Enhanced Brain Tumor Classification: A Transfer Learning Approach with Pre-trained Models

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ABSTRACT

The categorization and prediction of brain tumors are crucial in facilitating the timely identification and management of brain-related disorders. The significance of brain tumor detection and analysis for any indication system is supported by a substantial body of research and ongoing methodological advancements. The investigation necessitates precise identification of tumors, thereby necessitating the implementation of an effective automated methodology. A variety of segmentation algorithms have been developed to facilitate and enhance the categorization of brain tumors. Brain imaging segmentation is well recognized as a challenging topic within the domain of medical image processing. The study proposes a novel automatic detection and categorization method based on the findings. The proposed methodology is comprised of many sequential phases, encompassing the preprocessing of magnetic resonance imaging (MRI) scans, the segmentation of these scans, the extraction of pertinent characteristics, and the subsequent categorization of these features.

This work introduces a transfer learning methodology that aims to achieve the precise classification of brain tumors and accurate prediction of their malignancy through the utilization of sophisticated deep learning techniques. The MRI scans underwent feature extraction, followed by the utilization of a deep learning model to categorize the pictures into several classes, including gliomas, meningiomas, non-tumors, and pituitary tumors. To facilitate categorization, the researchers employed pre-trained VGG-16 Net models. To improve the performance of the VGG-16 Net model, data augmentation approaches are employed to mitigate the issue of overfitting and boost generalization capabilities. The model that has undergone training demonstrates exceptional accuracy in the categorization of brain tumors, surpassing previous benchmarks. It exhibits notable sensitivity and specificity in identifying the presence of tumors and properly predicting their grades. The VGG-16 Net, when utilized for the analysis of MRI images of brain tumors, had a commendable accuracy rate of 97.21 percent.

Keywords—: Brain tumor; disease prediction; disease classification; deep learning; detection model; MRI images.

I. INTRODUCTION

The medical community has major hurdles in the realm of diagnosis and therapy when dealing with brain tumors. The diagnosis of brain tumors at an early stage and with a high degree of accuracy is essential for the efficient planning of therapy and the improvement of patient outcomes. Throughout the years, medical imaging methods have been essential in playing a crucial part in the identification of brain tumors. Additionally, advances in technology have revolutionized the diagnosis and classification of brain tumors [1]. In the past, imaging procedures like computed tomography (CT) and magnetic resonance imaging (MRI) were utilized for the diagnosis of brain tumors. CT scans were able to offer useful information on the location and size of the tumor, but they frequently lacked the requisite sensitivity to differentiate between the various types and grades of tumors. MRI scans, on the other hand, provided improved soft-tissue contrast, which enabled clearer visualization of tumor borders as well as adjacent brain structures [2]. Nevertheless, manual interpretation of MRI images remained subjective and time-consuming, which resulted in the need for automatic and effective brain tumor categorization methods.

The most recent advancements in machine learning, namely deep learning algorithms, have transformed medical image analysis in several different areas. One of these areas is the categorization of brain tumors. Deep learning models, such as convolutional neural networks (CNNs), when applied to medical imaging, have the potential to learn patterns and properties that are very complex. CNNs can discriminate between normal brain tissues and tumor areas, hence enabling accurate and automated brain tumor classification [4]. This is accomplished by the automatic extraction of pertinent information by CNNs. Additionally, the availability of large-scale labelled datasets as well as advancements in processing capacity have encouraged the creation of advanced CNN architectures that are specifically specialised for medical image analysis. Researchers have made use of these improvements to develop robust models that are capable of properly discriminating between distinct types of tumors and predicting grades of tumors [5].

In addition, data augmentation strategies have been implemented to overcome issues associated with restricted datasets, to improve the model's generalization and lower the risk of overfitting. The classification accuracy and reliability of brain tumors have been greatly improved thanks to the application of deep learning models in conjunction with data augmentation. In addition, the incorporation of sophisticated machine learning models with user-friendly interfaces has made their use in clinical practice much simpler [6]. Utilizing web-based software, medical personnel can quickly submit MRI images and obtain fast data about the categorization of brain tumors. These kinds of apps provide doctors with effective tools for early identification and treatment planning, which ultimately leads to improved patient care and results.

