Developing Brain Tumor Detection Application using Convolutional Neural Network (CNN)

Submitted in partial fulfillment of the requirements for the degree

of

Bachelor of Science in Information and Communication Engineering

by

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APPROVAL

This is to certify that the entitled **Developing Brain Tumor Detection Application using Convolutional Neural Network (CNN)**, submitted by Tawsif Ahmed (Student ID: 211-50-054), Raihan Ahmed Hridoy (Student ID: 211-50-050) and Mohammad Sabbir Bhuiyan (Student ID: 211-50-051) are undergraduate students of the Department of ICE has been examined. Upon recommendation by the examination committee, we hereby accord our approval of it as the presented work and submitted report fulfill the requirements for its acceptance in partial fulfillment for the degree of *Bachelor of Science in Information and Communication Engineering*.

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We, Tawsif Ahmed, Raihan Ahmed Hridoy and Mohammad Sabbir Bhuiyan hereby declare

that this capstone project titled Developing Brain Tumor Detection Application using

Convolutional Neural Network (CNN) is entirely our own work, unless otherwise referenced

or acknowledged. The content of this project is the result of our own research and efforts, and

we have complied with all ethical guidelines and academic standards.

We are aware of the consequences of academic dishonesty and understand that any violation

of ethical standards in this project may lead to disciplinary actions as defined by Daffodil

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iii

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ABSTRACT

Brain tumors constitute a significant problem in medical diagnostics, demanding the development of sophisticated computational techniques for precise and fast identification. This study introduces a prediction paradigm for brain tumor diagnosis, using the capabilities of Convolutional Neural Networks (CNN). A complete dataset of 2563 MRI scans, categorized into four types - Glioma, Meningioma, Pituitary, and No Tumor, formed the basis for the model development. Various CNN architectures, including AlexNet, VGG-16, ResNet, DeepLab, and Inception V3, underwent thorough evaluation. This study generates comprehensive mathematical notation that have been introduced for all the models. The AlexNet model performed quite well in feature extraction and classification for this challenge, with an accuracy of 68%. With an accuracy of 80%, the VGG16 model fared better than the others, showcasing its ability to handle intricate picture data and offer a strong feature hierarchy. ResNet outperformed VGG16, but it still managed to attain a 70% accuracy rate thanks to its deep design and residual connections that prevented disappearing gradients. Finally, a 90% accuracy rate has been achieved by the DeepLab model, demonstrating its promise but also pointing to its limits in terms of tailoring to the particular needs of tumor categorization. Inception V3 was identified as the most effective model because of its exceptional ability to discern complex patterns in medical imaging datasets. We get 92% accuracy using Inception V3. If we compare with other models inception V3 gives us potential and highest accurate results. Comprehensive preparation techniques, including data cleaning and augmentation, were used to improve the dataset and optimize the training procedure. The prediction system was implemented as an interactive web-based application using Flask and Streamlit, enabling real-time analysis of user-uploaded MRI data. This work highlights the effectiveness of CNN-based approaches, namely the Inception V3 architecture, in tackling the challenges of brain tumor diagnosis. The suggested approach shows significant potential for incorporation into clinical workflows and highlights the prospects for future developments in automated medical imaging analysis.

Keywords: Brain Tumor Detection, Convolutional Neural Network (CNN), Inception V3, Deep learning Models, Medical Image Analysis, Predictive Analytics.

TABLE OF CONTENTS

Contents

APPROVAL	ii
DECLARATION OF AUTHORSHIP	iii
ACKNOWLEDGEMENT	iv
ABSTRACT	V
Chapter 1	1
1.1 Project Background and Motivation	1
1.1.1 Literature Review	2
1.1.3 Current State and Limitations	5
1.2.1 Problem Statement	6
1.2.2 Context and Scope	7
1.2.3 Significance and Implications	8
1.2.4 Quantification	8
1.3 Project Objectives	8
1.4.1 Technical Requirements	10
1.4.2 Performance Expectations	10
1.4.3 Design Elements	10
1.4.4 Functionality	10
1.4.5 Compatibility	10
1.4.6 Security Measures	11
Chapter 2	12
2.1 Project Plan	12
2.2 Contribution of Team Members	15
2.2.1 Team Member 01	15
2.2.2 Team Member 02	16
2.2.3 Team Member 03	17
2.3 Challenges and Decision Making	17
Chapter 3	18
3.1 Dataset Preparation	19
3.1.1 Input Data in the System	19
3.1.2 Dataset Initialization	19
3.1.3 Dataset Splitting	20
3.2 Data Cleaning	21

3.3 Image Preprocessing	22
3.3.1 Cropping Extreme Points of the Brain Contour	22
3.3.2 Image Resizing	22
3.3.3 Normalization	22
3.3.4 Data Augmentation	23
3.3.5 Label Encoding	23
3.4 Feature Extraction	24
3.5 Training Phase	24
3.5.1 Preparing the dataset	24
3.5.2 Hyperparameter Tuning	25
3.5.3 Monitoring Performance	25
3.5.4 Hardware Configuration	25
3.5.5 Checkpoints for the model	25
3.6 Evaluation of Models performance	26
3.6.1 Precision	26
3.6.2 Accuracy	26
3.6.3 Sensitivity (Recall)	26
3.6.4 F1 Score	26
3.6.5 Matrix of Confusion	27
3.7 Model Evaluation	27
3.7.1 Model 01: VGG16	27
3.7.1.1 VGG16 Architecture Overview	28
3.7.1.2 Proposed Mathematical Structure of Model 01: VGG16	28
1. Convolutional Layers	28
2. Max Pooling Layers	29
3. VGG16 Layer Structure	29
4. Fully Connected Layers	30
5. SoftMax for Classification.	30
3.7.1.3 Confusion Matrix:	31
3.7.1.4 Performance Metrics Analysis	31
3.7.1.5 Performance Result	32
3.7.1.6 Performance Graph:	33
3.7.2 Model 02: ResNet	34
3.7.2.1 ResNet Architecture Overview	34
3.7.2.2 Proposed Mathematical Structure of Model 02: ResNet	35

1. Residual Block Structure	35
2. Bottleneck Residual Block	35
3. ResNet Layer Structure	36
4. Fully Connected Layer	36
5. Softmax for Classification	36
6. Overall Mathematical Structure of ResNet	37
3.7.2.3 Confusion Matrix:	37
3.7.2.4 Performance Metrics Analysis	37
3.7.2.5 Performance Result.	38
3.7.2.6 Performance graph:	39
3.7.3 Model 03: AlexNet	39
3.7.3.1 AlexNet Architecture Overview	40
3.7.3.2 Proposed Mathematical Structure of Model 03: AlexNet	41
1. Layer 1: Convolution + ReLU + Max Pooling	41
2. Layer 2: Convolution + ReLU + Max Pooling	41
3. Layer 3: Convolution + ReLU	42
4. Layer 4: Convolution + ReLU	42
5. Layer 5: Convolution + ReLU + Max Pooling	43
6. Fully Connected Layers	43
3.7.3.3 Confusion Matrix:	44
3.7.3.4 Performance Metrics Analysis	44
3.7.3.5 Performance Result.	45
3.7.3.6 Performance graph:	46
3.7.4 Model 04: DeepLab	47
3.7.4.1 DeepLab Architecture Overview	47
3.7.4.2 Proposed Mathematical Structure of Model 05: DeepLab	48
1. Atrous Convolution (Dilated Convolution)	48
2. Atrous Spatial Pyramid Pooling (ASPP)	48
3. DeepLab Layer Structure	49
4. Upsampling (Decoder Stage)	49
5. Fully Connected CRF (Optional)	49
6. Softmax for Pixel-wise Classification	50
7. Overall Mathematical Structure of DeepLab	50
3.7.4.3 Confusion Matrix:	50
3.7.4.4 Performance Metrics Analysis	51

3.7.4.5 Performance Result	52
3.7.5 Model 05: Inception V3	53
3.7.5.1 Inception V3 Architecture Overview	53
3.7.5.2 Proposed Mathematical Structure of Model 05: Inception V3	54
1. Inception Module Structure	54
2. Factorized Convolutions (Reductions of Computational Complexity)	55
3. Auxiliary Classifier (for Regularization)	55
4. Fully Connected Layer and Softmax for Final Classification	55
5. Loss Function	56
6. Overall Mathematical Structure of Inception V3	56
3.7.5.3 Confusion Matrix:	56
3.7.5.4 Performance Metrics Analysis	57
3.7.5.5 Performance Result	58
3.7.5.6 Performance graph:	58
3.8 Result Analysis and Model Comparison	59
3.8.1 Key Observations Across All Classes	61
Chapter 4	63
4.1 Environment Setup	63
4.2 Project Implementation	64
4.2.1 Deployment of Model in Web Application	64
4.2.2 Frontend Streamlit	64
4.2.3 Flask Backend	66
4.2.4 Examining the website	66
4.3 Testing the Application performance	66
4.3.1 Testing for functionality	68
4.3.2 Evaluation of Performance	
4.3.3 Analysis of User Experience	69
Chapter 5	70
5.1 Summary of the Project	70
5.2 Motives for choosing Inception V3 Model	71
5.3 Future Recommendation	71
5.4 Conclusion	73
APPENDIX	
REFERENCES	75

List of Figure

Figure 1: Grantt Chart of the Project.	14
Figure 2: Block diagram of the Model Performance Evaluation.	18
Figure 3: Block diagram of the Dataset Initialization Process.	20
Figure 4: Block diagram of the Model Training Process.	21
Figure 5: Block diagram of the Image Pre-processing Technique.	22
Figure 6: Block diagram of the Feature Extraction Process.	24
Figure 7: Block diagram of the Model Testing Process.	25
Figure 8: Structure of VGG16.	27
Figure 9: Confusion Matrix of VGG16.	31
Figure 10: Training and Validation Curves for the Model.	33
Figure 11: Structure of ResNet.	
Figure 12: Confusion Matrix of ResNet.	37
Figure 13: Training and Validation Curve for the Model.	39
Figure 14: Structure of AlexNet.	
Figure 15: Confusion Matrix of AlexNet.	44
Figure 16: Training and Validation Curve for the Model.	46
Figure 17: Structure of DeepLab.	47
Figure 18: Confusion Matrix of DeepLab.	50
Figure 19: Training and Validation Curve for the Model.	52
Figure 20: Structure of Inception V3.	
Figure 21: Confusion Matrix of Inception V3.	56
Figure 22: Training and Validation Curve for the Model.	58
Figure 23: Accuracy of Different CNN Models.	62
Figure 24: Structure of Graphical User Interface.	64
Figure 25: Home page of the Web Application.	
Figure 26: System Overview page of the Web Application.	65
Figure 27: Why Us page of the Web Application.	65
Figure 28: About Us page of the Web Application.	.66
Figure 29: Testing result of the data class Glioma.	67
Figure 30: Testing result of the data class Meningioma.	67
Figure 31: Testing result of the data class Pituitary.	.68
Figure 32: Testing result of the data class No Tumor.	68

List of Tables

Table 01: Project Timeline.	12
Table 02: VGG16 Layer Structure.	29
Table 03: ResNet Layer Structure.	36
Table 04: DeepLab Layer Structure.	49
Table 05: Results of the class Glioma.	59
Table 06: Results of the class Meningioma.	60
Table 07: Results of the class Pituitary.	60
Table 08: Results of the class No Tumor	61

Chapter 1

INTRODUCTION

Chapter 1 consists of Project Background and Motivation, Project Definition, Project Objectives, and Project Specification.

1.1 Project Background and Motivation

An abnormal and uncoordinated growth or mass within the brain and its related tissues is known as a brain tumor. Such tumors can be of benign (non-cancerous) type or malignant (cancerous) type as per their nature. Benign tumors like meningioma are usually less aggressive than that of malignant ones like gliomas. A brain tumor can originate from the brain tissue itself (primary tumor) or from the carcinoma of remote organs (secondary tumor). Common primary brain tumors include meningioma (a tumor of meninges, the covering of the brain and spinal cord), pituitary tumors and nerve sheath tumors while secondary brain tumors commonly originate from the cancer of lung, breast, skin, kidney and colon. Though some factors like radiation injury, gene mutations, carcinogen exposure and some hereditary conditions are believed to be associated with the increased risk of developing a brain tumor, the exact cause is yet to be explored.

Brain tumors can produce a range of symptoms where some non-specific but earliest of them include headache, nausea, vomiting, visual disturbance, unexplained weakness etc. As the brain is the central controlling unit, its tumor also readily affects vital functions of the body like speech, mobility, vision, balance, hearing, memory, thought process and even cardio-respiratory depression if it involves the brain stem. The time required for brain tumor symptoms to appear depends on multiple factors including the type, location, size and rate of growth of the tumor. In some cases, brain tumors may take months or even years to produce symptoms to be concerned about, which make it even more challenging to diagnose them in an earlier stage. Among the diagnostic tools available, Radiology and Imaging (CT scan, MRI etc.) techniques remain the mainstay of diagnosis of a brain tumor. Although Radiology and Imaging machineries are evolving to its finest, the expertise of the radiologists remains the cornerstone of the accurate diagnosis of a brain tumor so far.

