Advancing brain tumor diagnosis with Deep Learning-Driven image segmentation techniques

Zeinab Khadra, Ammar Asad, Mohammed Hammoud, Ola Haydar, Sergey S. Lupin

Abstract— **Early diagnosis of brain tumors is critical for improving patient outcomes. This study presents a novel AI-driven framework for the early detection of brain tumors utilizing magnetic resonance imaging (MRI) scans. The core of the framework is a U-Net, a deep learning model specifically designed for image segmentation. Leveraging a substantial dataset of annotated MRI images, the U-Net is trained to accurately segment and identify tumor regions within the brain, even in their early stages where subtle abnormalities may be present. The proposed framework is evaluated on a diverse dataset of MRI scans, demonstrating its capability to achieve high accuracy in tumor segmentation and detection. Moreover, we explore the potential of incorporating explainable AI techniques to provide insights into the model's decision-making process, thereby enhancing the clinical interpretability of the results. Our findings suggest that the AI-powered framework, based on the Unet architecture, holds substantial promise for improving the early detection of brain tumors, potentially leading to better patient management and prognosis.**

Keywords— Artificial Intelligence, Brain Tumor, Unet, Deep learning, Image segmentation.

I. INTRODUCTION

Brain tumors pose a significant threat to human health, demanding prompt and accurate diagnosis for optimal treatment and patient outcomes. The early detection of brain tumors is crucial, as it allows for timely intervention, potentially leading to improved survival rates and reduced morbidity. However, the early stages of brain tumor development can be characterized by subtle abnormalities that are often challenging to identify using conventional diagnostic methods. This challenge underscores the need for innovative approaches that can enhance the sensitivity and accuracy of brain tumor detection, particularly in the early stages. Magnetic resonance imaging (MRI) has emerged as a cornerstone in brain tumor diagnosis, providing high resolution images of brain structures and facilitating the visualization of abnormalities. However, manual interpretation of MRI scans by radiologists can be time-consuming, prone to inter-observer variability, and potentially overlooks subtle changes indicative of early tumor development.

The advent of artificial intelligence (AI), specifically deep learning, has opened new avenues for automating and enhancing the analysis of medical images, including MRI scans.

Deep learning algorithms, particularly convolutional neural networks (CNNs), have demonstrated remarkable success in various image recognition and segmentation tasks, offering the potential to revolutionize medical image analysis. This study proposes a novel AI-driven framework for the early detection of brain tumors using MRI scans. The core of our framework is a U-Net, a powerful deep learning architecture specifically designed for image segmentation. The U-Net's ability to capture both local and global features within an image makes it particularly well-suited for segmenting complex anatomical structures like the brain and identifying subtle tumor regions.

By leveraging a large dataset of annotated MRI images, we train the U-Net to accurately segment and identify tumor regions, even in their early stages when the tumor may be small and the associated changes subtle. Furthermore, we explore the potential of incorporating explainable AI (XAI) techniques into our framework. XAI aims to provide insights into the decision-making process of AI models, enhancing the transparency and interpretability of their predictions. In the context of brain tumor detection, understanding the model's rationale for identifying a potential tumor can be invaluable for clinicians, fostering trust and facilitating the integration of AI into clinical workflows.

The proposed framework holds the potential to significantly improve the early detection of brain tumors, leading to earlier interventions and potentially better patient outcomes. By automating the process of tumor identification and providing valuable insights into the model's predictions, our framework aims to empower clinicians with a powerful tool for enhancing their diagnostic capabilities and ultimately improving patient care. The following sections detail the methodology, results, and discussion of our findings, highlighting the potential of this AI-driven approach for revolutionizing brain tumor diagnosis.

II. RELATED WORKS

Early detection of brain tumors is crucial for improving patient outcomes. Researchers explores the advancements in medical imaging, specifically the segmentation of brain tumors using MRI technology [1]. It emphasizes the critical role of accurate image segmentation in improving diagnostic precision and treatment outcomes. In another study [2], the researchers focused on automatic brain tumor segmentation, employing various machine learning algorithms to enhance accuracy and efficiency. They analyzed and optimized algorithms such as Hidden Markov Random Field and active contour methods. BRATS 2020 is utilized to evaluate the models' performance in this study.

