CHAPTER 1

1.1 Introduction

Brain tumors represent a significant health concern, affecting thousands of individuals worldwide. Brain tumor diagnosis and classification complexity necessitate advanced medical imaging techniques and robust analytical methods. Traditional diagnostic approaches often rely on the expertise of radiologists, which can be time-consuming and subject to human error. As a result, there is a growing demand for automated systems that can assist in detecting and classifying brain tumors with high accuracy.

1.2 Problem Statements

Despite advancements in medical imaging technologies such as Magnetic Resonance Imaging (MRI), the manual interpretation of MRI scans remains challenging due to the intricate nature of brain tumors. The key problems addressed in this project include:

- **Inconsistency in Diagnosis:** Variability in radiologists' interpretations can lead to inconsistent diagnoses.
- **Time Constraints:** The increasing volume of imaging data can overwhelm healthcare professionals, delaying diagnosis and treatment.
- **Need for Automation:** There is an urgent need for automated systems that can accurately detect and classify brain tumors to support clinical decision-making.

1.3 Motivation

The motivation behind this project stems from the critical need for timely and accurate brain tumor diagnosis. Early detection significantly improves treatment outcomes and patient survival rates. By leveraging advanced machine learning techniques, particularly Convolutional Neural Networks (CNNs), this project aims to develop an automated system that enhances the accuracy and efficiency of brain tumor detection and classification. The integration of AI into medical imaging promises to reduce the burden on healthcare professionals while ensuring reliable diagnostic support.

1.4 Background: Brain Tumors

Brain tumors are abnormal growths of cells within the brain or surrounding tissues. They can be classified into two main categories: primary tumors, which originate in the brain, and secondary tumors, which spread from other parts of the body. The World Health Organization (WHO) classifies brain tumors into different grades based on their malignancy and growth rates:

- **Grade I:** Benign tumors with slow growth.
- **Grade II:** Low-grade malignant tumors that may recur.
- **Grade III:** Malignant tumors with aggressive growth.
- **Grade IV:** Highly malignant tumors, such as glioblastomas.

The complexity of tumor types necessitates advanced imaging techniques for accurate diagnosis, with MRI being the most widely used modality due to its high-resolution images.

1.5 Project Goals

The primary goal of this project is to develop a robust automated system for detecting and classifying brain tumors using deep learning techniques. Specific goals include:

- To preprocess MRI images effectively for optimal model performance.
- To construct a CNN model capable of accurately classifying different types of brain tumors.
- To evaluate the model's performance against existing diagnostic methods.

1.6 Objectives

To achieve the project goals, the following objectives have been set:

- Implement a comprehensive image preprocessing pipeline that includes noise reduction, normalization, and augmentation.
- Design and train a CNN model tailored for brain tumor classification.
- Assess the model's accuracy, precision, recall, and F1-score using standard evaluation metrics.
- Develop a user-friendly interface for clinicians to utilize the model in real-world scenarios.

1.7 Proposed Idea

This project proposes a hybrid approach that combines advanced image processing techniques with deep learning algorithms to enhance brain tumor detection and classification accuracy. By utilizing transfer learning with pre-trained models such as EfficientNet or VGGNet, we aim to leverage existing knowledge while minimizing training time on limited datasets. The proposed system will not only improve diagnostic efficiency but also provide visual explanations through techniques like Grad-CAM, allowing clinicians to understand model decisions better.

1.8 Importance of Early Detection

Early tumor detection can significantly improve patient outcomes. Automated detection methods can assist radiologists, reduce diagnosis time, and improve treatment efficiency.

CHAPTER 2

2.1 Existing Approaches in Brain Tumor Detection

Existing methods for brain tumor detection often leverage various imaging techniques, with MRI being the most popular due to its non-invasive nature and excellent soft tissue contrast. Traditionally, manual segmentation of 3D MRI images relies on the expertise of healthcare professionals. However, automated methods are increasingly being explored to improve efficiency and reduce variability. Machine learning-based techniques, including those using supervised approaches and principal component analysis for feature extraction, have shown promise in detecting the presence of tumors. Deep learning approaches, particularly those employing Convolutional Neural Networks (CNNs), have demonstrated outstanding efficacy in medical image processing tasks, including brain tumor detection, often outperforming other machine learning classifiers. Recent studies have fine-tuned state-of-the-art models like YOLOv7 using transfer learning to accurately identify the presence and location of brain tumors in MRI images. Hybrid approaches combining CNNs with other techniques like Long Short Term Memory (LSTM) networks and Vision Transformers (ViT) with Gated Recurrent Units (GRU) are also being explored to enhance detection accuracy.

2.2 Existing Approaches in Brain Tumor Classification

Brain tumor classification aims to categorize tumors into different types, such as glioma, meningioma, and pituitary tumors, or grades based on their malignancy. Traditional methods involve histopathological analysis, but machine learning and deep learning techniques offer automated alternatives. Supervised learning methods with feature extraction using techniques like principal component analysis have been employed for classification. Deep learning-based automatic multimodal classification techniques, utilizing pre-trained CNN networks like VGG16 and VGG19 for feature extraction, have also been proposed. These methods often involve multiple stages, including image preprocessing, feature extraction, feature selection, and classification using algorithms like Extreme Learning Machine (ELM). More recent approaches use AI techniques and pre-trained models (e.g., Xception, ResNet50, InceptionV3, VGG16, MobileNet) to enhance MRI-based brain tumor classification.

2.3 Deep Learning Methods for Brain Tumor Analysis

Deep learning methods, especially CNNs, have become prominent in brain tumor analysis due to their ability to automatically learn complex features from medical images. These methods have shown superior performance compared to traditional machine learning techniques in both detection and classification tasks. Deep learning models are used for segmentation, feature extraction, and classification. Techniques such as fine-tuning pre-trained models, using attention mechanisms like CBAM, and incorporating spatial pyramid pooling (SPPF) and bi-directional feature pyramid networks (BiFPN) are employed to improve the accuracy and sensitivity of deep learning models in detecting and classifying brain tumors. Hybrid models combining CNNs with other deep learning architectures like LSTMs and Vision Transformers are also being explored to leverage the strengths of different approaches.

2.4 Functional Requirements

Based on the code provided, the core functional requirements of the brain tumor detection and classification system are as follows:

- **Image Input**: The system must accept MRI images as input.
- **Preprocessing**: The system must preprocess the images to enhance relevant features and standardize the input. This includes:
    - Grayscale conversion
    - Noise reduction using median filtering
    - Resizing to a standard dimension (240x240)
    - Normalization
    - Thresholding
    - Morphological operations (dilation)
- **Tumor Detection**: The system must accurately detect the presence or absence of a brain tumor in the input image.
- **Tumor Classification**: If a tumor is detected, the system must classify it into one of the specified categories (glioma, meningioma, notumor, pituitary).
- **Result Output**: The system must provide clear and interpretable results, including:
    - The detected presence or absence of a tumor.
    - The predicted class of the tumor, if detected.
- **User Interface**: A graphical user interface (GUI) must allow users to easily:
    - Load MRI images & View the loaded image.
    - Trigger the detection and classification process & View the results.

2.5 Non-Functional Requirements

- **Accuracy**: The system must achieve a high level of accuracy in both tumor detection and classification.
- **Speed**: The system should provide results in a reasonable time frame to be useful in a clinical setting.
- **Reliability**: The system must consistently produce accurate results.
- **Usability**: The GUI must be intuitive and easy to use for healthcare professionals.
- **Scalability**: The system should be able to handle a large volume of images.
- **Maintainability**: The code should be well-structured and documented to facilitate maintenance and updates.
- **Interpretability**: The model should be interpretable, providing insights into the factors influencing its decisions, which can be achieved using techniques such as LIME, SHAP, and Attention Maps.

2.6 Brain Tumor Types

Brain tumors are classified based on their growth rate, location, and potential to spread. The two main types are:

Benign Tumors

These tumors grow slowly and do not spread to other tissues. They are typically non-cancerous and can often be removed with surgery. However, depending on their location, they may still pose risks by compressing surrounding brain structures.

Examples of benign brain tumors include:

- **Meningiomas:** Originate in the meninges (protective layers covering the brain and spinal cord). They account for about 30% of brain tumors and are usually non-cancerous.
- **Pituitary Adenomas:** Develop in the pituitary gland, affecting hormone production. Most are benign but can cause hormonal imbalances.
- **Schwannomas:** Affect the Schwann cells of the nervous system, commonly occurring in the vestibular nerve (also known as acoustic neuromas).

