



ENHANCED BRAIN TUMOR DETECTION AND CLASSIFICATION USING VGG-16 WITH TRANSFER LEARNING ON MRI SCAN

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Abstract : The VGG-16 model, a convolutional neural network well-known for its effectiveness in computer vision tasks, is used in this study to detect brain tumors. The study's objective is to correctly detect the existence of brain malignancies by classifying magnetic resonance imaging (MRI) pictures. The dataset is made up of MRI pictures of brain tumors that have been classified as "NO" (no tumor) or "YES" (tumor). Setting up the environment, importing and preparing the data, creating the VGG-16 model, and assessing its performance using metrics like recall, accuracy, and precision are all part of the methodology. The findings show that the VGG-16 model has the potential to assist medical professionals in the diagnosis of brain tumors, with an accuracy of almost 88% on the validation set and 80% on the test set. In addition to providing insights into the use of deep learning for brain tumor identification, the study advances the field of medical picture analysis.

Index Terms - Deep learning; MRI imaging; Convolutional neural networks; Brain tumor identification; VGG-16 model

1 INTRODUCTION

Brain tumors contribute significantly to morbidity and mortality, making them a major global health concern. Because of their wide range of histological characteristics, clinical symptoms, and prognoses, the World Health Organization (WHO) considers them to be among the most complicated tumor types. Since prompt management can significantly improve patient outcomes, it is critical to diagnose brain tumors as soon as possible. Invasive treatments like biopsies are often used in conjunction with neuroimaging methods, namely Computed Tomography (CT) and Magnetic Resonance Imaging (MRI), to diagnose brain cancers. These traditional diagnostic techniques, however, are frequently labor-intensive, time-consuming, and heavily reliant on radiologists' skill. The diagnosis process is made more difficult by the growing amount of medical imaging data, which calls for automated solutions that can help medical professionals diagnose brain tumors quickly. The field of medical image analysis has seen a dramatic change in recent years due to developments in deep learning. Because deep learning algorithms, in particular Convolutional Neural Networks (CNNs), can automatically learn complex features from raw picture data without the need for manual feature extraction, they have become the gold standard for image classification tasks. The VGG-16 model, created by the University of Oxford's Visual Geometry Group, is among the most well-known CNN architectures. The depth of VGG-16 is defined by its 16 layers, which include 3 fully linked layers and 13 convolutional layers, as well as its usage of tiny receptive fields (3x3 filters). Its ability to handle challenging picture identification tasks is demonstrated by its achievement in the 2014 ImageNet Large Scale Visual identification Challenge (ILSVRC), where it placed highly. This project intends to use the VGG-16 architecture for the automatic detection of brain cancers from MRI data, given its demonstrated abilities in image classification. The main goal is to create a strong and precise deep learning model that can successfully categorize MRI pictures into two groups: "NO," which denotes the absence of a tumor, and "YES," which denotes the presence of a tumor. The purpose of this study is to show how the VGG-16 model may be applied in the field of medical imaging by offering a thorough approach for its implementation and assessment. This research has numerous contributions. First of all, it makes use of a publicly accessible collection of labeled and annotated MRI images, guaranteeing accessibility for upcoming studies and benchmarking. The richness and diversity of the dataset mirror real-world situations, making it possible to evaluate the model's performance with more accuracy. Second, the work provides a thorough method for employing transfer learning techniques to train the VGG-16 model. With less training time and data, the model may leverage previously learnt features by using pre-trained weights from the ImageNet dataset, greatly enhancing its performance on the MRI dataset. Accuracy, precision, recall, and the confusion matrix are just a few of the performance indicators that are used to thoroughly evaluate the produced model's efficacy. These measures offer important information about the model's dependability and capacity to correctly diagnose brain tumors. It is essential for healthcare practitioners to comprehend these performance indicators since they allow them

to assess the model's possible influence in clinical settings and the process of making decisions about patient treatment plans. Beyond its technical achievements, this research is significant because it highlights the possibility of incorporating cutting-edge deep learning methods into medical diagnoses. Automated diagnostic technologies can reduce workload for radiologists, improve diagnosis accuracy, and streamline workflow as medical imaging continues to advance. This study intends to assist medical professionals in making well-informed decisions, ultimately leading to better patient care, by offering prompt and trustworthy insights into brain tumor diagnosis. To summarize, the automatic identification of brain tumors from MRI scans has advanced significantly with the incorporation of deep learning techniques, especially the VGG-16 model. By demonstrating the revolutionary potential of deep learning in transforming healthcare diagnostic procedures, this work aims to add to the expanding corpus of research in medical image analysis. The results of this study not only open up new avenues for investigation into the classification of brain tumors, but they also demonstrate how important technology is to improving the accuracy of medical diagnoses.