In this inquiry, we intend to follow the history of brain tumor classification and prediction methods, beginning with traditional methods such as CT and MRI and progressing up to state-of-the-art deep learning models utilized in medical image analysis today. Our objective is to develop a dependable classification model for brain tumors by utilizing cutting-edge convolutional neural network (CNN) architectures and various ways of data augmentation. The findings of this study may have far-reaching consequences for neuroimaging [7], which would provide physicians with access to cutting-edge tools for the earlier diagnosis and treatment of brain tumors at a period when they are in their early stages.

The remaining content of the article is organized as described in the following paragraphs. In the next section, "Section 2," we will investigate the several methods that have been devised for recognizing and predicting the discovery of brain tumors. In Section 3, we talk about the deep learning framework that was constructed for the classification and prediction of transfer learning-based brain tumor detection. The findings of the investigation as well as potential future directions are discussed in Section 4.

II. LITERATURE SURVEY

During the initial stages, the classification of brain tumors predominantly depended on the visual examination of medical imaging modalities, including computed tomography (CT) and magnetic resonance imaging (MRI) scans. The images were manually analyzed by radiologists, who identified tumor sites by analyzing their visual characteristics, dimensions, and spatial coordinates. Nevertheless, these methodologies exhibited a lack of objectivity and proved to be excessively time-consuming. With advancements in processing capacity, researchers have begun to investigate approaches for the automated classification of brain tumors. Various image processing approaches, including thresholding, region expanding, and feature extraction, were utilized to detect tumor patches and differentiate them from normal brain tissues. The aforementioned approaches have shown potential, although encountered difficulties when confronted with intricate tumor forms and the presence of overlaying tissues [8].

Support vector machines (SVMs) and random forests, which are both machine learning methods, gained significant popularity in the early 2010s to classify brain tumors. The algorithms employed in this study utilized texture, intensity, and shape features that were manually extracted from MRI images to differentiate between tumorous and healthy tissue. Although the accuracy of these approaches was improved compared to conventional procedures, their effectiveness was limited due to the requirement of manually designed features [9].

In this particular aspect of the study, a comprehensive examination of existing literature is undertaken to explore the subject of convolutional neural network (CNN)-based multi-classification of brain tumors. The investigations documented in the existing literature can be examined from several viewpoints. In the context of brain tumor classification, several researchers have employed individually developed convolutional neural network (CNN) models, whilst others have opted for the transfer learning methodology. The same objective of these two research groups is evident. Several scientists have developed their convolutional neural network (CNN) models specifically designed for the categorization of brain tumors. Bada and Barjaktarovi (2010) employed a dataset consisting of 3064 T1-weighted contrast-enhanced MRI images to construct a convolutional neural network (CNN) model with 22 layers. The purpose of this model was to classify different types of brain tumors. The tumors were classified utilizing the aforementioned structural framework. The model that was put up demonstrated the capability to accurately classify meningioma, glioma, and pituitary as the three distinct types of brain tumors, with a precision rate of 86.56%.

In a separate investigation, Mzoughi et al. [11] proposed a comprehensive multi-scale 3D convolutional neural network (CNN) architecture to classify brain cancers based on volumetric 3D magnetic resonance imaging (MRI) data. The approach developed in this study achieved a classification accuracy of 87.49% in distinguishing between low-grade glioma and high-grade glioma based on brain cancer pictures. Ayadi et al. (2012) proposed the utilization of a computer-assisted diagnostic (CAD) system that relies on convolutional neural networks (CNNs) to categorize various forms of brain tumors. The studies conducted utilizing the 18-weighted layered CNN model yielded a classification accuracy of 84.74% for brain cancer kinds and 90.35% for tumor grades. The conclusions obtained from the investigations done on the three distinct datasets are as follows.

Pereira et al. [13] obviated the necessity for expert assessments of regions of interest by employing Convolutional Neural Networks (CNNs) to directly forecast cancer grades based on imaging data. Consequently, the acquired data was utilized to enhance their predictive analysis. This study examined and contrasted two prediction approaches: one using the entire brain and the other focusing on an automatically detected cancer site. By using comprehensive brain data, the researchers achieved a predictive accuracy of 89.5% for cancer grade. Similarly, by utilizing tumor region of interest (RoI) data, they achieved a predictive accuracy of 92.98% for tumor grade.

