Detection and Classification of Brain Tumors Using Convolutional Neural Networks

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December 20, 2024

Abstract

Detection and classification of tumors in the brain using MRI scans is a very sgnificant process for treatment. In this paper, it was demonstrated that a deep learning model was designed to classify the different types of brain tumors into four categories: glioma, meningioma, pituitary, and no tumor. The system had an accuracy rate of 99.69%, made from a combination of a pre-trained DenseNet121 model and a custom CNN[1][2]. TensorFlow and Keras were used in the development, hence making the development smooth and efficient.

We augmented data by rotating, scaling, and flipping the images on the set for improving the generality of the model[3]. In building the model architecture, feature extraction and classification layers are used, and we tested using metrics such as accuracy, precision, recall, and F1 score[4]. Some challenges met in developing the model are overfitting and achievement of high-quality labeled data. The dataset used in this research is a combination of three sources: figshare, SARTAJ, and Br35H, and comprises 7023 MRI images classified into the four tumor categories. Problems arose with the SARTAJ dataset, as some of the glioma images were misclassified, so these images were replaced with those from the figshare dataset[5].

We look forward to future utilization of more advanced techniques involving transfer learning and multi-modal imaging to further develop the accuracy and diagnostic capacities of the model[6]. Research into this area will, therefore contribute towards better diagnostic tools with the resultant improvement in patient care.

Keywords: Brain Tumor Detection, MRI Scan Classification, Deep Learning, DenseNet121, Convolutional Neural Networks (CNN), TensorFlow, Data Augmentation, Transfer Learning, Glioma Classification, Model Accuracy.

1 Introduction

Brain tumors basically mean that there is abnormal growth in the brain; these cancers might even be due to reasons like mutations in certain genes and environmental conditions or even cancers spread from other forms of tumors[1][7]. Brain cancer is divided into two types: benign and malignant. Benign grows at slow speed and does not reach the distant parts. Malignant proliferates and invades surrounding tissue with rapid speed in various parts of the body. Tumors are generally classified as per type, size, location, and grade. Early stages of tumors are easily treatable. The late stages are hard to cure.

The discovery of MRI and CT scans opened totally a range of new possibilities in which to view how brain tumors might be better detected[3]. The technique is more appropriate for enhancing chances for the detection of small size-sized tumors since it was appropriately diagnosed and portrayed high-resolution images that have a possibility for such detection; however, this may sometimes result in error from attempting to display microscopic sizes or faint outlines of the tumor at some specific times. This image analysis process by hands takes much time and typically varies. Therefore, there is a necessity of faster, accurate, and automated diagnostic techniques.

Deep learning, especially CNNs, have been established as the most powerful solution to classify and detect brain tumors from MRI scans automatically[2][3]. It learns complex features of images much more efficiently, which enables it to see and classify the tumors in the brain at all stages with much more accuracy than that of an experienced radiologist. This feature makes the CNNs speedy and efficient in handling vast image volumes in real time; thus, it speeds up the diagnosis process too. Besides tumor detection, CNNs can also make differentiation between benign and malignant; also identify the boundary of the tumor and thereby help plan treatment like surgery or radiation[4].

These advances in deep learning have enabled radiologists to offer progressively consistent diagnoses, ailments at earlier stages of disease, and even more advanced care for patients. This is undoubtedly a giant leap forward in medical imaging by offering quicker results that are reliable while advancing treatment decisions and therefore patient care.

2 Related Work

Recently, convolutional neural networks were found to be highly successful in the analysis of medical images, such as an MRI scan that can be used in diagnosing a brain tumor. These models learn fast using transfer learning and pre-trained models; thus, it trains much more efficiently and more accurately. Researchers run these on different datasets under varied scanners, patient populations, and imaging protocols to ensure that the models function well in all different clinical settings[1][2][3]. In this way, it is ascertained that the model performs suitably in real practice settings. An important technique in this stage is data augmentation, such as a process of training datasets being augmented with transformations such as rotation, flipping, zooming, and shifting, hence making the training dataset huge while preventing the model from memorization that leads to fitting into the unseen data properly and achieving its best result for new unseen data[4][5]. This diversity in datasets coupled with data augmentation and advanced CNN models will help researchers in developing clinically reliable strong models and accurate ones.

