

Automated Segmentation and Classification of Brain Tumor Using Deep Learning: Improving Healthcare Efficiency and Patient Outcomes

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Abstract

Introduction: Brain tumors are a significant cause of morbidity and mortality worldwide, making early diagnosis essential for improving patient outcomes. Manual segmentation and classification of brain tumors from MRI scans are time-consuming processes that are often subject to variability. This highlights the need for automated solutions to enhance diagnostic efficiency and accuracy.

Methods: This study presents an automated system for the segmentation and classification of brain tumors using deep learning techniques. The proposed model integrates a pre-trained U-Net for segmentation and utilizes various CNN-based models, specifically ResNet-50, VGG-16, and Inception-V3, for classification. Developed and validated with a dataset of MRI brain scans categorized into four tumor types: glioma, meningioma, pituitary tumor, and no tumor—the process involves several stages: in the data preprocessing phase, target masks were manually created, followed by data augmentation to enhance the dataset. To accurately delineate tumor regions, the U-Net model then applied on the augmented dataset. The segmented images were subsequently processed through the CNN-based models for classification, and optimization techniques such as batch normalization, dropout, regularization, and dense layers were incorporated to improve overall model performance.

Results: Experimental results demonstrated that the implementation of thresholding technique significantly enhanced the performance of the U-Net model, achieving an accuracy of 97% and a Dice coefficient of 0.91. Among the classification models, ResNet-50 emerged as the top performer, achieving the highest accuracy of 98%.

Conclusion: The findings of this study underscore the potential of deep learning techniques in the automated diagnosis of brain tumors. While the results are promising, further research is recommended to improve the model's capability to handle multi-class tumors within individual MRI scans. This approach aims to support healthcare professionals by providing accurate diagnostic information and potential treatment recommendations.

Keywords: UNet Segmentation, Image Classification, Brain Tumor Diagnosis, MRI Scan Images, CNN Based Models

Introduction

Brain tumors are a significant cause of mortality and morbidity worldwide. Accurate and timely diagnosis is crucial to improving patient outcomes, particularly as the survival rates of patients are heavily dependent on early intervention [1,2]. Magnetic Resonance Imaging (MRI) is the primary imaging modality used for diagnosing brain tumors, offering non-invasive and high-resolution views of brain tissues [3]. However, manual segmentation of brain tumors from MRI scans remains labor-intensive and prone to human error, especially

when considering the complex and heterogeneous nature of tumor tissues. This makes automation of both segmentation and classification a critical step in streamlining the diagnostic process in clinical settings, minimizing variability between radiologists, and improving the accuracy of diagnosis.

In recent years, deep learning, particularly Convolutional Neural Networks (CNNs), has emerged as a powerful tool for automating the segmentation and classification of medical images. U-Net, a CNN-based architecture developed by [4], has become a widely adopted



model for medical image segmentation tasks due to its encoder-decoder structure, which allows the preservation of both local and global image features. U-Net has proven effective in segmenting brain tumors from MRI images, ensuring that tumor boundaries are accurately delineated even in complex cases [5]. However, while segmentation is crucial for identifying the tumor, classification is equally important for determining the tumor type, such as Glioma, Meningioma, Pituitary and No Tumor. This helps guide clinical treatment and therapeutic decisions.

Deep learning models, such as ResNet-50, VGG-16, and Inception V3, have been used extensively for tumor classification based on segmented MRI regions. These models are capable of extracting hierarchical features from segmented images, allowing for accurate classification of tumor types [6]. Deep Medic, A Deep Learning Framework for Automated MRI Brain Tumor Segmentation by [7] demonstrated the effectiveness of deep learning for brain tumor segmentation, achieving state-of-the-art performance on the BRATS challenge.