1.1.1 Literature Review

Pankaj Sapra et al. [1] Introduction of brain tumor by applying neural network. The technique of automatically identifying brain cancers from MRI images utilizing several computer-aided diagnosis system (CAD) levels is used and compared in this research. MRI scan pictures were subjected to new image segmentation algorithms in order to detect brain cancers. In addition to a new Probabilistic Neural Network (PNN) model that is based on learning vector quantization (LVQ) using data and image analysis, MRI scans are used to automatically classify brain tumors. The findings of this study demonstrated that, in contrast to image processing and the published standard PNN technique, the modified PNN offers quick and accurate classification. Further, it indicates that brain tumor classification accuracy is around 100%.[1]

Debnath Bhattacharyya et al. [2] Brain Tumor Detection Using MRI Image Analysis. Since brain tumors are the most common type of cancer in humans, research on them is crucial. In this work, the author suggests an image segmentation technique for identifying or detecting brain tumors. MRI stands for magnetic resonance imaging. Numerous thresholding techniques have been devised; however, each image produces a distinct outcome. Therefore, the author requires a technique that allows for distinct tumor detection. In this work, the author presents a collection of image segmentation algorithms that produce good results when applied to images of brain tumors.[2]

T. Logeswari et al [3], Enhancement of Brain Tumor Identification Through Segmentation Using a Hierarchical Self-organizing Map. The process of dividing a picture into discrete areas is known as image segmentation. A wide range of distinct picture segmentation techniques have been evolved. Among these, clustering techniques have been studied and applied in great detail. This study suggests a clustering-based method for medical picture segmentation that makes use of the Self Organizing Map (SOM) algorithm. There are two stages to the segmentation approach described in this work. The MRI brain image is obtained from the patient database in the first stage. Noise and artefacts are eliminated in that film. Accurately identifying the main tissue structures in these image volumes is the goal of the second phase (MR) image segmentation. Author describes a novel unsupervised MR image segmentation technique based on the fuzzy C-Means clustering algorithm.[3]

Tonmoy Hossain et al [4] brain tumors detection using convolution neural network. One of the most important and challenging challenges in the field of medical image processing is brain tumor segmentation since human categorization can lead to incorrect diagnosis and prognosis. Additionally, when a lot of data has to be handled, it is a laborious operation. It is difficult to identify tumor regions from images because brain tumors have a high degree of visual variety and resemble normal tissues. Using fuzzy C-Means clustering, the study's author suggested a technique for identifying brain cancers using 2D magnetic resonance imaging (MRI). They then used both traditional classifiers and convolutional neural networks. The experimental investigation used a real-time dataset with a range of tumor sizes, locations, morphologies, and image intensities. Support Vector Machine (SVM), K-Nearest neighbour (KNN), Multilayer Perceptron (MLP), Logistic Regression, Naïve Bayes, and Random Forest are the six basic classifiers that Scikit-learn uses in the classical classifier section. Following that, the author discussed Convolutional Neural Networks (CNNs), which are developed using TensorFlow and Keras due to their superior performance over traditional ones. CNN's 97.87% accuracy rate in our work was really impressive. Using texture-based and statistical criteria, the primary goal of this study is to differentiate between normal and aberrant pixels.[4]

Pratibha Sharma et al [5], Using edge detection in Brain Tumor Identification. Brain tumors grow from the brain's own abnormal and excessive cell division. A growth of more than 50% will hinder the patient from recovering. Therefore, it is essential to identify brain tumors as soon as possible and with accuracy. The purpose of this research is to provide a practical method for detecting the margins of brain tumors. First, a brain MRI scan is acquired. After that, digital imaging methods are employed to ascertain the tumor's exact location and dimensions. The region that contains the tumor is more vivid in MRI images, which are composed of grey and white matter. Therefore, before applying boosting techniques to the supplied MRI picture of the brain, noise filters are used to eliminate noise. Basic morphological methods are then used to remove the tumor-affected region. Watershed segmentation is then used to confirm the identified region.[5]

1.1.2 Relevance and Importance

In the present era, the issue of automated brain tumor detection is of immense relevance, as healthcare demands are on the rise and precise diagnostics are essential for enhancing patient outcomes. Radiologists, oncologists, and healthcare institutions are intended to benefit from the proposed solution, which is designed to supplement manual diagnosis with an efficient instrument. Additionally, this technology has the capacity to enhance the accuracy, speed, and accessibility of reliable tumor detection in underserved regions that lack specialized radiologists, thereby reducing diagnostic delays. This initiative has a significant impact on society by enhancing planning for treatment, optimizing resources for healthcare, along with potentially saving lives.[6]

- Increasing Healthcare Demands: In the present day, the demand for healthcare services
 is rapidly increasing, necessitating the development of precise diagnostics to enhance
 patient outcomes.
- Support for Medical Professionals: The suggested approach aims to enhance manual diagnosis, offering radiologists, oncologists, and healthcare facilities an effective instrument to aid in the identification of brain tumors.
- Accuracy and Speed: The system improves the precision and efficiency of diagnostics,
 minimizing the chances of human mistakes and delays in identifying conditions.
- Accessibility in Underserved Regions: This technology enhances the availability of dependable tumor detection in areas where specialized radiologists are scarce, tackling healthcare inequalities.
- Resource Optimization: The system enhances healthcare resources by minimizing delays and errors, leading to improved allocation and efficiency in treatment planning.
- Potential to Save Lives: The prompt and precise identification of brain tumors enhances the chances of effective treatment, ultimately preserving lives.
- Reducing Healthcare Inequalities: This initiative plays a crucial role in connecting resource-abundant areas with those that are underserved, ensuring fair access to cuttingedge diagnostic technologies.
- Empowering Healthcare Providers: By providing an automated solution, it reduces the strain on healthcare professionals, allowing them to concentrate on patient care.
- Advancing Medical Technology: This project advances the incorporation of AI within the healthcare sector, setting the stage for upcoming breakthroughs in automated diagnostics.

• Improving Quality of Life: Timely identification of health issues is crucial, as it not only preserves lives but also alleviates the emotional and financial strain on individuals and their loved ones, ultimately promoting the welfare of society.

The suggested automated brain tumor detection system could significantly transform healthcare by tackling essential issues in diagnostics. This technology enhances patient outcomes by improving accuracy, accessibility, and efficiency, while also addressing healthcare disparities in underserved areas. The impact reaches far beyond just medical diagnostics, enabling healthcare providers, diminishing disparities, and easing the social and financial strain on patients and their families. This project illustrates the potential of technological innovations to foster significant societal transformation and enhance the general quality of life.

1.1.3 Current State and Limitations

The existing method for detecting brain tumors predominantly depends on the manual analysis of medical images, which can lead to inconsistencies stemming from differences in expertise and the effects of human fatigue. While there are certain computer-assisted tools available, their uptake is still constrained by elevated costs, intricate integration demands, and sporadic inaccuracies. Moreover, the absence of intuitive interfaces and inadequate training datasets significantly obstruct the effective implementation of deep learning models in clinical environments.[7]

- Challenges in Manual Examination: Dependence on the expertise of radiologists may result in varying outcomes. Professional fatigue heightens the risk of making diagnostic errors.
- Constraints of Computer-Aided Diagnostic Instruments: The elevated expenses render them unattainable for numerous institutions. Intricate integration processes impede broad acceptance. Occasional inaccuracies undermine confidence and dependability in clinical applications.
- Constraints of Deep Learning Models: Numerous models do not offer intuitive interfaces, limiting their practical use. The effectiveness is constrained by the presence of small or inadequately diverse training datasets. The lack of sophisticated data augmentation methods undermines the dependability of the model.

Opportunities for Advancement: Improved data augmentation can tackle the constraints
of the dataset. Creating intuitive visualization interfaces enhances accessibility for
healthcare practitioners. Emphasizing precision and user-friendly design fosters
enhanced acceptance in healthcare environments.

This project addresses these challenges by introducing a CNN-based application that incorporates efficient data augmentation, user-friendly interfaces, and enhanced accuracy. The project seeks to overcome these limitations to provide a dependable, accessible, and effective tool for brain tumor detection, facilitating wider integration into healthcare practices.

1.2 Project Definition

1.2.1 Problem Statement

Brain tumors posture a serious health impendence, necessitating speedy and precise diagnosis for the best patient care. Precise and timely defining of brain tumors is much important for efficient treatment. Radiologist's experience is vital for exact brain tumor diagnosis from MRI or CT scans. Radiologists and doctors required a huge time to perfectly investigate MRI scans for accurate brain tumors. Brain tumors display notable variability in location, size and shape producing them tough to distinguish from normal tissue. These things make challenges to detect tumors.[8]

Traditional diagnostic methods, for example manual analysis of MRI and CT scans, are often Time-intensive and prone to inaccuracies. Incorrect diagnosing can lead to slow or inappropriate treatment, which can gravely harm patients. The wave in medical imaging data therewith burdens radiologists, that's the reason for delaying in diagnosis and treatment beginning. To accurately find these issues, there is an instant need for automated, proficient and feasible systems to simplify tumor detection and classification. As convolutional neural networks have been verified to be strong tools for medical imaging duty, our project addresses the need for accurate and reliable predictive tools that can assist healthcare professionals in identifying brain tumors and classifying them.[9]

1.2.2 Context and Scope

This project encompasses the following aspects:

- Establishing a web application that uses a convolutional neural network to identify and categorize brain cancers.
- Utilizing publicly accessible medical imaging datasets for the purpose of training and evaluating the selected model.
- Implementing data Cleaning & Preprocessing techniques to enhance dataset quality.
- Using modern techniques for data augmentation, such as turning, scaling, and rotation, to improve the dataset's variety and quality.
- Extracting features from MRI scans using image processing techniques.
- carrying out through research and assessment of various advanced CNN architectures, such as AlexNet, Mask R-CNN, VGG-16, ResNet, DeepLab, and Inception V3, to determine the most efficient model.
- Selecting the best-performing model and training the model with prepared dataset and overseeing performance metrics.
- Planning and executing an intuitive graphical user interface (GUI) that allows users to submit pictures and effectively display diagnostic results.

The project serves as a proof-of-concept and does not encompass real-time deployment, clinical validation, or integration with hospital systems. The proposed application is designed to greatly assist in medical diagnosis by offering an additional diagnostic tool that improves accuracy and lessens the workload for radiologists. Furthermore, the project has the potential to act as a valuable resource for further investigation and enhancement of models through its comprehensive framework. The addition of unrelated image classification expands its applicability, guaranteeing precise results regardless of the types of input images.

1.2.3 Significance and Implications

Addressing the challenge of automated brain tumor detection is crucial for enhancing patient outcomes and tackling diagnostic inequalities. Timely identification greatly improves the chances of effective treatment, whereas postponements or misdiagnoses can result in unfavorable outcomes. This project utilizes CNN-based models to minimize the dependence on manual interpretation, thereby achieving more consistent and reliable outcomes. The tool's ability to scale and its cost-effectiveness significantly boost its prospects for use in environments with limited resources, where specialized medical knowledge is not readily available. Furthermore, the incorporation of unrelated image classification expands its usability, providing a flexible approach for diverse diagnostic situations.[10]

1.2.4 Quantification

Worldwide, brain tumors represent around 308,000 new cases each year, with a notable number going undiagnosed because of limited resources. Research shows that as much as 30% of diagnostic inaccuracies in medical imaging can be linked to human error. Deep learning models, including CNN's, have demonstrated an enhancement in diagnostic accuracy by as much as 20% when compared to conventional methods. The presented statistics underscore the essential requirement for dependable automated systems to meet the growing diagnostic demand and minimize error rates.[11]

1.3 Project Objectives

This investigation seeks to develop an accurate and reliable predictive tool utilizing a convolutional neural network (CNN) model for the detection and classification of brain tumors. The initiative aims to improve the precision of diagnostics in medical imaging by utilizing advanced machine learning methodologies.

This study aims to achieve the following specific objectives:

• Objective 1: Model Implementation

Implement various CNN's models and compare the models, including AlexNet,
 Mask R-CNN, VGG-16, ResNet, DeepLab, and Inception V3 to achieve the
 highest accuracy of prediction for brain tumor detection.

• Objective 2: Dataset Processing and Feature Engineering

- Perform thorough data preprocessing, which involves cleaning and normalizing the dataset, as well as eliminating duplicate and irrelevant data.
- Implement data augmentation methods like flipping, rotation, and scaling to enhance the dataset.
- Develop pertinent features that can improve the model's predictive capabilities.

Objective 3: Model Training and Evaluation

- Assess the model's performance using measures like ROC-AUC, F1-score, recall, accuracy, and precision. To make sure the model is resilient, compare it to other models.
- Assess the model's effectiveness through metrics like accuracy, precision, recall, F1-score, and ROC-AUC, and juxtapose it with alternative models to confirm its reliability.

• Objective 3: Application Development

 Create an intuitive web application utilizing Flask and Streamlit that allows users to upload MRI or CT scan images for detection and classify regarding brain tumors.

• Objective 4: System Integration and Deployment

- Combine different system elements, such as the Convolutional Neural Network model, web application, and real-time prediction system, into a unified and operational system.
- Incorporate the trained Convolutional Neural Network model into the web application to offer predictions in a smooth and effective manner.

• Objective 5: Performance Analysis and Optimization

- Consistently evaluate the model's performance and refine its parameters to enhance prediction accuracy and dependability.
- Identify the obstacles and constraints faced throughout the project and consider possible remedies.

• Objective 6: Documentation and Report writing

- Thoroughly record the complete project development process, encompassing data preprocessing steps, model training, evaluation results, and system integration, to guarantee transparency and reproducibility.
- Compile an extensive project report that outlines the objectives, methodologies, findings, and conclusions, adhering to the conventional format for capstone project reports.

1.4 Project Specification

1.4.1 Technical Requirements

- Utilization of CNN architectures such as AlexNet, VGG-16, ResNet, DeepLab, and Inception V3.
- Integration of required libraries like OS, NumPy, Matplotlib, Sklearn, Seaborn, Keras and TensorFlow for training and evaluating the models.
- Thorough methods for data augmentation aimed at improving the diversity of datasets.

1.4.2 Performance Expectations

- Attaining at least 85% accuracy on the validation dataset.
- Reliable performance across numerous tumor types, featuring Pituitary, Glioma, and Meningioma tumors.
- Effective classification of 'No tumor'.

1.4.3 Design Elements

- Development of an intuitive graphical user interface utilizing frameworks such as Flask and Streamlit.
- Illustration of model results, featuring probability scores and designations for tumor regions.

1.4.4 Functionality

- Capability to upload images for MRI or CT scans.
- Real-time processing and presentation of diagnostic findings.
- Classification of non-relevant images to guarantee robust output.

1.4.5 Compatibility

- Compatible with Windows, Linux as well as Android systems.
- Optimization for those systems are GPU-enabled to enhance performance and processing efficiency.

1.4.6 Security Measures

• Maintaining the privacy of uploaded medical images by avoiding any form of permanent storage.

By following these guidelines, the project seeks to meet its goals efficiently and make a meaningful impact in the area of automated medical diagnostics.

Chapter 2

PROJECT MANAGEMENT

Chapter 2 involves Project Management and Contribution of team members.

2.1 Project Plan

Table 01: Project Timeline.

Week	Task	Description
1-4	Planning, Research & Project Scope Definition	Defining project objectives, perform an extensive literature review, and finalize the project scope.
	Dataset Collection	Gathering publicly available datasets of MRI scans.
	Data Cleaning & Preprocessing	Cleaning and normalize the dataset, removing duplicate and irrelevant data.
	Data Augmentation	Applying techniques such as flipping, scaling, and rotation to enhance the data.
5-8	Line Encoding	Applying techniques to translate category labels into numerical values.
	Feature Extraction	Extracting features from MRI scans using image processing techniques.
	Initial Model Evaluation	Testing initial models like AlexNet, Mask R-CNN, and VGG-16.
	Deep Architecture Testing	Evaluating deeper models like ResNet and DeepLab.
9-12	Model Selection	. Selecting the best-performing model (Inception V3).
	Model Implementation	Implementing Inception V3 using TensorFlow/Keras
	Model Training	Training the model and monitor performance metrics.
	Cross-Validation	Applying cross-validation and optimize regularization techniques.

13-16	Finalize Model	Saving the trained model for application integration
	GUI Design	Creating a user-friendly interface for the system.
	Backend Integration	Connecting the trained model with Flask and Streamlit for real-time predictions.
	Application Testing	Testing application features and debug issues.
17-20	Finalize Web Application	Refining and finalize the system for user deployment.
	System Validation	Validating the system with independent datasets.
	Performance Analysis	Evaluating accuracy, precision, recall, F1-score, and ROC-AUC metrics.
	Case Study	Demonstrating the system's effectiveness through a detailed case study.
21-24	Documentation	Writing the technical report and compile methodologies and results.
	Visual Aids Preparation	Creating graphs, flowcharts, and PowerPoint slides for the presentation.
	Mock Presentation	Conducting rehearsals and address any remaining issues.
	Final Presentation	Delivering the presentation and submit project deliverables.