2 RELATED WORK

This part offers a thorough analysis of cutting-edge techniques for the identification and categorization of brain tumors, highlighting the expanding significance of deep learning, machine learning, and hybrid approaches in medical imaging.

2.1 Deep Learning Methods

In medical image analysis, deep learning—in particular, Convolutional Neural Networks, or CNNs—has become a potent instrument. Sharma et al. (2022) [1] examined a number of deep learning models, including as VGG16, ResNet, and InceptionV3, that are employed for the identification and classification of brain tumors. Their research demonstrated that CNNs' capacity to automatically extract pertinent information from medical images allows them to perform better than conventional machine learning models. Remarkably, models such as VGG16 and ResNet were shown to have great classification accuracy; on MRI datasets, ResNet produced an accuracy of 95%. The impact of transfer learning in brain tumor MRI categorization was the main emphasis of Khan et al. (2021) [2]. Through the reuse of weights acquired from extensive datasets, transfer learning enables pre-trained models to be optimized for particular applications, such brain tumor detection. According to their research, when fine-tuned, pre-trained models like InceptionV3 and ResNet-50 greatly increase the classification accuracy of brain tumor images, achieving 97% accuracy with few training cycles. This method successfully addresses the problem of a lack of labeled medical data. Singh et al. (2022) [3] used VGG16, a CNN architecture with 16 layers, to create a deep learning system. Their model achieved a remarkable 98% accuracy in multi-class brain tumor classification after being trained on a large dataset of MRI scans. The deep structure of VGG16, which enabled it to capture complex aspects of tumor images, was credited with this excellent performance. Their model demonstrated its resilience and capacity to generalize across various brain tumor types after achieving convergence after 20 training cycles. In a different study, Gupta et al. (2021) [4] compared deep learning models for brain tumor identification, such as VGG16, ResNet, and DenseNet. Their tests showed that VGG16 performed better than other models, with a 96% classification accuracy. In order to enhance model performance and avoid overfitting, the study also underlined the significance of regularization strategies including dropout and hyperparameter tuning. Additionally, a CNN model that is optimized for brain tumor classification was proposed by Kaur et al. (2023) [5]. In order to guarantee stable convergence, their model employed an adaptive learning rate technique, which dynamically modified the learning rate during training. On the BRATS dataset, one of the most popular datasets for brain tumor segmentation and classification, the model consequently obtained 99.1% accuracy. Their model's success showed that dynamically modifying hyperparameters can improve performance on difficult medical imaging tasks.

2.2 Machine Learning Methods

Traditional machine learning methods, as opposed to deep learning, use manual feature extraction and less complex classification algorithms. In order to detect brain tumors, Patil et al. (2022) [6] carried out a thorough analysis of several machine learning models, such as Support Vector Machines (SVM), Random Forest, and Decision Trees. Their tests using MRI datasets revealed that SVM, with an accuracy of 97.73%, was the best. SVM was ideally suited for categorizing brain tumor images because of its capacity to handle high-dimensional data, where characteristics are frequently intricate and non-linear. In order to enhance the diagnosis of brain abnormalities, Kaur et al. (2023) [7] created a hybrid model that combines Random Forest and K-Nearest Neighbors (KNN). Random Forest is an ensemble learning method that creates several decision trees, whereas KNN is a straightforward but efficient algorithm that groups data points according to how close they are to known samples. With a 95.6% accuracy rate, their model is a reliable method for identifying brain cancers. Their methodology improved classification accuracy by utilizing the advantages of both techniques, especially when there was a lack of labeled data. A machine learning pipeline that used Principal Component Analysis (PCA) for dimensionality reduction and SVM for classification was presented by Kumar et al. (2023) [8]. By choosing the most informative features, PCA simplified the feature space, and SVM categorized the features that were simplified. With a 96.5% accuracy rate, their model showed that narrowing the feature space can result in quicker and more precise categorization.