Despite the success of deep learning models in brain tumor segmentation and classification, existing methods face several limitations such as manual segmentation of MRI images, which is time-consuming and subject to interobserver variability [8,9]. Although automated techniques using deep learning models have shown potential, there are still several challenges. Many existing models focus solely on segmentation or classification, without integrating the two processes [10,11]. Additionally, there is a need for models that can generalize well across various tumor types and imaging conditions while maintaining high accuracy and low computational complexity.

This research aims to develop a comprehensive system for brain tumor segmentation and classification using deep learning techniques. Specifically, to leverage U-Net for accurate tumor segmentation and integrate it with CNN based pre-trained models such as ResNet-50, VGG-16, and Inception V3 for classifying segmented regions into different tumor types. By automating both tasks, the system is expected to improve the speed and accuracy of brain tumor diagnosis. The performance of the model will be evaluated using standard metrics such as Dice similarity coefficient for segmentation and accuracy, precision, recall, and F1-score for classification. Additionally, transfer learning and data augmentation techniques will be used to improve the generalization of the model across different types of tumors and MRI conditions.

This study focuses on the segmentation and classification of brain

tumors from MRI images. While other imaging modalities, such as CT and PET scans, also play a role in brain tumor diagnosis, this research is limited to MRI scans due to their higher resolution and ability to provide detailed information on brain tissues. The model is designed to be scalable and adaptable for future clinical use. By integrating segmentation and classification into a single model, the study aims to develop a system that can be deployed in various healthcare environments to enhance the diagnostic workflow.

In terms of methodology, this research uses a hybrid approach combining U-Net and CNN based pre-trained models such as ResNet-50, VGG-16, and Inception V3. The U-Net model is first trained on MRI scans to perform tumor segmentation. Data augmentation techniques such as rotation, flipping, and scaling are employed during training to enhance model robustness. The segmented tumor regions are then passed through a pre-trained CNN model classifier, which categorizes the tumors based on predefined labels such as Glioma, Meningioma, Pituitary and No Tumor. The models are trained and evaluated using common performance metrics, and the results are benchmarked against existing approaches to ensure that the system offers competitive accuracy and efficiency.

Methods

Dataset Description

For model training, we utilized the brain tumor dataset sourced from Kaggle, which is the world's largest data science community with powerful tools and resources to help achieve data science goals. This dataset contains MRI images of the brains of 7,023 individuals, including cases of glioma, meningioma, no tumor, and pituitary tumors. The dataset is pre-classified by domain experts and organized into training and testing folders. In general this dataset consists of 7,023 MRI images, distributed across four classes: 1,621 images in the glioma class, 1,645 in the meningioma class, 2,000 in the no tumor class, and 1,757 in the pituitary class. See Figure 1 However, we were unable to use all of the data since we employed an automatic segmentation technique that required manual preparation of mask, making the process time-consuming.

Architecture of the Model

The model's architecture is composed of four key stages: the data pre-processing stage, the segmentation stage, the classification stage, and the treatment planning stage. Refer Figure 2 for details.

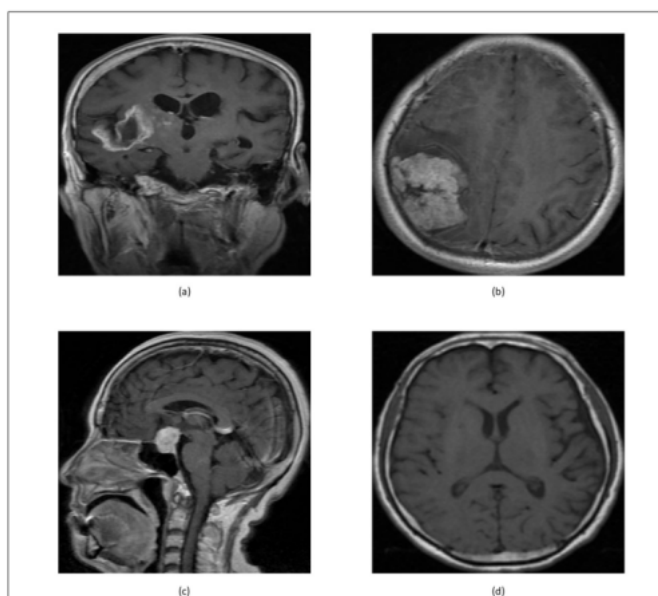


Figure 1: MR images (a) Glioma, (b) Meningioma, (c) Pituitary and (d) No Tumor.