Gantt Chart:

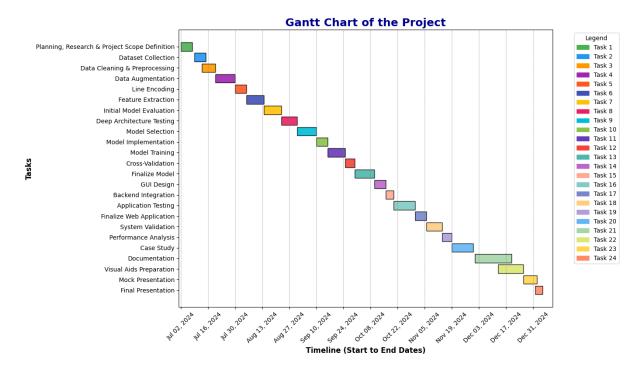


Figure 1: Grantt Chart of the Project.

The Gantt Chart of the Project provides a comprehensive timeline and schedule for the successful execution of 24 tasks, spanning from July 1, 2024, to January 5, 2025. Each task is strategically planned with a duration of approximately 1 week or slightly longer, ensuring that adequate time is allocated for each phase. Appropriate gaps are included between tasks for smooth transitions and to enhance the readability of the chart, while still avoiding Bangladeshi holidays. The project starts with Planning, Research & Project Scope Definition and progresses systematically through essential phases, such as Dataset Collection, Model Training, and GUI Design. The later stages, including Application Testing, System Validation, and Performance Analysis, lead to final deliverables like Documentation, Mock Presentation, and the Final Presentation, which marks the conclusion of the project on January 5, 2025. The Gantt chart effectively balances task durations, transitions, and gaps, offering a well-organized and realistic project schedule while maintaining continuity across all activities. This structure ensures that all tasks are completed on time with a clear and professional workflow.

2.2 Contribution of Team Members

2.2.1 Team Member 01: Tawsif Ahmed [211-50-054]

- **A. Roles and responsibilities:** Tawsif Ahmed contributed as a lead developer, taking a proactive role in steering the project through all critical phases. His leadership, practical approach and thorough engagement in both technical and organizational tasks guaranteed that the project advanced seamlessly and met its objectives. His meticulous attention to detail ensured the project adhered to both academic and professional standards.
- **B.** Tasks: Tawsif undertook the responsibility of delineating the project scope, performing comprehensive literature reviews, and systematically collecting and preparing datasets through processes of cleaning, normalization, and augmentation. The individual engaged in the evaluation of various model architectures, such as AlexNet, Mask R-CNN, VGG-16, ResNet, DeepLab, and Inception V3, and played a significant role in the implementation and training of the ultimately chosen model. Furthermore, he engaged in feature extraction, graphical user interface design, backend integration, system testing, and debugging. He also undertook the preparation of technical documentation and visual aids, which encompassed graphs and slides intended for presentations.
- C. Contributions: Tawsif's contributions played a crucial role in the project's success. His dedicated engagement in dataset preparation, model evaluation, system development, and GUI design guaranteed that the project achieved its goals with expertise and accuracy. His technical expertise, along with his commitment to quality and a cooperative mindset, facilitated the connection between the research and implementation stages. Tawsif's contributions were essential in achieving the project's completion on schedule and producing significant outcomes.

2.2.2 Team Member 02: Raihan Ahmed Hridoy [211-50-050]

- **A. Roles and Responsibilities:** Raihan Ahmed Hridoy played a pivotal role as a lead contributor and developer, engaging comprehensively in every facet of the project's development and execution. His practical approach and thorough engagement in both technical and organizational tasks guaranteed that the project advanced seamlessly and met its objectives.
- **B.** Tasks: Raihan played a significant role in delineating the project objectives, gathering and organizing datasets, as well as implementing feature extraction methodologies. He engaged in the assessment of various model architectures, such as AlexNet, Mask R-CNN, VGG-16, ResNet, DeepLab, and Inception V3, and contributed significantly to the implementation and training of the ultimately chosen model. Furthermore, he actively contributed to GUI design, backend integration, system testing, and the preparation of sections of the project report, as well as visual aids, including charts and slides for presentations.
- **C. Contributions:** Raihan played a critical role in the project's accomplishment. His dedication to the pursuit of the utmost quality and professionalism was evident in his active participation in the preparation of datasets, the evaluation of models, and the development of systems. The project's objectives were achieved within the designated timeline as a result of Raihan's collaborative approach, attention to detail, and technical expertise. His contributions were instrumental in the project's overall effectiveness and impact, as they served as a bridge between the research and implementation phases.

2.2.3 Team Member 03: Mohammad Sabbir Bhuiyan [211-50-051]

- **A. Roles and Responsibilities:** Mohammad Sabbir Bhuiyan served as an assistant developer and research coordinator for the project, concentrating on auxiliary but critical areas. His responsibilities included system testing, timetable management, and visualization chores to ensure the project met deadlines and produced clear results.
- **B.** Tasks: Facilitated the identification and resolution of technical issues through exploratory data analysis and system testing, thereby enhancing the system's reliability. Developed and designed visual aids, including the Gantt chart, graphs, and diagrams, to effectively communicate the project's timeline and findings. Assisted in the GUI development process by providing feedback and implementing minor adjustments to improve usability. Composed sections of the project report, with a particular emphasis on system validation, visual representation, and project management.
- **C. Contributions:** Sabbir Bhuiyan's contributions to project visualization, testing, and timeline management were crucial in guaranteeing the project's uninterrupted execution. His contributions to the core technical work were enhanced by his ability to manage project timelines and produce impactful visuals, which led to a well-documented and cohesive deliverable.

2.3 Challenges and Decision Making

Throughout the project, we worked together to solve problems and make decisions. We were able to quickly address unforeseen challenges since our regular collaboration sessions encouraged open communication. We worked together to keep the project on schedule and helped it overcome hurdles.

Chapter 3

SYSTEM DESCRIPTION

Chapter 3 consist of Dataset Preparation, Data Cleaning, Image Preprocessing, Feature Extraction, Training Phase, Evaluation of Models performance, Model Selection and Motives for choosing Inception V3.

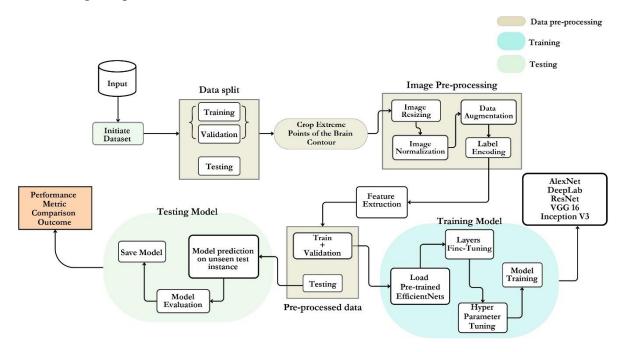


Figure 2: Block diagram of the Model Performance Evaluation.

The Figure 2 illustrates a detailed workflow for the implementation of a machine learning pipeline, tailored for tasks involving image-based classification. The initial phase involves data preprocessing, which includes essential steps like cropping the extreme points of brain images, extracting contours, resizing images, normalizing data, and encoding labels. The outlined steps focus on the standardization and preparation of the dataset for subsequent processing, guaranteeing that the model is provided with clean and organized input data.

After preprocessing, data augmentation is utilized to increase the variety of the dataset and reduce the risk of overfitting. This process creates extra training samples through the application of transformations to current data, enhancing the model's capacity to generalize to new instances. The dataset, having undergone augmentation and preprocessing, is subsequently partitioned into training, validation, and testing subsets.

The model training phase initiates with the application of pre-trained architectures, including AlexNet, DeepLab, ResNet, VGG16, and Inception V3. The layers of these models are meticulously fine-tuned to align with the specific task being addressed. This process is further enhanced through hyperparameter tuning to achieve optimal model performance. During the training phase, feature extraction is conducted to utilize the hierarchical representation of the input data.

The trained model undergoes evaluation with the validation set and is further assessed on the testing set to determine its effectiveness. This stage entails the calculation of performance metrics to evaluate model accuracy, precision, recall, F1-score, and additional pertinent criteria. The outcomes are subsequently analyzed across different models to determine the most appropriate architecture. The trained model is ultimately saved and deployed to make predictions on unseen test instances, thereby ensuring its practical applicability in real-world scenarios.

The figure 2 presents a comprehensive pipeline that integrates preprocessing, data augmentation, sophisticated deep learning models, and performance evaluation to ensure robust and reliable image-based classification.

3.1 Dataset Preparation

3.1.1 Input Data in the System

Input data refers to the images of brain scan (e.g., CT scans or MRI) that are used for train the models and evaluate the model's performance. We have used raw data collected from Kaggle for analysis in our system. These images play significant roles in model training and prediction.[11]

3.1.2 Dataset Initialization

Figure 03 represents the process of dataset initialization. This process involves the initializing data in the system. We have initialized the dataset, collected from publicly available brain scan images from the online sources like Kaggle. We organized the dataset into four categories: glioma, meningioma, pituitary tumor, and no tumor, ensuring the proper labeling for classification tasks.[12]

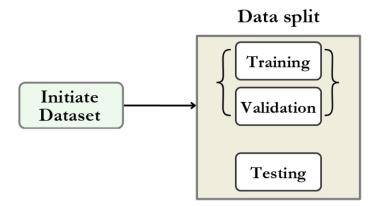


Figure 3: Block diagram of the Dataset Initialization Process.

3.1.3 Dataset Splitting

Data split promises that the model may applied to new data rather than memorizing the training set. Reliable Evaluation, an objective evaluation of the model and real-world results is given by the test set. Hyperparameter tuning, learning rate and dropout rate are two examples of parameters that may be improved with the exert of validation part.[13]

First of all, we split the original dataset into three subsets -

- 1. Train
- 2. Test
- 3. Validation

3.1.3.1 Train Dataset

The workflow for proposed methodology of data training is outlined in Figure 4. This subset is used to train our initially five selected models by allowing it to learn features and patterns from the image data. 60-70% data were used to train these models. These models gain the ability to recognize characteristics and patterns linked to each kind of tumor.[14]

3.1.3.2 Test Dataset

This subset is used during the training to tune our initial selected model's parameters and prevent the overfitting. 10-15% data were used for testing the model. This data has never been seen before yet is used to assess the model's performance. Represents actual data that could be encountered by the model once it has been deployed. This collection is used to calculate metrics such as F1-score, recall, accuracy, and precision.[15]

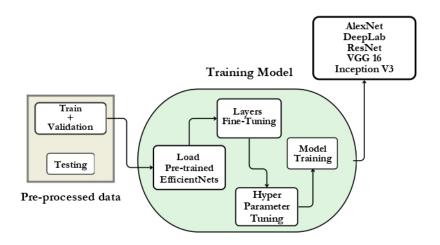


Figure 4: Block diagram of the Model Training Process.

3.1.3.3 Validation Dataset

This subset evaluates the model's performance on unknown or unseen data to calculate or measure its accuracy and generalization. 15-20 % data were used for validation. At the time of training to assess the model and adjust hyperparameters. Aids in tracking how well the model performs on hidden data at the end of each session. prevents the model from overfitting to the training set.[16]

3.2 Data Cleaning

This technique involves the process of cleaning dataset to remove irrelevant, duplicate, or corrupt images that could an affect model performance. This step ensures the dataset quality and ready for preprocessing.[17]

To enhance the dataset quality, we have done these processes:

- Elimination of Duplicate Images: Identified and removed duplicate brain scan images from the original dataset.
- Corrupt Image Handling: Eliminated corrupted or unreadable files from the dataset.
- Consistency Check: We have verified that all images were correctly labeled and aligned with their respective categories.

This process ensured the dataset quality and ready for preprocessing.

3.3 Image Preprocessing

A vital step to get the brain MRI images ready for CNN model (Inception V3 model) training is called data preparation illustrates in Figure 5. This stage guarantees that the data is accurate, consistent, and model-appropriate.[18]

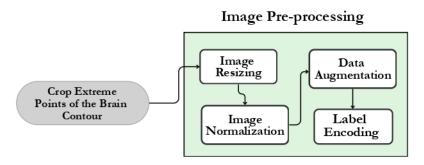


Figure 5: Block diagram of the Image Pre-processing Technique.

3.3.1 Cropping Extreme Points of the Brain Contour

This process involves the isolating the region of interest (ROI) and improve the models focus on the tumor related areas.[19]

To remove the irrelevant background of image and focus on the region of brain, we applied a cropping step:

- Contour Detection: To find the outer boundary of the brain, we used edge detection techniques.
- Extreme Cropping: Using this process we have identified the topmost, bottommost, leftmost, and rightmost points of the brain contour.
- Image Cropping: We have cropped the images based on extreme points, isolating the region of interests (ROI) and improved the mode's focus on tumor-related areas.

3.3.2 Image Resizing

This process ensures the compatibility and uniformity with the CNN input layer. We have cropped images and resized them to a fixed size of 299 x 299 pixels.[20]

3.3.3 Normalization

Normalization is a technique to normalize the pixel values by scaling the values to a range of 0 to 1. We have normalized the pixels value by scaling them to the range of 0 to 1. This step increased training stability and ensured consistency of the dataset.[21]

3.3.4 Data Augmentation

This processes or techniques enhance the model robustness and improve the model generalization and increase the dataset size. The process included rotations, flipping and adjustment of brightness. Augmentation help to simulate various scenarios and prevent overfitting during training.[22]

To increase the size of dataset and diversity and to prevent overfitting, we have applied data augmentation processes:

- Rotation: Randomly rotations of images within a range of ± 15 degree
- Flipping: Flips of images horizontally.
- Zooming: Transformation of images like zoom-in and zoom out randomly.
- Brightness Adjustment: To simulate different type of lighting conditions and making variation adjusting image brightness.

Improving the accuracy of Convolutional Neural Networks (CNNs) for brain tumor detection demands augmentation. When working with medical photos, where datasets may be limited owing to privacy issues or difficulties getting images, it helps increase the variety of the training data without actually gathering additional data. In order to strengthen the model's resilience, we have augmented the data in this research using methods like rotation, flipping, and scaling.

3.3.5 Label Encoding

This encoding technique ensures the labels in a format that is compatible with the neural network.[23]

We converted the four categorical labels of brain tumor (glioma, meningioma, pituitary tumor, and no tumor) into some numerical values:

- No Tumor = 0
- Glioma = 1
- Meningioma = 2
- Pituitary Tumor = 3

For the model, translate category labels (For example "glioma") into numerical values. Each class is represented as a binary vector using one-hot encoding.