Malignant Tumors

Malignant tumors are aggressive, grow rapidly, and can invade surrounding brain tissues. They are cancerous and may require intensive treatment, including surgery, chemotherapy, and radiation therapy.

Examples of malignant brain tumors include:

- **Glioblastoma Multiforme (GBM):** The most aggressive primary brain tumor, highly infiltrative, and difficult to treat. It has a poor prognosis despite intensive therapy.
- **Astrocytomas:** Arise from astrocytes, a type of glial cell. They can range from low-grade (slow-growing) to high-grade (fast-growing, like glioblastomas).
- **Medulloblastomas:** Common in children, these tumors develop in the cerebellum and can spread through the cerebrospinal fluid.

2.7 Existing Detection Techniques

Brain tumor detection relies on imaging techniques such as MRI and CT scans. Various methods exist to analyze these images, ranging from manual interpretation to automated AI-based systems.

Manual MRI Analysis

- Traditionally performed by radiologists using MRI scans.
- Requires expert interpretation to differentiate between normal and abnormal brain tissue.
- Prone to **human errors**, misinterpretation, and **subjectivity** in diagnosis.
- time-consuming and expensive.

Machine Learning-Based Detection

- Uses algorithms to extract meaningful features from MRI images.
- Common classifiers include:
    - **Support Vector Machines (SVM):** Separates tumor and non-tumor regions using hyperplanes.
    - **Decision Trees:** Classifies tumors based on extracted features like texture and intensity.
    - **Random Forests:** Uses multiple decision trees for better classification accuracy.
- Performance depends on the quality of feature extraction and dataset size.

Deep Learning-Based Detection

- Uses **Convolutional Neural Networks (CNNs)** for automatic feature extraction and classification.
- Learns from large datasets without requiring handcrafted features.
- Offers higher accuracy than traditional machine learning models.
- Can handle complex patterns and variations in tumor appearance.

2.8 Deep Learning in Medical Imaging

Deep learning, a subset of AI, has transformed medical imaging by enabling automated diagnosis and decision-making. In brain tumor detection, deep learning models process MRI scans to identify abnormalities with high accuracy.

Convolutional Neural Networks (CNNs) in Tumor Detection

CNNs are the most widely used deep learning architectures for medical imaging. They work by processing images through multiple layers:

- **Convolutional Layers:** Extract important features (edges, textures, patterns).
- **Pooling Layers:** Reduce the spatial dimensions, improving efficiency.
- **Fully Connected Layers:** Combine extracted features for classification.

Advantages of CNN-based tumor detection:

- Eliminates the need for manual feature extraction.
- Can detect subtle patterns in MRI scans that are difficult for humans to recognize.
- Provides **faster and more accurate** results than traditional methods.

Applications of Deep Learning in Medical Imaging

- **Tumor Segmentation:** Identifying and outlining tumor regions in MRI scans.
- **Classification:** Differentiating between benign and malignant tumors.
- **Prediction:** Assessing tumor progression and treatment response.

Deep learning continues to evolve, with new architectures like **U-Net** and **Transformers** improving medical image analysis. With sufficient data and computational power, these models can assist radiologists in making quicker and more reliable diagnoses.

CHAPTER 3

3.1 Hardware Requirements

- **Processor**: Intel Core i7 (or higher) / AMD Ryzen 7+
- **RAM**: Minimum 16 GB (32 GB recommended for deep learning)
- **GPU**: NVIDIA RTX 3060 / 3080 (or equivalent) with CUDA support
- **Storage**: At least 512 GB SSD for faster data processing
- **Other**: High-resolution display for visualization

3.2 Software Requirements

- **Operating System**: Windows 10/11, Ubuntu 20.04+, or macOS
- **Programming Language**: Python 3.x
- **Libraries and Frameworks**:
    - TensorFlow / PyTorch (for deep learning models)
    - OpenCV (for image processing)
    - NumPy, Pandas (for data handling)
    - Matplotlib, Seaborn (for visualization)
    - SciPy, Scikit-learn (for additional preprocessing)
    - Keras (for CNN implementation)

3.3 Dataset Description

The dataset consists of MRI images for brain tumor detection and classification. It is divided into two subsets: detection and classification. The detection dataset labels images as "Tumor" or "No Tumor," while the classification dataset categorizes tumor types. Images are sourced from open medical databases and hospitals. Data annotation ensures high-quality labels. Various preprocessing techniques are applied to standardize images. The dataset is balanced to prevent bias. Image resolution and format are kept consistent. Augmentation techniques enhance model robustness. Proper dataset handling ensures better generalization in real-world applications.

Dataset collection is a crucial step in developing an accurate and efficient brain tumor detection system. The quality and quantity of the dataset directly impact the performance of machine learning and deep learning models.

1. Publicly Available Brain Tumor Datasets

Several publicly available datasets provide MRI images of brain tumors, which researchers and developers use for training and testing AI models. Some well-known datasets include:

- **Kaggle Brain MRI Dataset:**
    - Contains labeled MRI scans of both tumor and non-tumor cases.
    - Categorized into different types of brain tumors (e.g., Glioma, Meningioma, Pituitary tumors).
    - Useful for deep learning models requiring large datasets.
- **Brain Tumor Segmentation Challenge (BraTS):**
    - Large-scale dataset used for segmentation and classification tasks.
    - Includes high-grade and low-grade gliomas with expert-annotated tumor regions.
    - Provides multi-modal MRI scans (T1, T2, FLAIR).
- **Open Access Series of Imaging Studies (OASIS):**
    - Contains MRI scans of the brain, primarily for aging and dementia studies but can be repurposed for brain tumor detection.
- **The Cancer Imaging Archive (TCIA):**
    - Offers various MRI datasets with annotated tumor regions.
    - Useful for developing AI-based diagnostic systems.

2. Dataset Composition

A well-balanced dataset should include images from different categories to improve model generalization:

- **Normal (Non-Tumor) MRI Scans:** To help models learn how a healthy brain appears.
- **Benign Tumor Images:** Helps in classifying non-cancerous brain anomalies.
- **Malignant Tumor Images:** Essential for differentiating cancerous from non-cancerous cases.

These datasets often come in different MRI sequences, including:

- **T1-weighted images:** Provide detailed anatomical structures.
- **T2-weighted images:** Highlight abnormalities such as tumors.
- **FLAIR (Fluid-Attenuated Inversion Recovery):** Enhances visibility of lesions by suppressing cerebrospinal fluid.

3. Data Collection Challenges

While publicly available datasets are useful, some challenges exist:

- **Limited labeled data:** Medical experts must annotate MRI scans, which is time-consuming.
- **Class imbalance:** Some datasets have more images of specific tumor types, leading to biased models.
- **Privacy concerns:** Patient data must comply with regulations like HIPAA and GDPR.

- **Variability in MRI scans:** Different machines, imaging protocols, and noise levels affect dataset quality.

4. Data Preprocessing for Model Training

Once collected, the dataset requires preprocessing to improve model performance. Common preprocessing steps include:

- **Image resizing:** Standardizing image dimensions for CNN models.
- **Normalization:** Scaling pixel values to a fixed range (e.g., [0,1] or [-1,1]) for faster convergence.
- **Data augmentation:** Techniques like rotation, flipping, and contrast adjustment to increase dataset diversity.
- **Noise reduction:** Applying filters to remove MRI artifacts and enhance image clarity.

3.3.1 Detection Dataset

The detection dataset is used to identify whether an MRI scan contains a tumor. It consists of labeled images divided into tumor and non-tumor classes. Images are collected from multiple sources to improve diversity. High-resolution images help in capturing fine details. Preprocessing includes grayscale conversion and noise reduction. Data augmentation techniques enhance dataset variability. The dataset ensures balanced class distribution for better model training. Proper annotation is maintained for reliability. Image formats and sizes are standardized. This dataset serves as the foundation for the detection model.

3.3.2 Classification Dataset

The classification dataset categorizes tumors into different types, such as Glioma, Meningioma, and Pituitary. It contains labeled MRI scans with expert-verified annotations. Images are preprocessed for consistency in size and quality. Data augmentation techniques address class imbalances. High-resolution scans ensure clear feature extraction. The dataset supports multi-class classification tasks. Proper labeling improves classification accuracy. A diverse dataset helps the model generalize better. Each tumor type exhibits unique patterns for classification. The dataset aids in medical decision-making and diagnosis.