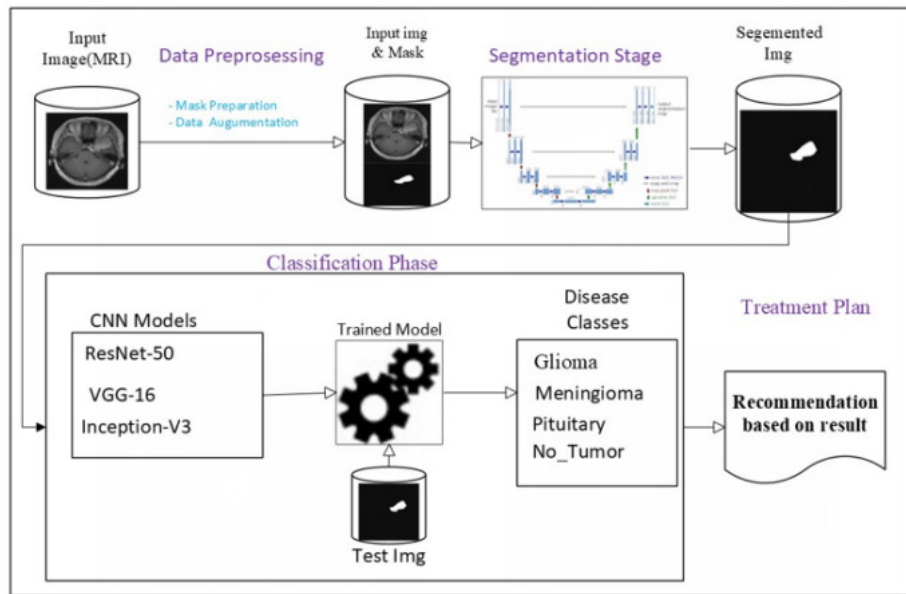


Figure 2: Architecture of the model.

Data Preprocessing Phase

This phase encompasses two key steps: target mask preparation and data augmentation, both essential for enhancing the quality and quantity of the training dataset.

Target Mask Preparation

Target masks for the input images were generated manually using tools like ITK Snap and ImageJ (Fiji). In total, 105 masks were prepared for each of the four classes: Glioma, Meningioma, Pituitary and No Tumor, leading to 420 target masks. Given the time-consuming nature of manual mask creation, we limited the number of masks and instead relied on augmentation techniques to enrich the dataset. The manual preparation of these masks ensures that the model has a solid foundation for identifying critical features, though this labor-intensive process was supplemented by data augmentation to ensure scalability.

Data Augmentation

To expand the dataset, we used the Albumentations library for both input images and their corresponding masks. Five different augmentation techniques were applied: Center Crop, RandomRotate90, Grid Distortion, Horizontal Flip, and Vertical Flip. These methods collectively increased the dataset size to 2520 images, with each of the original 420 images and masks being augmented five times. For every input image and its associated target mask, five additional variants were created, effectively increasing the dataset's diversity. To further enhance the accuracy of segmentation, a threshold value of 0.5 was applied to the augmented masks, reducing noise and improving the precision of the segmentation model by focusing on relevant areas of the image.

This strategic combination of manual preparation and augmentation not only increases the dataset's volume but also improves its quality, ensuring the model is trained with varied and noise-reduced data for better generalization.

