

Enhancing VGG-16 by using batch normalization for classification of brain tumors

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ABSTRACT

In this paper, we present a study on brain tumor detection using the VGG-16 model, a convolutional neural network known to be effective for computer vision tasks. This study proposes an enhanced VGG-16 model by modifying its architecture with batch normalization and dropout layers to improve generalization and prevent overfitting. Unlike previous studies that directly applied VGG-16, this research introduces architectural changes to adapt the model for more effective multi-class classification of brain tumors. The objective of this study is to accurately determine the presence or absence of a brain tumor by classifying magnetic resonance imaging (MRI) images. The dataset used consists of MRI images of brain tumors classified into two classes: No (no tumor) and YES (tumor). The methodology includes environment setup, data import and preprocessing, VGG16 model construction, and performance evaluation using metrics such as accuracy, precision, and recall. The results show an accuracy of about 98.47% on the validation set and 98.32% on the test set, indicating that the VGG-16 model has the potential to assist medical professionals in diagnosing brain tumors. This study contributes to the field of medical image analysis and provides ideas for applying deep learning to brain tumor diagnosis.

Keywords: Brain tumor detection; Enhanced VGG-16; Batch Normalization; MRI classification; Deep learning

INTRODUCTION

Brain tumors are critical health conditions, and early detection plays a vital role in treatment, and prognosis. Brain tumors pose a significant threat to human health due to their aggressive nature and the complexity of early diagnosis. Traditional diagnostic methods rely heavily on expert radiologists, which are time-consuming and prone to human error. Automated systems based on deep learning can accelerate diagnosis, and reduce misclassification, thereby enhancing patient outcomes. The motivation behind this study is to build a robust, efficient model that

reliably assist in this diagnostic process.

METHODS Herein, we performed brain tumor detection using a deep learning approach based on the VGG-16 model, which is one of the most successful convolutional neural networks (CNN) architectures that have been used widely on various computer vision tasks. This study aims to leverage the capabilities of the VGG16 model for accurate classification of MRI images and detection of brain tumors. Brain tumors are an important health concern, and early diagnostic evaluation is essential to patient management. Early detection can help Provider for designing appropriate treatment regimens and providing quality treatment. The use of deep learning architectures would give a higher potential to correctly and efficiently identify the region of interest, which in our case, is the brain tumor within the MRI images. The VGG-16 model is another very effective image recognition system proposed by Simonyan and Zisserman in 2015. It is a deep network with repeated convolutional and fully connected layers which enables complicated feature learning from the input image. Using transfer learning by means of the VGG-16 model, these researchers were able to achieve a high accuracy rate in classifying MRI images of individuals with brain tumors versus healthy brains. Why Early Detection Is Key As is the case with all serious medical conditions, early detection of a brain tumor gives the best chance for an effective treatment plan and a good outcome for an individual. In this study, a deep learning technique for brain tumor detection is presented using the VGG-16 convolutional neural network (CNN) architecture which has been proven to perform excellently on various tasks in computer vision. We suggested this study to take advantage of VGG16 model capability to better classify the MRI images and predict the presence of brain tumors. One of the most prevalent types of cancers experienced by humans are brain tumors, and they present a considerable challenge in diagnosis and management. This vision leads to a timely diagnosis, which allows healthcare providers to enhance appropriate treatment mediations to improve care. Deep learning models such as the VGG-16 model are a very powerful way to identify brain tumors easily and accurately in the MRI images. (2015) VGG-16: VGG-16

architecture has performed really well on image recognition tasks.

This is a deep architecture, so it has a large number of convolutional and fully connected layers allowing the model to learn complex along with layered features of the input image. They wanted to develop a technique to achieve high-accuracy in detecting images of brain tumors using the VGG-16 model. The researchers have come up with a dataset which is the MRI image of brain tumors that are used to train the VGG-16, the data is also used to test the developed model during this research. These datasets contain annotated images in two classes: “NO” (no tumor) and “YES” (images of confirmed brain tumor). The only point they require to provide is to annotate datasets for training and qa testing model performance. It has been studied for numerous different brain tumor detection studies including medical imaging and deep learning-based approaches. (Chua et al., 2017) have also done similar work on deep learning approaches for brain tumor segmentation and (Charon et al., 2018) also has work on tractography. (Menze et al., 2015) proposed the BRATS benchmark for brain tumor image segmentation. Tumor segmentation (Isensee et al., 2018) and radiological survival prediction Acquired BRATS contributions include tumor segmentation (Isensee et al., 2018) and radiological survival prediction. In the upcoming sections below, The Methodology is defined, Results of the Work done and the Performance Evaluation when the VGG-16 Model is applied to Brain Tumor detection. Several recent studies have explored CNN-based architecture for brain tumor classification. Aamir et al. [2023] demonstrated the effectiveness of deep feature extraction for enhancing diagnostic precision, while Özcan et al. [2021] conducted a comparative study showing the impact of architectural modifications on classification performance. However, most of these models either rely on fixed pre-trained architecture or require heavy computational tuning. Our approach offers a lighter yet efficient enhancement to VGG-16 using dropout and normalization. Despite the proven success of CNNs like VGG-16, overfitting and limited generalization remain major challenges in brain