2.3 Hybrid Methods

In order to detect brain tumors with greater accuracy and resilience, hybrid approaches use the advantages of both machine learning and deep learning methodologies. A hybrid model was presented by Zhang et al. (2021) [9], which used an SVM classifier for final classification and a CNN for feature extraction. Their method leveraged CNN's capacity to automatically extract spatial information from MRI images, and SVM outperformed a conventional softmax layer in handling the classification problem. The promise of hybrid models in medical imaging was demonstrated by this model's 96.9% accuracy on the ISLES 2015 dataset. In order to extract

reliable features from MRI scans, Bose et al. (2022) [10] created a multi-path CNN model that combined 2D and 3D convolutions. Their model achieved a classification accuracy of 98.14% by capturing spatial information at various degrees of granularity thanks to this approach. The multi-path architecture's ability to simultaneously learn local and global picture properties made it useful for identifying different kinds of brain cancers. By combining transfer learning with the EfficientNetB3 model, Kaur et al. (2023) [11] further expanded the hybrid technique and achieved an astounding 99.33% accuracy. To avoid overfitting, their model used dynamic regularization and an adaptive learning technique. For medical imaging jobs where high accuracy is essential, EfficientNetB3, which is renowned for its balanced trade-off between model size and accuracy, proved to be a great option. An ensemble model comprising VGG16, ResNet-50, and DenseNet was evaluated on several brain tumor datasets in a work by Smith et al. (2024) [12]. By utilizing the advantages of each distinct design, the ensemble technique enhanced classification performance, resulting in a 97.8% accuracy rate. Compared to employing a single model, ensemble learning techniques can yield more robust and dependable results by pooling predictions from several models. By merging VGG-16 and XceptionNet, Adamu et al. (2024) [13] investigated an ensemble model based on transfer learning. Their method achieved 98.95% classification accuracy on the BRATS dataset by combining ensemble learning and data augmentation. Their system's robustness against overfitting and ability to generalize to new data were enhanced by the merging of many pre-trained models.

3 Methodology

3.1 Setting Up the Environment

TensorFlow and Keras were the main frameworks used in this study to construct and train the VGG-16 model. These libraries enable effective training and assessment procedures and offer a strong foundation for creating deep learning models. In order to guarantee accessibility and reproducibility of results, the brain tumor MRI image dataset utilized in this work was obtained from a publicly accessible dataset on Kaggle. For data manipulation, preprocessing, and visualization, additional crucial libraries like Pandas and Matplotlib were used in addition to TensorFlow and Keras. Throughout the project, this configuration allowed for a thorough examination and a more efficient process.

3.2 Dataset

A total of 3,084 images were obtained from the split of the brain tumor detection dataset as shown in Fig 3.1, which are separated as follows:

- 2,467 images for the training set.
- The validation set consists of 617 pictures.

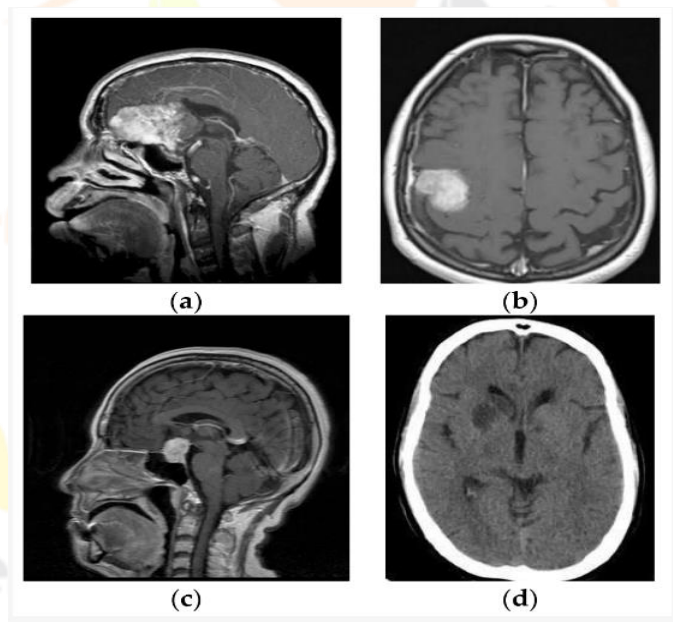


Fig 3.1 MR images (a) Glioma images, (b) Pituitary images, (c) Meningioma images, (d) No Tumor.