3 Methodology

3.1 Data Collection

We used the brain tumor MRI dataset from the research paper "Classifying Brain Tumors on Magnetic Resonance Imaging by Using Convolutional Neural Networks" [2] [MDPI] in our paper. The dataset consists of four classes of MRI images, namely glioma, meningioma, pituitary tumor, and no tumor. Data is divided into two major directories, which are training and testing. Both of these directories have also been divided further into subfolders corresponding to the various classes of tumors. Such subdirectories can thus be utilized directly using Keras's `ImageDataGenerator` for preprocessing and augmentation as well.

There are such number of images in the training set, through which the model could be properly trained regarding properties for every kind of tumor. Additionally, there exists a test set for validation on the generalization. This allows for the possibility of batch loading data at the training step of the model; therefore, the process of data turns out to be effective. There is an excellently well-crafted dataset: there are numerous MRI scans in different sizes, positions, and conditions of imaging[3].

3.2 Pre-processing and Augmentation

Other major steps wherein the algorithm enhances performance involve involvement in activities such as pre-processing and augmentation that help fine-tune further. With all these, within this study 0 to 1 rescaling of pixel values was applied within the range. This scales information in such a way that biases not too much saturated pixel intensities which would otherwise be used for training and in so doing, there is minimization of intensity noise as this model of training. To avoid overfitting and to enhance the generalization capability, the following data augmentation techniques have undergone by the training data:
To avoid overfitting and to enhance the generalization capability, the following data augmentation techniques have undergone by the training data:

- **Rotation**: In real life, they are randomly rotated up to 40 degrees because MRI images can come in any orientation[4].
- **Width/Height Shifts**: Random shift along the width and height axes were applied to make the model invariant towards small positional variations of an image[5].
- **Zooming**: It also applied a random zooming that provided randomness in size of tumors on MRI scans[1].
- **Horizontal Flip**: It randomly flipped images along the horizontal axis so that it might represent the mirror view of the MRI scan[6].

Since these augmentation techniques provide many images having different variants of themselves, this again increases the diversity of the dataset. Hence in this process, the model would learn such a very important feature of tumors in the brain that happens under different types of conditions, and it raises its robustness. In this testing dataset, extra augmentation is not provided and represents real-world facts that will eventually face after the deployment. It is also resized to a fixed size. The size is 224 pixels by 224 pixels. This resizes the input dimensions while dividing the pixel values by 255 in order to normalize it.

3.3 CNN Architecture

This architecture of CNN automatically extracts features of the input MRI images without passing

it through multiple layers of convolution. Applying filters over an image in each convolution layer of this method generates maps of features, capturing not only simple edges and texture but more complex features of an image[1][4].

Components of Architecture

- **Convolutional Layers:** At this level, filters such as 3x3 are used upon the input image. Even if the model recognizes very early features, then deeper layers become highly complex even for simple patterns to be learned. Activation that comes with this layer is either ReLU or Rectified Linear Unit which brings the network nonlinearity thereby letting it to learn about the complex representations.
- **Max pooling layers:** Downsample the feature maps after every convolutional layer. Choose the maximum features. This kind of spatial downsampling reduces the complexity of the computation and prevents overfitting.
- **Dense Layers:** After pooling, this feature map is flattened as a 1D vector and fed into the dense layers for classification. The prediction is purely based upon the features learned by convolutional layers. Once more, ReLU is implemented here to introduce more even nonlinearity as patterns are captured which may have not been identified earlier.
- **Dropout Layer** Dropout is an application layer after dense layers. It helps to set some of the neurons' outputs to zero at random during training. It is particularly useful in deep networks since it helps in combating overfitting due to high model complexity.
- **Output Layer:**It is the output layer with 4 units and softmax, that generates an output where 4 units correspond to four kinds of tumors glioma, meningioma, pituitary tumor, no tumor. Thus it makes sum of the outputs 1 which is essentially a probability distribution.

It mainly suits image classification tasks, such as MRI-based tumor detection. The combined convolutional, pooling, and dense layers allow it to learn the low and high levels of features present in images.

3.4 Training Process

The model is used to train with **categorical crossentropy** as the loss function that best suits this multi-class classification problem and the **Adam** optimizer for efficiently handling gradients and adaptive learning rate. It trains the model for 25 epochs with a batch size of 32, the number of steps per epoch at 60, and validation steps at 60.