In another study [3], the authors proposed a categorization approach to detect and classify benign tumors using a two-step technique that involves feature extraction followed by classification. A gray-level co-occurrence matrix was applied for feature extraction, while the K-Nearest Neighbors algorithm was used for image classification. This method enhances precision in analyzing a large volume of medical images, particularly in tumor research and other areas of medical decision support.

A recent study extracted tumor area using Fuzzy C-Mean-based clustering and classified it using CNN. It detected different brain tumors with 96.56% accuracy, proving its ability to be used in radiologists. Another research group evaluated the performance of Conditional Random Fields combined with a full-CNN and assessed the impact of post-processing steps, training patches number, and patch sizes [5]. The study also compared segmentation models based on different imaging modalities, demonstrating that models using fewer modalities could achieve competitive performance. An efficient methodology was developed for automatic brain tumor detection and classification. Feature were extracted using Wavelet Transform and then fed into ML and DL models: SVM and DNN. The DNN classifier, when combined with DWT, outperformed other classifiers in all performance measures [6]. SAM3D is built upon the Segment Anything Model (SAM) encoder [7], utilizing a simple 3D CNN decoder, while using the SAM encoder as feature extraction step.

Another study processes the entire 3D volume image as input, avoiding the need for extensive parameter training and slice-by-slice predictions [8]. It integrates CNNs and transformers by merging them into a unified framework. It used ANN and MobileNet and achieved an accuracy of 89%, emphasizing the applicability of DL. Another approach was proposed to detect brain tumors from MRI [9]. It extracted features using key algorithms, including the Berkeley Wavelet Transform for segmentation and the Gray Level Co-occurrence Matrix, and fed them into different models: SVM, Naive Bayes, and CNN for classification. The methodology emphasizes preprocessing, feature selection via a genetic algorithm, and achieving high precision in identifying tumor regions. In [10], an article introduced a novel U-Net-inspired CNN for automated brain tumor segmentation, outperforming other studies with high Dice scores for different tumor parts. Furthermore, it explored the use of radiomic features derived from the segmented images for survival prediction, achieving a promising correlation (Spearman's = 0.496). This work demonstrated the potential of integrating automated segmentation with radiomics for enhanced clinical decision-making in brain tumor management.

A novel approach is introduced to segment glioma in MRI scans using a densely connected 3D-CNN. The authors effectively addressed class imbalance and variability in tumor morphology by employing a hierarchical segmentation structure and multi-scale receptive fields [11]. The model achieves competitive Dice scores on the dataset, demonstrating its potential for improved performance in segmenting brain tumors. The authors segmented the brain tumor through the One-pass Multitask Network (OM-Net), tackling the class imbalance issue. Their approach significantly reduced computational complexity while maintaining high accuracy by integrating multiple segmentation tasks into a single model with shared parameters.

The introduction of Cross-task Guided Attention (CGA) enhances feature recalibration [12]. Multiple models for brain tumor segmentation were compared and a biophysics guided prognostic model was introduced to enhance overall accuracy [13]. A multi-task contextual atrous residual network was used to address the challenge of class imbalance in medical imaging by proposing a cascaded structure that localizes tumor regions and segments them accurately. Their use of a contextual detection network enhances the focus on relevant areas, while the 3D atrous residual network ensures robust feature extraction and gradient propagation, leading to superior performance on benchmark datasets compared to existing methods [14].

Incomplete segmentation was addressed by the Region-aware Fusion Network (RFNet) [15]. The authors develop a way to handle different sensitivities of various MRI modalities to specific tumor areas adaptively, enabling feature aggregation.

A novel two-pathway CNN architecture [16] is proposed that effectively captures both local and contextual features, resulting in a remarkable speed improvement over existing methods. Additionally, the implementation of a double-phase training addressed the data imbalance issue and enhanced the model's robustness. The authors highlight the effectiveness of CNNs [17], with their proposed model demonstrating 93.3% and 98.43% for accuracy and AUC, respectively.