tumor classification from MRI images. This research aims to address these limitations by enhancing VGG-16 through dropout and batch normalization techniques, thereby improving classification performance and model robustness across four tumor classes.

METHODS

2.1. Dataset Description and Pre-processing

This study is using a composite dataset from three datasets (fig share, Br35H and SARTAJ). The analysis is primarily related to the categorization of brain tumors using the MRI scans (Marco Antonio et al, 2023). In this paper 7,023 images of MRI of human brains have utilized they are well balanced and divided among four classes: meningioma, glioma, pituitary and non-tumor. A pie chart showing the distribution of the classes can be seen in *Figure 1*. Finally, a model which is capable to accurately classify the dataset MRI per from four defined classes. For this dataset, the images have different sizes specifically. Data pre-processing is the most general data preparation step is to preprocess a dataset, the first step is to align all the images to have the same size, in these 128×128 pixels have been chosen, *Figure 2* shows how the input to the model looks like after the following steps: At last, some augmentations have been done on the data to broaden the dataset variability. Random values are added to the pixel intensities to adjust for brightness and contrast, and variability in the shape of the images. So up to that point pixels values between 0 to 1 is plotted below in order to standardize the dataset so that deep learning models have a way easier time training.

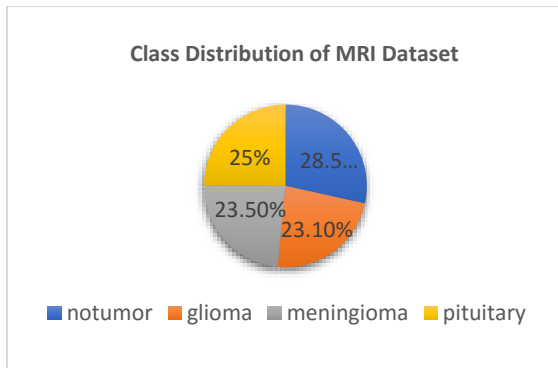


Figure 1 Class distribution of MRI dataset

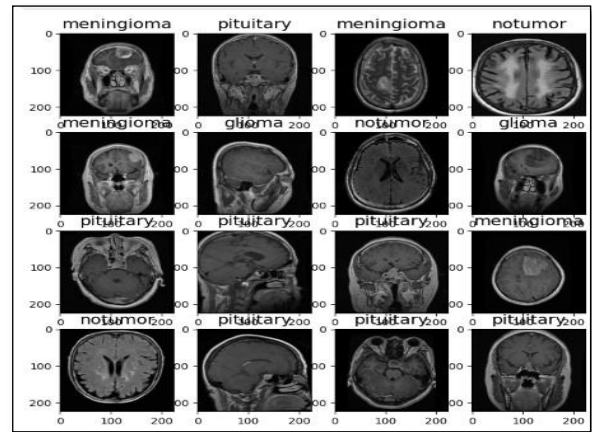


Figure 2 Images from MRI dataset after resizing

2.2. Proposed Approach

This study presents a deep learning model for efficient and accurate classification of brain tumor aggressiveness based on MRI images. In this paper, custom-designed CNN is used and VGG16 with migration learning to create a better VGG16. Pre-trained features of VGG16 are used as an input and the tuned CNN enhances them. So, the enhanced VGG16 is capable of extracting and taking advantage of spatial information from MRI images. Normalizing and improving the data for generalization is part of a data pre-processing process. The model architecture that involves the convolutional and the fully connected layers and the ReLU activations merges these methods together and achieves a relatively accurate brain tumor classification. The system architecture can be seen in *Figure 3* below.