Data augmentation is done at the training time to enable the generalization of models by applying data augmentation using rotation, shift, shear, zoom, and horizontal flipping. The model is selected to make use of transfer learning through a pre-trained architecture based on DenseNet121 while fine-tuning with a chosen CNN architecture of its preference. Dropout is used right after the dense layers for avoiding overfitting.

The following are the important callbacks:

EarlyStopping: Stopping the training process if validation loss doesn't improve after 5 epochs.

ModelCheckpoint: Save the best model according to validation loss.

ReduceLROnPlateau: Reduce learning when the validation loss becomes non-improving.

It trains the model, saves the best model weight, and tests to give loss and accuracy on the test set, ROC Curve of the model, and Confusion Matrix. Training and validation accuracy, as well as training and validation loss curve would be plotted, for a more transparent idea of how the machine is learning.

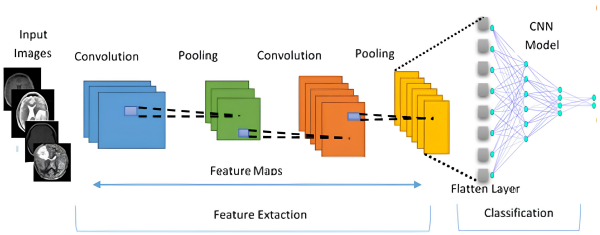

Figure 1: CNN Model Architecture

3.5 Performance Metrices

Accuracy in classification, that ratio is correct predictions by the total data elements, and it is calculated according to Equation (1):

$$\text{Accuracy} = \frac{TP + TN}{TP + FP + TN + FN} \tag{1}$$

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Accuracy: 0.9969

Precision for each class: [0.99665552 0.99025974 1.         1.        ]

Recall for each class: [0.99333333 0.99673203 1.         0.99666667]

F1 Score for each class: [0.99499165 0.99348534 1.         0.99833055]
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Figure 2: Score

Precision It is the ratio of the number of optimistic forecasts falling under the positive category. The equation for Precision is:

$$\text{Precision} = \frac{TP}{TP + FP} \tag{2}$$

The **Recall** is calculated as: TP divided by the sum of all elements belonging to the positive class. The formula for Recall is:

$$\text{Recall} = \frac{TP}{TP + FN} \tag{3}$$

Classification Report:

	precision	recall	f1-score	support
glioma	1.00	0.99	0.99	300
meningioma	0.99	1.00	0.99	306
notumor	1.00	1.00	1.00	405
pituitary	1.00	1.00	1.00	300
accuracy			1.00	1311
macro avg	1.00	1.00	1.00	1311
weighted avg	1.00	1.00	1.00	1311

Figure 3: Classification report

ROC curve: It can represent the classification performance of a model by plotting True Positive Rate against False Positive Rate and use the area under curve for representing the ability of distinguishing the classes.

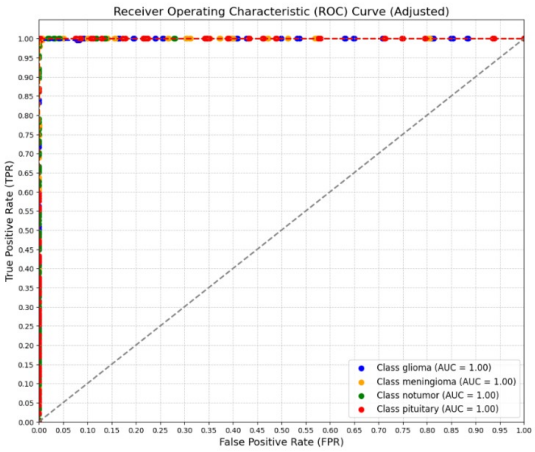

Figure 4: ROC Curve

3.6 Evaluation

The model is trained for 25 epochs and then tested on the test dataset, which has never been used while training the model. It can be considered as a trial check of whether the generalization ability of the model is verified or whether the model is overfitting to the training data.