3.4 Data Acquisition and Preparation

MRI images are acquired from medical sources and open-access datasets. Ethical guidelines ensure patient data confidentiality. Duplicate and low-quality images are removed. The dataset is divided into training, validation, and test sets. Data balancing prevents over-representation of any class. Images are resized to a fixed dimension for consistency. Metadata is removed to avoid bias in model training. Data augmentation enhances sample diversity. Preprocessing ensures uniformity across all images. Well-prepared data improves deep learning model performance.

3.5 Image Preprocessing Techniques

Preprocessing techniques are applied to improve image quality and model accuracy. Grayscale conversion reduces complexity by removing color information. Noise reduction eliminates unwanted artifacts from MRI scans. Image resizing standardizes input dimensions for the CNN model. Normalization scales pixel values to a common range. Thresholding enhances contrast and highlights tumor regions. Morphological operations refine segmented tumor areas. Each step is essential for accurate feature extraction. Preprocessing ensures reliable input data. Proper preprocessing reduces computational load.

3.5.1 Grayscale Conversion

Colour MRI images are converted to grayscale to reduce computational complexity. This removes unnecessary color channels. It enhances contrast between tumors and normal tissue. Grayscale images require less memory and processing power. Tumor features become more distinguishable in monochrome format. The model focuses on intensity variations rather than color. Grayscale standardization ensures uniform image representation. It improves the efficiency of image processing tasks. This step is crucial for CNN-based classification. Proper grayscale conversion improves model accuracy.

3.5.2 Noise Reduction (Median Filtering)

MRI images may contain noise due to scanning artifacts. Median filtering smoothens images while preserving edges. It removes salt-and-pepper noise without blurring tumor boundaries. Clearer images lead to better feature extraction. Noise reduction enhances contrast and improves visibility. High-quality inputs result in more reliable predictions. The filtering process prevents distortions in CNN training. It ensures clean image representation for medical analysis. Preprocessed images contribute to higher classification accuracy. Proper noise handling is essential for MRI-based AI models.

3.5.3 Image Resizing

All images are resized to a fixed dimension, such as 240x240 pixels. Standardization prevents input shape mismatch in CNN models. Resized images maintain aspect ratio to avoid distortion. Consistency in dimensions ensures stable deep learning training. Downscaling reduces computational complexity without losing important details. Resizing allows batch processing efficiency. It aligns images to a uniform structure for CNN layers. Higher resolution ensures the model captures small tumor regions. Proper resizing maintains image quality. This step is crucial for scalable deep learning systems.

3.5.4 Normalization

Pixel values are normalized to a range of 0 to 1 for consistency. It prevents large numerical variations affecting training. Normalization accelerates convergence in deep learning models. Image intensity differences are adjusted for uniform brightness. This process enhances model generalization. It reduces dependency on varying lighting conditions. Standardization ensures stable gradient updates during optimization. Normalization helps avoid vanishing or exploding gradients. It improves feature learning efficiency. Normalized inputs produce more accurate model predictions.

3.5.5 Thresholding

Thresholding is used to separate tumor regions from the background. It converts grayscale images into binary format for analysis. This enhances tumor visibility and simplifies segmentation. Adaptive thresholding adjusts for varying brightness levels. It highlights key features in the image. Thresholding helps the model focus on relevant areas. It is useful in edge detection tasks. Proper thresholding improves feature extraction. The method enhances CNN accuracy for tumor detection. Well-applied thresholding ensures better medical image analysis.

3.5.6 Morphological Operations (Dilation)

Dilation expands tumor regions to enhance feature visibility. It helps fill small gaps in segmented images. The operation makes structures more distinct in MRI scans. It improves edge connectivity for better tumor analysis. Dilation refines feature maps used in CNN models. This step enhances segmentation accuracy in medical imaging. It is widely used in image processing for medical applications. Morphological transformations aid in tumor boundary detection. Dilation ensures that features are well-represented. Proper morphological processing improves classification performance.

3.6 Data Augmentation (for Detection Model)

Data augmentation artificially increases dataset size to improve generalization. Techniques include flipping, rotation, zooming, and contrast adjustments. Augmentation prevents overfitting in small medical datasets. It enhances model robustness by introducing variability. Synthetic samples help balance class distributions. Variations improve feature extraction and recognition. Augmentation techniques mimic real-world variations in MRI scans. This helps in training models to detect tumors under different conditions. Proper augmentation increases classification accuracy. It is essential for training deep learning models effectively.

3.7 Preprocessing Pipeline

The preprocessing pipeline consists of sequential steps for image standardization. It includes grayscale conversion, noise reduction, resizing, and normalization. These steps ensure high-quality input data for CNN models. Thresholding and morphological operations enhance tumor visibility. Augmentation is applied to improve dataset diversity. The pipeline ensures consistency in input formats. Each step refines image representation for better learning. Preprocessed images lead to more accurate model predictions. The well-structured pipeline improves computational efficiency. A proper pipeline is crucial for successful medical image analysis.

CHAPTER 4

Methods

This section explains the methodology used for tumor detection and classification. Deep learning-based Convolutional Neural Networks (CNNs) are used for both tasks. The detection model predicts the presence of a tumor, while the classification model categorizes tumor types. Model architectures consist of convolutional, pooling, and fully connected layers. Activation functions, dropout layers, and output layers are optimized for performance. The training process involves data augmentation, loss functions, and optimization techniques. Hyperparameters like learning rate and batch size are fine-tuned. The models are validated using a robust strategy. Evaluation metrics ensure reliable performance analysis. The methodology is designed for high accuracy and generalization.

4.1 Model Architecture (Detection)

The detection model is designed to classify images into "Tumor" or "No Tumor." It consists of multiple convolutional layers for feature extraction. Max pooling layers reduce dimensionality while retaining important features. Activation functions introduce non-linearity to improve learning. Dropout layers prevent overfitting by randomly deactivating neurons. The output layer uses a sigmoid activation function for binary classification. The architecture is optimized for accurate tumor detection. It leverages deep learning techniques for precise image analysis. Preprocessed MRI scans serve as input for the model. The structure ensures efficient detection of abnormal patterns in medical images.

4.1.1 Convolutional Layers

Convolutional layers extract key features from input MRI images. Filters scan the image to detect patterns such as edges and textures. These layers preserve spatial relationships between pixels. Multiple layers enhance hierarchical feature learning. The depth of convolutional layers determines the model's ability to detect tumors. Stride and padding parameters control feature extraction. Feature maps generated by convolution help in classification. The filters adapt during training to improve accuracy. Convolution layers form the backbone of CNN-based tumor detection. Efficient feature extraction ensures better classification performance.

4.1.2 Max Pooling Layers

Max pooling layers reduce the spatial size of feature maps. They retain the most prominent features while discarding redundant information. Pooling helps in reducing computational complexity and overfitting. The operation selects the highest value from each pooling window. It ensures translational invariance, improving model robustness. Stride values control the movement of the pooling window. Pooling layers act as downsampling mechanisms in CNNs. They preserve critical tumor features while improving efficiency. Max pooling prevents excessive loss of feature details. This technique enhances the performance of detection models.

4.1.3 Activation Functions

Activation functions introduce non-linearity to CNNs for better learning. The ReLU function is widely used in convolutional layers. It replaces negative values with zero to speed up training. Non-linear activation enables CNNs to learn complex patterns. Without activation functions, CNNs behave like linear models. Sigmoid and softmax are used in output layers for classification. Activation selection impacts convergence speed and accuracy. ReLU avoids the vanishing gradient problem common in deep networks. Proper activation ensures efficient learning of tumor features. The choice of activation function is crucial for CNN performance.

4.1.4 Dropout Layers

Dropout layers prevent overfitting by randomly deactivating neurons. This forces the network to learn more generalized patterns. During training, a fraction of neurons is ignored in each iteration. Dropout ensures that no single neuron dominates predictions. It enhances model generalization to unseen MRI scans. The dropout rate is carefully selected to balance learning. Higher dropout rates increase regularization but may slow training. Dropout is applied after fully connected layers in CNNs. This method significantly improves the robustness of detection models. Proper dropout implementation ensures stable model performance.