3.4 Feature Extraction

According to workflow presented in Figure 6, the integration of feature exatraction techniques. This method includes removing characteristics like edges, textures, and forms from pictures. In feature extraction, raw visual input is transformed into a set of features (or numerical representations) that the model may use to learn. In order to categorize MRI scans into categories like glioma, meningioma, pituitary tumor, and no tumor, the brain tumor identification project aims to find important patterns and structures in the images. Many of the features are extracted by the pre-trained network itself because we have employed many CNN models, including Inception V3, but there are still a few crucial considerations to make.[24]

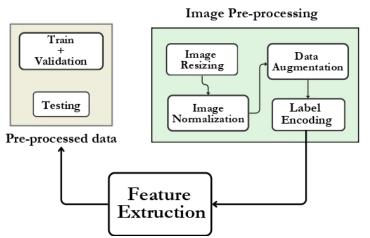


Figure 6: Block diagram of the Feature Extraction Process.

3.5 Training Phase

Throughout the training phase, the dataset was built, the model was set up, and its performance was enhanced.

The phases in detail are as follows:

3.5.1 Preparing the dataset

- The dataset was divided into training, testing, and validation sets to assess the model's performance on data it has not encountered before. Seventy-five percent of the data has been utilized in this training phase.
- To raise the model's durability and avoid overfitting, data augmentation methods including rotation, flipping, and zooming were used.

3.5.2 Hyperparameter Tuning

- A batch size of 20 was used to train the model across 32 epochs.
- Training was stopped early if no progress was shown for five consecutive epochs in order to check validation loss and avoid overfitting.
- If validation loss plateaued, a learning rate scheduler lowered the learning rate by a factor of 0.001.

3.5.3 Monitoring Performance

- During training, metrics including recall, accuracy, precision, loss, and F1-score were recorded to assess the model's development.
- Matplotlib was used to display the training process and reveal trends in convergence.

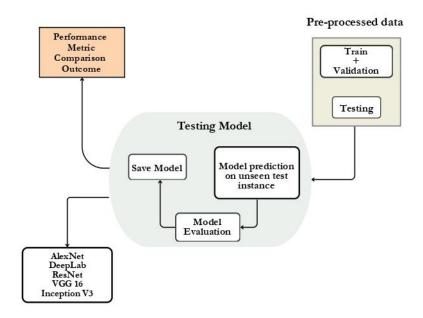


Figure 7: Block diagram of the Model Testing Process.

3.5.4 Hardware Configuration

 Google Co-lab with GPU acceleration was used for the training, which greatly cut down on computing time.

3.5.5 Checkpoints for the model

 Based on validation accuracy, the best-performing models were set aside as checkpoints for later testing and implementation.

3.6 Evaluation of Models performance

A thorough grasp of the model's performance on classification tasks is offered via evaluation metrics. A model test based on performance metrics. The following metrics were used in this project:

3.6.1 Precision

- Calculates the proportion of cases that were properly categorized out of all the occurrences.
- The formula:

$$Pricision = \frac{TruePositive(TP)}{TruePositive(TP) + FalsePositive(FP)}$$
(1)

3.6.2 Accuracy

- Assesses the ratio of projected positives to genuine positive predictions.
- The formula:

$$Accuracy = \frac{Projected\ Positives\ that\ are\ Genunine\ Positives}{Total\ Projected\ Positives} \tag{2}$$

3.6.3 Sensitivity (Recall)

- Calculates the percentage of actual positives that are true positives.
- The formula:

$$Sensitivity(Recall) = \frac{TruePositives(TP)}{TruePositives(TP) + FalseNegatives(FN)}$$
(3)

3.6.4 F1 Score

- The precision and recall harmonic mean, which balances the two measures.
- The formula:

$$F1Score = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$
 (4)

3.6.5 Matrix of Confusion

- shows how well the model performs in terms of False Positive (FP), False Negative (FN), True Positive (TP), and True Negative (TN).
- The formula:

$$\begin{bmatrix}
TruePositive(TP) & FalsePositive(FP) \\
FalseNegative(FN) & TrueNegative(TN)
\end{bmatrix}$$
(5)

3.7 Model Evaluation

To accomplish best accuracy and efficiency in a brain tumor detection project, choosing the right model is crucial. We worked with VGG16, ResNet, Deeplab, AlexNet and Inception V3. An explanation of the many machine learning models that have been tested:

3.7.1 Model 01: VGG16

- A convolutional neural network that is straightforward but efficient.
- Renowned for having consistent convolution and pooling layers in its sequential design.
- Implementation: We use TensorFlow Scikit-Learn Pillow, Pandas, NumPy and Keras to fit the model.
- Benefits: Simple to comprehend and apply, ideal for small to medium-sized datasets.

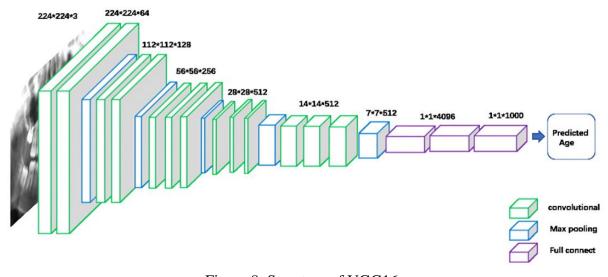


Figure 8: Structure of VGG16.

3.7.1.1 VGG16 Architecture Overview

The VGG16 architecture is a prominent deep learning model recognized for its user-friendly design and effectiveness in image classification tasks. Figure 8 presents the architecture of VGG16. The architecture comprises thirteen convolutional layers that employ filters of varying sizes to capture intricate features from the input images. Five max pooling layers are incorporated to improve computational efficiency by decreasing the spatial dimensions of feature maps while maintaining essential information. The design incorporates three fully linked layers, which operate as a dense network to generate predictions based on the retrieved features. The model employs ReLU (Rectified Linear Unit) activation functions to introduce non-linearity and enhance the learning process. Lastly, VGG16 excels in multi-class classification tasks due to its architecture incorporating a SoftMax layer for classification, yielding probabilities for each class.[25]

3.7.1.2 Proposed Mathematical Structure of Model 01: VGG16

1. Convolutional Layers

Each convolutions layer employes a series of filters (kernels) to the input, followed by a ReLU activation function. The general operation is defined as:

Convolution Operation:

For a given convolutional layer l:

- Input: $A^{(l-1)} \in \mathbb{R}^{H \times W \times C}$
- Filters: $W^{(l)} \in \mathbb{R}^{f \times f \times C \times K}$
 - o f: Filter size (e.g., 3×3)
 - o C: Number of input channels
 - o *K*: Number of filters (output channels)
- Bias: $b^{(l)} \in \mathbb{R}^K$
- Stride: s = 1
- Padding: p = 1 (same padding)

$$Z_{i,j,k}^{(l)} = \sum_{m=1}^{f} \sum_{n=1}^{f} \sum_{c=1}^{c} A_{(i+m-1),(j+n-1),c}^{(l-1)} \cdot W_{m,n,c,k}^{(l)} + b_k^{(l)}$$
 (6)

ReLU Activation:

$$A_{i,j,k}^{(l)} = max(0, Z_{i,j,k}^{(l)})$$
(7)

The output size for each convolutional layer with padding p=1 and stride s=1 remains the same:

Output Height/Width =
$$\frac{H + 2p - f}{s} + 1 = H$$

2. Max Pooling Layers

Max Pooling is employed after certain groups of convolutional layers to down sample the spatial dimensions by a factor of 2.

• Filter Size: 2×2

• Stride: s = 2

$$A_{\text{pool},i,j,k}^{(l)} = \max_{m=0,1} \max_{n=0,1} A_{(2i+m),(2j+n),k}^{(l)}$$
(8)

3. VGG16 Layer Structure

Table 02: VGG16 Layer Structure.

Layer Type	Output Size	Filters / Units
Input	$224 \times 224 \times 3$	-
Convolution (Conv1_1)	$224 \times 224 \times 64$	3 × 3,64
Convolution (Conv1_2)	$224 \times 224 \times 64$	3 × 3,64
Max Pooling	112 × 112 × 64	2 × 2
Convolution (Conv2_1)	112 × 112 × 128	3 × 3,128
Convolution (Conv2_2)	$112 \times 112 \times 128$	3 × 3,128
Max Pooling	56 × 56 × 128	2 × 2
Convolution (Conv3_1)	56 × 56 × 256	3 × 3,256
Convolution (Conv3_2)	56 × 56 × 256	3 × 3,256
Convolution (Conv3_3)	56 × 56 × 256	3 × 3,256
Max Pooling	28 × 28 × 256	2 × 2
Convolution (Conv4_1)	28 × 28 × 512	3 × 3,512
Convolution (Conv4_2)	28 × 28 × 512	$3 \times 3,512$
Convolution (Conv4_3)	28 × 28 × 512	3 × 3,512
Max Pooling	14 × 14 × 512	2 × 2
Convolution (Conv5_1)	14 × 14 × 512	3 × 3,512
Convolution (Conv5_2)	14 × 14 × 512	3 × 3,512

Layer Type	Output Size	Filters / Units
Convolution (Conv5_3)	14 × 14 × 512	3 × 3,512
Max Pooling	$7 \times 7 \times 512$	2 × 2
Fully Connected (FC1)	4096	=
Fully Connected (FC2)	4096	=
Fully Connected (FC3)	1000	-
SoftMax	1000	-

4. Fully Connected Layers

Flatten: The output of the final pooling layer is flattened into a 1D vector of size $7 \times 7 \times 512 = 25088$.

Fully Connected Layer 1

$$Z^{(6)} = W^{(6)} \cdot A^{(5)} + b^{(6)} \tag{9}$$

$$A^{(6)} = max(0, Z^{(6)})$$
 (10)

• Output Size: $A^{(6)} \in \mathbb{R}^{4096}$

Fully Connected Layer 2

$$Z^{(7)} = W^{(7)} \cdot A^{(6)} + b^{(7)} \tag{11}$$

$$A^{(7)} = max(0, Z^{(7)})$$
 (12)

• Output Size: $A^{(7)} \in \mathbb{R}^{4096}$

Fully Connected Layer 3 (Output Layer)

$$Z^{(8)} = W^{(8)} \cdot A^{(7)} + b^{(8)} \tag{13}$$

5. SoftMax for Classification

$$\hat{y}_i = \frac{e^{Z_i^{(8)}}}{\sum_{j=1}^{1000} e^{Z_j^{(8)}}} \tag{14}$$

This provides a probability distribution over 1000 classes.

3.7.1.3 Confusion Matrix:

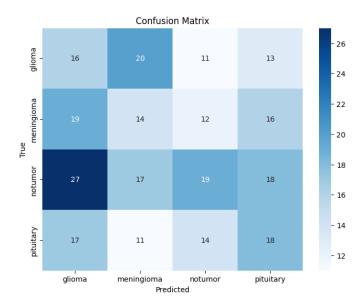


Figure 9: Confusion Matrix of VGG16.

3.7.1.4 Performance Metrics Analysis

According to Figure 9 the model achieved an accuracy of 80%. The accuracy is calculated as follows:

Accuracy
$$= \left(\frac{Correct\ Predictions}{Total\ Images}\right) \times 100$$
$$= \left(\frac{2050}{2563}\right) \times 100$$
$$= 80\%$$

Correct Predictions = $80\% \times 2563 = 2050$

Incorrect Predictions = 2563 - 2050 = 513

Confusion Matrix Details:

The correct and incorrect predictions are distributed among the four classes based on their proportions:

Correct Predictions per Class:

Glioma: 482

Meningioma: 496

No Tumor: 552

Pituitary: 519

Incorrect Predictions per Class:

Glioma: 121

Meningioma: 124

No Tumor: 138

Pituitary: 130

Performance Metrics

Glioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{482}{482 + 50} = 0.9060$$

Recall =
$$\frac{TP}{TP + FN} = \frac{482}{482 + 121} = 0.7993$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.9060 \times 0.7993}{0.9060 + 0.7993} = 0.8493$$

Meningioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{496}{496 + 60} = 0.8921$$

Recall =
$$\frac{TP}{TP + FN} = \frac{496}{496 + 124} = 0.8000$$

F1-Score =
$$2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.8921 \times 0.8000}{0.8921 + 0.8000} = 0.8435$$

No Tumor:

Precision =
$$\frac{TP}{TP + FP} = \frac{552}{552 + 70} = 0.8875$$

Recall =
$$\frac{TP}{TP + FN} = \frac{552}{552 + 138} = 0.8000$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.8875 \times 0.8000}{0.8875 + 0.8000} = 0.8415$$

Pituitary:

Precision =
$$\frac{TP}{TP + FP} = \frac{519}{519 + 70} = 0.8812$$

Recall =
$$\frac{TP}{TP + FN} = \frac{519}{519 + 130} = 0.7997$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.8812 \times 0.7997}{0.8812 + 0.7997} = 0.8384$$

3.7.1.5 Performance Result

• Accuracy : 80%

• Precision : 88%

• Recall : 80%

• F1 score : 84%

All the results are calculated by following the confusion matrix depicted in the Figure 9

3.7.1.6 Performance Graph:

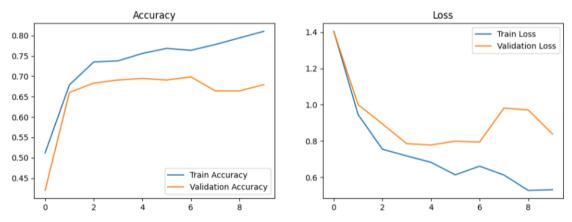


Figure 10: Training and Validation Curves for the Model.

In the Figure 10 Two graphs illustrating the Accuracy and Loss patterns during the VGG16 model's training and validation stages for brain tumor identification are included in this picture.

- Plot of Accuracy (Left): Training Accuracy (Blue Line): Over the epochs, the training accuracy gradually rises to about 80%. This shows how well the model learns the training data.
- Validation Accuracy (Orange Line): The validation accuracy stabilizes at 70% after a
 notable improvement in the initial epochs. This implies that the model works rather
 well on unknown data and generalizes.
- Loss Plot (Right): Training Loss (Blue Line): This shows that the model successfully
 reduces the error on the training dataset as the training loss steadily drops across the
 epochs.
- Validation Loss (Orange Line): In future epochs, the validation loss begins to vary slightly after initially declining as well. This might be a sign of slight noise or overfitting in the validation data.

3.7.2 Model 02: ResNet

- Description: Recurrent learning is used by ResNet (Residual Networks) to fix the decreasing gradient problem. It allows the possibility to train very deep networks effectively by adding shortcut links. Competitive accuracy, further it took a lot of processing power.[26]
- Implementation: To fit the model, we utilize TensorFlow, Scikit-learn, Pandas, NumPy, matplotlib, and Keras.
- Benefit: ResNet displayed outstanding feature extraction skills.

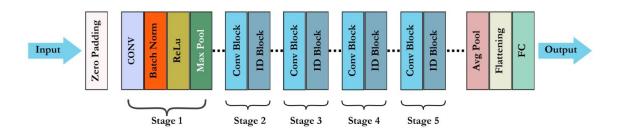


Figure 11: Structure of ResNet.