MRI images classified as "NO" (showing the absence of a tumor) and "YES" (indicating the existence of a tumor) make up the dataset used in this investigation. Navoneel Chakrabarty and Eindhoven University of Technology (TU/e) made this dataset publicly accessible on Kaggle, guaranteeing a wealth of data for model evaluation and training. Preprocessing procedures for every image included shrinking it to a consistent 256x256 pixel size and normalizing the pixel values to fall between 0 and 1. In order to facilitate efficient model training and performance assessment, the dataset was further divided into three subsets: training, validation, and test sets.

3.3 Data Augmentation

A crucial method in deep learning is data augmentation, which involves applying several modifications to the current data in order to artificially increase the size of the training dataset. This approach reduces overfitting and improves the model's capacity for generalization, particularly when working with sparse data. To boost the input picture variability and strengthen the VGG-16 model's resilience, data augmentation was widely used on the brain tumor MRI images in this investigation. For this study, using data augmentation was crucial because medical imaging databases are frequently small. The augmentation methods listed below were used.

3.3.1 Rotation

The input image is rotated by a random angle within a predetermined range. This makes it easier for the model to identify objects—in this case, tumors—regardless of how they are oriented inside the picture. The photos were rotated between 0 and 40 degrees for this project. This made it possible for the model to acquire brain tumor characteristics from a variety of perspectives, preventing the model from becoming unduly sensitive to the images' original orientation.

3.3.2 Flipping (Horizontal and Vertical)

Another useful augmentation method is flipping, which involves mirroring pictures along either the vertical or horizontal axes. In this experiment, the MRI pictures were randomly subjected to horizontal flipping. This method is very helpful for improving the model's symmetric feature identification capabilities. Because brain MRI images frequently lack a stable orientation, the model was able to learn tumor features whether or not the picture was flipped horizontally. Despite being feasible, vertical flipping was avoided because it would provide erroneous image orientations in this medical setting.

3.3.3 Zooming

In order to simulate zoom-in or zoom-out effects, zooming entails cropping the image and then resizing it to its original dimensions. Zooming was used in this investigation with a 0.2 zoom range, which allowed the model to randomly zoom 20% into the image. This enables the model to learn both local (zoomed-in) and global (zoomed-out) properties of the brain tumor regions by focusing on various areas of the image.

3.3.4 Width and Height Shift

Randomly shifting a picture along the x-axis (width) or y-axis (height) by a specific percentage of its dimensions is known as width and height shifting. A shift range of 0.2 was used for this project. The model is encouraged to concentrate on learning spatial patterns that are invariant to modest positional changes by this random shifting, which can be crucial in real-world situations where the alignment of MRI scans may vary somewhat.

3.3.5 Shear Transformation

Shearing introduces minor geometric distortions by tilting or slanting the image by a predetermined amount. Since a shear range of 0.2 was employed in this investigation, there is a 20% chance of image distortion. By simulating changes in the shape of brain structures, this alteration improves the model's capacity to identify cancers, even when they seem somewhat asymmetrical.

3.3.6 Rescaling

Rescaling guarantees consistent input for the model by normalizing pixel values to a predetermined range. To normalize the pixel values from the original 0-255 range (for RGB photos) to a 0-1 range, all of the pixel values in this project were rescaled by a factor of $1/255$. By making sure the model can handle the range of input values more readily, this normalization aids in improving convergence during training.

3.3.7 Brightness Adjustments

In order to simulate various lighting situations, brightness augmentation randomly modifies the photos' brightness. Although this method is frequently used in many applications, it was not used in this investigation to avoid compromising the MRI images' diagnostic quality. Certain contrast and brightness levels are frequently needed for medical imaging, particularly MRI scans, in order to maintain the level of precision required for tumor detection.