Segmentation Phase

In this phase, we applied automated segmentation to accurately identify the regions of interest (ROIs) in the input MRI images. Our approach leveraged the pre-trained U-Net model, originally developed by the University of Freiburg's Department of Computer Science. U-Net has been specifically designed for biomedical image segmentation tasks and is widely recognized for its ability to handle complex

medical images'-Net follows a U-shaped architecture, which consists of four key components: the contracting path (encoder), a central bottleneck, the expansive path (decoder), and skip connections [12]. The contracting path captures the high-level features through convolutional layers, while the expansive path reconstructs the spatial resolution of the image. The skip connections ensure that the high-resolution features from the encoder are directly passed to the decoder, thereby improving the precision of segmentation, especially in edge detection and finer details. Our segmentation model is designed to process two types of inputs: the original MRI images and their corresponding manually prepared target masks. The output of the model is a predicted mask that delineates the brain tumor region within the MRI scan. This predicted mask plays a crucial role in the next phase, serving as input to the classification model, which categorizes the brain tumor based on its characteristics.

Classification Phase

In this phase, the classification model operates using the predicted tumor masks generated from the segmentation process. For classification, we utilized several pre-trained CNN architectures, including VGG16, ResNet-50, and Inception-V3, each of which is well-established for image classification tasks. These models were used to classify the segmented MRI brain images into four distinct categories: glioma, meningioma, pituitary tumor, and no tumor.

VGG-16 is a 16-layer deep convolutional neural network comprising 13 convolutional layers and 3 fully connected layers. The convolutional layers are grouped into blocks, where each block consists of multiple convolutional layers followed by a max-pooling layer. This architecture processes input images of size 224×224 pixels and is pre-trained on the ImageNet dataset, which consists of over a thousand image classes [13]. The structure of VGG-16 is designed for feature extraction, leveraging deep representations of image data to identify the complex patterns characteristic of different tumor type.

ResNet-50 (Residual Network) is a deeper architecture, containing 50 layers, with 49 convolutional layers and a single fully connected layer. A unique feature of ResNet-50 is its use of residual blocks, which address the issue of vanishing gradients that commonly affect deep neural networks. Residual blocks allow the model to skip certain layers by adding the output of one layer directly to the input of another. This innovation enables better gradient flow during back-propagation, allowing ResNet-50 to achieve superior performance even with very

deep architectures. The network's ability to capture fine details and learn from deeper layers makes it highly effective for classifying complex medical images [14].

Inception-V3 is another widely used architecture, notable for its innovative Inception modules. These modules consist of parallel convolutional layers with different kernel sizes, allowing the network to capture features at multiple scales within the same layer. This multi-scale approach enhances the model's ability to identify both fine and coarse details in the image. Inception-V3 also incorporates advanced techniques such as batch normalization and factorized convolutions to improve both accuracy and computational efficiency. In total, Inception-V3 contains 42 layers, including 39 convolutional layers and 3 fully connected layers, and has proven to be highly effective in a wide range of image classification tasks [15].

Treatment Plan

After training, the automated brain tumor segmentation and classification model is deployed for clinical use, where it can be accessed by medical professionals such as radiologists, neurosurgeons, and oncologists. The system is designed to streamline the diagnostic process by enabling healthcare experts to upload new MRI brain scans into the platform. Once an MRI scan is input, the model proceeds to segment the tumor region and classify it into one of several categories, including glioma, meningioma, pituitary tumor, or no tumor.

Upon classification, the system generates diagnostic results and tailored recommendations, helping medical teams quickly assess the severity of the tumor and explore potential treatment options. This process not only accelerates the diagnostic workflow but also improves the accuracy of tumor identification, providing critical insights for the development of personalized treatment strategies.

By automating this process, the model reduces the reliance on manual segmentation and classification, allowing clinicians to focus on more complex decision-making aspects of patient care. The use of deep learning significantly enhances healthcare efficiency by minimizing human error, ensuring consistent results, and speeding up the diagnostic turnaround. This, in turn, improves patient outcomes by enabling early detection and prompt intervention, particularly for high-risk brain tumors.