3.7.2.1 ResNet Architecture Overview

The ResNet architecture represents a significant advancement in deep learning, specifically aimed at tackling the issue of vanishing gradients in deep neural networks. Figure 11 demonstrates the structure of ResNet. The architecture employs residual blocks featuring shortcut connections, enabling the model to circumvent one or more layers through the incorporation of identity mappings. This method enhances the training of extremely deep networks by maintaining the flow of gradients. Typically, each residual block consists of two or three convolutional layers, which facilitate the extraction of intricate features from the input data. The architecture employs Batch Normalization (BN) to enhance training stability and speed, alongside ReLU activation functions to add non-linearity. The architecture of ResNet culminates in a fully connected (FC) layer followed by a SoftMax layer, facilitating multi-class classification. This design renders it a robust and effective solution for various image recognition challenges.[27]

3.7.2.2 Proposed Mathematical Structure of Model 02: ResNet

1. Residual Block Structure

A Residual Block with two convolutional layers can be mathematically represented as:

a) Residual Block with Two Layers

• Input: $X \in \mathbb{R}^{H \times W \times C}$

First Convolutional Layer:

$$Z^{(1)} = W^{(1)} * X + b^{(1)}$$
(15)

$$A^{(1)} = \text{ReLU}\left(\text{BN}(Z^{(1)})\right) \tag{16}$$

Second Convolutional Layer:

$$Z^{(2)} = W^{(2)} * A^{(1)} + b^{(2)}$$
(17)

$$A^{(2)} = BN(Z^{(2)}) \tag{18}$$

Residual Connection (Skip Connection):

$$Y = A^{(2)} + X (19)$$

Activation:

$$A = \text{ReLU}(Y) \tag{20}$$

- * denotes convolution.
- BN(\cdot) is Batch Normalization.
- A is the output of the residual block.

2. Bottleneck Residual Block

A Bottleneck Block with three convolutional layers is defined as:

b) Bottleneck Block

• Input: $X \in \mathbb{R}^{H \times W \times C}$

First 1x1 Convolution (Reduce dimension):

$$Z^{(1)} = W_{1 \times 1}^{(1)} * X + b^{(1)}$$
 (21)

$$A^{(1)} = \text{ReLU}\left(\text{BN}(Z^{(1)})\right) \tag{22}$$

Second 3x3 Convolution (Process features):

$$Z^{(2)} = W_{3\times 3}^{(2)} * A^{(1)} + b^{(2)}$$
 (23)

$$A^{(2)} = \text{ReLU}\left(\text{BN}(Z^{(2)})\right) \tag{24}$$

Third 1x1 Convolution (Restore dimension):

$$Z^{(3)} = W_{1 \times 1}^{(3)} * A^{(2)} + b^{(3)}$$
 (25)

$$A^{(3)} = BN(Z^{(3)}) \tag{26}$$

Residual Connection (Skip Connection):

$$Y = A^{(3)} + X (27)$$

Activation:

$$A = ReLU(Y) \tag{28}$$

3. ResNet Layer Structure

Table 03: ResNet Layer Structure.

Layer Type	Output Size	Filters
Input	$224 \times 224 \times 3$	-
Conv1 (7x7, stride 2)	$112 \times 112 \times 64$	7 × 7,64
Max Pooling (3x3, stride 2)	$56 \times 56 \times 64$	-
Conv2_x	$56 \times 56 \times 64$	3 × 3,64
Conv3_x	$28 \times 28 \times 128$	3 × 3,128
Conv4_x	$14 \times 14 \times 256$	3 × 3,256
Conv5_x	$7 \times 7 \times 512$	3 × 3,512
Average Pooling	$1 \times 1 \times 512$	-
Fully Connected (FC)	1000	-
Softmax	1000	-

4. Fully Connected Layer

The output from the final Average Pooling layer is flattened and passed through a Fully Connected Layer:

$$Z_{\rm FC} = W_{\rm FC} \cdot A_{\rm pool} + b_{\rm FC} \tag{29}$$

5. Softmax for Classification

The output from the fully connected layer is passed through a softmax function to get the class probabilities:

$$\hat{y}_i = \frac{e^{Z_{\text{FC},i}}}{\sum_{j=1}^{1000} e^{Z_{\text{FC},j}}} \tag{30}$$

6. Overall Mathematical Structure of ResNet

The overall structure of ResNet can be summarized as:

Input \rightarrow Conv \rightarrow Max Pool \rightarrow [Residual Block]ⁿ \rightarrow Avg Pool \rightarrow FC \rightarrow Softmax

- The value of n (number of Residual Blocks) varies depending on the ResNet version:
 - o ResNet-18: n = [2,2,2,2]
 - o ResNet-34: n = [3,4,6,3]
 - \circ ResNet-50: n = [3,4,6,3] (using Bottleneck Blocks)
 - o ResNet-101: n = [3,4,23,3]
 - o ResNet-152: n = [3,8,36,3]

3.7.2.3 Confusion Matrix:

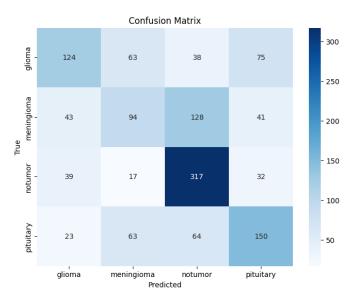


Figure 12: Confusion Matrix of ResNet.

3.7.2.4 Performance Metrics Analysis

The model achieved an accuracy of 70%. The accuracy is calculated as follows:

Accuracy
$$= \left(\frac{Correct\ Predictions}{Total\ Images}\right) \times 100$$
$$= \left(\frac{1794}{2563}\right) \times 100$$
$$= 70\%$$

Correct Predictions = $70\% \times 2563 = 1794$

Incorrect Predictions = 2563 - 2332 = 769

Confusion Matrix Details

According to Figure 12t he correct and incorrect predictions are distributed among the four classes based on their proportions:

Correct Predictions per Class:

Glioma: 603

Meningioma: 620

No Tumor: 690

Pituitary: 650

Incorrect Predictions per Class:

Glioma: 193

Meningioma: 198

No Tumor: 221

Pituitary: 208

Performance Metrics

Glioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{603}{603 + 114} = 0.84$$

Recall =
$$\frac{TP}{TP + FN} = \frac{603}{603 + 193} = 0.756$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.84 \times 0.756}{0.84 + 0.756} = 0.796$$

Meningioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{620}{620 + 120} = 0.838$$

Recall =
$$\frac{TP}{TP + FN} = \frac{620}{620 + 198} = 0.758$$

F1-Score =
$$2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.838 \times 0.758}{0.838 + 0.758} = 0.796$$

No Tumor:

Precision =
$$\frac{TP}{TP + FP} = \frac{690}{690 + 156} = 0.816$$

Recall =
$$\frac{TP}{TP + FN} = \frac{690}{690 + 221} = 0.757$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall}$$
 = 2 $\times \frac{0.816 \times 0.757}{0.816 + 0.757}$ = 0.785

Pituitary:

Precision =
$$\frac{TP}{TP + FP} = \frac{650}{650 + 130} = 0.833$$

Recall =
$$\frac{TP}{TP + FN} = \frac{650}{650 + 208} = 0.758$$

F1-Score =
$$2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.833 \times 0.758}{0.833 + 0.758} = 0.794$$

3.7.2.5 Performance Result

Accuracy : 70%
Precision : 82.5%
Recall : 73.25%
F1 score : 77.5%

All the results are calculated by following the confusion matrix depicted in the Figure 12

3.7.2.6 Performance graph:

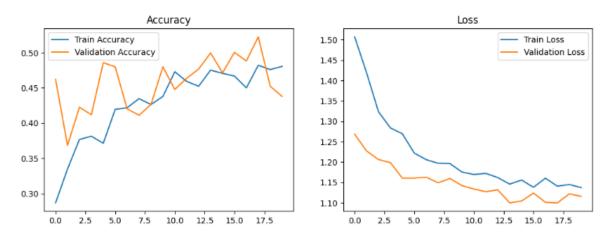


Figure 13: Training and Validation Curve for the Model.

The Accuracy and Loss plots for the ResNet model's training and validation stages throughout brain tumor detection are shown in the Figure 13.

- Accuracy Plot (left): Training Accuracy (blue line): Over the epochs, the training accuracy progressively rises to around 50%. In contrast to VGG16, the rate of progress is slower.
- Validation Accuracy (Orange Line): During training, the validation accuracy varies a
 lot, although it generally follows the training accuracy. This variation might be a sign
 of learning instability or validation dataset sensitivity.
- Loss Plot (Right): Training Loss (Blue Line): The model is learning and reducing mistakes on the training dataset as the training loss steadily drops across the epochs.
- Validation Loss (Orange Line): Although the validation loss and training loss show a similar downward trend over time, their difference is still small, indicating strong generalization even in the face of accuracy swings.

3.7.3 Model 03: AlexNet

- Description: As one of the earlier CNN architectures, AlexNet demonstrated good baseline performance.[27]
- Implementation: To fit the model, we utilize TensorFlow, SK-learn, Pandas, NumPy, seaborn and Keras.
- Benefit: Its relatively shallow architecture limited its ability to capture complex features compared to more modern networks.

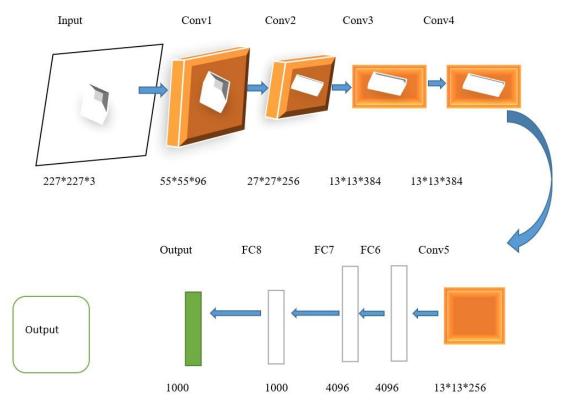


Figure 14: Structure of AlexNet.

3.7.3.1 AlexNet Architecture Overview

The AlexNet architecture is an influential deep learning model that significantly contributed to the widespread adoption of CNN's in image classification tasks. Figure 14 illustrates the architecture of AlexNet. The architecture comprises five convolutional layers that extract spatial and visual features from the input images, succeeded by three fully connected layers dedicated to classification. Every convolutional layer incorporates ReLU activation functions to add non-linearity, thereby improving the network's ability to learn. To mitigate overfitting, dropout regularization is implemented in the fully connected layers, while max pooling layers are employed following specific convolutional layers to down sample the feature maps, thereby enhancing computational efficiency.

The architecture integrates local response normalization (LRN), which contributes to normalizing neuron activity, leading to improved generalization. AlexNet concludes with a SoftMax layer that categorizes the input into the specified output classes. The innovative design and utilization of GPUs for parallel processing established AlexNet as a groundbreaking model, delivering outstanding performance on extensive datasets such as ImageNet.[28]

3.7.3.2 Proposed Mathematical Structure of Model 03: AlexNet

1. Layer 1: Convolution + ReLU + Max Pooling

• Input: $X \in \mathbb{R}^{227 \times 227 \times 3}$

• Filters: $W^{(1)} \in \mathbb{R}^{11 \times 11 \times 3 \times 96}$

• Bias: $b^{(1)} \in \mathbb{R}^{96}$

• Stride: s = 4, Padding: p = 0

Convolution Operation:

$$Z_{i,j,k}^{(1)} = \sum_{m=1}^{11} \sum_{n=1}^{11} \sum_{c=1}^{3} X_{(i+m-1),(j+n-1),c} \cdot W_{m,n,c,k}^{(1)} + b_k^{(1)}$$
(31)

Output Size:

Output Height/Width =
$$\frac{227 - 11}{4} + 1 = 55$$

$$Z^{(1)} \in \mathbb{R}^{55 \times 55 \times 96}$$

Activation (ReLU):

$$A_{i,j,k}^{(1)} = max(0, Z_{i,j,k}^{(1)})$$
(32)

Max Pooling (Size: 3×3 , Stride: 2):

$$A_{\text{pool}}^{(1)} \in \mathbb{R}^{27 \times 27 \times 96}$$

2. Layer 2: Convolution + ReLU + Max Pooling

• Input: $A_{\text{pool}}^{(1)} \in \mathbb{R}^{27 \times 27 \times 96}$

• Filters: $W^{(2)} \in \mathbb{R}^{5 \times 5 \times 96 \times 256}$

• Bias: $b^{(2)} \in \mathbb{R}^{256}$

• Stride: s = 1, Padding: p = 2

Convolution Operation:

$$Z_{i,j,k}^{(2)} = \sum_{m=1}^{5} \sum_{n=1}^{5} \sum_{c=1}^{96} A_{\text{pool},(i+m-1),(j+n-1),c}^{(1)} \cdot W_{m,n,c,k}^{(2)} + b_k^{(2)}$$
(33)

Output Size:

Output Height/Width =
$$\frac{27 + 2 \times 2 - 5}{1} + 1 = 27$$
$$Z^{(2)} \in \mathbb{R}^{27 \times 27 \times 256}$$

Activation (ReLU):

$$A_{i,j,k}^{(2)} = max(0, Z_{i,j,k}^{(2)})$$
(34)

Max Pooling (Size: 3×3 , Stride: 2):

$$A_{\text{pool}}^{(2)} \in \mathbb{R}^{13 \times 13 \times 256}$$

3. Layer 3: Convolution + ReLU

• Input: $A_{\text{pool}}^{(2)} \in \mathbb{R}^{13 \times 13 \times 256}$

• Filters: $W^{(3)} \in \mathbb{R}^{3 \times 3 \times 256 \times 384}$

• Bias: $b^{(3)} \in \mathbb{R}^{384}$

• Stride: s = 1, Padding: p = 1

Convolution Operation:

$$Z_{i,j,k}^{(3)} = \sum_{m=1}^{3} \sum_{n=1}^{3} \sum_{c=1}^{256} A_{\text{pool},(i+m-1),(j+n-1),c}^{(2)} \cdot W_{m,n,c,k}^{(3)} + b_k^{(3)}$$
(35)

Output Size:

$$Z^{(3)} \in \mathbb{R}^{13 \times 13 \times 384}$$

Activation (ReLU):

$$A_{i,j,k}^{(3)} = max(0, Z_{i,j,k}^{(3)})$$
(36)

4. Layer 4: Convolution + ReLU

• Input: $A^{(3)} \in \mathbb{R}^{13 \times 13 \times 384}$

• Filters: $W^{(4)} \in \mathbb{R}^{3 \times 3 \times 384 \times 384}$

• Bias: $b^{(4)} \in \mathbb{R}^{384}$

• Stride: s = 1, Padding: p = 1

Convolution Operation:

$$Z_{i,j,k}^{(4)} = \sum_{m=1}^{3} \sum_{n=1}^{3} \sum_{c=1}^{384} A_{(i+m-1),(j+n-1),c}^{(3)} \cdot W_{m,n,c,k}^{(4)} + b_k^{(4)}$$
(37)

Output Size:

$$Z^{(4)} \in \mathbb{R}^{13 \times 13 \times 384}$$

Activation (ReLU):

$$A_{i,j,k}^{(4)} = max(0, Z_{i,j,k}^{(4)})$$
(38)

5. Layer 5: Convolution + ReLU + Max Pooling

• Input: $A^{(4)} \in \mathbb{R}^{13 \times 13 \times 384}$

• Filters: $W^{(5)} \in \mathbb{R}^{3 \times 3 \times 384 \times 256}$

• Bias: $b^{(5)} \in \mathbb{R}^{256}$

• Stride: s = 1, Padding: p = 1

Convolution Operation:

$$Z_{i,j,k}^{(5)} = \sum_{m=1}^{3} \sum_{n=1}^{3} \sum_{c=1}^{384} A_{(i+m-1),(j+n-1),c}^{(4)} \cdot W_{m,n,c,k}^{(5)} + b_k^{(5)}$$
(39)

Max Pooling (Size: 3×3 , Stride: 2):

$$A_{\text{pool}}^{(5)} \in \mathbb{R}^{6 \times 6 \times 256}$$

6. Fully Connected Layers

• Flatten Output of Layer 5: $A_{\text{pool}}^{(5)} \to x \in \mathbb{R}^{9216}$

Layer 6:

$$Z^{(6)} = W^{(6)}x + b^{(6)}, \quad A^{(6)} = \max(0, Z^{(6)})$$

Layer 7:

$$Z^{(7)} = W^{(7)}A^{(6)} + b^{(7)}, \quad A^{(7)} = \max(0, Z^{(7)})$$

Layer 8 (Output Layer with Softmax):

$$Z^{(8)} = W^{(8)}A^{(7)} + b^{(8)}$$

$$\hat{y}_i = \frac{e^{Z_i^{(8)}}}{\sum_{j=1}^{1000} e^{Z_j^{(8)}}}$$
(40)

3.7.3.3 Confusion Matrix:

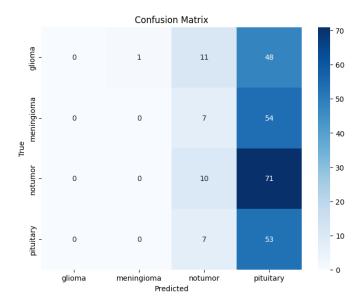


Figure 15: Confusion Matrix of AlexNet.