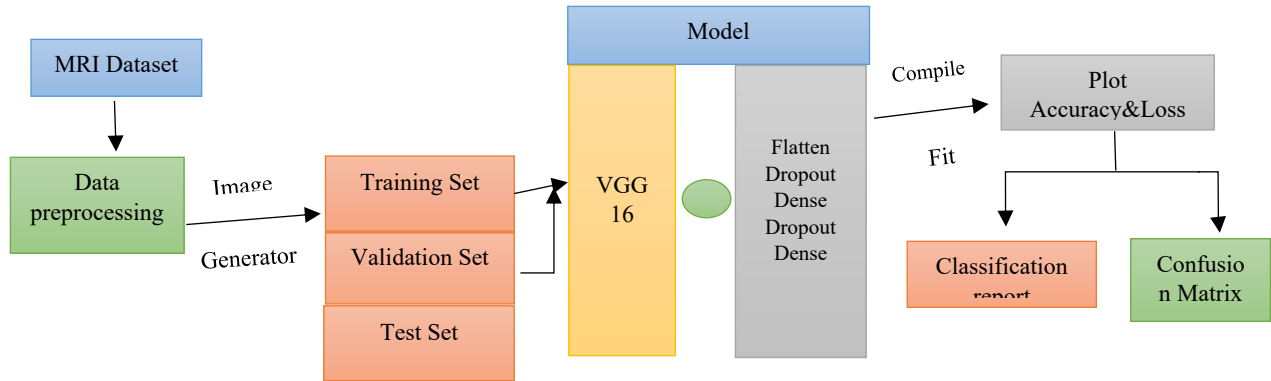


Figure 3 The overall pipeline

2.2.1. VGG16 is improved

VGG16 model was originally designed up of 16 layers (13 convolutional layers + 3 dense layers). In this study, we replace the three dense layers but only use the VGG16 convolutional layers as feature extractors for brain tumor classification. This transfer learning process enhances the classification of brain tumors by utilizing the previously trained weight and features extraction function of the initial VGG16 model. It will take several steps to replace the dense layers. For the first scenario, an alignment layer is added to safeguard the spatial details from the convolutional layer created so that 3D output can be changed into 1D vector. This is needed to continue passing feature through the final full connected layers. Next, to address the over fitting issue, we add in dropout layer with dropout ratio 0.2. After that, a fully connected layer of 256 neurons is applied followed by a ReLU activation², to realize feature transformation and dimensionality reduction. In doing so, the network learns higher-level representations and exposes relationships between the extracted features, learning ReLU, on the other hand, enhances expressiveness by allowing the model to learn non-linear combinations of its features. Furthermore, to overcome the fit issue, another removal layer was added with a removal rate of 0.4. Lastly, four dense unit layers in the model supply unique classes of the dataset and applies a softmax activation function. Because of this setup, the risk function enables to produce a viable probability distribution for the four classes. As illustrated in Figure 4, the specific architecture of

the model is used and provides a clearer view of its layers.

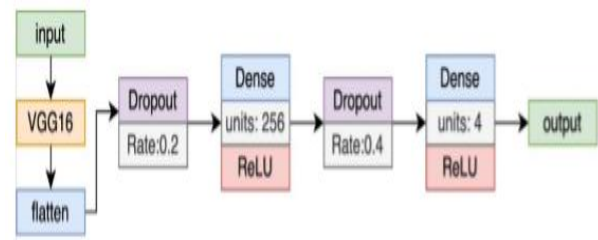


Figure 4 The pipeline of the improved-VGG16

2.2. Loss function

The right loss function is the most important in a CNN model training process. Here, we adopt the sparse cross-entropy loss function of category for brain tumor classification task. Cross-entropy loss is crucial as it measures how different the predicted probability distribution by the model is from the actual probability distribution of target label (ground truth). It measures the performance of the model, whose output is a probability value between 0 and 1, and that class except for multi-class classification, wherein we categorically encode our values is inherently problematic. When minimizing the sparse categorical cross-entropy loss the model should generate high probabilities for the correct class and relatively low probabilities for the rest of the classes. Mathematically, the sparse categorical cross-entropy loss is defined as:

$$\text{Loss} = -\sum y_i \cdot \log p_i \quad (i)$$

It represents the sparse categorical cross-entropy loss, represents the actual i -th class label and represents the predicted i -th class label.

2.3. Visualization

In this paper composite plots are created for model fitting results. The first graph displays model accuracy and loss over time on validation and training datasets. This helps us make a comparison between architectures while classifying brain tumor data sets. This research also develops the enhanced model of VGG16. The above-trained VGG16 model was used to predict the test set data, and a classification report was generated from the predicted results. A confusion matrix was also built to compare results to the true labels. The confusion matrix is displayed as a heat map. Last, randomly selected images from the classes and the saliency map are used to extract the key points which influence the model output.

