Enhanced Brain Tumor Detection: Integrating Deep Learning with Chatbot Support

Team 8

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AIT 736 – DL1 (Spring 2024), Applied Machine Learning

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November 3, 2024

CHAPTER 1
INTRODUCTION

1.1 Objective

Brain tumors are known to be deadly diseases, just like many other illnesses that can kill people. For the condition to be treated, an early diagnosis is crucial. This project's primary goal is to create a system that can identify whether a human brain has a tumor by employing convolutional neural networks, which make it simple and highly accurate to identify an infected brain.

1.2 Introduction

A brain tumor is an abnormal growth of cells within the brain or skull that can be benign (non-cancerous) or malignant (cancerous). Tumors can either originate in the brain (primary tumors) or spread from other parts of the body (metastatic tumors). Treatment approaches vary depending on the tumor's type, size, and location, with goals that range from cure to symptom management. Among the 120+ types of brain tumors, many are treatable, and advancements in therapies are improving patient survival and quality of life.

Primary brain tumors start within the brain and usually don't spread to other parts of the body, though they can still pose serious risks if they affect critical areas. Malignant tumors grow rapidly, have irregular borders, and can invade nearby brain regions, causing symptoms like persistent morning headaches, abnormal eye movements, and visual difficulties. Metastatic brain tumors, on the other hand, develop when cancer from different organs, such as the lungs or breasts, spreads to the brain. These tumors can cause damage by destroying or compressing healthy tissue and raising intracranial pressure, with symptoms varying based on the tumor's type, size, and location. Early diagnosis improves the chances of survival.

1.3 Motivation

Brain Tumor and other CNS (Central Nervous System) cancers are the 10th most significant cause of mortality in both men and women. It is anticipated that 18,280 people in the US will die from primary malignant brain and central nervous system tumors this year (10,710 men and 7,570 women). An estimated 251,329 people worldwide lost their lives to primary malignant brain and central nervous system tumors in 2020. Therefore, it is essential to thoroughly diagnose a condition based on scientific data to save the patient's life by implementing early measures. Quickly and efficiently, this model will let the person determine whether or not a brain tumor impacts them.

1.4 Scope for the Work

Expert radiologists have historically examined patient brain MRIs to identify the existence of brain tumors, a procedure that can take a long time. Deep learning has the potential to significantly accelerate diagnostics in this area. Automated diagnostic systems can be developed using convolutional networks and pre-trained models such as VGG16, VGG19, and Densenet, considerably speeding up the detection process. The speed and effectiveness of brain tumor identification are improved by these automated technologies. Nevertheless, the proposed algorithm can only identify brain cancers from the provided brain MRI image.

CHAPTER 2
PROJECT OVERVIEW

2.1 Description of the project

The project aims to detect the presence of tumors in the Human Brain. We detected the presence of tumors by employing VGG16, VGG19, and Densenet models from the Keras package, part of Deep Learning. As shown in the flow diagram, various methods are implemented, such as data pre-processing, model training, and model testing.