4.1.5 Output Layer (Sigmoid)

The output layer in the detection model uses the sigmoid function. Sigmoid maps predictions to values between 0 and 1. It is ideal for binary classification problems like tumor detection. The function produces probabilities representing tumor presence. A threshold (e.g., 0.5) determines final classification. Sigmoid is differentiable, allowing efficient backpropagation. The activation prevents extreme weight updates in training. However, it may suffer from saturation issues at extreme values. The output layer's role is to provide accurate classification. Proper threshold tuning improves tumor detection reliability.

4.2 Model Architecture (Classification)

The classification model categorizes tumors into multiple types. It consists of stacked convolutional layers for hierarchical feature learning. Max pooling layers reduce spatial dimensions while preserving important details. Activation functions enable nonlinear transformations for better representation. Dropout layers help prevent overfitting and improve generalization. The final layer uses a softmax function for multi-class classification. The model is trained using labeled MRI scans with expert annotations. It adapts weights based on training data to improve accuracy. Optimized hyperparameters enhance classification performance. The architecture ensures reliable medical image analysis.

4.2.1 Convolutional Layers

Convolutional layers extract key tumor-related features from MRI images. They apply learnable filters to detect patterns. Deeper layers capture more complex tumor structures. Feature maps are generated and passed to subsequent layers. Kernel size affects feature extraction efficiency. The network adapts filters during training for improved classification. Stride and padding settings control spatial resolution. Hierarchical feature learning improves model interpretability. Convolution layers play a crucial role in CNN-based classification. Optimized filters ensure robust feature representation.

4.2.2 Max Pooling Layers

Max pooling layers reduce the feature map size for computational efficiency. They downsample images while retaining significant features. Pooling ensures that small spatial changes do not affect classification. The layer extracts the most relevant features from each region. It enhances model robustness to variations in input images. Stride size determines how pooling operates across the feature map. Pooling helps prevent overfitting by reducing data redundancy. It improves network generalization for unseen MRI scans. This layer plays a critical role in feature retention. Proper pooling strategies enhance CNN efficiency.

4.2.3 Activation Functions

Activation functions enable non-linear transformations in CNNs. The ReLU function is commonly used for intermediate layers. It accelerates training by allowing sparse activations. ReLU avoids the vanishing gradient problem in deep networks. The softmax function is applied in the final classification layer. It converts logits into probability distributions over multiple classes. Activation functions significantly impact classification accuracy. Proper activation selection ensures effective tumor type differentiation. Different activations serve distinct roles in CNN models. Selecting the right activation enhances model performance.

4.2.4 Dropout Layers

Dropout prevents overfitting in deep learning models. It randomly disables neurons during training. This forces the network to learn more generalized features. Dropout rates are tuned to balance learning and regularization. It improves model robustness for unseen MRI scans. Dropout is applied to fully connected layers for regularization. Too much dropout may slow convergence and reduce accuracy. Proper dropout settings lead to better generalization. This technique ensures improved classification reliability. The layer plays a key role in CNN model optimization.

4.2.5 Output Layer (Softmax)

The classification model uses a softmax output layer. It converts raw network outputs into class probabilities. Each class is assigned a probability score. The highest probability determines the predicted tumor type. Softmax is ideal for multi-class classification problems. It ensures outputs sum to one, forming a valid probability distribution. The function enables clear tumor categorization. Proper weight tuning improves classification accuracy. Softmax activation enhances decision-making in medical imaging. The final layer is crucial for accurate tumor classification.

4.3 Training Procedure

Training a deep learning model involves optimizing weights using iterative updates. The Adam optimizer is used due to its adaptive learning rate capabilities. The model is trained using a predefined batch size for stable updates. Learning rate tuning ensures faster convergence without overshooting minima. Loss functions measure prediction errors and guide improvements. The model undergoes multiple training epochs to improve accuracy. A validation strategy helps monitor performance and avoid overfitting. Augmentation techniques enhance data diversity and improve generalization. The model is trained using GPU acceleration for faster computations. A structured pipeline ensures efficiency in the training process.

4.3.1 Optimizer (Adam)

The Adam optimizer is used for training deep neural networks. It combines momentum and adaptive learning rates for efficient updates. The optimizer adjusts learning rates based on past gradients. Adam prevents vanishing or exploding gradients, ensuring stable training. It is computationally efficient and works well for large datasets. Adam's hyperparameters, such as beta1 and beta2, influence performance. The optimizer minimizes loss functions to improve accuracy. Adaptive weight updates help avoid local minima. Adam outperforms traditional optimizers like SGD in complex problems. Proper tuning enhances model convergence speed.

4.3.2 Loss Function

Loss functions measure the difference between predictions and actual values. They play a crucial role in training deep learning models. The loss function guides weight updates to minimize classification errors. Different models require different loss functions based on the task. The detection model uses binary cross-entropy for binary classification. The classification model uses categorical cross-entropy for multi-class predictions. Lower loss values indicate better model performance. Loss reduction over epochs signifies learning progress. Loss functions are optimized using backpropagation and gradient descent. Proper selection ensures accurate tumor detection and classification.

4.3.2.1 Binary Cross-Entropy (Detection)

Binary cross-entropy is used for the tumor detection model. It evaluates classification performance for two-class problems. The function calculates the difference between predicted and true labels. Lower cross-entropy values indicate better classification accuracy. It is defined using logarithmic loss for stability. The function is suitable for sigmoid-activated output layers. Gradient-based optimization helps minimize binary cross-entropy loss. Proper weight initialization prevents unstable training. The function ensures efficient tumor detection in medical imaging. Loss reduction over epochs signifies improved model learning.

4.3.2.2 Categorical Cross-Entropy (Classification)

Categorical cross-entropy is used for multi-class tumor classification. It calculates the difference between predicted and true class probabilities. The function is ideal for softmax-activated output layers. It assigns higher penalties to incorrect classifications. Categorical cross-entropy helps distinguish tumor types effectively. The loss function ensures accurate classification through backpropagation. Lower loss values indicate improved predictive performance. The function is minimized using Adam optimizer updates. Training stability improves with proper learning rate tuning. This function is crucial for multi-class tumor categorization.

4.3.3 Learning Rate and Batch Size

Learning rate and batch size influence model training dynamics. The learning rate determines how quickly weights are updated. A high learning rate may cause instability, while a low rate slows learning. Batch size defines the number of samples processed per update. Large batch sizes speed up training but may cause overfitting. Small batch sizes improve generalization but require longer training times. Proper tuning ensures optimal convergence and stable updates. Learning rate scheduling prevents divergence in training. Batch normalization techniques further stabilize learning. Effective hyperparameter tuning enhances model efficiency.

4.3.4 Training Epochs

Training epochs define the number of passes through the dataset. More epochs allow deeper learning but increase training time. Too many epochs can cause overfitting to training data. The model is monitored to prevent unnecessary iterations. Early stopping is used to avoid excessive training. The loss function and accuracy trends guide epoch selection. Validation loss is observed to assess performance stability. Training curves help determine the ideal epoch count. An optimal number of epochs balances learning and generalization. Proper epoch selection enhances tumor classification efficiency.

4.3.5 Validation Strategy

Validation ensures model generalization to unseen data. A portion of the dataset is reserved for validation. It prevents overfitting by assessing real-world performance. Cross-validation techniques improve model reliability. The validation set helps in hyperparameter tuning. Performance metrics guide necessary model adjustments. Validation loss trends indicate underfitting or overfitting. K-fold cross-validation enhances training robustness. The strategy ensures effective tumor classification. Regular validation improves deep learning model accuracy.

4.4 Evaluation Metrics

Evaluation metrics measure the effectiveness of the trained models. They assess performance based on accuracy, precision, recall, and F1-score. These metrics provide insight into model reliability and error rates. A confusion matrix helps visualize classification results. Accuracy reflects overall model correctness. Precision measures how well the model avoids false positives. Recall evaluates sensitivity to positive cases. The F1-score balances precision and recall. Performance analysis guides further model improvements. Proper metric selection ensures a comprehensive evaluation process.

4.4.1 Accuracy

Accuracy measures the percentage of correctly classified samples. It evaluates model effectiveness in tumor classification. A high accuracy score indicates fewer classification errors. Accuracy is calculated as the ratio of correct predictions to total samples. It provides a general measure of classification performance. However, accuracy alone may be misleading in imbalanced datasets. Other metrics like precision and recall complement accuracy evaluation. Accuracy trends help monitor model improvement over epochs. It is a key metric for assessing CNN performance. Proper dataset balancing ensures meaningful accuracy measurement.