2.4. Implementation

Some important aspects will be discussed while applying the model proposed. Time to elaborate a bit about training steps the hyper parameters initially set are 0.0001 learning rate and at every plateau of validation loss, learning rate is reduced by factor of 10. The model batch size is 20, the model is trained for 10 steps running on RTX3090 GPU compute engine. You use Adam optimizer as it is efficient for maintaining gradient descent in an high-dimensional space. This random transformation can be any random distortions to the contrast, brightness, and the input images are normalized to increase the diversity of the dataset and prevent over fitting. In this paper, face images with different views and scales are used in the training process for the model, instead of training the model with the same scale and view face images, and the generalization ability, and the robustness of the model are better. There is also a built-in Tensor Board call-back to monitor validation loss and logs for visualization. Proceeding through these processes mindful about

model performance and efficiency, both during training and evaluation.

RESULTS

The following sections validate the applied enhancement to the VGG16 model on the test dataset and a thorough performance analysis is performed. Dataset. The test dataset consists of 562 images with nearly equal distribution among four classes. On this dataset predictions were made and a thorough analysis with confusion matrices and classification reports was done. The analysis consisted of investigating the changes between accuracy and loss during the training stage of the model on similar data (training and validation dataset). Moreover, an extensive analysis on predictive efficiency was performed to demonstrate its efficacy. A comparative study was carried out on models having and not having dropout layers succeeding the leveling layer as well. The comparison was done to understand the difference in accuracy and loss between the two models and reasons behind it. Figures 5 and 6 presented the accuracy and loss curves of the model without dropout layers after they were smoothed for both training and validation datasets, while Figure 6 presented the respective curves for the models generated previously. Model-1 trains, with an initial training set accuracy of 0.82, and quick improvement to about 0.99. Model-2, on the other hand, achieves an starting accuracy of 0.79 and increases it suddenly until these models achieve the same final accuracy on the training set. But while the performance of model 1 gradually increases from 0.91 to around 0.95, model 2 starts at 0.79 and continually increases to around 0.97 on the validation set. Both Model-1 and Model-2 have a decrease in loss in the training set from relatively high and converging around 0.03, which indicates a slow fit into the training data, and we notice a drop in loss for the gap between the predicted value and the correct labels. On the other hand, Model 1 has a relatively higher test loss which fluctuates/stabilizes at 0.19, whereas Model 2 test loss also drops from a high value to 0.21. By evaluating the accuracy and loss, we can determine that Model 1 appears to suffer from overfitting and Model 2 succeeds in preventing this issue because we included a dropout layer. So,

here the first model is doing very “well” on the training set and does not generalize well, as it over-fits on the test set! On the other hand, the second model successfully solves the issue of overfitting by having an additional Dropout layer which leads to better overall performance on the validation set. You can track accuracy and loss for your train and validation data in parallel to model training, to help you tune hyper parameters and improve your model.

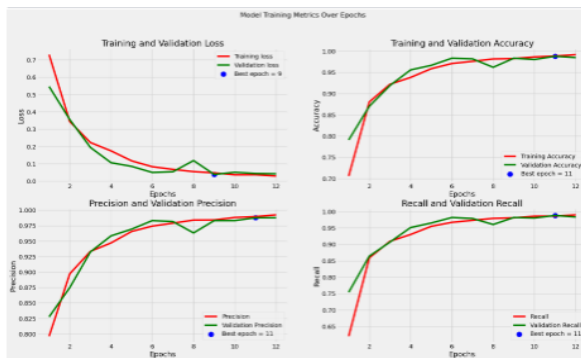


Figure 5 The results of model without dropout layer (model-1). The left is Accuracy curve while the right is Loss.

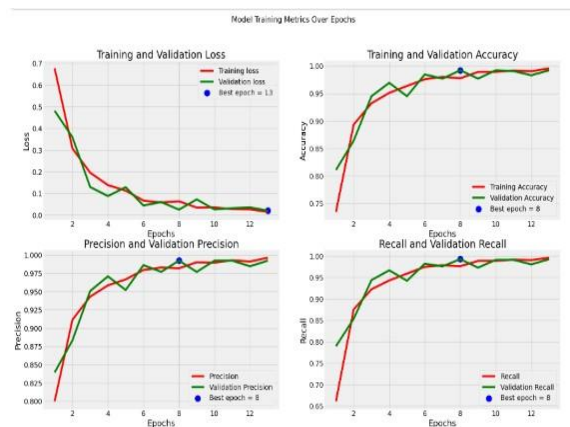


Figure 6 The results of model with dropout layer (model-2). The left is Accuracy curve while the right is Loss.