In another work, a two-step approach [18] was proposed. Synthetic data was generated using a generative model to create a larger and balanced dataset, followed by training a convolutional classifier on the synthesized data. The framework achieved high accuracy of 96.88%, demonstrating its performance as a robust solution for accurate brain tumor detection. The integration of Mask R-CNN with Fuzzy C-Means clustering enhanced diagnostic efficiency and accessibility, particularly for patients without immediate access to radiologists. By leveraging the strengths of both Mask R-CNN for precise segmentation and FCM for managing data uncertainty [19], this study demonstrates significant improvements in classification accuracy using an ensemble deep learning model that combines CNN and Long Short-Term Memory (LSTM) networks [20], achieving 99.1% accuracy along with high precision and recall rates.

Using data augmentation techniques, the study [21] addressed the challenge of limited datasets in medical imaging, demonstrating that augmenting MRI images through methods such as flipping, rotation, and translation significantly improved the model's performance metrics, including accuracy, precision, and recall. The findings highlight the effectiveness of the VGG16 architecture in classifying brain tumors.

By integrating CNN with Gray Level Co-occurrence Matrix (GLCM) features [22], researchers proposed a feature fusion model that effectively distinguished between various brain tumor types and non-tumor cases, achieving impressive accuracy rates of 98.22% and 98.01% on binary and multi-class datasets, respectively. The study highlighted the potential of deep learning techniques in enhancing diagnostic accuracy and offered a robust framework for future research in automated medical image analysis.

III. METHODS AND METHODOLOGY

A. Dataset

The Br35H dataset [1] is a collection of medical images specifically focused on brain tumors. These images are likely MRI (Magnetic Resonance Imaging) scans, a common tool for visualizing the brain and detecting abnormalities like tumors. The dataset is designed to help researchers and AI developers train and test algorithms that can automatically detect and classify brain tumors in these images. We divided the images into three sections: 500 for training, 200 for validation and 100 for testing.

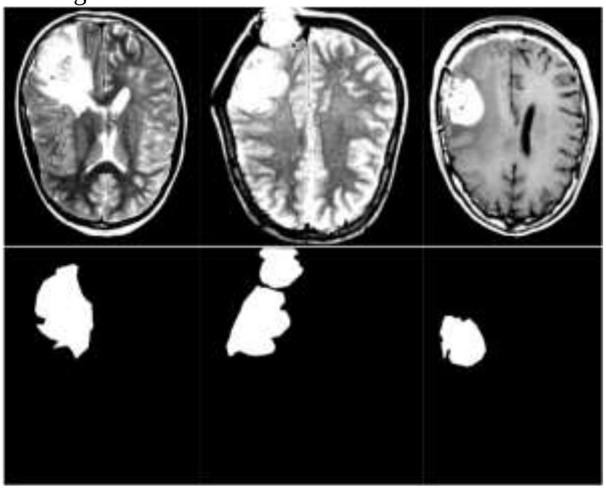

Fig. 1. Samples from the dataset

B. Model architecture

The U-Net architecture stands out as a significant deep learning framework in the realm of image analysis, particularly excelling in tasks related to semantic segmentation. This model is adept at capturing intricate details from visual data, enabling accurate recognition and demarcation of specific regions and contours.

The construction of U-Net is founded on the dual principle of contraction and expansion, resembling the shape of the letter "U". During the contraction phase, convolutional layers are utilized to progressively decrease the spatial dimensions of the image while extracting critical feature representations. As the dimensionality reduces, the model enhances its capacity to discern more abstract and complex features.

Conversely, the expansion phase reverses this process. The image dimensions are successively enlarged while assimilating features gleaned from earlier stages. In this context, skip connections are crucial for the transference of intricate information from the contraction layers to the expansion layers. These connections ensure that meticulous details regarding object boundaries and finer characteristics within the image are preserved, leading to improved accuracy in segmentation outcomes.

In simpler terms, U-Net can be conceptualized as a "focused beam" illuminating particular sections of an image. In the contraction phase, the beam initially highlights broad features and progressively narrows down to finer details in the expansion phase. Thanks to the utilization of skip connections, all captured information is amalgamated to create a comprehensive and precise depiction of the target segment.