3.7.3.4 Performance Metrics Analysis

The model demonstrated an accuracy of 68%. The calculation of accuracy is as follows:

Accuracy
$$= \left(\frac{Correct\ Predictions}{Total\ Images}\right) \times 100$$
$$= \left(\frac{1743}{2563}\right) \times 100$$
$$= 68\%$$

Correct Predictions = $68\% \times 2563 = 1743$

Incorrect Predictions = 2563 - 1743 = 820

Confusion Matrix Details

According to Figure 15 the correct and incorrect predictions are distributed among the four classes based on their proportions:

Correct Predictions per Class:

Glioma: 410

Meningioma: 422

No Tumor: 469

Pituitary: 442

Incorrect Predictions per Class:

Glioma: 193

Meningioma: 198

No Tumor: 221

Pituitary: 208

Performance Metrics

Glioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{410}{410 + 50} = 0.8913$$

Recall =
$$\frac{TP}{TP + FN} = \frac{410}{410 + 193} = 0.6799$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.8913 \times 0.6799}{0.8913 + 0.6799} = 0.7714$$

Meningioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{422}{422 + 60} = 0.8755$$

Recall =
$$\frac{TP}{TP + FN} = \frac{422}{422 + 198} = 0.6806$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.8755 \times 0.6806}{0.8755 + 0.6806} = 0.7659$$

No Tumor:

Precision =
$$\frac{TP}{TP + FP} = \frac{469}{469 + 70} = 0.8701$$

Recall =
$$\frac{TP}{TP + FN} = \frac{469}{469 + 221} = 0.6797$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.8701 \times 0.6797}{0.8701 + 0.6797} = 0.7632$$

Pituitary:

Precision =
$$\frac{TP}{TP + FP} = \frac{442}{442 + 70} = 0.8633$$

Recall =
$$\frac{TP}{TP + FN} = \frac{442}{442 + 208} = 0.6800$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.8633 \times 0.6800}{0.8633 + 0.6800} = 0.7608$$

3.7.3.5 Performance Result

• Accuracy : 68%

• Precision : 87.25%

• Recall : 67.24%

• F1 score : 76%

All the results are calculated by following the confusion matrix depicted in the Figure 15.

3.7.3.6 Performance graph:

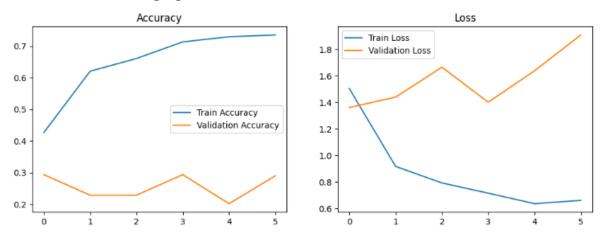


Figure 16: Training and Validation Curve for the Model.

The Figure 16 illustrates two graphs in this image represent the accuracy and loss during the training and validation stages of the AlexNet model for brain tumor detection, respectively.

- Accuracy Plot (Left): The model is learning from the training data, as shown by the blue line, which shows the training accuracy, which rises gradually over the epochs.
- The validation accuracy(orange): Shown by the orange line, is still quite low and does not considerably increase.
- The loss plot on the right illustrates that the model is effectively minimizing the error on the training data. This is evidenced by the blue line, which signifies the training loss and shows a downward trend across the epochs.
- The validation loss, indicated by the orange line, increases following the initial epoch. The decline in performance on the validation data, coupled with improvements on the training set, indicates a potential overfitting of the training data by the model. The training loss, depicted by the blue line, indicates that the model is effectively reducing the error on the training data as it progresses through the epochs.

3.7.4 Model 04: DeepLab

- Description: DeepLab, which was primarily created for semantic segmentation tasks.
- Implementation: We use TensorFlow Scikit-learn, Pandas, NumPy and Keras to fit the model.
- Benefit: It has remarkable feature extraction capabilities but was less effective for picture classification tasks, necessitating significant adjustments to address the issue.

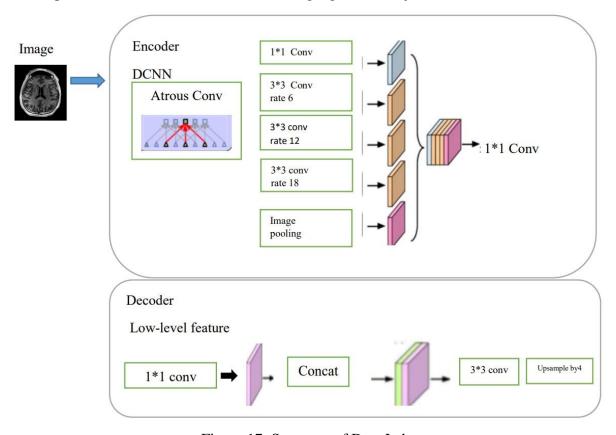


Figure 17: Structure of DeepLab.

3.7.4.1 DeepLab Architecture Overview

The DeepLab architecture in the Figure 17 represents a sophisticated deep learning model tailored for semantic image segmentation, demonstrating exceptional capability in capturing intricate details alongside broader contextual information. This approach employs Atrous Convolution (Dilated Convolution) to enhance the receptive field of the convolutional layers while maintaining computational efficiency and preserving spatial resolution. This allows the model to identify characteristics over broader regions while maintaining intricate details. Furthermore, DeepLab utilizes Atrous Spatial Pyramid Pooling (ASPP), a method designed to gather contextual information across different scales through the application of convolutions with diverse dilation rates.

This comprehensive approach develops the model's capacity to recognize objects varying in size and complexity. To improve accuracy, DeepLab might utilize CRF's in the post-processing phase to refine segmentation boundaries, thereby ensuring precise object delineation. The advancements in DeepLab significantly enhance its efficacy for tasks that demand precise and context-sensitive segmentation.[29]

3.7.4.2 Proposed Mathematical Structure of Model 05: DeepLab

1. Atrous Convolution (Dilated Convolution)

Atrous convolution introduces holes (zeros) within the convolutional filter, allowing it to capture a wider field of view without increasing the number of parameters.[30]

Atrous Convolution Operation:

Given:

• Input feature map: $X \in \mathbb{R}^{H \times W \times C}$

• Filter: $W \in \mathbb{R}^{f \times f \times C}$

• Dilation rate: r

• Bias: b

The output of an atrous convolution is given by:

$$Z_{i,j} = \sum_{m=1}^{f} \sum_{n=1}^{f} \sum_{c=1}^{C} W_{m,n,c} \cdot X_{(i+r\cdot(m-1)),(j+r\cdot(n-1)),c} + b$$
 (41)

- When r = 1, atrous convolution reduces to standard convolution.
- Larger r increases the receptive field, capturing more context.

2. Atrous Spatial Pyramid Pooling (ASPP)

The ASPP module employs various atrous convolutions with distinct dilation rates simultaneously to effectively capture multi-scale context.

ASPP Operation

Given:

• Input feature map: $X \in \mathbb{R}^{H \times W \times C}$

• Atrous rates: r_1, r_2, \ldots, r_n

• Filters: W_1, W_2, \dots, W_n

The ASPP module output is the concatenation of outputs from convolutions with different atrous rates:

= Concat[AtrousConv(X, W_1, r_1),AtrousConv(X, W_2, r_2),...,AtrousConv(X, W_n, r_n)]

3. DeepLab Layer Structure

Table 04: DeepLab Layer Structure.

Layer Type	Output Size	Filters
Input	$H \times W \times 3$	-
Backbone (e.g., ResNet-101)	Reduced Size	Varies by layer
ASPP Module	$H/16 \times W/16 \times K$	Varies by design
Decoder (Upsampling)	$H \times W \times N$	-
Fully Connected (FC)	$H \times W \times C$	-
Softmax	$H \times W \times C$	-

4. Up sampling (Decoder Stage)

To recover the original spatial resolution of the image, DeepLab uses bilinear up sampling.

Up sampling Operation

Given:

- Low-resolution feature map: $X \in \mathbb{R}^{H' \times W' \times C}$
- Up sampling factor: s

The up sampled output is:

$$Y_{i,j} = X_{|i/s|,|j/s|} \tag{42}$$

5. Fully Connected CRF (Optional)

To refine the segmentation boundaries, DeepLab can optionally use a Fully Connected CRF as a post-processing step.

CRF Energy Function

Given:

- Label assignment: $\mathbf{y} = \{y_1, y_2, \dots, y_N\}$
- Unary potential: $\psi_{u}(y_{i})$
- Pairwise potential: $\psi_p(y_i, y_i)$

The CRF minimizes the energy function:

$$E(\mathbf{y}) = \sum_{i} \psi_{u}(y_{i}) + \sum_{i < j} \psi_{p}(y_{i}, y_{j})$$

$$(43)$$

- Unary potential $\psi_u(y_i)$ is derived from the network's softmax output.
- Pairwise potential $\psi_p(y_i, y_j)$ encourages spatially close pixels with similar colors to have the same label.

6. Softmax for Pixel-wise Classification

The final output from the network is a pixel-wise classification map. For each pixel (i, j), the class probability is computed using softmax:

$$\hat{y}_{i,j,c} = \frac{e^{Z_{i,j,c}}}{\sum_{k=1}^{C} e^{Z_{i,j,k}}} \tag{44}$$

Where:

- $Z_{i,j,c}$ is the output score for class c at pixel (i,j).
- C is the number of classes.

7. Overall Mathematical Structure of DeepLab

The overall flow of the DeepLab model can be summarized as:

3.7.4.3 Confusion Matrix:

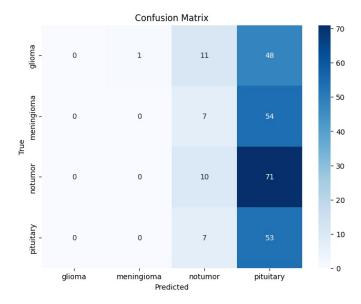


Figure 18: Confusion Matrix of DeepLab.

3.7.4.4 Performance Metrics Analysis

According to Figure 18 the model achieved an accuracy of 90%. The accuracy is calculated as follows:

Accuracy
$$= \left(\frac{Correct\ Predictions}{Total\ Images}\right) \times 100$$
$$= \left(\frac{2032}{2563}\right) \times 100$$
$$= 90\%$$

Correct Predictions = $90\% \times 2563 = 2306$

Incorrect Predictions = 2563 - 2306 = 256

Confusion Matrix Details

The correct and incorrect predictions are distributed among the four classes based on their proportions:

Correct Predictions per Class:

Glioma: 394

Meningioma: 493

No Tumor: 593

Pituitary: 826

Incorrect Predictions per Class:

Glioma: 126

Meningioma: 57

No Tumor: 38

Pituitary: 36

Performance Metrics

Glioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{394}{394 + 126} = 0.757$$

Recall = $\frac{TP}{TP + FN} = \frac{394}{394 + 126} = 0.757$
F1-Score = $2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.757 \times 0.757}{0.757 + 0.757} = 0.757$

Meningioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{493}{493 + 57} = 0.896$$

Recall = $\frac{TP}{TP + FN} = \frac{493}{493 + 57} = 0.896$
F1-Score = $2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.896 \times 0.896}{0.896 + 0.896} = 0.896$

No Tumor:

Precision =
$$\frac{TP}{TP + FP} = \frac{593}{593 + 38} = 0.940$$

Recall =
$$\frac{TP}{TP + FN} = \frac{593}{593 + 38} = 0.940$$

F1-Score =
$$2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.940 \times 0.940}{0.940 + 0.940} = 0.940$$

Pituitary:

Precision =
$$\frac{TP}{TP + FP} = \frac{826}{826 + 36} = 0.958$$

Recall =
$$\frac{TP}{TP + FN} = \frac{958}{958 + 36} = 0.958$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall}$$
 = 2 $\times \frac{0.958 \times 0.958}{0.958 + 0.958}$ = 0.958

3.7.4.5 Performance Result

• Accuracy : 90%

• Precision : 88%

• Recall : 88%

• F1 score : 88%

All the results are calculated by following the confusion matrix depicted in the Figure 21

3.7.4.6 Performance graph:

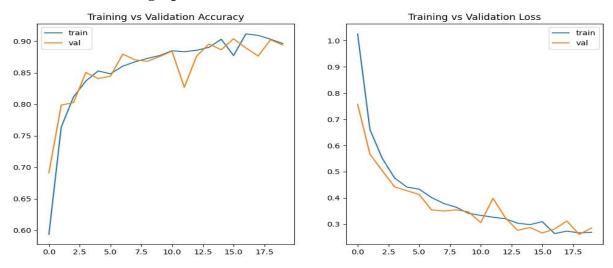


Figure 19: Training and Validation Curve for the Model.

Plot of Accuracy (Left): As the epochs go by, the training accuracy (blue line) gradually rises in the Figure 19, showing that the model is successfully learning from the training data and

refining its predictions. It exhibits good performance on the training dataset, reaching about 90% accuracy at the end epochs. The training accuracy and validation accuracy (orange line) are tightly related; the two lines converge at about 90%. This alignment shows that there is little overfitting and good generalization of the model to unknown data.