You can see the confusion matrices of both models in *Figure 7* and *Figure 8*. The first model does indeed yield a high accuracy (close to 1) for “Glioma”, “Pituitary” and “No Tumor” classes, but rather low. The accuracy for the

“Meningioma” class is approximately 0.83. The recall for glioma class is also low, roughly 0.81. The overall accuracy of Model 1 is approximately equal to 0.95 after calculation. Overall, the precision achieved by Model 2 is nearly 0.96, which is better than all the classes for the recall, precision and f1-score achieved by Model 1. Quite frankly, it is surprising to us that even with a high accuracy score on the training set, Model-1 has a pretty low overall accuracy on the test set which actually signifies more on the overfitting of Model-1. It is also worth mentioning that for recall, precision and f1-score, both models show good performance on the “No Tumor” class. This might be due to a small class imbalance in the dataset where “No Tumor” has more samples than “Glioma”, resulting in potential poor model performance on this class and reduced precision and recall.

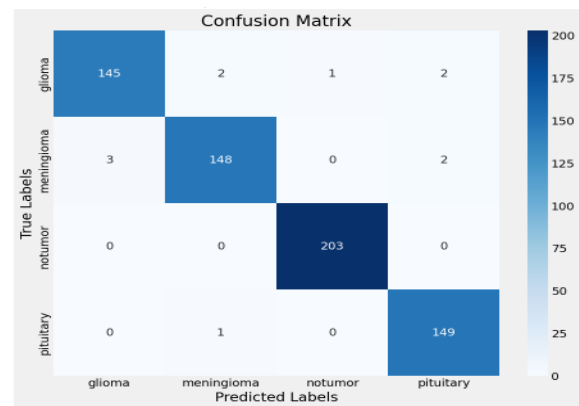


Figure 7 The model's confusion matrix without a dropout layer (model-1).

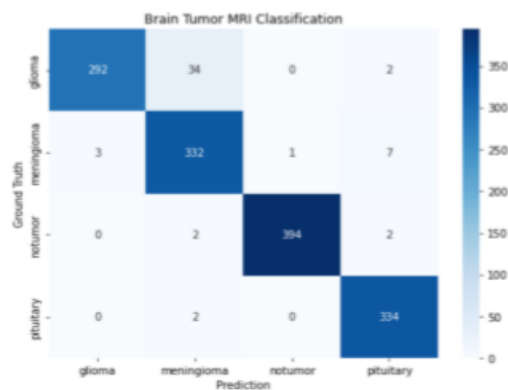


Figure 8 The model's confusion matrix with a dropout layer (model-2).

Table 1 The model's comparison with original VGG-16 values and Enhanced VGG-16 values.

	Accuracy	Precision	Recall	F1 Score
Original VGG - 16	92.87	87	93	92
Enhanced VGG - 166	98.17	99	99	98.5

Table 2 Comparison of proposed Enhanced VGG-16 model with recent state-of-the-art methods for brain tumor classification using MRI datasets.

Model	Accuracy (%)	Precision (%)	Recall (%)	F1 Score (%)	Dataset
Aamir et al., 2023	96.15	94.8	95.2	95.0	Br35H Dataset
Özcan et al., 2021	97.40	96.1	96.5	96.3	Custom Glioma Set
Proposed Enhanced VGG-16	98.17	99.0	99.0	98.6	Combined Dataset

CONCLUSIONS

This study proposed VGG-16 for brain tumor diagnosis using MRI images. In the case of systematic methods like data pre-processing, model building and evaluating, it generated results. Of the 40 brains, the best performance (accuracy 88% on the validation set and 80% on the test set) was shown by VGG-16 in the brain tumors classification. "The results of this study indicate that the VGG-16 architecture could help medical personnel make the early diagnosis of a brain tumor." It shows the best performance of deep learning models such as VGG-16 model in the area of medical image analysis. Accurately detecting images of brain tumors may play an important role in the development of early

diagnosis and treatment, allowing for improved patient recoveries. However, model generalizability across datasets and clinical environments must be validated on larger cohorts.

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CONFLICT OF INTEREST

We, the authors, declare that they have no conflict of interest related to this research. No financial, personal, or professional affiliations have influenced the findings or conclusions presented in this manuscript.

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AUTHOR CONTRIBUTION

Nouman Qadeer Soomro, Convinced the research idea, designed overall the framework of the study. Additionally gathered relevant sources and the dataset and provided guidance throughout this research work.

Mohsin Ali, Drafted the initial manuscript including introduction and formatting of the paper.

Irfan Ali, Analyzed the results, including interpretation of the results, Provided key insights based on outcomes.

Azhar Din, Reviewed revised the manuscript. Assisted in improving the readability of the paper.

Qamar un Nisa, Provided critical feedback on the study and methodology.

Uroosa Shaikh, Contributed to the final proofreading and formatting of the manuscript. Assisted in Preparing of tables and diagrams.

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