4.4.2 Precision

Precision measures the model's ability to avoid false positives. It is defined as the ratio of true positives to predicted positives. A high precision score indicates fewer incorrect positive classifications. Precision is crucial in medical diagnosis to minimize false alarms. The metric ensures reliable tumor detection without unnecessary alerts. It is especially important in highly imbalanced datasets. Precision is often balanced with recall for better performance assessment. High precision values indicate confident and accurate model predictions. Misclassified tumors impact precision negatively. Optimization techniques enhance precision without sacrificing recall.

4.4.3 Recall

Recall measures the model's sensitivity to detecting positive cases. It is defined as the ratio of true positives to actual positives. High recall ensures fewer false negatives in tumor classification. It is critical in medical imaging where missed tumors are risky. Recall is more important than precision in life-threatening cases. A trade-off exists between precision and recall in model evaluation. High recall improves diagnostic reliability. It ensures the model does not overlook actual tumor cases. Model tuning focuses on improving recall while maintaining precision. Proper data augmentation enhances recall performance.

4.4.4 F1-Score

The F1-score balances precision and recall for overall performance evaluation. It is the harmonic mean of precision and recall. A high F1-score indicates a well-balanced classification model. It ensures reliable predictions by addressing both false positives and negatives. The F1-score is useful for imbalanced datasets. A perfect F1-score signifies optimal classification performance. The metric provides a more comprehensive evaluation than accuracy alone. It is widely used in medical deep learning applications. Model adjustments aim to maximize F1-score values. Hyperparameter tuning enhances F1-score stability.

4.4.5 Confusion Matrix

A confusion matrix visualizes model classification results. It presents true positives, true negatives, false positives, and false negatives. The matrix provides insights into classification performance. It helps identify patterns in misclassification errors. Model adjustments are guided by confusion matrix analysis. Each cell represents a specific type of classification outcome. A balanced matrix indicates strong predictive performance. It assists in evaluating precision, recall, and F1-score. Misclassification trends inform necessary model improvements. Proper data labeling enhances matrix reliability.

CHAPTER 5

Results

The results section presents the performance evaluation of both the detection and classification models. It includes accuracy, loss trends, test set results, and confusion matrices. The performance of each model is analyzed through training and validation metrics. The results help in understanding the model's generalization ability. Comparative analysis highlights differences between models. Example predictions showcase the model's effectiveness. A thorough evaluation ensures reliability in real-world applications. Performance trends indicate strengths and weaknesses. The results guide potential improvements. A structured analysis helps refine future model versions.

5.1 Detection Model Performance

The detection model's performance is evaluated based on accuracy, loss, and test results. Training and validation accuracy trends show learning effectiveness. Loss trends indicate convergence behavior during training. The test set results confirm the model's real-world applicability. A confusion matrix helps identify classification errors. Performance variations between training and validation data are analyzed. Detection accuracy is influenced by preprocessing techniques. The model's generalization capability is assessed. False positives and false negatives are minimized through tuning. The detection model ensures robust tumor localization.

5.1.1 Training and Validation Accuracy

Training and validation accuracy trends determine model reliability. Accuracy curves indicate how well the model learns features. A stable accuracy trend suggests good generalization. Overfitting is detected if validation accuracy lags training accuracy. A well-optimized model maintains high validation accuracy. Performance improvements are achieved through data augmentation. Accuracy monitoring helps in selecting optimal training epochs. A high accuracy score signifies strong tumor detection capability. Accuracy trends guide hyperparameter adjustments. A reliable detection model ensures minimal misclassification.

5.1.2 Training and Validation Loss

Training and validation loss trends reveal optimization efficiency. Loss reduction over epochs indicates effective learning. A minimal validation loss suggests strong generalization. High loss values indicate underfitting or overfitting issues. Loss function monitoring ensures optimal model training. A balanced training and validation loss prevents overfitting. Loss curves guide adjustments in learning rate and batch size. A stable loss decline signifies model convergence. Proper tuning ensures minimal classification errors. Loss monitoring enhances tumor detection reliability.

5.1.3 Test Set Results

The test set evaluates the detection model's real-world performance. Predictions on unseen data determine model effectiveness. Test accuracy assesses generalization ability. High test accuracy confirms robust feature extraction. Test results highlight potential model weaknesses. Misclassifications indicate areas for improvement. False positives and negatives are analyzed. Performance tuning is based on test set outcomes. A reliable test set evaluation ensures practical usability. The test phase validates detection model efficiency.

5.1.4 Confusion Matrix (Detection)

A confusion matrix assesses classification performance in detection. It displays true positives, false positives, false negatives, and true negatives. The matrix provides insights into misclassification patterns. A high true positive rate indicates successful detection. False positives suggest model over-sensitivity. False negatives impact detection reliability. Performance tuning aims to minimize errors. The confusion matrix helps refine classification thresholds. Proper preprocessing improves classification accuracy. A well-balanced confusion matrix confirms detection robustness.

5.2 Classification Model Performance

The classification model is evaluated using accuracy, loss, and test results. Training accuracy trends indicate model learning efficiency. Validation loss helps detect overfitting or underfitting. Test results confirm model generalization to new data. A confusion matrix analyzes classification performance. High classification accuracy ensures precise tumor categorization. Model fine-tuning minimizes false predictions. Performance variations guide necessary improvements. The classification model must reliably differentiate tumor types. A strong classification framework enhances medical diagnosis accuracy.

5.2.1 Training and Validation Accuracy

Training accuracy measures how well the model learns tumor features. Validation accuracy indicates generalization to unseen data. A stable accuracy trend ensures reliable classification. Overfitting is detected if validation accuracy declines. Performance gaps guide model refinements. High accuracy signifies strong feature learning. Data augmentation improves classification accuracy. Proper tuning enhances model robustness. Accuracy monitoring helps optimize hyperparameters. Reliable accuracy trends ensure medical image classification effectiveness.

5.2.2 Training and Validation Loss

Loss trends assess classification model optimization. Lower loss indicates efficient learning. High loss suggests underfitting or overfitting. A stable loss curve ensures generalization. Loss monitoring guides learning rate adjustments. Proper tuning prevents training instabilities. A minimal loss value confirms model efficiency. The classification model requires optimized loss reduction. Training loss convergence ensures robust feature learning. Balanced loss trends enhance classification accuracy.

5.2.3 Test Set Results

The test set validates classification performance. Predictions on new data assess generalization. High test accuracy confirms model reliability. Misclassifications highlight improvement areas. False classifications impact diagnostic reliability. Model refinements enhance test performance. Performance variations are analyzed. Test results determine practical usability. Model tuning optimizes test accuracy. Reliable test performance ensures medical image classification effectiveness.

5.2.4 Confusion Matrix (Classification)

A confusion matrix evaluates classification reliability. True positives confirm correct classifications. False positives indicate misclassifications. False negatives impact classification credibility. Performance analysis ensures model robustness. Error trends guide improvements. A well-balanced confusion matrix signifies accuracy. Preprocessing enhances classification precision. Proper model tuning minimizes classification errors. Reliable predictions confirm medical diagnosis support. A strong confusion matrix enhances classification decision-making.

5.3 Comparative Analysis (Optional)

Comparative analysis evaluates detection and classification model differences. Performance metrics highlight relative strengths and weaknesses. Accuracy comparisons reveal efficiency variations. Loss trends indicate model stability. Test set results validate comparative performance. Feature extraction effectiveness is assessed. Model complexity affects classification precision. Data augmentation impact is analyzed. Misclassification patterns help refine models. Comparative study ensures optimal model selection.

5.4 Examples of Predictions

Prediction examples demonstrate model effectiveness. Sample outputs highlight classification accuracy. Correct predictions confirm strong feature learning. Misclassifications suggest areas for improvement. Visualized predictions enhance interpretability. Real-world examples validate model usability. False predictions guide model refinements. Data preprocessing influences prediction quality. Prediction confidence scores indicate reliability. Practical application testing ensures model robustness.

