Classification Of Brain Images For Identification Of Tumors

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***Abstract*—Early detection of brain tumors is very crucial as they grow extremely fast. To extend patients' life expectancy, correct treatment planning and precise diagnoses are critical. Manual diagnosis can be prone to errors and is a time-consuming and complex task for radiologists because of how minute variations in the tumor could lead to a completely different diagnosis. The proposed method is focused on creating an automated way of classifying brain MRI images by using SOTA models like VGG-16 and InceptionV3 and building on them. The brain MRI images are classified into four classes by extracting significant features and experimented with and without pre-processing. The experimental results have shown that the VGG-16 model used, although without any image augmentation, has given a high validation accuracy of 74%. The inceptionV3 model without image augmentation techniques reported a worse validation accuracy of 69%, defining VGG-16 to be the better classifier.**

***Index Terms*—Transfer learning, Brain MRI processing, VGG -16, Inception v3 model**

I. Introduction

Brain tumors are caused by the proliferation of aberrant cells in the brain's tissues [1]. It can be categorized as benign or malignant, depending on how dangerous it is for the person who has the tumor. Brain and nervous system cancer are thought to affect 25,050 people in the United States, according to the "Surveillance, Epidemiology, and End Results Program" (SEER). This number is 1.3% of all new cancer cases in the US in the year 2022. On a grim note, the estimated deaths amount to 18,280 in 2022. This is 3% of all cancer deaths reported in the United States in 2022 [2]. These harrowing statistics highlight the urgency for early detection of brain tumors to enable treatment to cure them. But there exist many different types of brain tumors. There are at least 120 different forms of brain tumors known to exist [3]. The availability of a multi-class brain tumor detection model is necessary to detect and catch hold of any possible brain tumors that may lead to the death of a person.

This paper includes the classification of three brain tumor classes, with the fourth class being a "no tumor" class for the detection of healthy patients. The three different categories of brain tumors are pituitary, meningioma, and glioma. The dataset is made up of numerous brain regions that were photographed from various angles [4]. Multiple state-of-the-art models are implemented to find the optimal multi-class brain tumor detection model between the implemented models. VGG-16 and inceptionV3 models are used to define a multi-class classifier. This is done in conjunction with and also without pre-processing techniques to observe and validate the difference that the techniques bring while training the aforementioned dataset. The models have also undergone class balancing to mitigate the effect of an imbalanced dataset. The multiple pre-processing techniques include different image augmentation techniques such as scaling, rotation, flipping, and zooming. The final accuracy of all the models is compared to estimate the best model among the implemented ones for multi-class classification of brain tumor.

Manual feature extraction is a very tedious task in the traditional approach. As we can see in Fig. 1, different types of tumors are strongly correlated with their surrounding tissues, and they vary in their location relative to the skull.

Deep learning overcomes this type of problem with an auto-

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mated feature extraction mechanism. But becomes inefficient when the amount of data is small, and the scarcity of human expert annotations is more [5]. Transfer learning is an efficient strategy under the base of deep learning when the training samples are limited. Since the network is already fine-tuned for the larger dataset, by transferring the knowledge to the target dataset, the network becomes faster with less complex in the training stage [6].

Fig. 1. (a) Meningioma tumor (b) Glioma tumor (c) Pituitary

II. Literature Review

Utilizing Edge-Based Histogram Equalization and DCT, Khan et al. [7]'s automated multimodal classification method proposes linear contrast stretching. For feature extraction, a joint learning method based on correntropy and transfer learning were applied. ELM received the composite matrix with resilient covariant features based on partial least squares for final classification. On the BraTs dataset, an accuracy of 93.4% was attained.

CNN networks that are only simple have also been proven to work well. They worked on the categorization of three different forms of brain tumors for the implementation in Abiwinanda et al. [8]. Convolution, max-pooling, and flattening each had one layer in the CNN. The accuracy and validation accuracy the authors achieved while working with the dataset made accessible on figshare Cheng were 98.51% and 84.19%, respectively. There was no prior segmentation of the job based on regions.