2.1.1 Flow Diagram

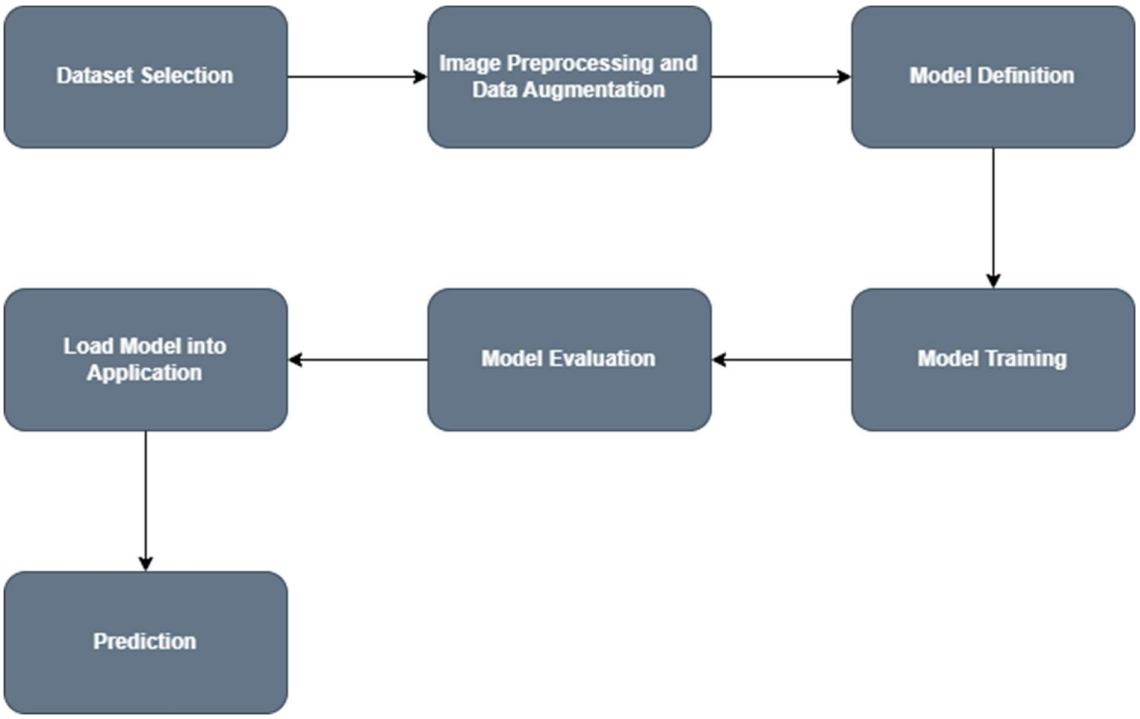

Fig: 2.1.1 Model Flowchart

The above figure depicts the flowchart of the model employed in this project, including Data Acquisition, Data Pre-processing, Model Training, Model Testing, Validation loss, Accuracy Metrics, and finally, Model Evaluation for the test data.

2.2 Brain Tumor

A brain tumor is a growth of abnormal cells in the brain that can be either malignant (cancerous) or benign (non-cancerous). Despite being benign, brain tumors can still cause severe issues due to the skull's rigidity; as the tumor grows, it presses on parts of the brain, affecting functions like thinking, behavior, and sensation, depending on its location. Tumors that originate in the brain are known as primary brain tumors, with meningiomas and gliomas being the most common types. Secondary brain tumors, or metastases, occur when cancer spreads to the brain from other organs, like the lungs or skin.

Brain tumor symptoms vary based on the tumor's type and location, potentially causing unusual behavior, confusion, balance issues, vision and hearing problems, nausea, and seizures. Brain tumors can affect people of any age, but they are most common in older adults and children. Tumors in the brain are a leading cause of cancer-related death in children under 14

and a common cancer in young adults aged 15 to 39. The median age for primary brain tumor diagnosis in adults is 59, with symptoms and types often differing between adults and children.

2.2.1 How are brain tumors detected?

Doctors use various tests to diagnose a brain tumor, determine its type, and check if it has spread from another part of the body. For primary brain tumors, this spread (metastasis) is rare. Imaging tests, like MRI and CT scans, are essential in diagnosis, providing internal images of the body to help identify the tumor's nature. An MRI is typically the first test to detect a brain tumor, offering detailed images through magnetic fields rather than X-rays.

MRIs are preferred over CT scans due to their higher image quality, especially for diagnosing brain tumors. An MRI can show the tumor's size and may involve a contrast dye to enhance clarity. CT scans, which use X-rays, create a 3D image and can help detect bleeding, fluid-filled spaces, and bone changes in the skull. While MRIs are more detailed, CT scans can be helpful for specific observations, such as detecting bleeding or ventricular enlargement.

CHAPTER 3
METHODOLOGY

3.1 Data Preparation

3.1.1 Data Description

One of the most severe conditions that can impact both adults and children is a brain tumor. Brain tumors make for 85 to 90 percent of all occurrences of primary Central Nervous System (CNS) malignancies. Every year, over 11,700 patients receive a brain tumor diagnosis. The 5-year survival rate for individuals with a malignant brain or central nervous system tumor is approximately 36% for women and 34% for men. Brain tumors are divided into benign, malignant, pituitary, and other categories. Appropriate treatment, preparation, and accurate diagnosis should be used to extend the patient's life expectancy. Magnetic resonance imaging, or MRI, is the best technique for identifying brain cancers. The scans produce an enormous amount of picture data.

For our study, we've chosen the Brain tumor dataset from Kaggle. This dataset contains **7023** images of human brain MRI images, which are classified into four classes:

Glioma, **meningioma**, **no tumor** and **pituitary**.

