMax activation function:
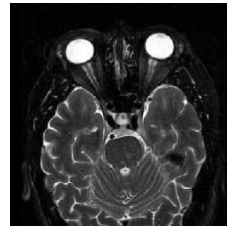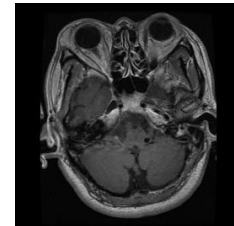
$$\sigma(x_i) = \frac{e_i^x}{\sum_j e_j^x} \qquad (2)$$

Dense Layer

The dense layer operates on an input that has been flattened so that every input should be interconnected to every neuron. A straightforward method of detecting nonlinear mixtures of the high-level data retrieved using earlier CNN layers is to allocate a dense layer. The design classifies the irregularity using a single dense layer.

$$d(x) = \text{Activation } (wTx + b) \qquad (3)$$

The dense layer, $w = [w1, w2, \ldots, wn]T$ indicates the weight matrix, and b indicates its bias value. The nonlinear activation function defines the outcome for a particular input. The proposed network utilizes a thick layer at the end to classify the brain tumor and illness type. The SoftMax function is utilized as an activation function in the dense layer. The best parameters are mentioned for the experiments in Table 1.

| Glioma Tumor | Meningioma Tumor | No Tumor | Pituitary Tumor |

Figure 1. Tumor Multiclass Dataset Samples

Table 1. Best Parameters of the Experiments

Hyperparameters	Values
Batch Size	32
Number of epochs	10
Hidden Layers	Pretrained Considered model layers of Last Convolutional Block + (256, 4)
Learning rate	0.001 with Reduce Learning Rate function
Dropout	0.2
Optimizer	ReLU & SoftMax
Freeze Layers (ResNet50)	Trainable False (0-142) Trainable True (143- So on)

Results & Discussion

The effectiveness of trained models was evaluated in the research work for classifying brain tumor images. The dataset is split into 80% training and 20% testing, and this testing we have considered as for validation for brain tumor classification. There are separate test data that are available for testing. We applied different variations of CNN models in this research for brain tumo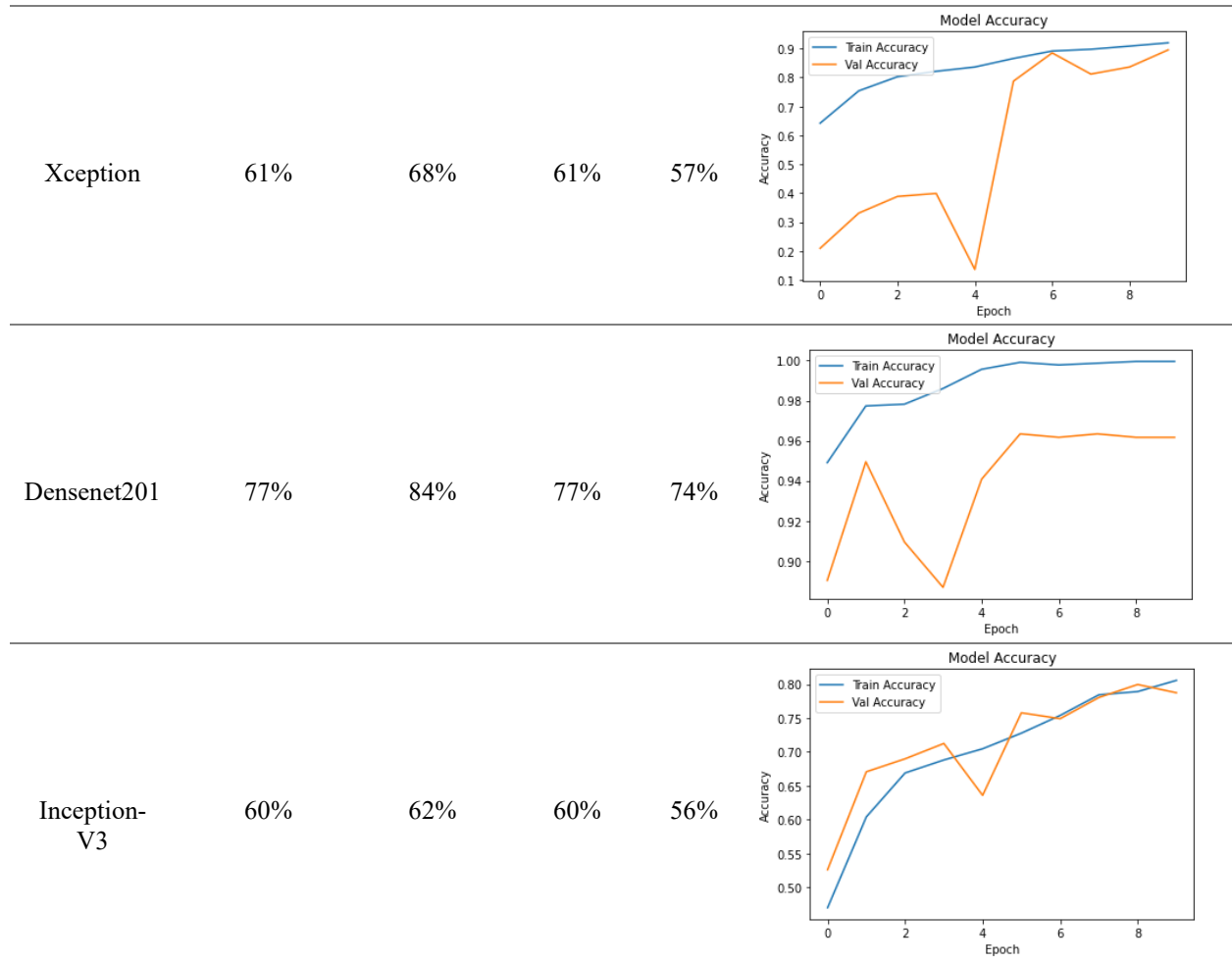r classification. MRI scan images were trained using the pre-trained networks for brain tumor detection. It was noted that Vgg-16, Vgg-19, ResNet-50, ResNet-152, DenseNet-201, Xception, and Inception V3 models were picked as these are the most widely used CNN architectures. All CNN architectures allow us to retrieve details from images. We used the ReLU activation function and Adam optimizer for these pre-trained models. We trained