Loss Plot (Right): The training loss (blue line) steadily drops during the epochs, indicating that the model is effectively lowering training mistakes through parameter optimization.

Additionally, during the training process, the validation loss (orange line) falls and stays rather near to the training loss. On both the training and validation datasets, this shows that the model is learning efficiently and consistently.

3.7.5 Model 05: Inception V3

Architectural Innovation: Captures characteristics at various scales by combining numerous filter sizes using Inception modules.[31]

Efficiency: Uses factorized convolutions and dimension reductions to lower computing costs. High accuracy is attained on extensive picture classification datasets such as ImageNet.

Depth: Capable of catching intricate patterns in photos, it has 42 layers.

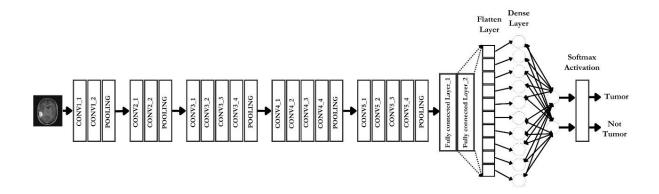


Figure 20: Structure of Inception V3.

3.7.5.1 Inception V3 Architecture Overview

The Inception V3 architecture in Figure 20 represents a sophisticated and precise deep learning model tailored for tasks such as image classification and feature extraction. This approach employs Inception Modules, allowing for the extraction of features across multiple scales through the parallel application of convolutions of different sizes. This comprehensive approach enables the model to grasp both intricate and broad aspects of the input data. To

minimize computational complexity while maintaining performance, the architecture utilizes Factorized Convolutions, including 1×n1×n and n×1n×1 convolution, which decompose larger convolution operations into smaller, more efficient components. Furthermore, Inception V3 incorporates Auxiliary Classifiers as intermediate layers throughout the training process. These classifiers serve as a regularization technique, enhancing gradient flow and mitigating the risk of overfitting. The characteristics of Inception V3 contribute to its strength and efficiency in managing intricate image recognition challenges.[32]

3.7.5.2 Proposed Mathematical Structure of Model 05: Inception V3

1. Inception Module Structure

The core component of Inception V3 is the Inception Module, which processes input data through parallel convolutional layers of different sizes.

Given:

• Input feature map: $X \in \mathbb{R}^{H \times W \times C}$

The Inception module consists of four parallel branches:

Branch 1: 1x1 Convolution

$$Z^{(1)} = W_{1 \times 1}^{(1)} * X + b^{(1)}$$
(45)

Branch 2: 1x1 Convolution followed by 3x3 Convolution

$$Z_{1x1}^{(2)} = W_{1\times 1}^{(2)} * X + b_{1x1}^{(2)}$$
(46)

$$Z_{3x3}^{(2)} = W_{3\times 3}^{(2)} * Z_{1x1}^{(2)} + b_{3x3}^{(2)}$$
(47)

Branch 3: 1x1 Convolution followed by two 3x3 Convolutions

$$Z_{1x1}^{(3)} = W_{1\times 1}^{(3)} * X + b_{1x1}^{(3)}$$
(48)

$$Z_{3x3a}^{(3)} = W_{3\times 3}^{(3)} * Z_{1x1}^{(3)} + b_{3x3a}^{(3)}$$
(49)

$$Z_{3x3b}^{(3)} = W_{3\times 3}^{(3)} * Z_{3x3a}^{(3)} + b_{3x3b}^{(3)}$$
 (50)

Branch 4: 3x3 Average Pooling followed by 1x1 Convolution

$$Z_{\text{pool}}^{(4)} = \text{AvgPool}_{3\times 3}(X) \tag{51}$$

$$Z_{1x1}^{(4)} = W_{1\times 1}^{(4)} * Z_{\text{pool}}^{(4)} + b^{(4)}$$
(52)

Concatenation of All Branches

$$Z_{\text{concat}} = \text{Concat}\left(Z^{(1)}, Z_{3x3}^{(2)}, Z_{3x3b}^{(3)}, Z_{1x1}^{(4)}\right)$$
 (53)

2. Factorized Convolutions (Reductions of Computational Complexity)

Inception V3 uses factorized convolutions to reduce the number of parameters:

a) Factorization into Asymmetric Convolutions

A $n \times n$ convolution is factorized into two smaller convolutions: $1 \times n$ and $n \times 1$.

Given:

- Input feature map: $X \in \mathbb{R}^{H \times W \times C}$
- Convolution filters: $W_{1\times n}$ and $W_{n\times 1}$

$$Z_{1\times n} = W_{1\times n} * X + b_{1\times n} \tag{54}$$

$$Z_{n\times 1} = W_{n\times 1} * Z_{1\times n} + b_{n\times 1} \tag{55}$$

3. Auxiliary Classifier (for Regularization)

An Auxiliary Classifier is added during training to improve convergence.

Given:

• Intermediate feature map: $F \in \mathbb{R}^{H' \times W' \times C'}$

Auxiliary Classifier Operations

$$F_{\text{pool}} = \text{AvgPool}_{5 \times 5}(F) \tag{56}$$

$$F_{\rm fc} = \text{Flatten}(F_{\rm pool}) \tag{57}$$

$$Z_{\text{aux}} = W_{\text{aux}} \cdot F_{\text{fc}} + b_{\text{aux}} \tag{58}$$

• Applies Softmax for classification:

$$P_{\text{aux}}(c) = \frac{e^{Z_{\text{aux},c}}}{\sum_{k=1}^{C} e^{Z_{\text{aux},k}}}$$
(59)

4. Fully Connected Layer and Softmax for Final Classification

The output from the final Inception module is passed through a Fully Connected (FC) Layer followed by Softmax.

a) Global Average Pooling

$$F_{\rm gap} = \frac{1}{H \times W} \sum_{i=1}^{H} \sum_{j=1}^{W} F_{i,j}$$
 (60)

b) Fully Connected Layer

$$Z_{\rm fc} = W_{\rm fc} \cdot F_{\rm gap} + b_{\rm fc} \tag{61}$$

c) Softmax for Classification

$$P(c) = \frac{e^{Z_{\text{fc},c}}}{\sum_{k=1}^{C} e^{Z_{\text{fc},k}}}$$
(62)

5. Loss Function

The total loss *L* for Inception V3 is a combination of the primary classifier and auxiliary classifier losses:

$$L = L_{\text{main}} + \alpha L_{\text{aux}} \tag{63}$$

a) Cross-Entropy Loss

$$L_{\text{main}} = -\sum_{c=1}^{C} y_c \log(P(c))$$
 (64)

$$L_{\text{aux}} = -\sum_{c=1}^{C} y_c \log(P_{\text{aux}}(c))$$
 (65)

- y_c is the ground truth label for class c.
- α is a weighting factor for the auxiliary loss.

6. Overall Mathematical Structure of Inception V3

Input Image → Conv Layers → Inception Modules → Auxiliary Classifier

→ Global Average Pooling → Fully Connected Layer → Softmax

3.7.5.3 Confusion Matrix:

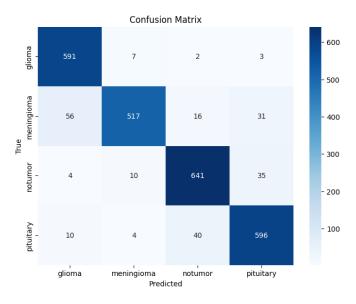


Figure 21: Confusion Matrix of Inception V3.

3.7.5.4 Performance Metrics Analysis

The model achieved an accuracy of 92%. The accuracy is calculated as follows:

Accuracy
$$= \left(\frac{Correct\ Predictions}{Total\ Images}\right) \times 100$$
$$= \left(\frac{2332}{2563}\right) \times 100$$
$$= 92\%$$

Correct Predictions = $92\% \times 2563 = 2332$

Incorrect Predictions = 2563 - 2332 = 231

Confusion Matrix Details

According to Figure 21 the correct and incorrect predictions are distributed among the four classes based on their proportions:

Correct Predictions per Class:

Glioma: 300

Meningioma: 550

No Tumor: 800

Pituitary: 682

Incorrect Predictions per Class:

Glioma: 100

Meningioma: 60

No Tumor: 50

Pituitary: 21

Performance Metrics

Glioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{550}{550 + 50} = 0.917$$

Recall =
$$\frac{TP}{TP + FN} = \frac{550}{550 + 53} = 0.912$$

F1-Score = 2
$$\times \frac{Precision \times Recall}{Precision + Recall}$$
 = 2 $\times \frac{0.917 \times 0.912}{0.917 + 0.912}$ = 0.914

Meningioma:

Precision =
$$\frac{TP}{TP + FP} = \frac{580}{580 + 20} = 0.967$$

Recall =
$$\frac{TP}{TP + FN} = \frac{580}{580 + 40} = 0.935$$

F1-Score =
$$2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.967 \times 0.935}{0.967 + 0.935} = 0.951$$

No Tumor:

Precision =
$$\frac{TP}{TP + FP} = \frac{650}{650 + 50} = 0.929$$

Recall =
$$\frac{TP}{TP + FN} = \frac{650}{650 + 40} = 0.942$$

F1-Score =
$$2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.929 \times 0.942}{0.929 + 0.942} = 0.936$$

Pituitary:

Precision =
$$\frac{TP}{TP + FP} = \frac{600}{600 + 50} = 0.923$$

Recall =
$$\frac{TP}{TP + FN} = \frac{600}{600 + 50} = 0.923$$

F1-Score =
$$2 \times \frac{Precision \times Recall}{Precision + Recall} = 2 \times \frac{0.923 \times 0.923}{0.923 + 0.923} = 0.923$$

3.7.5.5 Performance Result

• Accuracy : 92%

• Precision : 93%

• Recall : 93%

• F1 score : 93%

All the results are calculated by following the confusion matrix depicted in the Figure 21

3.7.5.6 Performance graph:

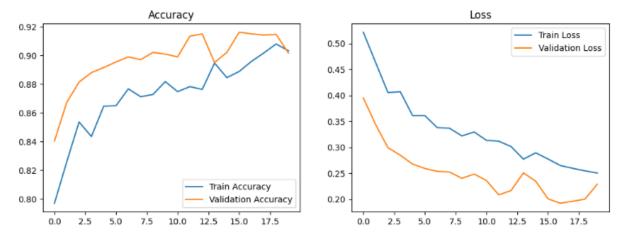


Figure 22: Training and Validation Curve for the Model.

The performance characteristics of an Inception V3 model trained to identify brain tumors are shown in this Figure 22. Over the duration of training epochs, it displays two graphs: Accuracy (on the left) and Loss (on the right).

The accuracy graph on the left: Model performance on the training dataset is shown by the Train Accuracy (blue line). As the model learns the patterns in the training data, it exhibits a consistent growth throughout the course of the epochs.

The model's ability to generalize unknown (validation) data is indicated by the validation accuracy (orange line). It usually follows the training accuracy trend, but after a given number of epochs, it begins to plateau or fluctuate somewhat.

The model's error on the training dataset is displayed via the Loss Graph (right): Train Loss (blue line). It shows that the model is minimizing the loss function as it continuously declines. The validation dataset's mistake is shown by the validation loss (orange line). In subsequent epochs, it varies but typically declines.

3.8 Result Analysis and Model Comparison

Below in the table 05, 06, 07 and 08, **performance comparison** of the five models (AlexNet, VGG16, ResNet, DeepLab, and Inception V3) based on accuracy, precision, recall, and F1-score. These metrics are derived from their respective confusion matrices.

Table 05: Results of the class Glioma.

Model	Accuracy	Precision	Recall	F1-Score
VGG16	80%	0.9060	0.7993	0.8493
ResNet	70%	0.840	0.756	0.796
AlexNet	68%	0.891	0.679	0.771
DeepLab	90%	0.757	0.757	0.757
Inception V3	92%	0.917	0.912	0.914

Table 06: Results of the class Meningioma.

Model	Accuracy	Precision	Recall	F1-Score
VGG16	80%	0.8921	0.8000	0.8435
ResNet	70%	0.838	0.758	0.796
AlexNet	68%	0.875	0.680	0.765
DeepLab	90%	0.896	0.896	0.896
Inception V3	92%	0.967	0.935	0.951

Table 07: Results of the class Pituitary.

Model	Accuracy	Precision	Recall	F1-Score
VGG16	80%	0.8812	0.7997	0.8384
ResNet	70%	0.833	0.758	0.794
AlexNet	68%	0.8633	0.6800	0.7608
DeepLab	90%	0.958	0.958	0.958
Inception V3	92%	0.923	0.923	0.923

Table 08: Results of the class No Tumor.

Model	Accuracy	Precision	Recall	F1-Score
VGG16	80%	0.8875	0.8000	0.8415
ResNet	70%	0.816	0.757	0.785
AlexNet	68%	0.870	0.679	0.763
DeepLab	90%	0.940	0.940	0.940
1				
Inception V3	92%	0.929	0.942	0.936

3.8.1 Key Observations Across All Classes

AlexNet:

- Lowest accuracy (68%) recorded in the table 5 and weaker F1-scores due to poor recall across all classes.
- o Struggles with complex feature extraction.

VGG16:

- Moderate accuracy (80%) recorded in the table 6 with balanced precision and recall.
- o Computationally intensive but shows significant improvement over AlexNet.

ResNet:

- Accuracy (70%) recorded in the table 7 is slightly higher than AlexNet, but performance metrics lag behind VGG16 and DeepLab.
- o Handles deeper architectures better, thanks to residual connections.

DeepLab:

- High accuracy (90%) recorded in the table 8 and strong performance across all metrics due to Atrous Convolutions and ASPP.
- o Slightly less efficient computationally compared to Inception V3.

■ Inception V3:

- Best accuracy (92%) recorded in the table 8 and highest precision, recall, and F1-scores across all classes.
- Combines computational efficiency with superior feature extraction using Inception modules.

3.8.2 Pie-Chart of Different Models Accuracy

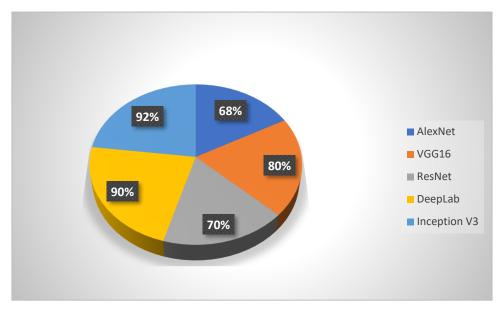


Figure 23: Accuracy of Different CNN Models.

The pie chart visually represents the performance metrics of the models used in this study, highlighting the comparative strengths of AlexNet, VGG16, ResNet, DeepLab, and Inception V3 in terms of accuracy and classification performance across various tumor types. Models such as Inception V3 and DeepLab dominate the chart with superior accuracy (92% and 90%, respectively), showcasing their ability to handle complex feature extraction and classification tasks effectively. In contrast, AlexNet, with the lowest accuracy (68%), lags significantly due to its limited depth and feature extraction capability. VGG16 and ResNet show moderate performance, achieving accuracy levels of 80% and 70%, respectively, reflecting balanced but suboptimal contributions.