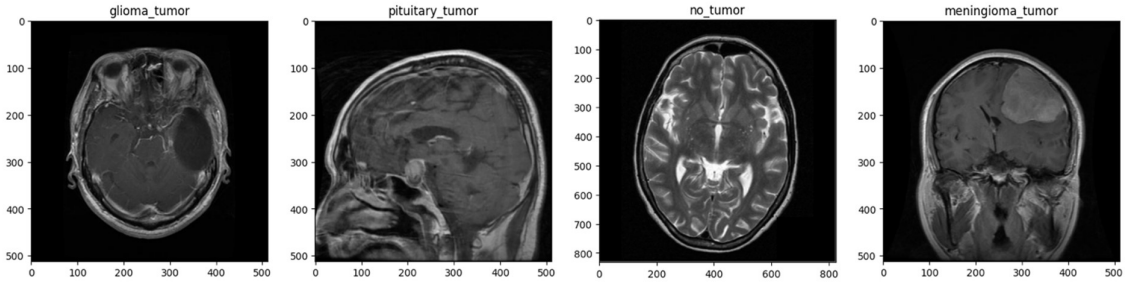

Fig 3.1.1: Images in the dataset

3.1.2 Data Pre-processing

To optimize the performance of our deep learning model, we implemented a series of data preprocessing and augmentation techniques, as detailed below.

To prepare our images for training, we applied several preprocessing steps:

Image Rescaling: All images were rescaled by a factor of 1/255 to normalize the pixel values. This step converts the original pixel values, which range from 0 to 255, into a scale between 0 and 1, making the data suitable for training deep learning models and ensuring faster convergence.

Image Resizing: The MRI images were resized to 224x224 pixels to match the input size requirements of our deep learning models, such as VGG16. Consistent image size helps maintain uniformity and efficiency during training.

Data Augmentation

We used data augmentation to artificially increase the diversity of our training dataset and reduce overfitting. By introducing random transformations, the model can generalize better to unseen data. Our data augmentation techniques included:

Rotation: Images were randomly rotated within a range of 20 degrees to make the model robust to the orientation of tumors.

Width and Height Shifts: We applied random horizontal and vertical shifts of up to 20% of the image size to account for positional variations in the MRI scans.

Shear Transformation: A shear range of 0.2 was used to distort the images slightly, simulating different viewing angles and shapes of tumors.

Zoom: Random zooming in and out by 20% helped the model learn features at different scales.

Horizontal Flip: We included horizontal flipping to address symmetry variations, further improving the model's generalization capabilities.

Data Generators

We created separate data generators for training, validation, and testing:

Training Data Generator: This generator incorporated all the augmentation techniques mentioned above to train the model on diverse images.

Validation and Testing Data Generators: These generators only rescaled the images, without augmentation, to accurately evaluate the model's performance on unseen data.

This comprehensive data preprocessing and augmentation approach ensures our model is well-trained, generalizes effectively, and can perform highly in classifying brain tumor types.

3.2 Splitting the Dataset

Before sending the dataset to the model for training, it must be separated into training and testing data. The training data is given to the model to be trained, and the testing data is used to evaluate the model's performance on the final data. The training data is then divided into training and validation data once more. For each epoch, the model is trained on the training data before being tested on the validation data. When the model's performance or accuracy is low, it adjusts its parameters or tunes itself to improve performance and reduce loss. The dataset is split into train, test, and validation data.

3.3 Model Training

3.3.1 Model Selection

In this project, we have used Deep Learning techniques to detect the presence of tumors in the human brain. Various pre-trained models are available in deep learning, and they are available using Keras Library. The table below depicts the multiple models available in Keras.

We have studied many papers and developed three models that perform well for this project. They are VGG16, VGG19 and Densenet. Now, let us take a look at all of these models.

3.3.2 VGG16

ImageNet, a massive visual database project used in visual object recognition software research, uses VGG16, a simple and widely used Convolutional Neural Network (CNN) Architecture. Karen Simonyan and Andrew Zisserman of the University of Oxford created and launched the VGG16 Architecture in their article "Very Deep Convolutional Networks for Large-Scale Image Recognition" in 2014. The term 'VGG' stands for Visual Geometry Group, a group of scholars at the University of Oxford who designed this architecture, and the number '16' indicates that there are 16 layers in this architecture.

In ImageNet, a dataset of over 14 million images belonging to 1000 classes, the VGG16 model obtained 92.7 percent top-5 test accuracy. In 2014, it was one of the well-known models submitted to the ImageNet Large Scale Visual Recognition Challenge (ILSVRC). It outperformed AlexNet by substituting giant kernel-sized filters (11 and 5 in the first and second convolutional layers, respectively) with multiple three kernel-sized filters one after the other. NVIDIA Titan Black GPUs were used to train VGG16 for weeks.