With their suggested automated technique, Byale et al. [9] seek to differentiate between benign, malignant, and normal tumors. The proposed method consisted of four steps, the first of which was the use of adaptive median filtering during pre-processing to remove noise. To locate regions of interest, segmentation using the Gaussian mixture model is next used. The authors use a Grey Level Co-occurrence Matrix for feature extraction in the third stage, then neural networks for the final classification. The proposed model's accuracy was 93.33%, above the Adaboost model's accuracy of 89.90%.

Usman and Rajpoot [10] employed supervised classifiers to classify brain tumors and worked on creating wavelet texture feature to predict tumor labels. The edges of the feature images were highlighted using an absolute function and Gaussian smoothing. Among the features from which a candidate must be chosen are intensity, neighborhood data, and texture. Dice overlaps of 88% for the entire tumor region, 95% for the enhancing tumor region, and 75% for the core tumor region were achieved by the authors.

Many fuzzy models perform poorly at identifying non-enhanced tumors yet excel at detecting hyper-intensity tumors. The approach outlined by Saha et al. [11] offers a quick, automatic segmentation procedure. A set of MRI slices from a single patient study are taken by Fast Bounding Box (FBB), which produces a subset of the slices that contain tumors or edemas. Each slice is then labelled with an axis-parallel bounding box that encircles the tumor or edema region, achieving 92% accuracy, 81% recall, and 97% precision.

Brindha et al. [12] used both a self-defined ANN and CNN while comparing their overall prediction results on an MRI image dataset. The dataset contains two classes of MRI images-normal and tumors of different sizes that are resized. The ANN model uses 7 layers- a flatten layer, five dense(hidden) layers using relu, and a last dense layer. Their CNN sequential model uses different layers- the images pass through 5 sets of convolutional layers of varying filters, with a max-pooling of 2x2 and a dropout of 20%. They are then flattened and have a full connection using a single hidden layer. With CNN, the authors achieved a testing accuracy of 89% and higher precision, recall, and f1 scores compared to ANN, which provided a testing accuracy of 65.21%. In their conclusion, they assert that compared to ANN, CNN offers better analysis outcomes for an image dataset.

Bathe et al. [13] proposed a Depth wise Separable CNN model on a Kaggle MRI dataset. The images first undergo pre-processing like Image augmentation by cropping, rotating, flipping, and defining brightness range. The dataset is then split and passes through a MobileNet base model that uses Depth wise separable convolutions, to which global average 2D pooling is applied to reduce overfitting. After this, two hidden layers are applied, and the last layer using sigmoid is used to classify. The authors have found that Depth wise separable CNNs are a better choice and give a higher accuracy of 92% on the test set than simple CNNs, SNM, and Adaboost algorithm. This is because it provides more filters to detect patterns in MRI images, there is less data loss, and it takes less time in computation.

Logeswari and Karnan [14] focused on the segmentation of images by a self-organizing map that classifies the image row by row. HSOM was used to overcome the limitations of SOM. It is a hybrid of self-organization and graphic-mapping techniques. Calculating a neighborhood function, a weight vector, and a value for the winning neuron are all included in the mathematical implementation. If the current neuron is greater than the value required for the winning neuron, it is made the current neuron (suspicious region). Nine of the most well-liked and reliable machine learning models, including SVM, LR, KNN, NB, DT classifier, Random Forest classifier, XGBoost classifier, SGD classifier, and Gradient Boosting classifier, were tested by Ghosh and Kole [15]. The models were trained using MRI scans of brains with and without tumors from a binary class dataset for brain tumors, according to the authors. Based on a few performance metrics, a performance comparison of the various machine learning algorithms has been made. The best classifier among

all the other machine learning classifiers used, according to the authors, was gradient boosting. It reported an f1-score of 0.895 and an accuracy of 92.4%.

When a less-than-ideal number of MRIs were used, CNN experienced an overfitting problem, according to Gab Allah et al. [16]. To expand the dataset available for training the CNN models, they presented a progressive, growing adversarial network (PGGAN) augmentation technique to create realistic MRIs of brain tumors. This made it easier for the authors to train the model despite their lack of data. Following this step, they ran the resulting images through a number of model combinations, including VGG19+CNN, VGG19+GRU, and VGG19+Bi-GRU. With accuracy rates of 98.54% across all categories, the VGG19 and CNN combination was shown to be the best one.