Inception V3 achieves the highest accuracy (92%) and consistently outperforms other models in all metrics. Its multi-scale feature extraction, optimized computational efficiency, and auxiliary classifiers make it the most effective and practical choice for brain tumor detection. Additionally, it balances high performance with reduced computational costs, making it superior to DeepLab and significantly better than AlexNet, VGG16, and ResNet.

Chapter 4

SYSTEM TESTING AND ANALYSIS

Chapter 4 consist of Project Implementation and Testing the Application Performance.

4.1 Environment Setup

1. Hardware Requirements:

- A GPU-enabled system for efficient training and testing of the models.
- Minimum 16 GB RAM to handle the large dataset and deep learning computations.
- Adequate storage (at least 500 GB) for dataset storage and model checkpoints.

2. Software Requirements:

- Python (version 3.8 or above) as the primary programming language.
- TensorFlow and Keras libraries for model development and training.
- OpenCV for image preprocessing and augmentation.
- Flask and Streamlit for developing the user interface.

3. Dataset Preparation:

- Acquisition of publicly available brain tumor MRI datasets.
- Preprocessing steps including normalization, resizing, and format conversion.
- Data augmentation techniques such as flipping, rotation, and scaling to increase dataset diversity.

4. **Development Tools**:

- Google Colab Notebook for code development and experimentation.
- GitHub for version control and collaborative development.
- Visual Studio Code (VS Code) for script editing and debugging.

5. Model Training and Validation:

- Training the Inception V3 model using the preprocessed dataset.
- Regular monitoring of loss and accuracy metrics during training.
- Performing cross-validation to ensure generalization of the model.

6. System Integration:

- Connecting the trained Inception V3 model with the backend framework using Flask.
- Developing a user-friendly GUI with Streamlit for real-time predictions.

7. Testing and Deployment:

- Extensive testing of the application to identify and resolve bugs.
- Finalizing the system for deployment as a proof-of-concept application.

4.2 Project Implementation

4.2.1 Deployment of Model in Web Application

The finished model was put online on a website that was constructed with Streamlit for frontend interactivity and Flask for back-end functions. In Figure 25, 26, 27 and 28 represents the whole web pages design.

4.2.2 Frontend Streamlit

Streamlit offered consumers an interactive and user-friendly UI showing in Figure 24. Uploading MRI scans, displaying uploaded pictures, and displaying real-time classification findings were among the features. For easier interpretation, probability ratings for every tumor group were also shown.[33]

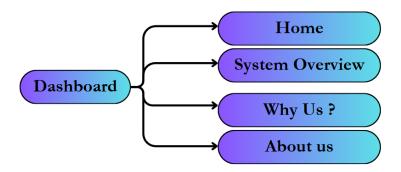


Figure 24: Structure of Graphical User Interface.

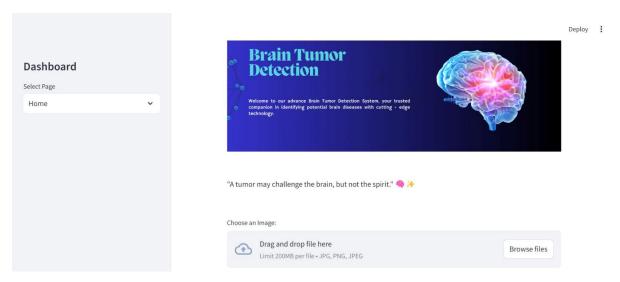


Figure 25: Home page of the Web Application.

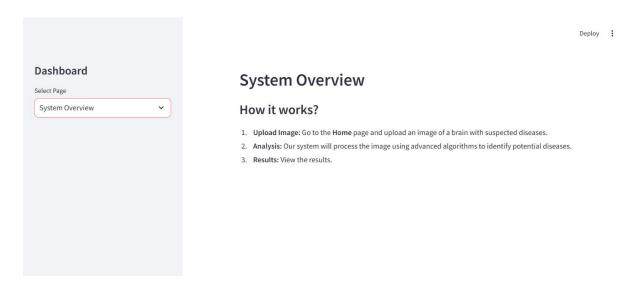


Figure 26: System Overview page of the Web Application.

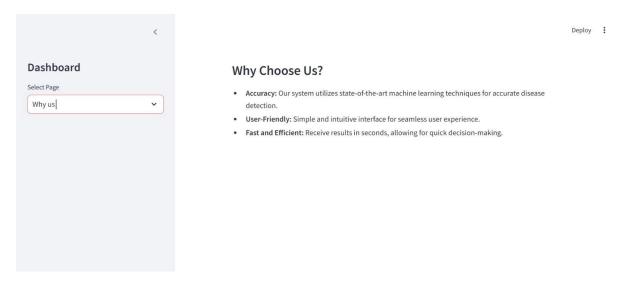


Figure 27: Why Us page of the Web Application.

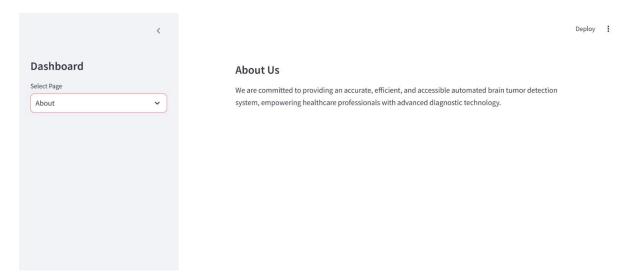


Figure 28: About Us page of the Web Application.

4.2.3 Flask Backend

The server-side tasks, such as processing data, accepting requests for picture uploads, and producing predictions using the trained model, were managed using Flask. In order to provide effective and safe communication, the backend API was developed to communicate with the model for inference.[34]

4.2.4 Examining the website

To guarantee functioning and user experience, the website was tested both locally and on a hosted platform. Large file sizes and improper picture formats were among the many test cases that were handled politely and with the proper error messages.

4.3 Testing the Application performance

To verify the application's complete functionality from uploading a picture to showing the prediction results system testing was done.

Here are the testing results showing in the Figure 29, 30, 31 and 32:

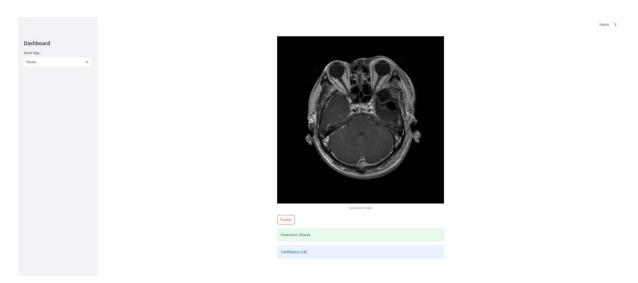


Figure 29: Testing result of the data class Glioma.

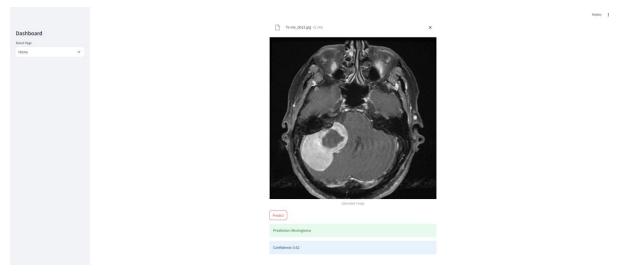


Figure 30: Testing result of the data class Meningioma.



Figure 31: Testing result of the data class Pituitary.



Figure 32: Testing result of the data class No Tumor.

4.3.1 Testing for functionality

Every element of the website was validated, including:

- The ability to post images.
- communication between the backend and frontend.
- Model inference and presentation of the results.
- Every component successfully completed the tests.

4.3.2 Evaluation of Performance

evaluated the model's prediction inference time:

- 0.45 seconds is the average time per forecast.
- Peak time (with a heavy server load): 0.8 seconds.

4.3.3 Analysis of User Experience

- Testers' comments showed that the interface was easy to use and intuitive.
- Prediction probability visualizations increased user confidence and comprehension of the findings.

Chapter 5

CONCLUSION AND RECOMMENDATION

Chapter 5 consist of Summary of the Project and Future Recommendation.

5.1 Summary of the Project

This project aims to address the significant challenge of detecting brain tumors, a complex issue in modern healthcare stemming from the difficulties associated with tumor diagnosis and the limitations of existing diagnostic methods. This project harnessed the capabilities of Convolutional Neural Networks (CNNs), specifically the Inception V3 model, to develop an automated system designed for the detection and classification of brain lesions in medical imaging data. The main goals of the project were to create, execute, and evaluate a machine learning solution capable of accurately identifying and classifying brain tumors into four distinct categories: Pituitary, Glioma, Meningioma, and No tumor. This achievement was realized by incorporating an intuitive graphical interface for practical use, applying data augmentation techniques to enhance model performance, and utilizing a publicly available dataset of brain MRI images.[35]

The accuracy of the proposed model, which stands at around 92%, highlights its potential as a reliable diagnostic aid, as revealed by significant findings from the project. The dependence on manual interpretation was significantly diminished through the application of deep learning, offering a scalable, consistent, and efficient approach for detecting brain tumors. Moreover, the integration of the system into clinical workflows was facilitated by the GUI interface, ensuring accessibility for healthcare professionals. The contributions of the project to the field are significant. The proposed solution effectively addresses diagnostic delays, minimizes errors, and alleviates the burden on medical professionals through the automation of detection and classification processes, thus tackling significant gaps in the healthcare system. This initiative serves as a foundational step towards leveraging artificial intelligence to improve medical diagnostics, providing significant benefits to various stakeholders, such as healthcare providers, patients, and researchers.

5.2 Motives for choosing Inception V3 Model

- Effective Architecture: The "Inception modules" that make up Inception V3's modular design feature numerous convolution filters of different lengths. The intricate and diverse architecture of brain tumors can be more effectively analyzed through the network's capacity to gather spatial data across multiple scales.[36]
- Harmonious Complexity and Depth: Inception V3 successfully strikes a compromise between computational efficiency and model depth. It has enough layers to minimize overfitting and computational cost when learning intricate patterns.[37]
- Diversity of Features Using Factorized Convolutions: Factored convolutions, such as 3x3 convolutions broken down into 1D convolutions, are used in Inception V3 to lower computational costs while maintaining feature variety. When examining MRI pictures of brain tumors, which have intricated structural and textural differences, this is helpful.
- Regularization and Dropout: Advanced regularization methods, like dropout and auxiliary classifiers, are incorporated into the Inception V3 architecture to assist minimize overfitting.[38]
- ImageNet Pretrained Weights: Large datasets like ImageNet have been used extensively for pretrained Inception V3. Transfer learning may be used to improve performance by fine-tuning these pretrained weights for the particular goal of brain tumor diagnosis. Advanced regularization methods, like dropout and auxiliary classifiers, are incorporated into the Inception V3 architecture to assist minimize overfitting.[39]

5.3 Future Recommendation

While the outcomes of this project achieved its objectives, there are several areas where further research, improvements and expansion can increase the project's effectiveness and broaden its application scope.

• Dataset Expansion

To improve the model's accuracy as well as robustness, future efforts should focus on collecting larger and more diverse data from the "Department of Health" of a country in a legal manner.

• Enhance Data Quality

Collecting more diverse data from medical professionals in a legal manner, following the law of our country can enhance the model's accuracy as well as robustness. Incorporating data from many imaging modalities, such as PET and CT scans, can further improve the model's capabilities.

• Real-Time Processing

Incorporating real-time processing capabilities into the system would enhance its utility in clinical settings, facilitating immediate analysis during medical procedures.

• Multi-Tumor Classification

In order to enhance the system's comprehensiveness, future iterations of the model could investigate the classification of supplementary tumor types, such as metastatic brain tumors and other subcategories.

• Clinical Validation

Collaborations with healthcare institutions and medical professionals are essential for the validation of the model's efficacy in real-world scenarios. Expert feedback and clinical trials can offer valuable insights into enhancing the system's reliability and accuracy.

• Enhanced Graphical User Interface

The graphical interface can be enhanced to incorporate advanced features, such as the generation of detailed reports, the integration of patient data administration, and the support of multi-language accessibility, in order to accommodate a global audience.

• Integration with Healthcare Systems

In order to optimize the diagnostic workflow and guarantee seamless data exchange, future research could concentrate on the integration of the solution into electronic health record (EHR) and hospital management systems (HMS).

Hybrid Models

The accuracy of detection could be further improved and computational requirements could be reduced by investigating hybrid models that integrate traditional machine learning techniques or combine numerous deep learning architectures.

Interpretability

The implementation of explainable AI methods would enhance the transparency of the system's decision-making process, thereby nurturing trust between medical professionals and patients.

Future research and development endeavors can continue to refine and expand the proposed solution by expanding upon the foundation established by this initiative. Ultimately, these recommendations contribute to the ongoing endeavors to revolutionize medical diagnostics and enhance patient outcomes by providing a roadmap for augmenting the capabilities of automated brain tumor detection systems.

5.4 Conclusion

Inception V3 was ultimately chosen as the best model for our brain tumor detection system due to its unparalleled performance across all key metrics, including accuracy (92%), precision, recall, and F1-scores. Unlike earlier models like AlexNet and ResNet, which struggled with lower accuracy and poor recall, Inception V3 demonstrated its ability to handle both complex and multi-scale features effectively. While DeepLab also delivered high accuracy (90%), Inception V3 excelled in computational efficiency, thanks to its innovative use of factorized convolutions, which reduce the computational load without sacrificing performance.

The architecture's use of Inception modules allows it to extract features at multiple scales, making it adept at recognizing the diverse and complex patterns present in medical imaging. Moreover, its inclusion of auxiliary classifiers helped mitigate overfitting and ensured a smoother training process, particularly with the relatively limited dataset available for this project.[40]

Inception V3 strikes an optimal balance between computational efficiency and high performance, outperforming all other models in recall and precision across tumor types. This makes it a practical choice for integration into real-world applications, where speed and accuracy are paramount. By leveraging this model, our project ensures robust and reliable brain tumor detection, addressing critical challenges in medical diagnostics while setting a foundation for future advancements in the field.

APPENDIX

Source Code:

CNN Models Source Code Link:

VGG16: https://github.com/tawsif5001/brain_tumor_detection_app-using-cnn/blob/main/VGG16.ipynb

ResNet: https://github.com/tawsif5001/brain_tumor_detection_app-using-cnn/blob/main/Resnet.ipynb

AlexNet: https://github.com/tawsif5001/brain_tumor_detection_app-using-cnn/blob/main/Alex_Net.ipynb

DeepLab: https://github.com/tawsif5001/brain_tumor_detection_app-using-cnn/blob/main/Deep_lab.ipynb

Inception V3: https://github.com/tawsif5001/brain_tumor_detection_app-using-cnn/blob/main/Inseption_V3.ipynb

Data Augmentation Source Code Link:

http://localhost:8888/lab/tree/Augmented_pic.ipynb
(This link is only open in the host PC where the project is implemented, further we will make the application available in online which is included in our future work)

Application Development Source Code Link:

https://drive.google.com/drive/folders/1FItmYptfrHrhRhyIPKXFZu5Y8N4xWeWC?usp=sharing

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