Many deep-learning image classification methods use VGG16, which is popular due to its ease of use. Because of its advantages, VGG16 is often employed in learning applications. VGG16 is a CNN Architecture, which was used to win the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) in 2014. It is still one of the best vision architectures to date.

3.3.3 VGG19

The Visual Geometry Group at the University of Oxford, led by Karen Simonyan and Andrew Zisserman, developed the VGG19 architecture to expand the VGG16 architecture. VGG19, first presented in their 2014 paper "Very Deep Convolutional Networks for Large-Scale Image Recognition," has 19 layers. Like VGG16, it gained impressive performance with a top-5 accuracy of 92.7% after being trained on ImageNet, a vast dataset containing over 14 million images in 1,000 classes. By incorporating extra layers, the architecture expands on the VGG16 model and enables it to recognize even more intricate picture patterns. Like VGG16, VGG19 improved feature learning while maintaining computing efficiency by substituting successive 3x3 filters for massive kernel-sized filters. Applications for feature extraction and picture classification extensively use VGG19, a benchmark architecture in deep learning.

3.3.4 Densenet

DenseNet (Dense Convolutional Network) is a unique deep learning architecture introduced by Gao Huang and his team in their 2017 paper, "Densely Connected Convolutional Networks." Unlike traditional architectures, DenseNet connects each layer to every other layer in a dense manner, allowing feature reuse across layers. This densely connected structure helps improve gradient flow, reduces the number of parameters, and makes the model highly efficient. DenseNet achieved state-of-the-art performance on several image classification tasks, including on datasets like ImageNet and CIFAR-10, due to its ability to learn more compact representations and efficiency. The model has become popular in applications that require deep networks without excessive computational costs, making it suitable for real-time applications such as medical image analysis. DenseNet's innovative connectivity makes it one of the most effective architectures for deep learning in vision tasks.

3.4 Llama Model Integration

Our initiative incorporates the Meta Llama 3.1-8B Instruct model, particularly the Q4_K_M GGUF variant. This model is tailored for instruction-based tasks, rendering it ideal for producing precise and informative responses in medical scenarios. The extensive architecture of the Llama model allows it to deliver nuanced and comprehensive answers, which is especially important in healthcare settings where accuracy and contextual understanding are vital.

3.4.1 Functionality and Usage in the Project

In our application, the Llama model drives the chatbot functionality, which offers users comprehensive explanations, concise summaries, and responses to subsequent questions related to brain tumor diagnostics. This arrangement enhances the interactivity of the user experience, allowing the system to address medical queries in real time and improving accessibility and user engagement.

3.4.2 LM Studio

LM Studio is the platform we utilize to manage and operate the Llama model on our local systems. It simplifies large language models' deployment and fine-tuning processes by offering an intuitive interface for setting configurations, selecting models, and managing API endpoints.

The integrated server features of LM Studio enhance the incorporation of Llama into our applications, allowing for compelling local inference without dependence on cloud services—crucial for maintaining privacy and optimizing performance in healthcare settings.