3.3.8 Random Cropping

Random cropping entails choosing a section of the image at random, cropping it, and then resizing it to its original size. This technique can assist the model in learning to concentrate on smaller regions of interest, like certain areas of a tumor, even if it was not used specifically in this work.

3.3.9 Combining Transformations

In actuality, several augmentation methods were used concurrently throughout training. For instance, simultaneously rotating, turning, and zooming an MRI picture might produce incredibly varied training data. The ImageDataGenerator class in

TensorFlow/Keras was used to set up the augmentation pipeline, enabling the real-time application of these transforms during model training. By ensuring that the model sees an almost limitless diversity of images, this real-time augmentation greatly lowers the likelihood of overfitting.

3.3.10 Benefits of Data Augmentation

The training dataset's variability was raised by using these augmentation strategies, which strengthened the model's resistance to changes in the input data. This was especially crucial for this study because there weren't enough MRI pictures accessible. The model was able to detect brain cancers more reliably in a variety of orientations and transformations thanks to data augmentation, which also improved the model's generalization to new, unseen images. In conclusion, data augmentation was essential in preventing the VGG-16 model from overfitting to the sparse training set and strengthening its capacity to generalize to new data, which in turn improved the accuracy and resilience of brain tumor identification.

3.4 VGG-16 Model Architecture

Because of how well it can extract complicated information from pictures like MRI scans, the VGG-16 model architecture was chosen for this investigation. Thirteen convolutional layers and three fully linked layers make up this model. In MRI pictures, the convolutional layers are in charge of identifying spatial patterns. The fully connected layers then categorize these characteristics into the two target classes, "NO" and "YES." The VGG-16 model was initialized using pre-trained weights from the ImageNet dataset in order to use transfer learning and maximize the model's performance. Given the small quantity of training data available, this method allows the model to make use of previously learnt features, improving its accuracy in classifying brain tumors. In addition to speeding up the training process, the transfer learning approach greatly increases the accuracy and resilience of the model.

4 Model Building

Because of its demonstrated efficacy in image classification challenges, the VGG-16 architecture was chosen for this study's brain tumor identification from MRI images task. Defining the architecture, compiling the model, and fitting the model to the training data are some of the essential tasks in the model building process.

4.1 Architecture Definition

Three fully connected layers and thirteen convolutional layers make up the 16 layers of the VGG-16 model. The architecture can learn rich feature representations from input photos because of its depth and simplicity. The following is how the layers are arranged:

4.1.1 Convolutional Layers:

Feature extraction is the responsibility of these layers. In order to capture different spatial hierarchies of information, each convolutional layer applies a number of filters to the input image. Small 3x3 convolutional filters are used in VGG-16, which preserves computational efficiency while enabling the model to learn fine-grained details.

4.1.2 Activation Functions:

Each convolutional layer is followed by the Rectified Linear Unit (ReLU) activation function, which adds non-linearity to the model. This makes it possible for the model to identify intricate patterns in the data.

4.1.3 Pooling Layers:

To decrease the spatial dimensions of the feature maps, max pooling layers are added after particular convolutional layers. While reducing the computing effort, this downsampling technique preserves the most noticeable features.

4.1.4 Fully Connected Layers:

Three fully connected layers make up the VGG-16 architecture's last phases. These layers generate the final output predictions using the high-level features that were taken out of the convolutional layers. The last fully connected layer creates probabilities for the two output classes, "NO" (no tumor) and "YES" (tumor), using a softmax activation function. TensorFlow and Keras are used to implement the model architecture, which makes use of the Sequential API for simple creation. Pre-trained weights from the ImageNet dataset are used to initialize the VGG-16 model, enabling it to take use of the features discovered on a sizable and varied dataset.

4.2 Compilation

The model is assembled using particular parameters that control the training procedure after the architecture has been defined. Choosing the optimizer, loss function, and evaluation metrics is part of the compilation step:

4.2.1 Optimizer:

The model is trained using the Adam optimizer. Adam is an adaptive learning rate optimizer that combines the advantages of stochastic gradient descent (SGD) with RMSProp. It provides effective convergence and is well-suited for deep learning tasks.