III. METHODOLOGY

A. Dataset

The dataset, which is accessible on Kaggle, consists of 3,264 high-quality photos divided into four classes: glioma tumor, meningioma tumor, pituitary tumor, and no tumor. With 926 photos for gliomas, 937 for meningiomas, 1001 for pituitary tumor, and 500 for no tumor, the collection is significantly skewed. With the image dataset from directory by Keras to load and split the sets, setting the size of the batch as the size of 64 for the training and validation sets, the proposed model uses 80% of the dataset for training and 20% for testing. Both models' images are 224 pixels in size.

B. Pre-processing

In this approach, the dataset is subjected to a number of pre-processing procedures before the model is trained in order to track statistical variations in the predictions. As seen in Fig. 2, the dataset's pixel values have been adjusted to fall within a predetermined range.

Multiple image augmentation techniques are applied, such as rotation of the image, zooming, and flipping. In order to increase the performance and results of deep learning models, image augmentation is used to create new variations of the images that are added to the dataset, highlight the significant features of an image that are crucial for our learning, and make up for the absence of variant data.

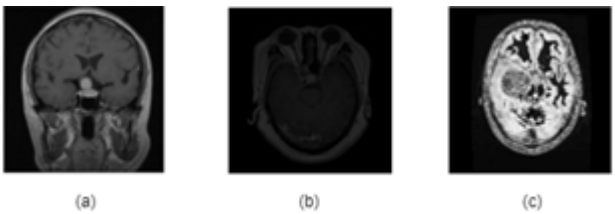

Fig. 2. (a) Original (b) Normalized UP (c) Normalized DOWN

C. Proposed Models

On this dataset, two models have been applied and contrasted. The VGG-16 and Inception-v3 [18]. Even while VGGNet's architectural simplicity is desirable, doing so comes at a high cost because doing so necessitates a substantial amount of computation [17].

VGG16 has 16 weighted layers, denoted by the number 16. VGG16 has 21 layers altogether—13 convolutional layers, 5 Max Pooling layers, 3 Dense layers—but only 16 of them are weight layers or learnable parameters layers [18]. The InceptionV3 model consists of 3 conventional Inception modules, 5 Inception modules that have been factorized, and 2 additional Inception modules that include an output filter bank that has been concatenated. The network of the model has 42 layers. Inception's processing cost is also considerably cheaper than that of VGGNet or its more effective descendants [6]. As a result, it is now feasible to use Inception networks in big-data applications.

Once the dataset has been received, two flows take place. In Fig. 3, the planned work is shown. In one flow, pre-processing methods are not used before the data is sent to the models. The second flow involves selecting and utilizing specific pre-processing methods, followed by model training and data passing through these models.

In both cases, we implemented class balancing by adjusting weights for each class, owing to the imbalanced nature of the no tumor class with respect to other tumor classes in the original dataset. The learning parameters for VGG 16 are shown in Table I.

Some additional layers are added to the Inception-v3 model to make it more relevant to our brain tumor dataset. Table II is the representation of the extra layers added over Inception-v3. The data is fed to the Inception model, considering its input format. The pre-trained weights have been loaded, and the dense layers have been replaced by custom layers to make them relevant to the data. In order to provide the output of the final trainable layer of the Inception Net as input to a dense layer utilizing the Relu activation function, a flatten layer is added. The output goes to a final dense layer that classifies data into the four classes using a simple SoftMax function. For VGG-16, the SoftMax function is added for classification. No extra layers have been added to the VGG-16 model.