In their study, Abiwinanda et al. (2014) employed a basic convolutional neural network (CNN) architecture to classify the predominant brain tumor types, namely glioma, meningioma, and pituitary. Their model achieved a maximum validation accuracy of 84.19%. This was feasible given the tumors were classified as glioma, meningioma, and pituitary tumors. In 2019, Hossam et al. [15] presented the utilization of a Convolutional Neural Network (CNN) architecture to distinguish between the three categories of glioma and categorize brain tumors as meningioma, glioma, or pituitary. The technique employed in this study was utilized to categorize the grades of glioma.

III. TRANSFER LEARNING BRAIN TUMOR CLASSIFICATION MODEL

This study aims to explore the use of the VGG-16 transfer learning model in the classification and prediction of brain cancers based on MRI data. The VGG-16 deep convolutional neural network (CNN) architecture was developed by the Visual Geometry Group (VGG) at Oxford University. The 2014 ImageNet Large Scale Visual Recognition Challenge (ILSVRC) garnered significant attention and impressed judges due to its exceptional performance in computer vision tasks, particularly in the domain of picture categorization.

The architectural components of the VGG-16 Net consist of many levels, which may be described as follows:

- Feeding the Input Images for Training and Testing
- Phase of Feature Extraction (Conv. Layer)
- Phase of Performing Non-Linearity Function (Activation Function)
- Phase of Feature Reduction (Down-sampling: Max or Min Layer)
- Phase of Flatten and Fully connected layer (Converting to 2D to 1D data)
- Phase of Soft-max classifiers (Final Classification)

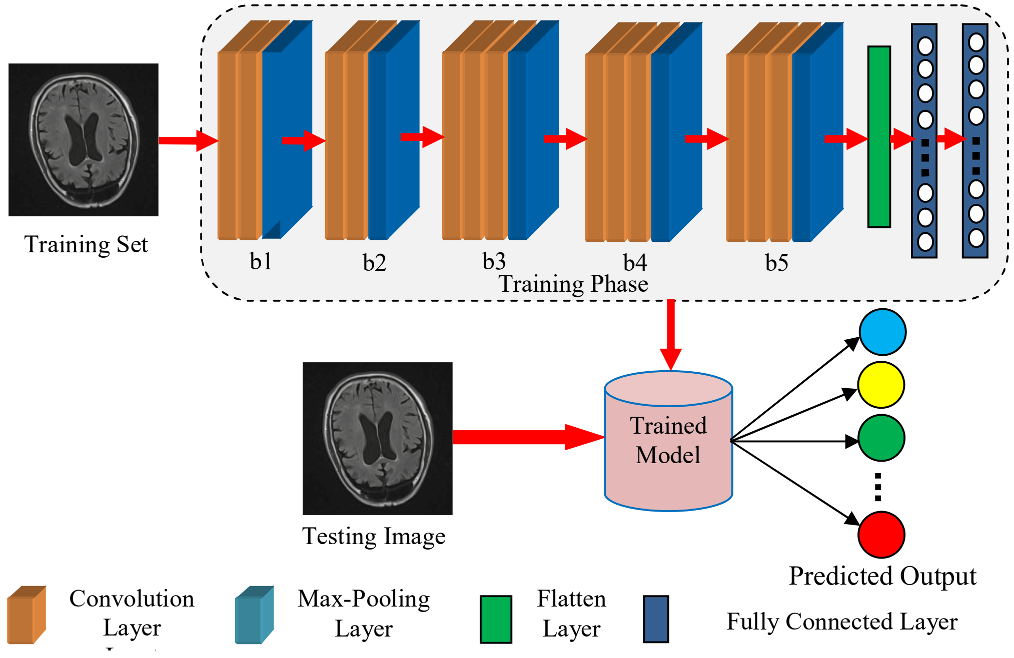

Figure 1: Architecture of VGG-16 Net Model

Image Input: The VGG-16 model requires an image as its first input to function properly. Before the image is uploaded to the network, it is traditionally preprocessed to a certain size.

