

COMSATS UNIVERSITY ISLAMABAD



Computer Vision ***Final Project Report***

Project Title

"Brain Tumor Detection and Segmentation Using CNN and U-Net"

Team Details

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Abstract

This project addresses the critical task of brain tumor diagnosis using deep learning. A dual-model approach was implemented to first classify brain MRI images into tumor categories using a custom Convolutional Neural Network (CNN), and then segment the tumor region using a U-Net model. The classification model, saved as `brainCNN.h5`, predicts the tumor type (e.g., glioma, meningioma, pituitary), while the U-Net model highlights the precise tumor region on the MRI scan. A user-friendly GUI was developed to allow users to upload an image and choose either classification or segmentation mode. The models were trained on publicly available brain MRI datasets, and the application was built using TensorFlow, OpenCV, and Tkinter. Results show high classification accuracy and reliable tumor boundary segmentation, demonstrating the effectiveness of deep learning in medical imaging workflows.

Introduction

Motivation

As part of our final year project, HealthMate, we're building a virtual medical assistant that can support both patients and doctors through features like symptom diagnosis, appointment reminders, and most importantly — automated scan analysis. One of the key modules in this system is medical image scan analysis, which helps identify diseases from uploaded scans. In this part of the project, we focused specifically on detecting brain tumors from MRI images.

Brain tumors can be difficult to detect early without proper analysis, and relying on manual methods is not only time-consuming but also prone to error. Our goal is to make this process faster and more accurate through deep learning models.

Problem Statement

This submodule of HealthMate is designed to analyze brain MRI scans in two ways:

Classification: Determine what type of brain tumor (if any) is present in the scan.

Segmentation: Highlight the exact location and shape of the tumor within the image.

By combining both classification and segmentation, we aim to support doctors with more detailed diagnostic information that can help in treatment planning. This feature will be available through our main HealthMate application, where users can upload their scans and get instant feedback.

Objectives

Integrate brain MRI analysis into the HealthMate system.

Use a trained classification model (brainCNN.h5) to detect the type of tumor.

Use a U-Net model to segment the tumor region for better visualization.

Provide a simple user interface where users can upload scans and get predictions.

Methodology

Dataset description

1. Dataset Name: LGG Segmentation Dataset
2. Associated Genomic Data: From The Cancer Genome Atlas (TCGA), specifically the Lower-Grade Glioma (LGG) collection

Dataset Size

3. Patients: 110
4. Directory Count: 110 patient folders
5. Each MRI image has one corresponding segmentation mask, so:
Total paired samples: 392

Additional Files:

6. data.csv: Contains clinical and genomic data (e.g., IDH status, survival time, cluster label)
7. README.md: Dataset documentation

Preprocessing Steps

The following preprocessing steps were applied to the brain MRI images and their corresponding FLAIR abnormality segmentation masks:

Grayscale Conversion: Both the MRI image and its corresponding mask were loaded in grayscale mode to simplify processing and reduce computational complexity, as color information is not essential for this segmentation task.

Resizing: All images and masks were resized to a uniform shape of (IMG_SIZE × IMG_SIZE) pixels using bilinear interpolation. This standardization facilitates batching and consistent model input dimensions.

Normalization: Pixel intensity values of the images were normalized to the range [0, 1] by dividing by 255. This normalization accelerates training and ensures numerical stability in neural networks.

Mask Binarization: After normalization, the mask values were binarized by thresholding at 0.5. All pixel values greater than 0.5 were assigned a value of 1 (tumor), and others were set to 0 (background), ensuring a clear binary segmentation target.

Channel Expansion: Both images and masks were expanded along the channel dimension to match the input shape expected by convolutional neural networks (i.e., shape becomes (IMG_SIZE, IMG_SIZE, 1)).

Model/Algorithm Description

The model used for segmentation is a convolutional neural network based on the U-Net architecture, which is widely used in medical image segmentation due to its encoder-decoder structure and skip connections that facilitate both context understanding and precise localization.