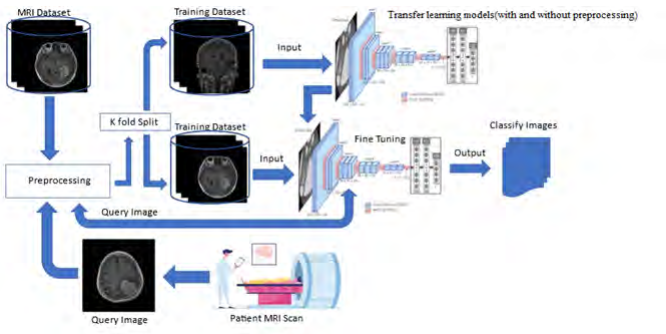

Fig. 3. Architecture of the system

TABLE I
SAMPLE LEARNING PARAMETERS VGG-16

VGG-16 Learning Parameters		
Layer(type)	***Output Shape***	***Param#***
block5_conv1(Conv2D)	(None, 14, 14, 512)	2359808
block5_conv2(Conv2D)	(None, 14, 14, 512)	2359808
block5_pool(MaxPooling2D)	(None, 7, 7, 512)	0
flatten(Flatten)	(None, 25088)	0
fc1(Dense)	(None, 4096)	102764544
dense(Dense)	(None, 4)	16388

TABLE II
ADDITIONAL PARAMETERS INCEPTION-V3

Inception-V3 Learning Parameters		
Layer(type)	***Output Shape***	***Param#***
flatten_3(Flatten)	(None, 110592)	0
dense_6(Dense)	(None, 512)	56623616
dropout_3(Droput)	(None, 512)	0
dense_7(Dense)	(None, 4)	2052

IV. RESULTS & DISCUSSION

Tables III, IV, V, and VI shows the classification reports generated on the validation part of the brain tumor dataset. Without any pre-processing, Inception-v3 has an accuracy of 69%, with f1-scores of 0.33 for pituitary tumor, 0.71 for meningioma, 0.85 for no tumor, and 0.64 for glioma. On the other side, the VGG-16 claimed an accuracy of 74% with f1-scores of 0.40, 0.73, 0.88, and 0.81 without any pre-processing. In the case of utilization of pre-processing techniques, an accuracy of 72% was observed in Inception-v3, and an accuracy of 69% was observed in VGG-16. Inception-v3 also reported f1-scores of 0.30, 0.90, 0.76, and 0.70, while the VGG-16 network produced f1-scores of 0.35, 0.70, 0.70, and 0.93. We observe that the best performance was reported in the VGG-16 network without pre-processing and in lower number of epochs compared to the Inception-v3 network in any scenario. However, there was a significant performance boost for the Inception-v3 network when pre-processing techniques were applied.

Observing the accuracy graphs and confusion matrix shown in Fig. 4 and Fig. 5, we find that the VGG-16 network was able to reach a good score in lesser number of epochs in comparison to the Inception-v3 network. The capacity of the model to learn the attributes of the images in the brain tumor dataset was demonstrated by the VGG network's smoother learning curve. Additionally, we can see how pre-processing affected the models with lower accuracy value deviations than their non-pre-processed counterparts. In all cases, the training set had an accuracy of about 95%, which indicates some overfitting during the training phase. These components must be made by the formatter using the relevant criteria that follow.

In comparison with Brindha et al. [12], we observe that our models predict more classes in a more balanced way and achieve higher scores in the majority of the classes when we compare their ANN model. While the ANN achieves 65.21% accuracy for their implementation, our implementation of VGG-16 and Inception-v3 achieves significantly higher accuracy in the range of 69% to 74%, with an f1-score reported over 0.7 for the majority of the classes. While Usman and Rajpoot [10], Saha et al. [11], and Logeswari and Karnan [14] focus on using more complex techniques to achieve optimum results, our proposed work offers a simple transfer learning implementation on an image-based dataset whose performance can be enhanced on the integration of other statistical techniques.