Convolutional Layers: The original input image is processed through a total of 13 convolutional layers before being output. It is the job of each convolutional layer to identify a distinct set of low-level to high-level characteristics inside the image. To generate feature maps, these layers convolve over the input data using tiny 3x3 filters. After each convolution operation, VGG-16 employs zero-padding to guarantee that the spatial dimensions of the feature maps stay unchanged. This is accomplished by adding zeros to the beginning and end of each dimension.

Pooling Layers: VGG-16 makes use of max-pooling layers periodically. Each of these layers has a 2x2 window and a stride of 2 pixels. The spatial dimensions of the feature maps may be reduced with the assistance of max-pooling, which helps to improve translation invariance while also reducing the amount of computational complexity.

Fully Connected Layers: After a large number of convolutional and pooling layers, the spatial dimensions of the feature maps are reduced by a significant amount. Following this step, the simplified feature maps are imported into three thick layers, also referred to as completely connected layers.

Soft-max Classifier: A softmax classifier is utilised in the final fully linked layer. This layer receives the findings of the layer that came before it, and based on those results, it calculates probabilities for each class. The model's final projection represents the category with the highest likelihood.

Dataset Description: The dataset utilised in this work comprises magnetic resonance imaging (MRI) scans obtained from patients diagnosed with various types of brain cancers, including gliomas, meningiomas, and pituitary tumours. The data collection encompasses malignant tumours of different stages, such as glioma, meningioma, notumor, and pituitary tumours. Prior to being fed into the model, the MRI images undergo a series of preprocessing and normalisation steps. The dataset has a grand total of 5,650 magnetic resonance imaging (MRI) images, which have been categorised into four distinct groups, each containing an equal number of 1,350 images. MRI is an acronym that stands for magnetic resonance imaging. The dimensions of each image are 176x208 pixels, and they are shown in a monochrome grayscale format. Figure 2 depicts the labelling of several entities: glioma is denoted as c1, meningioma is designated as c2, a non-tumor is identified as c3, and the pituitary gland is marked as c4.

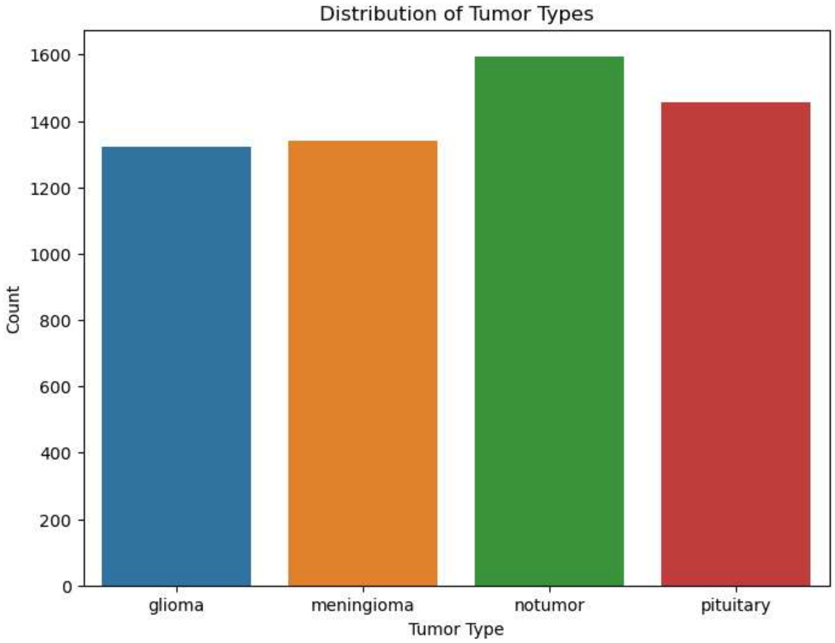

Figure 2: Brain Tumor Detection class distribution and categories

Figure 3 showcases a selection of MRI pictures derived from the kaggle repository dataset, serving as illustrative examples. The dataset was partitioned into three subsets: a training set, a validation set, and a test set. Table 1 presents the distribution of the dataset, indicating that 70% of the data is allocated for training the model, 20% is allocated for model validation, and the remaining 10% is reserved for model testing.