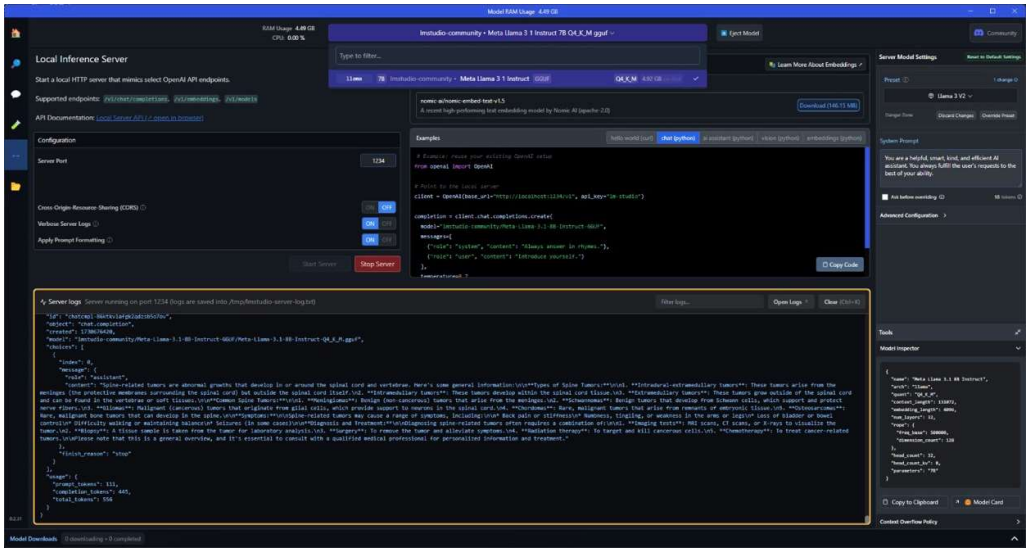

Fig: 3.5.2.1 Llama integration with LM studio

3.5 Web Application using Flask

The project focuses on developing a web application to classify brain tumors based on MRI scans, utilizing a deep learning model trained to identify four categories: Glioma, Meningioma, Pituitary Tumor, and No Tumor. Utilizing the Flask framework, the application enables users to upload their MRI images, which are then processed and analyzed using a pre-trained DenseNet model stored as `brain_tumor_detection_model.h5`. The model provides predictions regarding the type of tumor present and showcases the results to the user. Additionally, a feature allows users to test the model using a random MRI image from a selected collection. Before inputting the images into the model, they are resized to 224x224 pixels and normalized. The app displays the predicted type of tumor next to the uploaded or sample image, creating an intuitive platform for brain tumor identification and potentially assisting in initial diagnostic evaluations.

This Brain Tumor Prediction web application is designed to offer an engaging and user-friendly interface for analyzing MRI images to detect brain tumors. The application presents a professional appearance with an interactive layout featuring a collage of MRI scans. Its primary

function is to allow users to upload their MRI images, which are subsequently processed for tumor classification. Using a predictive model, the application analyzes these images to provide a streamlined and accessible method for preliminary tumor detection.

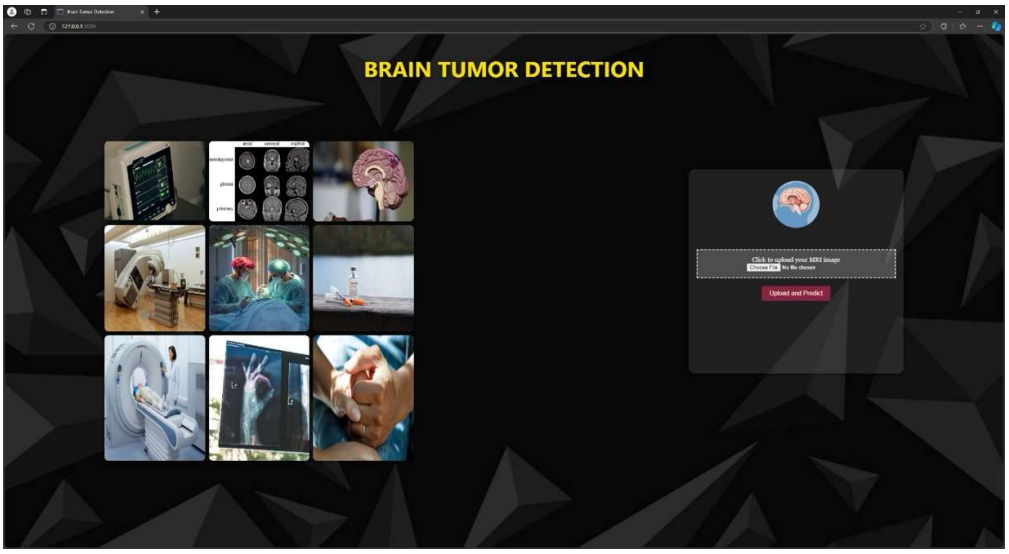

Fig: 3.5.1 Home page

The results page displays the outcome of the tumor prediction model, highlighting important information regarding the tumor type. Users can view their uploaded MRI scan on this page for reference. Additionally, a chatbot is available for interaction, enabling users to inquire about the prediction results or request more details about tumor characteristics.