our model by providing ten epochs with 32 batch sizes. We compared the suggested ResNet50 model with various well-known CNN architectures. The outcomes demonstrate that classifying using pre-trained CNN architectures typically yields mediocre results. When classifying brain tumor MRI images, only ResNet-50 provided a validation accuracy of 96% and a test accuracy of 80%. The comparison findings for the suggested ResNet50 model are shown in Table 2.

Table 2. Robustness of the Proposed Model

Models	Test Accuracy	Precision	Recall	F1	Graph
Resnet-50	**80%**	**84%**	**75%**	**75%**	
VGG16	75%	82%	75%	72%	
VGG19	29%	9%	29%	13%	
Resnet-152	78%	84%	78%	75%	

Xception	61%	68%	61%	57%

Densenet201	77%	84%	77%	74%

Inception-V3	60%	62%	60%	56%

It is observed that the proposed pre-trained CNN models, with the transfer learning approach, are more successful in finding tumors in brain MRI images and can also be used to detect other types of targets. Because of this, our suggested transfer learning (TL) method for the ResNet-50 model is adequate for identifying brain tumors in MRI images. Our goal was to effectively increase performance by applying the pre-trained CNN models with the TL approach for brain tumor classification in MRI images. Use the Transfer Learning approach to identify brain tumors without endangering them and give support to improving accuracy. The accuracy, F1-score, precision, and recall of each proposed methodology are assessed. The study's findings demonstrate that the ResNet-50 model gives an accuracy of 80%, which is better than all other architectures.

CONCLUSION

This paper presents even performance comparisons of different pre-trained classification models for classifying brain tumor MRI data. Due to changes in the brain's physical structure and disparities in neuroimaging, deep learning models have also been applied in processing brain MRI images. However, the automatic detection and classification of brain tumors are still challenging. High accuracy has been attained while lowering the new model's workload with the transfer model's learned parameters. In this research, brain tumor classifications were performed on a dataset containing 3264 MRI images with (tumor types) and without tumors using pre-trained VGG-16, VGG-19, ResNet-50, ResNet-152, DenseNet-201, Xception, and Inception V3 models. To ease the effort during training, raw MRI scan images were preprocessed. The evaluation metrics, including recall, precision, accuracy, and F1-score, were used to assess the classification process using seven distinct models. The ResNet-50 model performed the best with 80% accuracy, 75% recall, 84% precision, and 75% F1 score. In comparison, the VGG-19 model has the lowest accuracy rate. The ResNet-50 model, which was the most efficient approach in this research, was more effective than peer studies. The transfer learning approach was demonstrated to yield good outcomes with small data and fewer epochs. The classification analyses of MRI scan images will be more thoroughly studied in upcoming research. In this context, it aims to offer a novel technique and comprehensively analyze the existing literature.

CREDIT AUTHOR STATEMENT

Muhammad Asad Arshed: Research Experiments **Aqsa Shahzad** Writing Original Draft **Kamran Arshad:** Data Curation **Dianial Karim:** Results Comparison **Shahzad Mumtaz:** Data Visualization and Investigation **Muhammad Tanveer:** Evaluation

COMPLIANCE WITH ETHICAL STANDARDS

It is stated that all authors don't have any conflict of interest. Furthermore, informed consent was obtained from all individual participants included in the study.

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