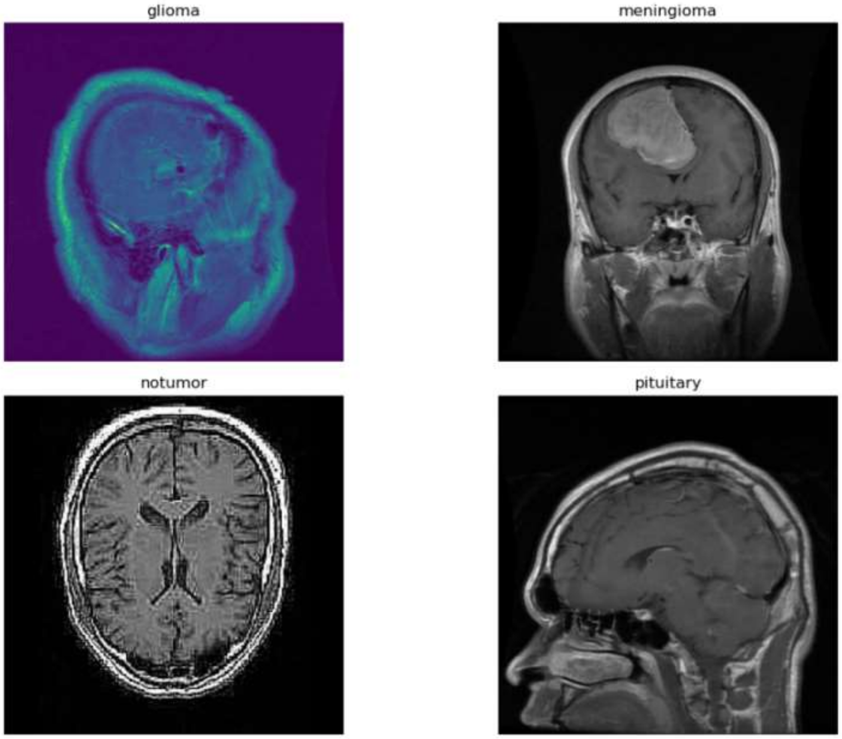

Figure 3: Sample Brain MRI Images for Prediction of Brain Tumors

Table 1: Dataset split ratio for Brain MRI Images

S. No.	Disease Type	Tr. Images	Val. Images	Test	Total	Category
1.	Glioma	1000	300	50	1350	C1
2.	Meningioma	1000	300	50	1350	C2
3.	Notumor	1100	405	95	1600	C3
4.	Pituitary	1000	300	50	1350	C4

IV. EXPERIMENTAL RESULTS OF BRAIN TUMOR PREDICTION MODEL

This part utilises transfer learning techniques with the VGG-16 Net model to investigate the detection and diagnosis of Alzheimer's disease in MRI scans. The results of the analysis are examined and discussed. The system under consideration was developed utilising the Python programming language and the Anaconda Integrated Development Environment (IDE). The data was analysed using a computing device equipped with an Intel Core i5 central processing unit, 8 gigabytes of random access memory, and a 1 terabyte hard disc drive.

A. Performance Metrics

The utilisation of classification performance measures is employed to assess the effectiveness of a statistical or machine learning model in accurately categorising data into several unique groups or classes. These metrics provide valuable information on the performance of the model and aid in the analysis of its accuracy, precision, recall, and other important characteristics.

Accuracy: The accuracy metric assesses the proportion of correctly classified instances (both positive and negative) in relation to the total number of instances in the dataset.

Precision: Precision referred to as positive predictive value, is a metric used to measure the accuracy of a model's positive predictions. It is calculated by dividing the number of correct positive predictions by the total number of positive predictions made by the model. This demonstrates the model's ability to effectively differentiate between instances classified as genuine positives and those classified as false positives.

Recall: The recall is utilised to assess the frequency with which a model accurately predicts a desirable outcome. The measure serves as a means of evaluating the model's efficacy in accurately detecting real positive instances while minimising the occurrence of false positive detections.

F1-Score: The F1 score is a metric that provides a balanced evaluation of accuracy and recall by condensing both into a single numerical value.

B. Result Analyse

In this article, we describe the findings of an experiment in which a deep learning model was used to diagnose and estimate the likelihood of brain tumours. The model will be evaluated to determine how well it can classify different types of tumours and rank the degree of their aggressiveness. The purpose of the experiment is to train the model using a series of MRI images taken from brain tumours and then evaluate the model using another set of data.