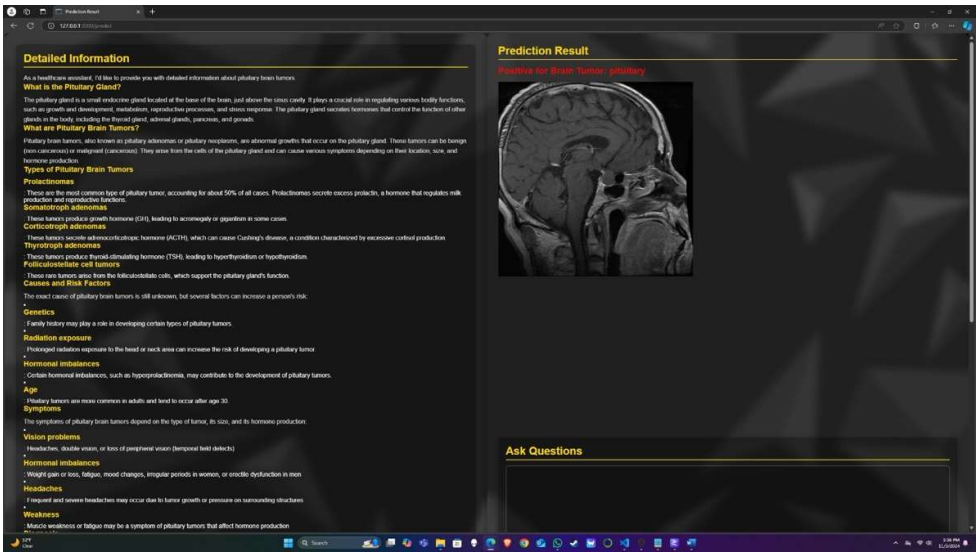

Fig: 3.5.2 Result page

CHAPTER 4

RESULTS AND DISCUSSIONS

4.1 Evaluation Metrics

4.1.1 Model Testing

The model is trained, and now it is time to send that model into the testing phase. The weights are adjusted in the training phase to get maximum performance. As the model is trained with VGG16, VGG19, and DenseNet, we have to test these models with the test dataset, which is a part of the dataset split during training. The evaluation metrics are analyzed after the model is tested on the test data.

4.1.2 Findings of Evaluation Metrics

The VGG16 model demonstrated strong performance in classifying brain tumors, achieving a high test accuracy of 93.82% and a low test loss of 0.178, indicating effective generalization to new data. The model's precision, recall, and F1 scores across classes were consistently high, with % overall accuracy of 94%. It excelled in identifying no-tumor cases with perfect recall and an F1-score of 0.99 while performing well on pituitary tumors. However, there is room to improve recall for glioma cases, which currently stand at 0.85. The ROC-AUC scores further highlight the model's discriminative capability, with AUC values of 0.99 for glioma, 0.98 for meningioma, and perfect scores of 1.00 for no-tumor and pituitary, demonstrating the model's ability to differentiate between classes effectively.

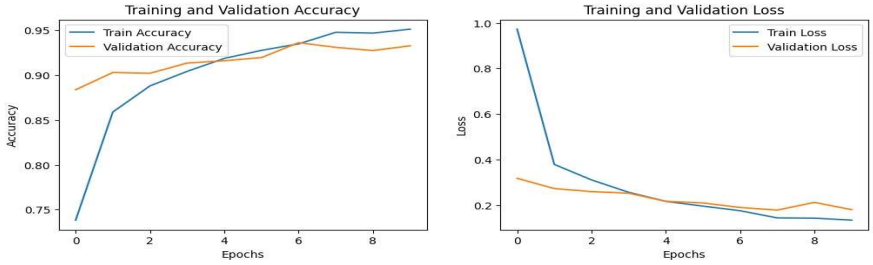

Fig: 4.1.2.1 VGG16-Training Accuracy and Validation Accuracy

```
41/41 ━━━━━━━━━━━━━━━━━━━━ 43s 1s/step - accuracy: 0.9066 - loss: 0.2479
Test Loss: 0.17869001626968384
Test Accuracy: 0.9382150769233704
```

Fig: 4.1.2.2 VGG16-Testing Accuracy and Test Loss

```
Classification Report:
              precision    recall  f1-score   support

      glioma       0.96      0.85      0.90       300
  meningioma       0.86      0.90      0.88       306
     notumor       0.98      1.00      0.99       405
   pituitary       0.95      0.98      0.96       300

    accuracy                           0.94      1311
   macro avg       0.94      0.93      0.93      1311
weighted avg       0.94      0.94      0.94      1311
```

Fig: 4.1.2.3 VGG16-Classification report

The VGG16 model shows exceptional reliability, especially in cases where precise identification is critical. Its balanced and consistent metrics make it a robust tool for brain tumor classification, though minor improvements in recall for specific classes could enhance overall performance further.

The VGG19 model demonstrated robust performance with a test accuracy of 93.44% and a low test loss of 0.174, indicating effective learning and strong generalization to unseen data. The training and validation accuracy curves show steady improvement and convergence, while the loss curves confirm minimal overfitting, highlighting the model's stability during training. The classification report reveals high precision, recall, and F1 scores across all classes, with an overall accuracy of 93%. The model performed exceptionally well in detecting cases with no tumor (perfect recall of 1.00 and an F1-score of 0.99) and showed reliable performance for glioma and pituitary tumors.