Evaluation Metrics

For the segmentation task, we used the Dice coefficient as the primary evaluation metric. This metric measures the overlap between the predicted segmentation mask and the ground truth, indicating how well the model is able to replicate the actual tumor region [16]. Dice coefficient scores range from 0 to 1, with higher values signifying superior model performance [17]. For evaluating the classification models, we applied a train-test split strategy. The dataset was divided into three parts: training, validation, and testing sets. The classification performance was assessed using several key metrics, including accuracy, precision, recall, and F1-score.

Table 1A: The classification result.

	Masks	%
Training set	1960	70%
Validation set	420	15%
Test set	420	15%

Results

The proposed model exhibited excellent performance in both the segmentation and classification tasks. In the segmentation stage, the model achieved an accuracy of 97% and a Dice coefficient of 0.91, indicating a strong overlap between the predicted masks and the ground truth. The classification phase similarly demonstrated a high degree of accuracy, with the model correctly classifying brain tumor types with 98% accuracy on the test dataset. These results underline the effectiveness of our approach in segmenting and classifying brain tumors from MRI images, showcasing its potential for improving diagnostic efficiency.

Segmentation Results

During the preprocessing phase, we manually created 420 target masks for the input MRI images, which were later augmented using the Albumentations library. Augmentation techniques such as Center Crop, Random Rotate 90, and Flip operations expanded the dataset to 2520 images and masks. From this dataset, 80% (2016 images) were allocated for training, while the remaining 20% (504 images) were set aside for validation and testing. The U-Net model, pre-trained for biomedical image segmentation, used for training. The input images were resized to (256, 256, 3) to match U-Net's required input size. Training was conducted over 20 epochs, utilizing the Adam optimizer with a learning rate of 0.0001 and a batch size of 16. To minimize overfitting and enhance generalization, early stopping was applied. The binary cross-entropy loss function was used during training to optimize the segmentation performance. At the conclusion of the segmentation phase, the model produced a segmented MRI image (predicted mask) with an impressive accuracy of 97% and a Dice coefficient of 0.91, reflecting its ability to accurately segment brain tumors from MRI scans.

Classification Result

The dataset used for classification comprised 2800 masks, generated from the segmentation stage. The dataset was divided into 70% training set (1960 masks), 15% validation set (420 masks), and 15% test set (420 masks). Each set had a balanced distribution, with 105 samples from each of the four tumor classes: glioma, meningioma, pituitary tumor, and no tumor (Table A1).

All three classification models: VGG-16, ResNet-50, and Inception-V3 were trained using the same hyper parameters, specifically, the models were trained over 50 epochs with a batch size of 16, using the Adam optimizer with a learning rate of 0.0001. The loss computed using categorical cross-entropy, as the classification task involved multiple classes (Figure 3).

To improve model performance and generalization, techniques like Batch Normalization, regularization, dropout layers, and dense layers were incorporated into the models. As a result, the classification models achieved a high accuracy of 98% on the test dataset (Table 1B), demonstrating robust performance in differentiating between the four tumor classes based on the segmented images.



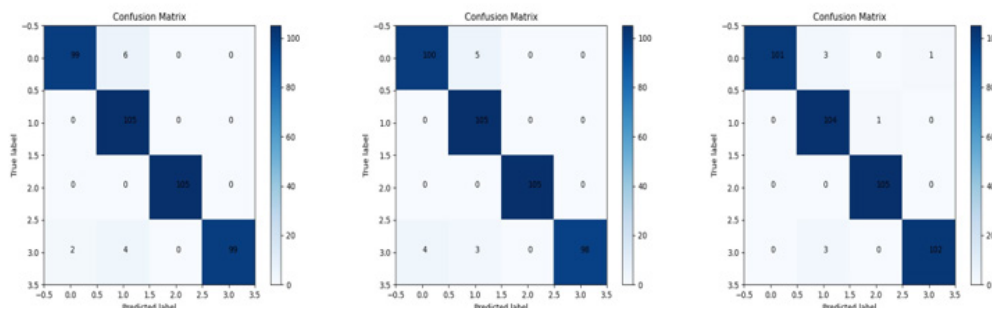


Figure 3: Confusion matrix (a) Inception-V3, (b) ResNet-50 and (c) VGG-16.