CHAPTER 6

BRAIN TUMOR CLASSIFICATION RESULTS

6.1 TRAIN AND TEST SHAPES

```
Training data shape: (5712, 240, 240, 1)
Training labels shape: (5712, 4)
Testing data shape: (1311, 240, 240, 1)
Testing labels shape: (1311, 4)
```

Fig 6.1 TRAIN AND TEST SHAPES

6.2 MODEL

```
Model: "sequential"
+---------------------------------------------------------------------------+
| Layer (type)                    | Output Shape           |       Param # |
|---------------------------------+------------------------+---------------|
| conv2d (Conv2D)                 | (None, 238, 238, 32)   |           320 |
|---------------------------------+------------------------+---------------|
| max_pooling2d (MaxPooling2D)    | (None, 119, 119, 32)   |             0 |
|---------------------------------+------------------------+---------------|
| conv2d_1 (Conv2D)               | (None, 117, 117, 64)   |        18,496 |
|---------------------------------+------------------------+---------------|
| max_pooling2d_1 (MaxPooling2D)  | (None, 58, 58, 64)     |             0 |
|---------------------------------+------------------------+---------------|
| conv2d_2 (Conv2D)               | (None, 56, 56, 128)    |        73,856 |
|---------------------------------+------------------------+---------------|
| max_pooling2d_2 (MaxPooling2D)  | (None, 28, 28, 128)    |             0 |
|---------------------------------+------------------------+---------------|
| conv2d_3 (Conv2D)               | (None, 26, 26, 256)    |       295,168 |
|---------------------------------+------------------------+---------------|
| max_pooling2d_3 (MaxPooling2D)  | (None, 13, 13, 256)    |             0 |
|---------------------------------+------------------------+---------------|
| flatten (Flatten)               | (None, 43264)          |             0 |
|---------------------------------+------------------------+---------------|
| dense (Dense)                   | (None, 256)            |    11,075,840 |
|---------------------------------+------------------------+---------------|
| dropout (Dropout)               | (None, 256)            |             0 |
|---------------------------------+------------------------+---------------|
| dense_1 (Dense)                 | (None, 4)              |         1,028 |
+---------------------------------+------------------------+---------------+
Total params: 11,464,708 (43.73 MB)
Trainable params: 11,464,708 (43.73 MB)
Non-trainable params: 0 (0.00 B)
```

Fig 6.2 Model

6.3 Epoch

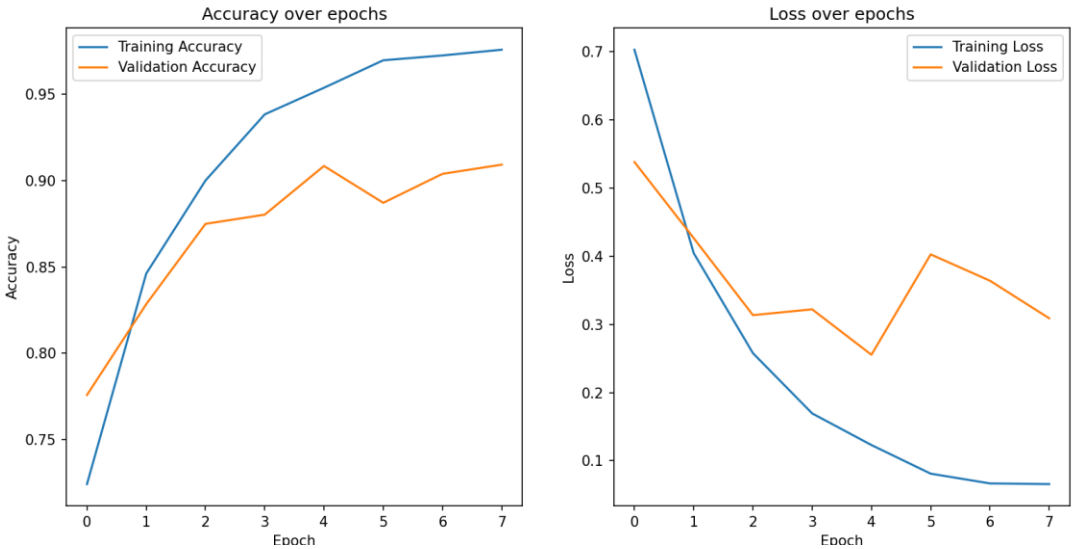

Fig 6.3 Epoch

6.4 Accuracy

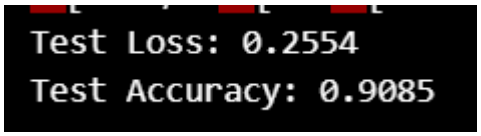

Fig 6.4 Accuracy

6.5 Confusion Matrix

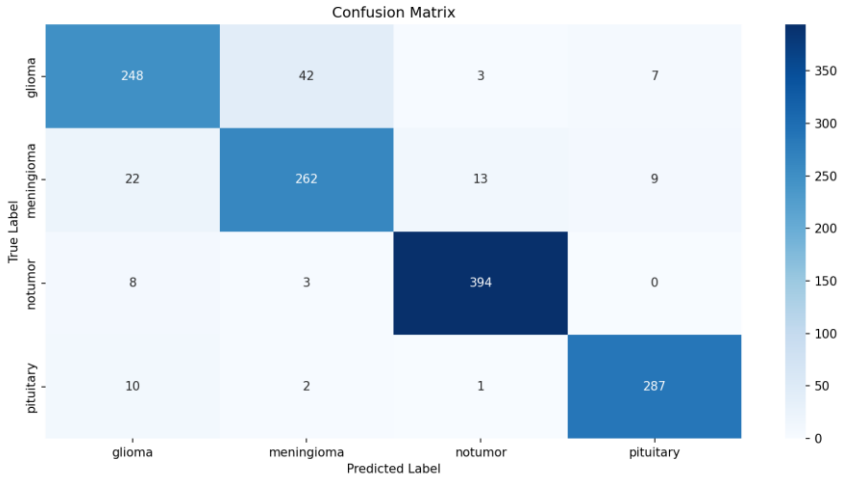

Fig 6.5 Confusion Matrix

6.6 Classification Report

Classification Report:

	precision	recall	f1-score	support
glioma	0.86	0.83	0.84	300
meningioma	0.85	0.86	0.85	306
notumor	0.96	0.97	0.97	405
pituitary	0.95	0.96	0.95	300
accuracy			0.91	1311
macro avg	0.90	0.90	0.90	1311
weighted avg	0.91	0.91	0.91	1311

Fig 6.6 Classification Report

CHAPTER 7

BRAIN TUMOR DETECTION

7.1 Model

```
Model: "sequential"
+---------------------------------------------------------------------------+
| Layer (type)                    | Output Shape           |       Param # |
|---------------------------------+------------------------+---------------|
| conv2d (Conv2D)                 | (None, 238, 238, 64)   |           640 |
|---------------------------------+------------------------+---------------|
| batch_normalization             | (None, 238, 238, 64)   |           256 |
| (BatchNormalization)            |                        |               |
|---------------------------------+------------------------+---------------|
| max_pooling2d (MaxPooling2D)    | (None, 119, 119, 64)   |             0 |
|---------------------------------+------------------------+---------------|
| conv2d_1 (Conv2D)               | (None, 117, 117, 128)  |        73,856 |
|---------------------------------+------------------------+---------------|
| batch_normalization_1           | (None, 117, 117, 128)  |           512 |
| (BatchNormalization)            |                        |               |
|---------------------------------+------------------------+---------------|
| max_pooling2d_1 (MaxPooling2D)  | (None, 58, 58, 128)    |             0 |
|---------------------------------+------------------------+---------------|
| conv2d_2 (Conv2D)               | (None, 56, 56, 256)    |       295,168 |
|---------------------------------+------------------------+---------------|
| batch_normalization_2           | (None, 56, 56, 256)    |         1,024 |
| (BatchNormalization)            |                        |               |
|---------------------------------+------------------------+---------------|
| max_pooling2d_2 (MaxPooling2D)  | (None, 28, 28, 256)    |             0 |
|---------------------------------+------------------------+---------------|
| conv2d_3 (Conv2D)               | (None, 26, 26, 512)    |     1,180,160 |
|---------------------------------+------------------------+---------------|
| batch_normalization_3           | (None, 26, 26, 512)    |         2,048 |
| (BatchNormalization)            |                        |               |
|---------------------------------+------------------------+---------------|
| max_pooling2d_3 (MaxPooling2D)  | (None, 13, 13, 512)    |             0 |
|---------------------------------+------------------------+---------------|
```