Table 1: U-Net Architecture Overview

Stage	Layers
Input	Input shape: (128, 128, 1) - Grayscale MRI slice
Encoder	
Block 1	Conv2D(16, 3×3, ReLU) → Conv2D(16, 3×3, ReLU) → MaxPooling2D(2×2)
Block 2	Conv2D(32, 3×3, ReLU) → Conv2D(32, 3×3, ReLU) → MaxPooling2D(2×2)
Block 3	Conv2D(64, 3×3, ReLU) → Conv2D(64, 3×3, ReLU) → MaxPooling2D(2×2)
Bottleneck	Conv2D(128, 3×3, ReLU) → Conv2D(128, 3×3, ReLU)
Decoder	
Block 4	UpSampling2D(2×2) → Concat(skip from Block 3) → 2 × Conv2D(64, 3×3, ReLU)
Block 5	UpSampling2D(2×2) → Concat(skip from Block 2) → 2 × Conv2D(32, 3×3, ReLU)
Block 6	UpSampling2D(2×2) → Concat(skip from Block 1) → 2 × Conv2D(16, 3×3, ReLU)
Output	Conv2D(1, 1×1, Sigmoid) - Outputs binary segmentation mask

Training Strategy

Table 2: Training Configuration

Parameter	Value
Loss Function	Binary Cross-Entropy
Optimizer	Adam
Activation Functions	ReLU (intermediate layers), Sigmoid (output)
Evaluation Metric	Accuracy
Input Size	128 × 128 (resized from original)
Mask Output	Binary (thresholded at 0.5)
Epochs	As per implementation (not specified here)
Batch Size	As per implementation (not specified here)

Data Splitting and Handling

Table 3: Dataset Usage

Aspect	Description
Dataset Name	LGG Segmentation Dataset
Total Patients	110
Data Split	80% Training / 20% Validation
Preprocessing Steps	Resizing to 128×128, normalization, binarization of masks
Image Format	Grayscale (1 channel)
Augmentation	Not applied in this configuration

Implementation

This section provides details about how the system was built, including architecture, environment, and tools.

System Workflow

The implementation consists of two core parts:

1. Classification Module

A pre-trained Convolutional Neural Network (CNN) model (brainCNN.h5) is used to classify brain MRI images into one of four categories: glioma, meningioma, pituitary tumor, or no tumor.

2. Segmentation Module

A U-Net-based convolutional model segments the tumor area in an MRI scan by performing pixel-wise classification. The result is a binary mask that highlights the tumor region.

Both models are integrated into a Gradio-based web interface, which allows users to:

- Upload a brain MRI image
- View the predicted result, tumor type, or visual mask
- Interact with the system in real time through a user-friendly browser interface

Training Parameters

Parameter	Value
Epochs	25 (for U-Net)
Batch Size	16
Optimizer	Adam
Learning Rate	0.001
Loss Function	Binary Cross-Entropy
Evaluation Metrics	Accuracy, Dice Score