Table 1B: Performance evaluation of the three CNN-based models.

Model Performance Evaluation				
Models	Accuracy	Precision	Recall	F1- score
Resnet-50	98%	98%	98%	98%
VGG-16	97%	97%	97%	97%
Inception-V3	96%	96%	96%	96%

Discussion

The evaluation of our classification model’s performance was conducted using standard metrics such as accuracy, precision, recall, F1-score, and the confusion matrix. These metrics provide a comprehensive understanding of the model’s ability to accurately identify various brain tumor types, as detailed in Table 1B and Figure 3. Additionally, training and validation accuracy curves, alongside their corresponding loss curves, are displayed in (Figures 4-6), which displays the learning dynamics of the models throughout the training process.

The confusion matrices, presented in Figure 3, offer a detailed comparison of the classification results for the four tumor categories: glioma, meningioma, pituitary tumor, and no tumor. Among the three models, ResNet-50 achieved the highest classification accuracy, especially for the meningioma and no tumor categories, where it attained near-perfect scores. However, performance slightly diminished in the classification of glioma and pituitary tumor cases, with 12 out of 105

glioma cases and 10 out of 105 pituitary tumor cases misclassified. These misclassifications suggest that some overlap in the visual characteristics of these tumor types could challenge even advanced models. Despite these minor errors, ResNet-50 consistently outperformed VGG-16 and Inception-V3, demonstrating superior precision, recall, and overall classification accuracy across all tumor categories, which is required for appropriate diagnosis.

The learning behavior of the models is further analyzed in (Figures 4-6) which display the training and validation accuracy curves over 50 epochs. The results indicated that, all models successfully converged, with ResNet-50 showing the most stable and reliable improvement in both training and validation phases. Its loss curve also demonstrates a steady decline, indicating that the model effectively learned the relevant features for tumor classification without overfitting. In comparison, VGG-16 and Inception-V3 displayed more fluctuation in their accuracy curves, suggesting these models may require additional epochs or further fine-tuning to achieve optimal performance.

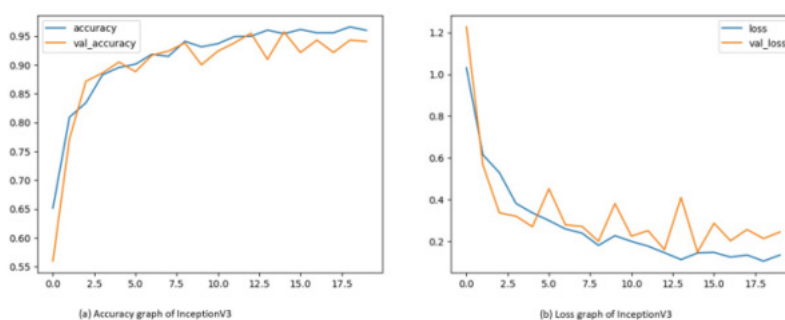


Figure 4: Accuracy and Loss graph of InceptionV3: (a) Accuracy graph and (b) Loss graph.

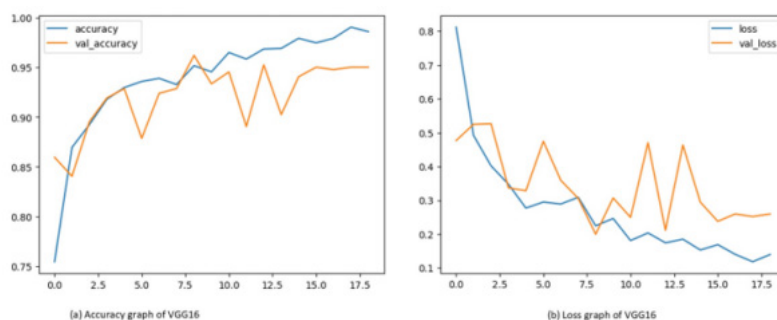


Figure 5: Accuracy and Loss graph of VGG16: (a) Accuracy graph and (b) Loss graph.