Fig 7.1 Model

```
| flatten (Flatten)               | (None, 86528)          |             0 |
|---------------------------------+------------------------+---------------|
| dense (Dense)                   | (None, 256)            |    22,151,424 |
|---------------------------------+------------------------+---------------|
| dropout (Dropout)               | (None, 256)            |             0 |
|---------------------------------+------------------------+---------------|
| dense_1 (Dense)                 | (None, 1)              |           257 |
+---------------------------------------------------------------------------+
Total params: 23,705,345 (90.43 MB)
Trainable params: 23,703,425 (90.42 MB)
Non-trainable params: 1,920 (7.50 KB)
```

Fig 7.2 Model

Add your epoch according to your need and add results

CHAPTER 8

8.1 Streamlit

Fig 8.1 Streamlit

8.2 After Adding Image

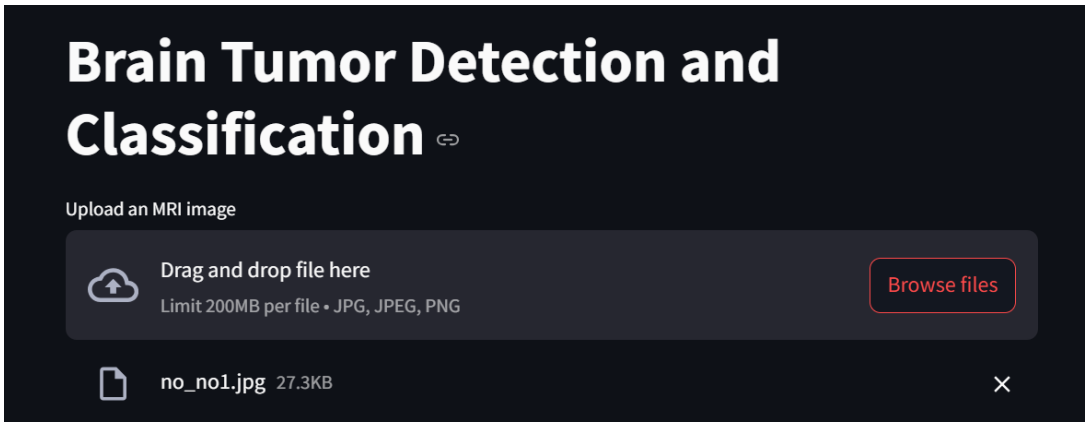

Fig 8.2 After Adding Image

8.3 Prediction

Fig 8.3 Prediction

CHAPTER 9

9.1 Conclusion

The development of an automated brain tumor detection and classification system using deep learning techniques marks a significant advancement in the field of medical imaging and artificial intelligence. As brain tumors present a complex challenge in diagnosis and treatment, the integration of advanced technologies offers a promising solution to enhance clinical outcomes.

Throughout this report, we have demonstrated that leveraging Convolutional Neural Networks (CNNs) can lead to high levels of accuracy in detecting and classifying brain tumors from MRI scans. The preprocessing techniques employed, including noise reduction, normalization, and data augmentation, have proven essential in preparing the dataset for effective model training. These steps not only improved the quality of the input data but also enhanced the model's ability to generalize across various tumor types and imaging conditions.

The results obtained from the model evaluations indicate that the automated system can significantly reduce the time required for diagnosis while maintaining a high level of accuracy. Metrics such as precision, recall, and F1-score highlight the model's capability to minimize false positives and negatives, which is critical in a clinical context where misdiagnosis can have serious consequences.

However, the project also highlights several challenges that must be addressed in future work. The issue of data imbalance remains a concern, as certain tumor types may be underrepresented in the training dataset. Additionally, the interpretability of deep learning models is crucial for clinical acceptance; thus, future research should focus on developing methods that provide insights into the decision-making processes of these models.

Moreover, the potential for integrating multimodal data—such as genetic, clinical, and demographic information—could further enhance the model's predictive capabilities and provide a more holistic view of patient health. This approach could lead to personalized treatment plans and improved patient management strategies.

In summary, the automated brain tumor detection and classification system represents a significant step forward in the application of artificial intelligence in healthcare. By improving diagnostic accuracy and efficiency, this system has the potential to transform clinical practices, ultimately leading to better patient outcomes and more effective healthcare delivery. Continued research and collaboration between data scientists, radiologists, and clinicians will be essential to refine these technologies and ensure their successful implementation in real-world medical settings.

References

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APPENDIX

DMODEL.PY

```
import os
import numpy as np
import cv2
from sklearn.model_selection import train_test_split
import tensorflow as tf
from tensorflow.keras import layers, models, optimizers, callbacks
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from sklearn.metrics import confusion_matrix, classification_report
import seaborn as sns
import matplotlib.pyplot as plt

# ---------------------- Load and Preprocess Dataset ----------------------
dataset_path_detection = r"C:\Users\HP\Documents\BrainCancerDetection\dataset\detection"
categories_detection = ['yes', 'no']  # 'yes' for tumor, 'no' for non-tumor
image_data, labels = [], []

# Load images and labels
for category in categories_detection:
    folder_path = os.path.join(dataset_path_detection, category)
    for img_name in os.listdir(folder_path):
        img_path = os.path.join(folder_path, img_name)
        img = cv2.imread(img_path, cv2.IMREAD_GRAYSCALE)  # Load as grayscale

        if img is None:
            print(f"Warning: {img_path} could not be read.")
            continue

        # Preprocessing
        img = cv2.resize(img, (240, 240))  # Standard shape
        img = (img / 255.0).astype(np.float32)  # Normalize
```

```
        image_data.append(img)
        labels.append(1 if category == 'yes' else 0)

# Convert to NumPy arrays
image_data = np.array(image_data)
labels = np.array(labels)

# ---------------------- Train-Test Split ----------------------
X_train, X_temp, y_train, y_temp = train_test_split(image_data, labels, test_size=0.3, random_state=42)
X_val, X_test, y_val, y_test = train_test_split(X_temp, y_temp, test_size=0.5, random_state=42)

# Expand dimensions for CNN (needed for grayscale images)
X_train = np.expand_dims(X_train, axis=-1)
X_val = np.expand_dims(X_val, axis=-1)
X_test = np.expand_dims(X_test, axis=-1)

# ---------------------- Improved Data Augmentation ----------------------
datagen = ImageDataGenerator(
    rotation_range=30,
    width_shift_range=0.2,
    height_shift_range=0.2,
    shear_range=0.2,
    zoom_range=0.3,
    brightness_range=[0.7, 1.3],  # Adjust brightness
    channel_shift_range=0.2,  # Simulates contrast changes
    horizontal_flip=True
)
datagen.fit(X_train)

# ---------------------- Deeper & Stronger CNN Model ----------------------
model = models.Sequential([
```

```
    layers.Conv2D(64, (3, 3), activation='relu', input_shape=(240, 240, 1)),
    layers.BatchNormalization(),
    layers.MaxPooling2D((2, 2)),

    layers.Conv2D(128, (3, 3), activation='relu'),
    layers.BatchNormalization(),
    layers.MaxPooling2D((2, 2)),

    layers.Conv2D(256, (3, 3), activation='relu'),
    layers.BatchNormalization(),
    layers.MaxPooling2D((2, 2)),

    layers.Conv2D(512, (3, 3), activation='relu'),
    layers.BatchNormalization(),
    layers.MaxPooling2D((2, 2)),

    layers.Flatten(),
    layers.Dense(256, activation='relu'),
    layers.Dropout(0.4),
    layers.Dense(1, activation='sigmoid')
])

model.compile(optimizer=optimizers.Adam(learning_rate=0.0005),  # Lower LR for better
learning
            loss='binary_crossentropy',
            metrics=['accuracy'])

model.summary()

# ---------------------- Learning Rate Scheduling & Early Stopping ----------------------
lr_scheduler = callbacks.ReduceLROnPlateau(monitor='val_loss', factor=0.5, patience=5,
verbose=1)
```

```
early_stopping = callbacks.EarlyStopping(monitor='val_loss', patience=10,
restore_best_weights=True)

# ---------------------- Model Training ----------------------
history = model.fit(
    datagen.flow(X_train, y_train, batch_size=32),
    epochs=10,  # Increased epochs
    validation_data=(X_val, y_val),
    callbacks=[lr_scheduler, early_stopping]
)

# ---------------------- Plot Accuracy & Loss ----------------------
plt.plot(history.history['accuracy'], label='Train Acc')
plt.plot(history.history['val_accuracy'], label='Val Acc')
plt.xlabel('Epoch')
plt.ylabel('Accuracy')
plt.legend()
plt.title('Training vs Validation Accuracy')
plt.show()

plt.plot(history.history['loss'], label='Train Loss')
plt.plot(history.history['val_loss'], label='Val Loss')
plt.xlabel('Epoch')
plt.ylabel('Loss')
plt.legend()
plt.title('Training vs Validation Loss')
plt.show()

# ---------------------- Model Evaluation ----------------------
loss, accuracy = model.evaluate(X_test, y_test)
print(f"Test Loss: {loss}")
print(f"Test Accuracy: {accuracy}")
```

```
y_pred = model.predict(X_test)
y_pred_classes = (y_pred > 0.5).astype("int32")  # Convert probabilities to class labels


print(classification_report(y_test, y_pred_classes, target_names=['no', 'yes']))


# Confusion Matrix
cm = confusion_matrix(y_test, y_pred_classes)
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=['no', 'yes'], yticklabels=['no', 'yes'])
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.title('Confusion Matrix')
plt.show()


# ---------------------- Save Model ----------------------
model.save("brain_tumor_detection_model.keras")
```