TABLE III
CLASSIFICATION REPORT OF VGG-16 WITH PRE-PROCESSING

Type of tumor	**Scores**				
	precision	***recall***	***f1-score***	***support***	***sensitivity***
glioma tumor	1	0.21	0.35	19	1
meningioma tumor	0.81	0.62	0.7	21	0.8
no tumor	0.53	1	0.7	23	0.49
pituitary tumor	0.93	0.93	0.93	15	0.92

TABLE IV
CLASSIFICATION REPORT OF INCEPTION-V3 WITH PRE-PROCESSING

Type of tumor	**Scores**				
	precision	***recall***	***f1-score***	***support***	***sensitivity***
glioma tumor	0.54	0.21	0.3	33	0.54
meningioma tumor	0.83	0.98	0.9	45	0.83
no tumor	0.62	0.97	0.76	34	0.62
pituitary tumor	0.83	0.6	0.7	25	0.83

TABLE V
CLASSIFICATION REPORT OF VGG-16 WITHOUT PRE-PROCESSING

Type of tumor	**Scores**				
	precision	***recall***	***f1-score***	***support***	***sensitivity***
glioma tumor	0.83	0.26	0.4	19	0.83
meningioma tumor	0.61	0.9	0.73	21	0.61
no tumor	0.79	1	0.88	23	0.79
pituitary tumor	0.92	0.73	0.81	15	0.92

TABLE VI
TABLE VI. CLASSIFICATION REPORT OF INCEPTION-V3 WITHOUT PRE-PROCESSING

Type of tumor	**Scores**				
	precision	***recall***	***f1-score***	***support***	***sensitivity***
glioma tumor	0.8	0.21	0.33	19	0.8
meningioma tumor	0.57	0.95	0.71	21	0.57
no tumor	0.74	1	0.85	23	0.74
pituitary tumor	1	0.47	0.64	15	1

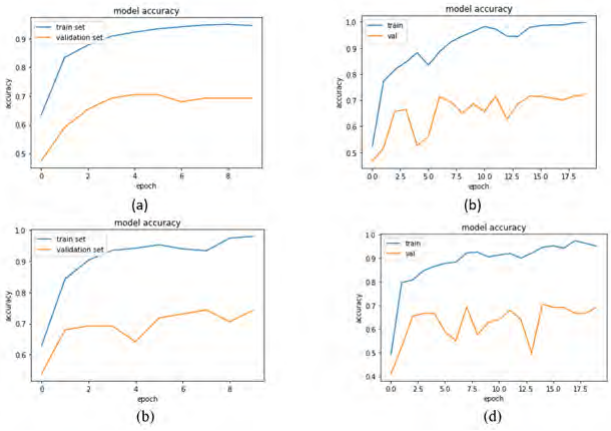

Fig. 4. Accuracy graphs – (a) VGG-16 with pre-processing, (b) Inception-v3 with pre-processing, (c) VGG-16 without pre-processing, (d) Inception-v3 without pre-processing

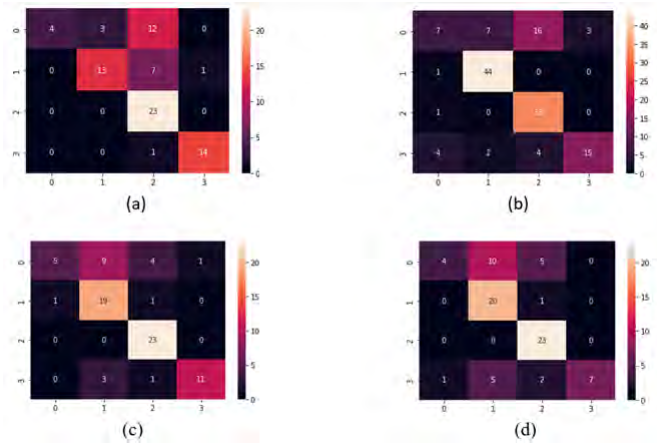

Fig. 5. Confusion Matrix – (a) VGG-16 with pre-processing, (b) Inception-v3 with pre-processing, (c) VGG-16 without pre-processing, (d) Inception-v3 without pre-processing

V. CONCLUSION

A brain tumor is a dangerous condition that can harm anyone. To enable the ability to save lives, brain cancers must be accurately and early detected. The proposed comparison of the high-quality datasets VGG-16, InceptionV3, and those models with pre-processing demonstrates the failure of using numerous augmentation strategies. Without the use of any pre-processing procedures, VGG-16 has reported the best accuracy performance out of all the models.

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