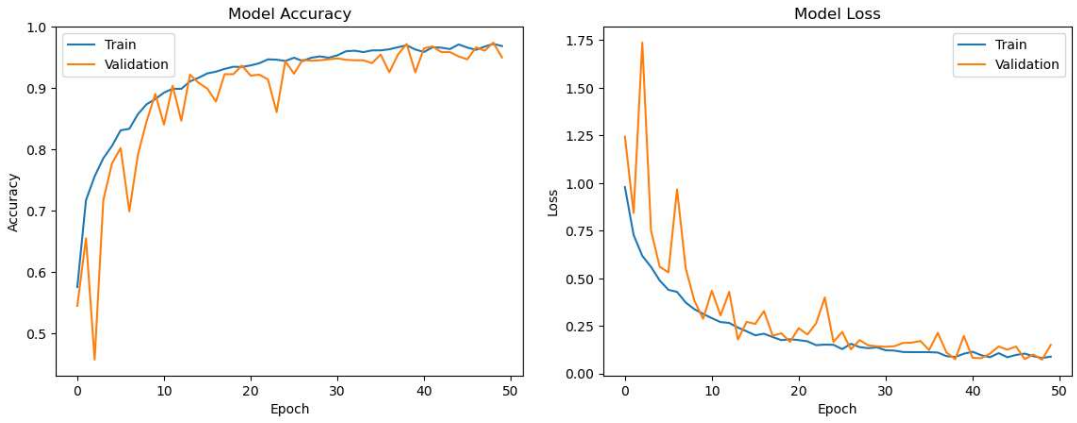

Figure 4: VGG-16 Net transfer learning accuracy and Loss

To begin, we have trained and evaluated the VGG-16 Net transfer learning model in order to categorise brain cancer disease in MRI images. This was done so that we can categorise brain tumours. The data shown in Table

2 and Figure 4 led us to the conclusion that the VGG-16 Net was the way that achieved the maximum achievable accuracy of 96.17 and was the most successful approach. This was determined by the fact that it was the method that acquired the best possible accuracy. Following a period of 50 epochs, the results of a VGG-16 Net transfer learning model are shown in Figures 3 in terms of standard metrics including trained accuracy, validated accuracy, trained loss, and validated loss. These metrics were calculated after the model had been subjected to training. These parameters are developed in order to provide the information in order to present an estimation of the trained models applying a learning rate of 0.00001 and SGD optimisation. These parameters are generated in order to provide an estimated of the degree to which the training models have been overfit in order to offer an estimate of the degree to which the models have been overfit. A visual representation of the characteristics of several exemplary examples of brain tumour pictures is shown in Figure 4. As can be seen in Figures 5 and 6, the outputs of the confusion matrix as well as the predictions provided for the sickness prediction and the classification of brain tumours are presented here.

Table 2: Performance Comparison of base models

S. No.	Model	Acc.	Pr.	Re.	F1- S
1.	CNN Model	89.23	89.1	89.2	89.0
2.	Alex Net Model	91.3	91.1	91.2	91.1
3.	VGG-16 Transfer Learning	96.17	96.3	96.2	96.2