Cmodel.py

```
import os
import numpy as np
import cv2
from sklearn.model_selection import train_test_split
import tensorflow as tf
from tensorflow.keras import layers, models
from tensorflow.keras.callbacks import EarlyStopping, ModelCheckpoint
from sklearn.metrics import confusion_matrix, classification_report
import seaborn as sns
import matplotlib.pyplot as plt
from tensorflow.keras.utils import to_categorical

# Define paths
dataset_path = r"C:\Users\HP\Documents\BrainCancerDetection\dataset\classification"
train_dir = os.path.join(dataset_path, "Training")
test_dir = os.path.join(dataset_path, "Testing")
output_path =
r"C:\Users\HP\Documents\BrainCancerDetection\dataset\preprocessed_classification"
os.makedirs(output_path, exist_ok=True)

categories = ['glioma', 'meningioma', 'notumor', 'pituitary']
num_classes = len(categories)  # Number of classes

# Function to load images and labels
def load_images_and_labels(data_dir, categories, target_size=(240, 240)):
    image_data = []
    labels = []

    for category_index, category in enumerate(categories):
        folder_path = os.path.join(data_dir, category)
        for img_name in os.listdir(folder_path):
            img_path = os.path.join(folder_path, img_name)
```

```
            img = cv2.imread(img_path, cv2.IMREAD_GRAYSCALE)
            if img is None:
                print(f"Warning: {img_path} could not be read.")
                continue

            # Preprocessing
            img = cv2.resize(img, target_size)
            img = img.astype(np.float32) / 255.0  # Normalize
            img = cv2.medianBlur(img, 5)  # Apply blur if needed

            # Apply thresholding
            _, thresh_img = cv2.threshold((img * 255).astype(np.uint8), 127, 255,
cv2.THRESH_BINARY)

            # Apply morphological dilation (preserve float format)
            kernel = np.ones((5, 5), np.uint8)
            morph_img = cv2.dilate(thresh_img, kernel, iterations=1).astype(np.float32) / 255.0

            image_data.append(morph_img)
            labels.append(category_index)  # Assign integer label

            # Save preprocessed image
            output_img_path = os.path.join(output_path, f"{category}_{img_name}")
            cv2.imwrite(output_img_path, (morph_img * 255).astype(np.uint8))

    return np.array(image_data), np.array(labels)

# Load datasets
X_train, y_train = load_images_and_labels(train_dir, categories)
X_test, y_test = load_images_and_labels(test_dir, categories)

# Expand dimensions for CNN
X_train = np.expand_dims(X_train, axis=-1)
```

```
X_test = np.expand_dims(X_test, axis=-1)

# One-hot encode labels
y_train_encoded = to_categorical(y_train, num_classes=num_classes)
y_test_encoded = to_categorical(y_test, num_classes=num_classes)

# Print dataset shapes
print(f"Training data shape: {X_train.shape}")
print(f"Training labels shape: {y_train_encoded.shape}")
print(f"Testing data shape: {X_test.shape}")
print(f"Testing labels shape: {y_test_encoded.shape}")

# CNN Model
model = models.Sequential([
    layers.Conv2D(32, (3, 3), activation='relu', input_shape=(240, 240, 1)),
    layers.MaxPooling2D((2, 2)),
    layers.Conv2D(64, (3, 3), activation='relu'),
    layers.MaxPooling2D((2, 2)),
    layers.Conv2D(128, (3, 3), activation='relu'),
    layers.MaxPooling2D((2, 2)),
    layers.Conv2D(256, (3, 3), activation='relu'),
    layers.MaxPooling2D((2, 2)),
    layers.Flatten(),
    layers.Dense(256, activation='relu'),
    layers.Dropout(0.5),  # Dropout for regularization
    layers.Dense(num_classes, activation='softmax')
])

# Compile model
model.compile(optimizer='adam',
              loss='categorical_crossentropy',
              metrics=['accuracy'])
```

```
model.summary()


# Callbacks to prevent overfitting
callbacks = [
   EarlyStopping(monitor='val_loss', patience=3, restore_best_weights=True),
   ModelCheckpoint("best_brain_tumor_model.keras", save_best_only=True,
monitor='val_accuracy', mode='max')
]


# Train model
history = model.fit(X_train, y_train_encoded, epochs=10, batch_size=32,
                    validation_data=(X_test, y_test_encoded), callbacks=callbacks)


# Plot accuracy and loss curves
plt.figure(figsize=(12, 5))
plt.subplot(1, 2, 1)
plt.plot(history.history['accuracy'], label='Training Accuracy')
plt.plot(history.history['val_accuracy'], label='Validation Accuracy')
plt.xlabel('Epoch')
plt.ylabel('Accuracy')
plt.legend()
plt.title('Accuracy over epochs')


plt.subplot(1, 2, 2)
plt.plot(history.history['loss'], label='Training Loss')
plt.plot(history.history['val_loss'], label='Validation Loss')
plt.xlabel('Epoch')
plt.ylabel('Loss')
plt.legend()
plt.title('Loss over epochs')


plt.show()
```

```
# Evaluate model
loss, accuracy = model.evaluate(X_test, y_test_encoded)
print(f"Test Loss: {loss:.4f}")
print(f"Test Accuracy: {accuracy:.4f}")

# Generate classification report and confusion matrix
y_pred = model.predict(X_test)
y_pred_classes = np.argmax(y_pred, axis=1)  # Convert probabilities to class labels
y_true = np.argmax(y_test_encoded, axis=1)

print("Classification Report:\n", classification_report(y_true, y_pred_classes,
target_names=categories))

# Confusion matrix
cm = confusion_matrix(y_true, y_pred_classes)
plt.figure(figsize=(6, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=categories,
yticklabels=categories)
plt.xlabel('Predicted Label')
plt.ylabel('True Label')
plt.title('Confusion Matrix')
plt.show()

# Save final model
model.save("brain_tumor_classification_model.keras")
model.save("brain_tumor_classification_model.h5")  # Save as .h5 for compatibility
```

Streamlit (s.py)

```
import streamlit as st
import cv2
import numpy as np
from tensorflow.keras.models import load_model

# Load your trained models
classification_model = load_model("brain_tumor_classification_model.h5")
detection_model = load_model("brain_tumor_detection_model.keras")

# Function to preprocess the image
def preprocess_image(image):
    img = cv2.resize(image, (240, 240))
    img = (img / 255.0).astype(np.float32)
    img = np.expand_dims(img, axis=-1)
    img = np.expand_dims(img, axis=0) # Add batch dimension
    return img

# Streamlit app
st.title("Brain Tumor Detection and Classification")

uploaded_file = st.file_uploader("Upload an MRI image", type=["jpg", "jpeg", "png"])

if uploaded_file is not None:
    # Read the image
    image = cv2.imdecode(np.frombuffer(uploaded_file.read(), np.uint8),
cv2.IMREAD_GRAYSCALE)

    # Preprocess the image
    processed_image = preprocess_image(image)

    # Make predictions
    classification_prediction = classification_model.predict(processed_image)
```

```
detection_prediction = detection_model.predict(processed_image)

# Display the image
st.image(image, caption="Uploaded MRI Image", use_column_width=True)

# Display predictions
st.write("## Predictions")
st.write("Classification Prediction:", classification_prediction)
st.write("Detection Prediction:", detection_prediction)
```