U-Net finds extensive application across various domains, including medical imaging (for delineating tumors or anatomical structures), autonomous vehicle systems (for recognizing objects within images), and satellite image interpretation (for detecting agricultural zones or urban areas). The model's capability to manage high-resolution imagery while sustaining segmentation precision is among its primary strengths, rendering it an optimal selection for a broad spectrum of practical uses.

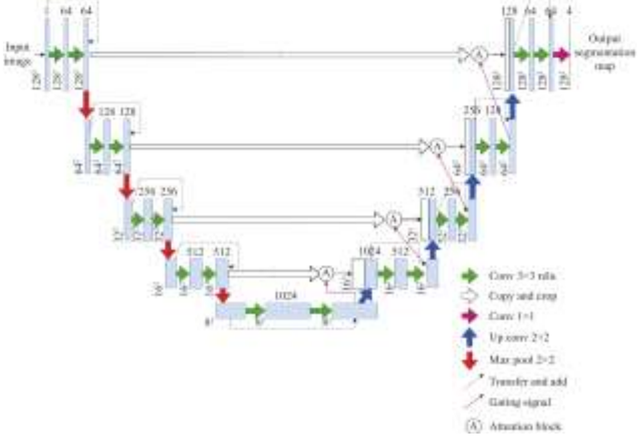

Fig. 2. U-Net Architecture Module

C. Implementation Details

Our methodology leverages the U-Net architecture for model training. The Adam optimizer, configured with a learning rate of 1e-4, is employed for model optimization. Experiments are conducted on the Brain Tumour Br35H dataset utilizing a batch size of 50 and input image dimensions of 256x256 pixels. No learning rate scheduling mechanisms are implemented. The proposed architecture comprises four convolutional layers. Model training is performed using binary cross-entropy loss, as well as a combination of binary cross-entropy loss functions. All models are implemented within the PyTorch framework and trained on a single NVIDIA RTX 3060 GPU for a total of 100 epochs. No pre-trained weights are utilized in any of the experiments. Both

[1] https://https://www.kaggle.com/datasets/ahmedhamada0/brain-tumor-detection

encoder and decoder pathways incorporate four layers each. Each encoder layer consists of two convolutional layers with a 3x3 kernel and 1-pixel padding, followed by a Batch Normalization 2D (BatchNorm2d) layer. The ReLU activation function is applied to introduce non-linearity. Analogously, each decoder layer comprises two convolutional layers and a BatchNorm2d layer, with identical kernel size and padding. Transposed convolutional layers (ConvTranspose2d) are employed in the decoder to facilitate up-sampling and reconstruction.

The performance of the model was evaluated using F1score/ Dice score coefficient (DCS), IoU/Jaccard Index, precision/ Positive Predictive Value, sensitivity/recall/true positive rate, and specificity/ True Negative Rate. Precision measures the accuracy of the positive predictions, while recall measures the ability of a model to find all the actual positives. Specificity measures the proportion of actual negatives that are correctly identified. All these equations are expressed below:

$$F1score/DSC = \frac{2 * TP}{2 * \mathrm{TP} + \mathrm{FP} + \mathrm{FN}} \quad (1)$$

$$IoU = \frac{|A \cap B|}{|A \cup B|} = \frac{TP}{\mathrm{TP} + \mathrm{FP} + \mathrm{FN}} \quad (2)$$

$$Precision = \frac{TP}{TP + FP} \quad (3)$$

$$Recall = \frac{TP}{TP + FN} \quad (4)$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (5)$$

IV. Results and Discussion

In Table I, we show the results we obtained from the training with recent techniques.

TABLE. I. TESTING RESULTS

Study	F1	IoU	Precision	Recall	Specificity	Acc
[23]	0.854	0.743	0.848	0.859	0.87	0.865
[24]	0.9314					0.934
[25]	0.79	-	-	-	-	-
[26]	-	0.94	-	-	-	0.914
[27]	0.95	0.95	-	-	-	0.951
[19]	0.95	-	-	0.96	-	0.96
Our	0.826	0.74	0.934	0.780	-	0.982

Our precision score of 0.934 is quite high, indicating that a large proportion of predicted positive tumor segments are indeed correct. However, our recall of 0.780 suggests that we are missing some true positive tumor segments, leading to a lower F1 score. Our accuracy of 0.982 is remarkably high, indicating that the model correctly identifies most of the pixels as either tumor or non-tumor. However, high accuracy can sometimes be misleading, especially in imbalanced datasets where the majority class dominates.