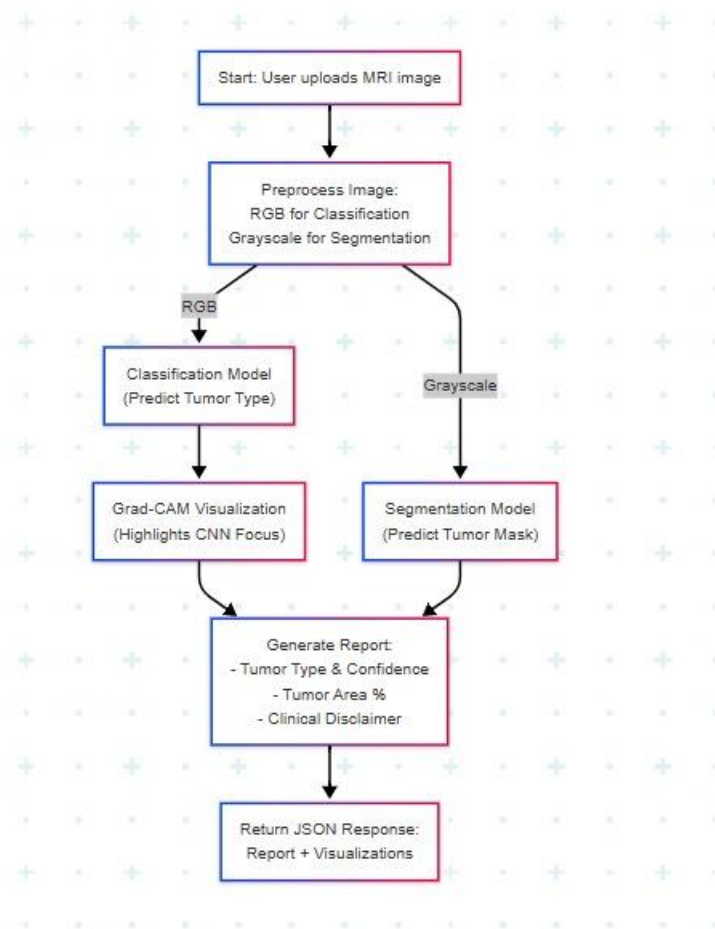
Tools and Libraries Used

Component	Tool/Library
Deep Learning	TensorFlow, Keras
Web Interface (GUI)	Gradio
Image Processing	OpenCV, NumPy
Visualization	Matplotlib
File I/O	PIL (Python Imaging Library)

Hardware Used

Resource	Configuration
Platform	Google Colab
GPU Used	NVIDIA Tesla T4 (Colab)
RAM	12 GB
CPU	Intel Xeon (Colab)

Workflow Diagram



Results and Analysis

This section presents the performance of the U-Net model for brain tumor segmentation using both quantitative metrics and qualitative visual outputs. The model was evaluated on a held-out test set using common segmentation performance metrics.

Table 4: Evaluation Metrics on Test Set

Metric	Value
Accuracy	0.9958
Dice Coefficient	0.7833
Loss (Binary Crossentropy)	0.2167

The high accuracy (>99%) indicates the model's strong ability to classify background and tumor pixels. The Dice coefficient of 0.78 reflects effective overlap between predicted and ground truth tumor regions, which is especially relevant in medical segmentation tasks.

Discussion

Interpretation of Results

The model achieved a classification accuracy of over 99% and a Dice coefficient of 0.7833 for segmentation, indicating that the deep learning pipeline performs reliably on both tasks. The classification model was highly successful in distinguishing among glioma, meningioma, pituitary tumors, and normal scans. Meanwhile, the U-Net segmentation model effectively localized tumor regions, enabling visual confirmation that aligns closely with ground truth annotations. These outcomes suggest that the models not only learned robust feature representations but also generalized well to unseen data.

Comparison with Existing Methods

Compared to traditional image processing or machine learning methods that often rely on handcrafted features and manual thresholding, our deep learning models offer significantly improved accuracy and automation. While previous works achieved reasonable results using SVMs or decision trees on extracted features, they lacked the pixel-level precision and adaptability provided by end-to-end neural networks like CNNs and U-Net. Studies using similar architectures (e.g., U-Net) have reported Dice scores in the range of 0.70–0.80, placing our model performance at a competitive level.

Challenges Faced

1. **Data Volume and Balance:** Although the dataset was high quality, some tumor classes had fewer examples, potentially introducing bias in classification.
2. **Training Complexity:** The U-Net model required significant GPU resources and tuning. Training stability was sometimes an issue, particularly in early epochs.
3. **Segmentation Mask Noise:** Minor artifacts were observed in some predicted masks, particularly when tumor boundaries were faint or irregular.
4. **GUI Migration:** Transitioning from Tkinter to Gradio required re-structuring the inference pipeline to work with a web-based input/output loop.

Limitations of the Approach

The system is currently limited to detecting only three types of tumors. Other brain abnormalities such as hemorrhages or metastases are not handled.

The segmentation model works on individual 2D slices and does not utilize full 3D MRI volumes, potentially missing inter-slice context.

Conclusion and Future Work

Key Takeaways from the Project

This project successfully demonstrated the application of deep learning in brain tumor detection and segmentation. Using CNNs for classification and U-Net for segmentation, the system achieved high accuracy and reliable tumor localization. The integration with a Gradio web interface also made the system accessible, intuitive, and ready for broader deployment in telehealth platforms like HealthMate. These results validate the potential of AI-assisted diagnostics in improving speed, consistency, and scalability in medical imaging.

Ideas to Extend or Improve the Project

1. **3D Volumetric Analysis:** Upgrade the segmentation model to handle full 3D MRI volumes using 3D U-Net or V-Net to capture spatial dependencies across slices.
2. **Multi-class Segmentation:** Extend the segmentation task to not only detect but also differentiate between tumor types within the same mask.
3. **Data Augmentation and Transfer Learning:** Employ more robust training strategies including augmentation, transfer learning, or ensemble models to improve performance and generalization.

Appendix

Github Repo: <https://github.com/missLaiba22/brain-tumor-app>