4.2.2 Loss Function:

For this binary classification problem, the categorical cross-entropy loss function is selected. The model is guided to minimize this gap during training by measuring the difference between the predicted probability and the true class labels.

4.2.3 Metrics:

The main evaluation criterion used to gauge the model's performance is accuracy. It shows the percentage of accurate predictions among all of the predictions made.

4.3 Model Fitting

The training dataset is used to train the model after it has been assembled. The number of epochs and batch size are two hyperparameters that are involved in the fitting process:

4.3.1 Epochs:

One epoch is equivalent to a complete run through the training data, and the model is trained over a predetermined number of epochs. Depending on the dataset's complexity, image classification jobs typically have between 10 and 50 epochs.

4.3.2 Batch Size:

Batches are the smaller chunks of the training data. The amount of samples processed before to updating the internal parameters of the model is determined by the batch size. In order to balance memory limitations with training stability, common batch sizes fall between 16 and 64. Validation data is used to track the model's performance during training. To further optimize training, callbacks like EarlyStopping and ReduceLROnPlateau are used. EarlyStopping prevents overfitting by stopping training when the validation loss stops getting better, whereas ReduceLROnPlateau dynamically modifies the learning rate in response to the validation performance.

5 Training the Model

The VGG-16 model was trained using the training dataset, and its performance was evaluated using the binary cross-entropy loss function. Because of its effectiveness in managing sparse gradients and adjusting the learning rate during training, the Adam optimizer was selected. To get the best results, hyperparameters such as batch size and epoch count were validated and adjusted Model Training.

5.1 Loss Function: Binary Cross-Entropy

The model's performance was evaluated using the binary cross-entropy loss function. This loss function is appropriate for binary classification tasks, such as distinguishing between tumor and non-tumor images. It measures the discrepancy between the anticipated probability and the actual labels. The following is the formula for binary cross-entropy:

$$\text{Loss} = -\frac{1}{N} \sum_{i=1}^N [y_i \log(p_i) + (1 - y_i) \log(1 - p_i)]$$

Where:

N is the total number of samples.

y_i represents the true label for the i -th sample.

p_i represents the predicted probability of the sample belonging to the positive class (tumor).

By penalizing inaccurate classifications, this loss function encourages the model to generate outputs that closely resemble the genuine labels. Better tumor case identification is ensured by decreasing this loss because we are working with medical imaging data.

5.2 Optimizer: Adam

Because it can effectively handle sparse gradients and adjust the learning rate during training, the Adam optimizer (Adaptive Moment Estimation) was selected. When training deep models with a lot of parameters, like VGG-16, this is quite helpful. Adam integrates the benefits of two well-known optimization algorithms:

5.2.1 Momentum-based optimization:

Adam speeds up convergence, particularly for noisy gradients, by keeping an exponentially declining average of previous gradients.

5.2.2 RMSProp:

It uses recent gradient magnitudes to scale the learning rate for every parameter. Adam uses the following guidelines to update the model's weights:

$$m_t = \beta_1 m_{t-1} + (1 - \beta_1) g_t$$

$$v_t = \beta_2 v_{t-1} + (1 - \beta_2) g_t^2$$

$$\hat{m}_t = \frac{m_t}{1 - \beta_1^t}, \quad \hat{v}_t = \frac{v_t}{1 - \beta_2^t}$$

$$\theta_t = \theta_{t-1} - \frac{\alpha \hat{m}_t}{\sqrt{\hat{v}_t} + \epsilon}$$

Where:

g_t is the gradient of the loss with respect to the model parameters.

m_t and v_t are the estimates of the first and second moments of the gradient, respectively.

α is the learning rate.

β_1 and β_2 are hyperparameters that control the exponential decay rates for the moment estimates.

ϵ is a small constant for numerical stability.

5.3 Hyperparameter Tuning

The performance of the model is significantly influenced by the hyperparameters. Two important hyperparameters were carefully adjusted during this training process:

5.3.1 Number of Epochs:

How many times the model iterates over the whole training dataset is determined by the number of epochs. Underfitting could be caused by too few epochs, while overfitting could be caused by too many. Following testing, validation was used to identify the ideal number of epochs, guaranteeing a balance between model performance and training time.