Our study shows strong precision and high accuracy, which are positive indicators. However, the lower recall highlights a potential area for improvement, suggesting that refining the model could help in detecting more tumor regions without sacrificing precision.

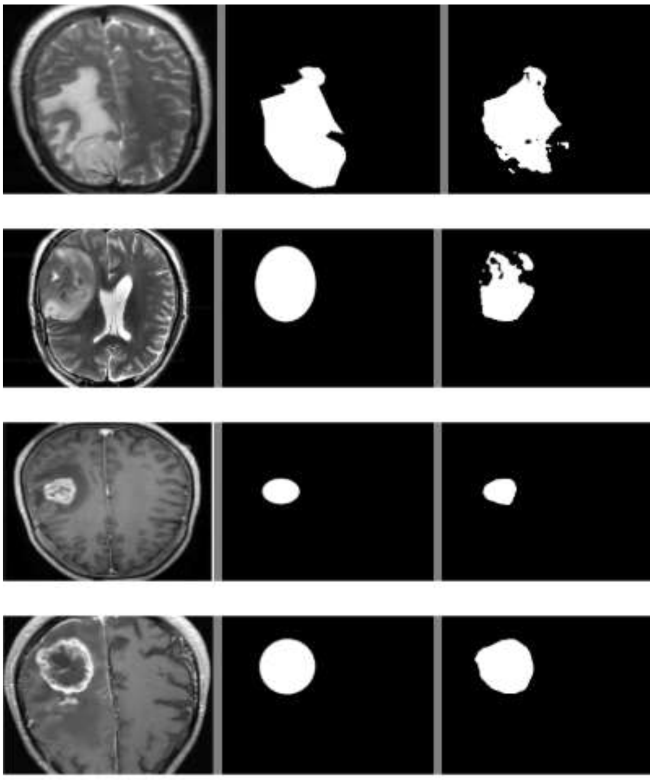

Fig. 3. Some samples from each dataset

The variation in results among studies emphasizes the importance of dataset characteristics, model architectures, and evaluation methodologies in achieving different performance outcomes in medical image segmentation tasks.

Unlike previous studies that employed pre-trained models or architectural modifications, our approach used unmodified, standard model architectures. This methodological difference may account for the discrepancies observed in our results compared to those reported in our article.

In Figure 3, we present the results for specific samples. It includes a set of output images corresponding to the input samples, along with their respective masks.

V. Conclusion

This study investigated the application of a standard U-Net-based model to detect tumors in MRI images. The model was trained without leveraging pre-trained weights or transfer learning techniques, Performance evaluation yielded satisfactory accuracy metrics, demonstrating the efficacy of the proposed methodology. However, the inherent limitations associated with the relatively small size of used benchmark (Br35H) warrant careful consideration. The limited dataset size may have introduced bias and hindered the model's ability to generalize on a new and unseen images, potentially impacting the model's robustness.

Finally, rigorous validation studies on independent, large-scale datasets are crucial to establish the clinical utility and reliability of the developed model before deployment in real-world diagnostic settings. These enhancements to both data acquisition and model architecture are anticipated to significantly improve the diagnostic capabilities and clinical translation potential of AI-driven brain tumor detection.

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Paper received 16 April 2026.

Zeinab Khadra, Ph.D. student, Moscow Polytechnic University, (e-mail: zeinabkhadrah@gmail.com).

Ammar Asad, Ph.D. student, Moscow Polytechnic University, (e-mail: ammarasad09@gmail.com).

Mohammed Hammoud, Ph.D. student, Skolkovo Institute of Science and Technology, (e-mail: Mohammed.Hammoud@skoltech.ru).

Ola Haydar, Ph.D. student, National Research University of Electronic Technology «MIET», (e-mail: oulahaider@gmail.com).

Sergey S. Lupin, Ph.D., Ass. Professor, National Research University of Electronic Technology «MIET», (e-mail: Sergeylupin.jr@gmail.com);