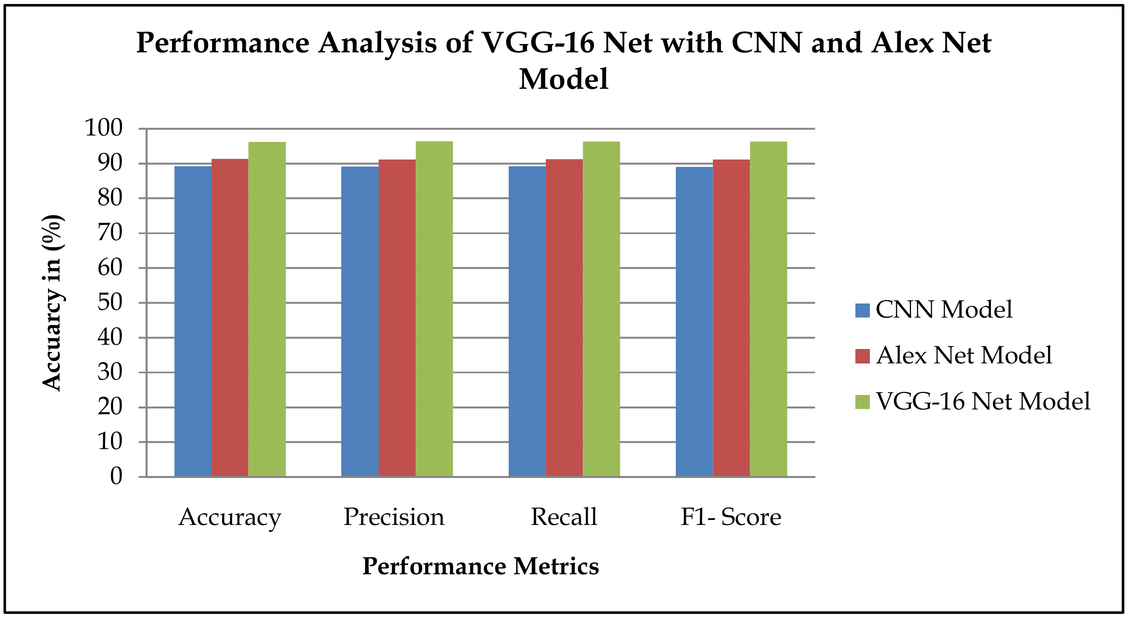

Figure 5: Performance Analysis of VGG-16 Net with CNN and Alex Net Model

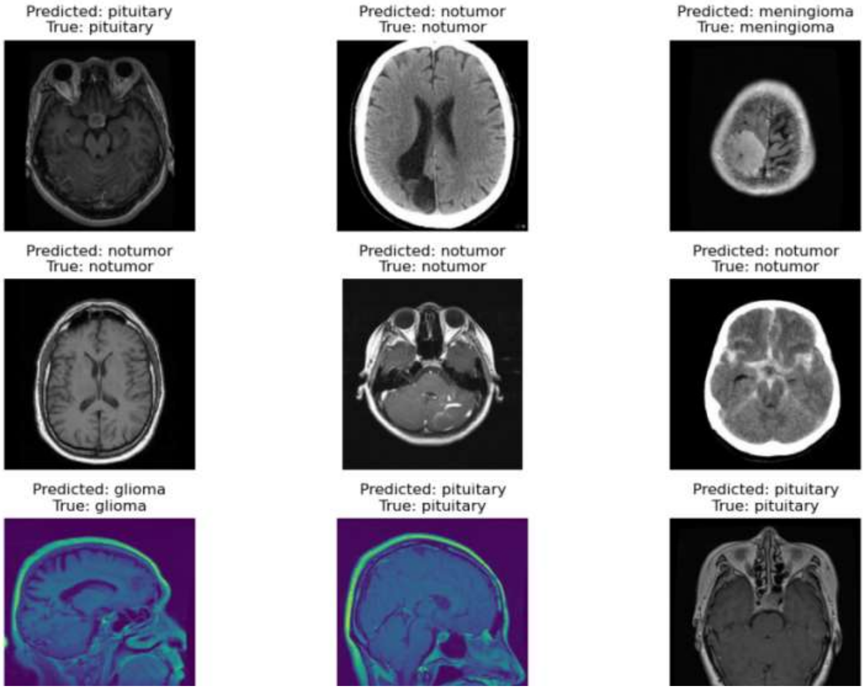

Figure 6: Brain tumor disease prediction and classification

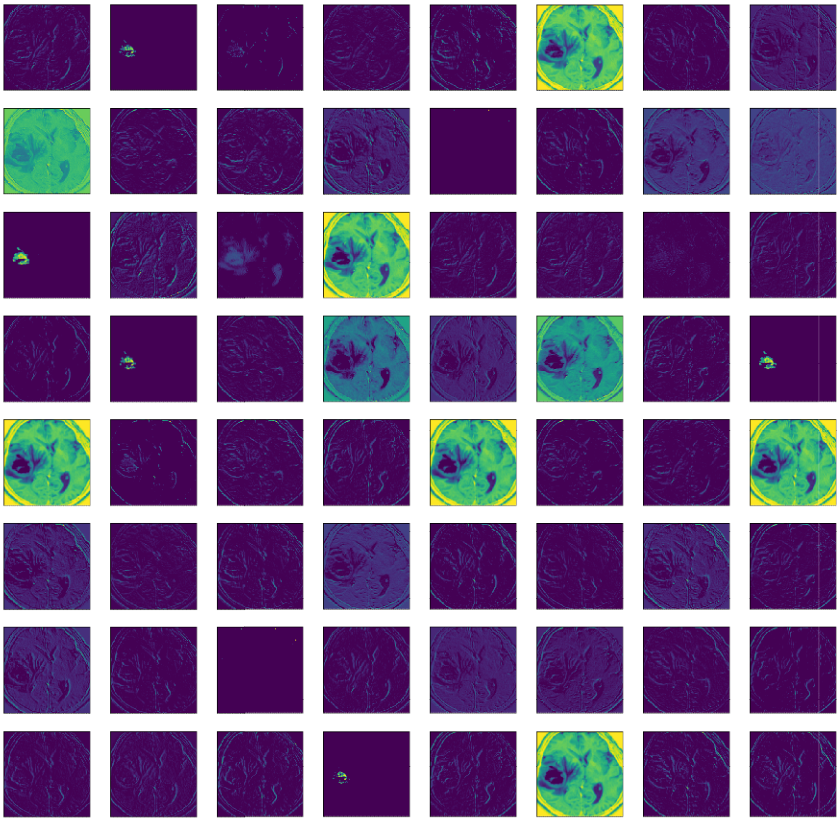

Figure 7: Feature Visualization of brain tumor disease images

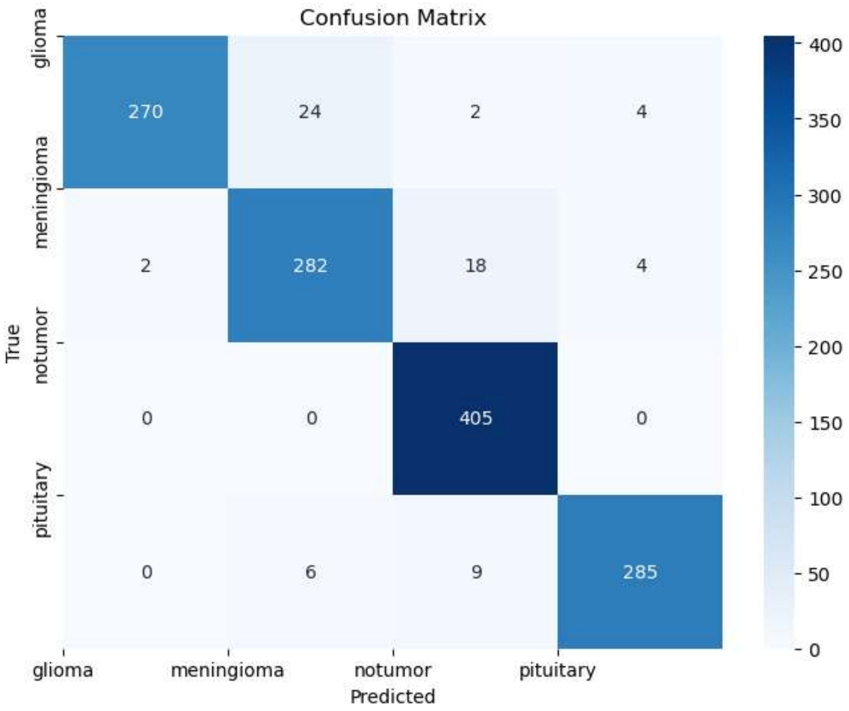

Figure 8: Confusion matrix of brain tumor images

V. CONCLUSIONS

Research and study in the field of machine learning have been expanded beyond the world of feature engineering and into the realm of architectural design as a result of recent developments in deep learning. This research presents a way for multi-classifying these disorders by utilising VGG-16 Net transfer learning models. The goal of this method is to facilitate the early detection of brain tumours. There are three robust CNN models that have been designated for use in the process of brain tumour identification in medical imaging. The diagnosis of brain tumours can achieve an extremely high degree of accuracy, at around 96.1%. The CNN models that were constructed as part of this research will allow medical professionals, such as doctors and radiologists, to assess the accuracy of their preliminary screening for numerous forms of brain tumours.

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