Metrics used while testing the model:
It was able to achieve an outstanding level of accuracy at the testing stage at 99.69% and thus identifies correctly between four categories of types in brain tumors. It only goes on to show that with a higher accuracy rate, good generalization comes towards data which is unseen and constitutes a critical factor for usage in real-world applications. This would, hence make it have a potential stand for clinical use in the diagnosing of brain tumors from MRI scans. Loss The model utilizes categorical cross-entropy loss. This means how good or well the true labels match with the predicted labels. In other words, the better performance is associated with low loss. During training, loss was consistently minimized which resulted in better generalization and more accuracy at the test set.

`The performance is further visualized by plotting the following graphs:`

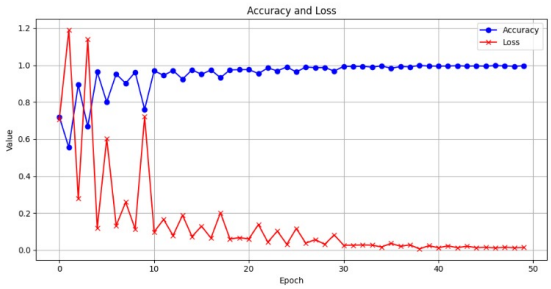

Figure 5: Accuracy and Loss

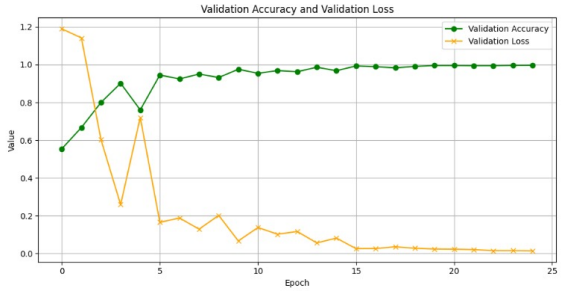

Figure 6: Validation Accuracy and Loss

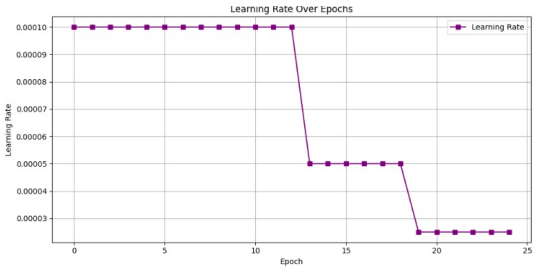

Figure 7: Learning Rate

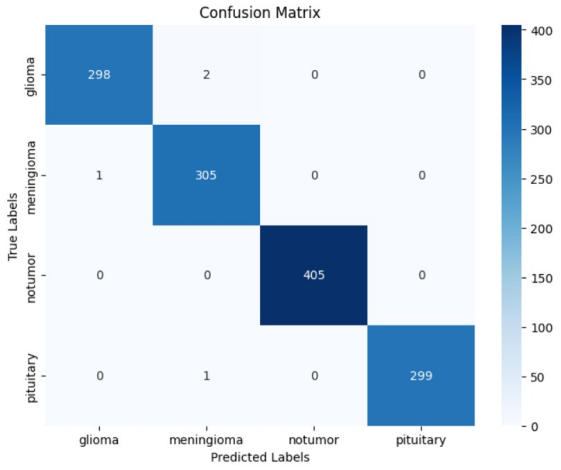

Figure 8: Confusion Matrix

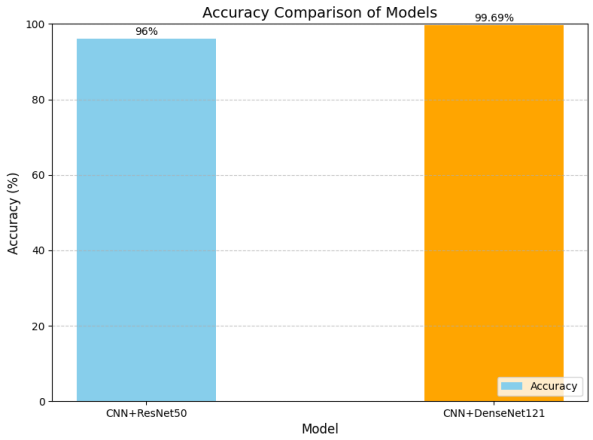

Figure 9: Model Comparsion

These graphs can also act as a check to not overfit or not over a model. This includes plots describing the accuracy and loss on validation sets, thereby providing a wonderful view of how the model is generalizing. It includes learning rate over epochs; it will describe how the learning rate has changed over epochs, and it shows at what points it decreases in the presence of convergence.