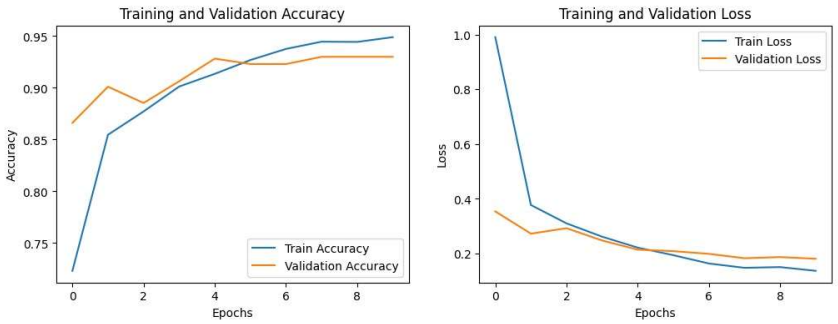

Fig: 4.1.2.4 VGG19-Training Accuracy and Validation Accuracy

```
41/41 ━━━━━━━━━━━━━━━━━━━━ 56s 1s/step - accuracy: 0.9208 - loss: 0.2088
Test Loss: 0.17425420880317688
Test Accuracy: 0.9344012141227722
```

Fig: 4.1.2.5 VGG19-Testing Accuracy and Test Loss

Classification Report:

	precision	recall	f1-score	support
glioma	0.90	0.92	0.91	300
meningioma	0.90	0.83	0.86	306
notumor	0.97	1.00	0.99	405
pituitary	0.95	0.97	0.96	300
accuracy			0.93	1311
macro avg	0.93	0.93	0.93	1311
weighted avg	0.93	0.93	0.93	1311

Fig: 4.1.2.6 VGG19-Classification report

The recall for meningioma was slightly lower at 0.83, which suggests an area for potential improvement. The macro and weighted precision, recall, and F1-score averages at 0.93 each confirm balanced performance across classes. Overall, the VGG19 model is highly effective for brain tumor classification, though further fine-tuning could enhance recall for more challenging cases like meningioma.

The DenseNet model achieved excellent performance with a fine-tuned test accuracy of 95.04% and a test loss of 0.151, demonstrating strong generalization and practical learning. The training and validation accuracy graphs show consistent improvements, with both metrics converging near 95%, while the loss curves reflect a steady decline, indicating minimal overfitting. The model's structure, which leverages dense connections for efficient feature learning, contributed to these results.