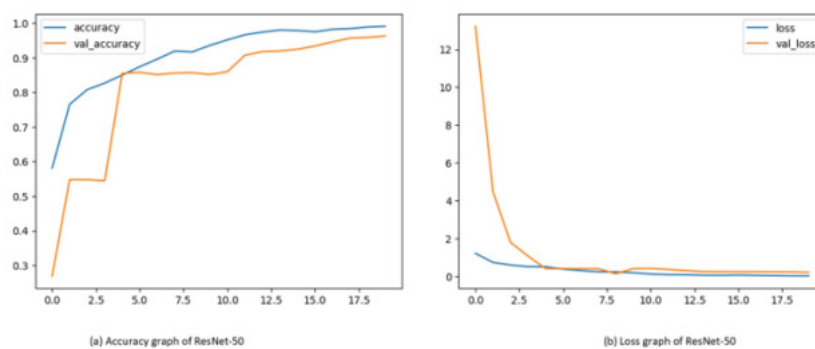


Figure 6: Accuracy and Loss graph of ResNet-50: (a) Accuracy graph and (b) Loss graph.

The implementation of techniques such as batch normalization, dropout layers, and regularization was critical in improving the models' generalization capabilities and reducing the risk of overfitting. These techniques allowed all three models to maintain robust performance on the validation and test datasets. However, ResNet-50's superior performance is attributed to its use of residual connections, which facilitate gradient flow and make training deep networks more efficient and effective, particularly for complex medical image classification tasks.

In summary, the ResNet-50 model demonstrated the best overall performance in both the segmentation and classification tasks, achieving high accuracy, precision, and recall. While there were minor misclassifications in the glioma and pituitary tumor classes, the model's consistent and robust performance across other tumor types underscores its potential for clinical application in brain tumor diagnosis. The stable convergence patterns and low loss values further validate ResNet-50's ability to generalize well across various tumor categories, reinforcing the feasibility of utilizing deep learning models like ResNet-50 for automated brain tumor classification, ultimately enhancing diagnostic accuracy and improving patient outcomes (Imrus and Dae-ki., 2023).

Conclusion

In this study, we developed an effective deep learning model for automated brain tumor segmentation and classification using CNN-based pre-trained networks on MRI scans. The segmentation model, based on U-Net, achieved notable performance with 97% accuracy, 97.7% (97.7% Not mentioned in the results) precision, and a Dice coefficient of 0.91. Performance improvements were realized by incorporating a thresholding technique to reduce noise in the MRI data.

We further applied the segmented images to train apply or test three classification models: VGG-16, ResNet-50, and InceptionV3. Among these, ResNet-50 achieved the best results, with a testing accuracy of 98%, though some misclassifications occurred, particularly in MRI images containing multiple tumor types labeled as a single class. This highlights the need for more advanced methods to handle multi-class data more effectively.

This research demonstrates the potential of deep learning techniques in improving the accuracy of brain tumor diagnosis. Future work should focus on enhancing the model's handling of complex data and exploring multi-label classification for more accurate tumor characterization.

Statement of Ethics

The use of a publicly available dataset for conducting this research does not require ethical approval, in accordance with local and national guidelines. The dataset utilized in this study is publicly accessible, and no personal or sensitive information is involved in this research.

Conflict of Interest Statement

The authors declare no conflicts of interest related to this study.

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This research received no specific funding or sponsorship from any organization.

Author Contributions

Author 1 was responsible for the design and execution of the experiments. Author 2 performed the data analysis. Both authors contributed to the writing and editing of the manuscript and have approved the final version for submission.

Data Availability

The dataset supporting the findings of this study is publicly available and can be accessed at kaggle.

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