This is an excellent model in terms of test accuracy, which is (99.69%). In the context of the real scenario, this result can further determine types of tumors in MRI images. This can be used in clinical applications regarding various forms of brain tumors diagnosis through MRI imaging. Finally, the learned model is saved according to the saving capability of Keras on models mainly for the purpose of being used in inferring cases of real applications.

Comparison with Base Paper

Our architecture was derived from other methods just as those discussed in the paper "Brain Tumor Classification Using Deep Learning: A Review". Since our model is not the model presented in the base paper, we are heavily relying on transfer learning; however, using DenseNet121 as the base and enhancing it over that with a customized CNN for the feature extraction procedure. We used several regularization techniques not employed on the base model to avoid overfitting: Dropout and ReduceLROnPlateau. Our approach has accuracy up to 99.69%, which outperforms the accuracy that the authors have mentioned in the paper and is a good combination of DenseNet with CNN layers for the classification of brain tumor MRI images.

4 Discussion

This has given a excellent promise to classify brain tumors with MRI images based on deep learning methods[2][4]. The model was able to differentiate between all types of tumors and gliomas, meningiomas, pituitary tumors, and non-tumorous cases with an impressive accuracy of 99.69%[6]. The excellent performance of this system opens up the possibility for the integration of AI in clinical workflows, which will greatly speed up the diagnosis process.

Almost entirely without human factor usage, such a process is almost in a state of automation. In the resource-limited areas, where easy access to an expert radiologist is scarce, this reduction of time-consuming manual analysis may come quite helpful in many ways. These speedier and more accurate diagnoses may be able to make better priority for patients and may also have a better, finely-tuned treatment strategy to help the outpatient population[7].

Data augmentation has been crucial to the application of such techniques as rotation, zooming, and horizontal flipping; it enhances the model's robustness and generalizability[3]. These simulate clinical scenarios and help avoid overfitting and ensure that the model does not lose accuracy when used in new, unseen datasets[5].

Although promising, there remain challenges with

such results. This means that the data class is very imbalanced[6]. Some tumor types would have a few samples when compared to others. As a result, this will cause a shift in model performance to perform better with those classes much more abundant to undermine the performance in other classes with few representations. Further research, therefore, is needed to balance this either through synthesis of data, or oversampling, or balanced learning techniques that would improve for all classes[1].

5 Conclusion

Conclusion As such, it would qualify among the best achievements until present in developing tumor-brain classification using the technology CNNs[4]. So efficiently, it has served, given the complexities about managing data from medical image-what would be needed especially scans from MRI-a development undertaken at remarkably higher velocities in accuracy. The accuracy reached about 99.69%, hence making it an excellent practical application of deep learning in the automation of and high-precision diagnosis of brain tumors.
With data augmentation techniques, the general capability of overall generalization by the model is improved. It will give a good performance on new unseen datasets as chances of overfitting are minimized. Transfer learning enhanced the feature extraction ability of the model along with the usage of pre-trained models like DenseNet121 along with the proposed architecture of CNN. This combined, further enabled the model to give effective detections and classifications with the different types of tumors found in the brain-gliomas, meningiomas, and pituitary tumors as well as non-tumorous conditions. However, an area for improvement of this model would be enriching the dataset with samples that can be more diverse than in the current set. This would clean away the biases there in the existing data, and it would make it more reliable for different populations and institutions. More complex architectures, such as EfficientNet, ResNet, ANN, Densenet201 or Vision Transformers, will help the model to recognize finer patterns within medical images and thus raise accuracy. Ensemble learning or transfer learning from larger pre-trained models would further increase performance if availability of data is limited.
Optimizing the model to work for healthcare workflows could mean the best optimization possible with regard to hardware usage and minimum latency. An enormous validation through clinical trials could also be considered essential, where the reliability will have to be ensured through extensive usage in high-stakes real-world applications. It must be explainable as its outputs need acceptance among the health professionals. It might involve techniques like Grad-CAM or SHAP in revealing the decision process in making it transparent.
Further researches and refinements can make it a giant leap toward getting early and accurate diagnoses that can be made for a brain tumor, improving results and quality of healthcare at the patient level[6].

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