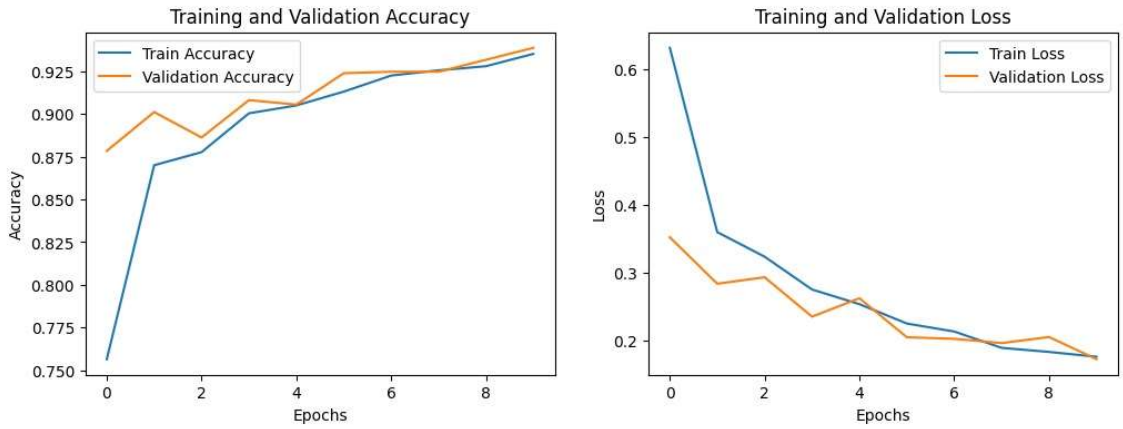

Fig: 4.1.2.7 DenseNet - Before Tuning

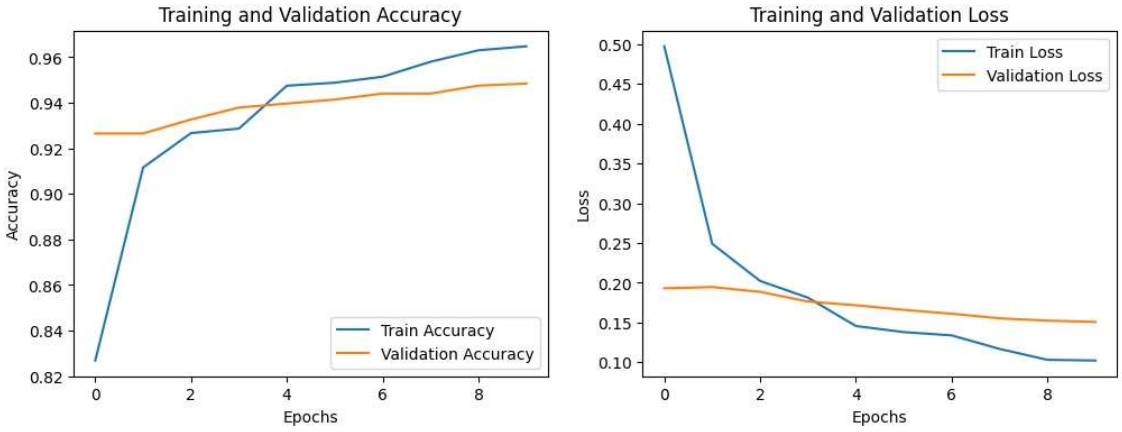

Fig: 4.1.2.8 DenseNet - After Tuning

```
Fine-tuned Test Loss: 0.1512228548526764
Fine-tuned Test Accuracy: 0.9504195451736455
```

Fig: 4.1.2.9 DenseNet-Testing Accuracy and Test Loss

The classification report highlights balanced and robust performance across all tumor classes. Precision, recall, and F1-scores for each class are above 0.90, with exceptionally high scores for no-tumor and pituitary cases (F1-scores of 0.99 and 0.98, respectively). The overall accuracy, macro average, and weighted average F1-scores all stand at 0.95, underscoring the model's reliability and suitability for brain tumor classification tasks.

```
Classification Report:
              precision    recall  f1-score   support

      glioma       0.96      0.90      0.93       300
  meningioma       0.88      0.91      0.90       306
     notumor       0.98      0.99      0.99       405
   pituitary       0.97      0.98      0.98       300

    accuracy                           0.95      1311
   macro avg       0.95      0.95      0.95      1311
weighted avg       0.95      0.95      0.95      1311
```

Fig: 4.1.2.10 DenseNet-Classification report

4.2 Discussions and Final Thoughts

Our project used MRI images to successfully leverage advanced deep learning models VGG16, VGG19, and DenseNet for brain tumor classification. All models demonstrated high accuracy, with DenseNet achieving the best performance at 95.04% test accuracy, followed closely by VGG19 and VGG16. The consistent reduction in training and validation loss, coupled with solid precision, recall, and F1 scores across classes, highlights the models' robust learning and generalization capabilities. The confusion matrix showed minimal misclassifications, further supporting the models' reliability. Overall, our results indicate that these models provide effective and efficient tools for brain tumor detection, with DenseNet's efficient feature reuse making it particularly impactful. Future work could explore optimizing recall for challenging cases and implementing real-time diagnostic systems to support medical professionals.

CHAPTER 5
CONCLUSION AND FUTURE SCOPE

5.1 Conclusion

The project involved collecting the data set and processing the collected data into various categories. Later, deep learning algorithms run on the pre-processed data to classify the disease that might have occurred to the patient. The project's purpose has been to assist the doctors with quick reference and get quick reports using the predictions as outputs generated by the model we designed. Lack of awareness and post-identification of disease will be the primary reason for higher death rates. Brain Tumor has recently become a significant public health concern in our culture. Advanced approaches for predicting this disease are used in this project. Deep learning is a new branch of artificial intelligence that has shown promise in improving the accuracy of medical diagnosis in all domains.

5.2 Future Scope

This model design, which acts as a computer-aided diagnosis, will be a perfect solution for all kinds of people to diagnose with accurate results. This system will not be an ideal replacement for professional doctors. Still, this aid will help them a lot by assisting practitioners in making a perfect decision by analyzing patient reports. Sometimes, practitioners may make some mistakes so that it will act as a better remedy for the current medical environment.

As we used VGG16, VGG19, and DenseNet, DenseNet yielded better results than VGG16, and with advanced methods such as GANs and Capsule Networks, the accuracy can be further increased. It can be detected in a very short interval of time.

This model can also be deployed as a web application so all lab practitioners worldwide can use it. Also, only Windows software can be made, as most poor countries still face many internet issues. It will benefit them, as the internet is not always available for most poorer countries.

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