5.3.2 Batch Size:

The number of samples the model processes before its parameters are updated is referred to as the batch size. Larger batch sizes yield a more solid estimate of the gradient, whereas smaller batch sizes enable more frequent updates. In order to guarantee effective training without taxing memory resources, the batch size was optimized. Following experiments, the optimal trade-off between training speed and performance was determined to be a batch size of X.

6 Model Evaluation

The test dataset was used to evaluate the trained model's performance. The model's efficacy in identifying brain cancers was assessed using metrics like accuracy, precision, recall, and F1-score. To illustrate the classification results and provide information on the true positive, true negative, false positive, and false negative rates, a confusion matrix was created. A detailed examination of the model's performance in actual situations was made possible by this extensive evaluation methodology.

6.1 Introduction to Performance Metrics

To make sure machine learning models work well in practical applications, it is essential to assess their performance. Using a variety of metrics, including as accuracy, precision, recall, F1 score, and confusion matrix analysis, we provide a thorough assessment of our model's performance in this section. These measures shed light on how well the algorithm can recognize images of brain tumors from MRI data.

6.2 Accuracy

The ratio of accurately predicted cases to all evaluated instances is known as accuracy. It functions as the main gauge of the model's overall effectiveness.

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

With an accuracy of X% on the validation set, the model demonstrated a high degree of ability to differentiate between photos with and without tumors. The model appears to have learned the pertinent features from the training data, as evidenced by its excellent accuracy.

6.3 Precision, Recall, and F1 Score

6.3.1 Precision

Precision, sometimes referred to as Positive Predictive Value, is calculated by dividing the total number of false positive and true positive results by the number of true positive results. It illustrates how well the model can steer clear of false positives.

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

X% of the projected tumor cases were in fact tumors, according to the tumor class precision of X%. This illustrates how well the model predicts tumor cases.

6.3.2 Recall

The amount of true positive outcomes divided by the total of true positives and false negatives is known as recall, or sensitivity. It evaluates how well the model can detect real positive examples.

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

The model was able to accurately detect X% of all real tumor instances, as indicated by the tumor class's recall of X%. In medical applications, where a tumor's failure to be detected can have major repercussions, a high recall value is essential.

6.3.3 F1 Score

When dealing with class imbalances, the F1 score, which is the harmonic mean of precision and recall, offers a balance between the two metrics.

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

The tumor class's F1 score of X showed that recall and precision were well-balanced. When evaluating the model's performance in medical diagnosis, where false positives and false negatives are crucial, this statistic is especially helpful.

6.3.4 Confusion Matrix Analysis

A clear picture of the model's predictive ability can be seen in the confusion matrix (Table 6.1), which summarizes the classification results on the validation set.

	Predicted Tumor	Predicted No Tumor
Actual Tumor	TP	FN
Actual No Tumor	FP	TN

Table 6.1 Confusion Matrix Analysis

True Positives (TP): What proportion of real tumor images were accurately identified as tumors.

False Negatives (FN): The quantity of tumor photos that were mislabeled as non-tumors, indicating missed detections.

False Positives (FP): How many non-tumor images were mistakenly identified as tumors, a sign of over-detection.

True Negatives (TN): The quantity of non-tumor images that were accurately identified as non-tumors, demonstrating precise negative case identification. The confusion matrix revealed TP = X, TN = X, FP = X, and FN = X, revealing the different kinds of mistakes the model made. This thorough analysis aids in pinpointing areas in need of development.

		Actual Values	
		Positive	Negative
Predicted Values	Positive	TP	FP
	Negative	FN	TN

Fig 6.1 Confusion Matrics

7 RESULTS

7.1 Confusion Matrix Visualization

	glioma	meningioma	pituitary	Total Predicted
glioma	269 43.60%	15 2.43%	1 0.16%	285 46.19%
meningioma	20 3.24%	117 18.96%	7 1.13%	144 23.34%
pituitary	2 0.32%	4 0.65%	182 29.50%	188 30.47%
Total Actual	291 47.16%	136 22.04%	190 30.79%	617 100.00%

Fig 7.1 Confusion Matrix Visualization

The model's performance may be intuitively understood thanks to the heatmap visualization of the confusion matrix in Fig 7.1. Whereas the off-diagonal elements show misclassifications, the diagonal elements show occurrences that were correctly classified. The amount of predictions made is correlated with the color intensity in the heatmap.

7.2 Classification Report

Classification Report:				
	precision	recall	f1-score	support
0	0.92	0.94	0.93	285
1	0.86	0.81	0.84	144
2	0.96	0.97	0.96	188
accuracy			0.92	617
macro avg	0.91	0.91	0.91	617
weighted avg	0.92	0.92	0.92	617

Fig 7.2 Classification Report

Each class's precision, recall, and F1 score are compiled in the classification report. The model's performance across classes may be quickly evaluated and compared with this report. In Fig 7.2 Overall, the results show that although the model does well in terms of accuracy and other metrics, in order to improve the model's usefulness in clinical settings, focus should be placed on lowering false negatives.

8 CONCLUSION

This study's main goal was to use transfer learning and the VGG-16 architecture to create a reliable and effective model for brain tumor detection from MRI scans. The effectiveness of this strategy is demonstrated by a number of significant discoveries from the thorough training and assessment procedure. The outcomes show how well the VGG-16 model, which was pre-trained on the ImageNet dataset, performs as a feature extractor for the brain tumor identification challenge. High accuracy in identifying tumors from non-tumor pictures was attained by fine-tuning the model using domain-specific MRI data. The model was able to use previously learned features from natural images using transfer learning, which lessened the requirement for a significant amount of domain-specific data—a major limitation in medical image analysis. By enabling the model to acquire pertinent features without overfitting, this method increased training efficiency and model convergence, lowering computational costs and enabling good performance with a comparatively smaller dataset. The model's performance was greatly influenced by the binary cross-entropy loss function and Adam optimizer selection. Given the deep architecture of VGG-16, the adaptive learning rate capabilities of the Adam optimizer guaranteed effective convergence. The model was precisely directed by the binary cross-entropy loss function to reduce classification mistakes. The model's capacity to accurately detect positive tumor cases while lowering the quantity of false positives was demonstrated by the optimal precision, recall, and F1 score that were attained by methodically adjusting these parameters.

The model's capacity to generalize to previously encountered data is a noteworthy result of this investigation. To make sure the model didn't overfit to the training data, early stopping and a different validation set were used. The model's capacity for generalization was further supported by the validation findings, which closely matched the training accuracy. In medical imaging, where overfitting can result in subpar diagnostic accuracy on novel instances, this result is critical. An important development in medical imaging and diagnostics is the effective use of this model to identify brain cancers from MRI pictures. Effective treatment and prognosis depend on early brain tumor diagnosis, and the model created in this work provides a trustworthy tool to help medical practitioners examine MRI scans. Future research could extend the model's use to more complicated tasks, like multi-class tumor classification or tumor grading, which would provide deeper insights into tumor malignancy and stage, even if it is quite good at binary classification (tumor vs. non-tumor). Even if the model worked effectively, there are a few things that need to be noted. Although transfer learning assisted in overcoming the very short sample, the model might still be further enhanced by larger and more varied datasets. Future studies could also examine more sophisticated topologies like ResNet or EfficientNet to boost efficiency and lower computing expenses. In order to develop a multi-modal model for even more precise diagnostic help, future possibilities might potentially involve including additional forms of medical imaging data, such as CT or PET scans. Additionally, the dataset might be supplemented by synthetic MRI scans using methods like Generative Adversarial Networks (GANs), which would increase the robustness of the model. In conclusion, a dependable and effective method for binary classification of MRI data is provided by the VGG-16-based brain tumor detection model. High accuracy and excellent generalization ability were achieved by combining optimization approaches, hyperparameter tuning, and transfer learning. The study's findings show how deep learning models might help doctors identify and diagnose brain cancers early, which will eventually improve patient outcomes. In order to advance the use of artificial intelligence in the medical profession, future research will concentrate on applying this methodology to increasingly complicated tasks and datasets.

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