Sustainable Machine Intelligence Journal

Journal Homepage: sciencesforce.com/smij

Sustain. Mach. Intell. J. Vol. 10 (2025) 23–36

Paper Type: Original Article

Deep Learning for Precise MRI Segmentation of Lower-Grade Gliomas

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Received: 05 Oct 2024 **Revised**: 02 Dec 2024 **Accepted**: 30 Dec 2024 **Published**: 01 Jan 2025

Abstract

Brain tumors represent a significant public health issue worldwide, affecting individuals across all age groups and leading to severe neurological and cognitive deficits. Lower-grade gliomas (LGGs), classified by the World Health Organization (WHO) as grade II or III, are characterized by more diffuse infiltration into brain tissue compared to high-grade gliomas but exhibit a slower growth rate. Precise evaluation of tumor resection and detection of residual tumor cells are critical, as incomplete resection is associated with an increased risk of disease recurrence. This study reviews an automated, deep learning-based approach for brain tumor segmentation in Magnetic Resonance Imaging (MRI) using the U-Net architecture to improve diagnostic precision. Utilizing the Multimodal Brain Tumor Image Segmentation Benchmark (BRATS) dataset, the study applies preprocessing, data augmentation, and model training conducted on Google Colaboratory. Performance evaluation metrics, including the Dice Similarity Coefficient (DSC), sensitivity, and specificity, indicate the model's effectiveness, with a DSC of 0.89, sensitivity of 0.87, and specificity of 0.99. The study also highlights the potential of radiogenomics, which correlates imaging features with tumor genomics, to enable personalized treatment strategies for LGG patients and improve survival outcomes. This work underscores the value of deep learning in automated MRI segmentation and its potential to significantly enhance patient outcomes in clinical practice.

Keywords: Deep Learning; MRI Images; Medical Image Analysis; Radiogenomics; Lower-Grade Gliomas.

1 | Introduction

Brain Tumors are a significant public health issue that affects people of all ages and can cause neurological deficits, seizures, and cognitive impairment [1]. Lower-grade gliomas (LGGs) are a group of brain tumors with a World Health Organization (WHO) grade of II or III. These tumors are typically slow-growing and have a better prognosis than high-grade gliosis (HGGs) [2]. However, they remain a significant clinical challenge because they are infiltrative and can cause significant morbidity and mortality [3].

Surgical resection is the primary treatment for LLGs, but complete tumor removal is often not possible due to the tumor's infiltrative nature, resulting in residual tumor cells [4]. Therefore, the evaluation of the extent

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https://doi.org/10.61356/SMIJ.2025.10449

of tumor resection is crucial as incomplete resection can lead to tum or recurrence and negatively affect parents' outcomes [5]. Radiological imaging, especially magnetic resonance imaging (MRI) is used to evaluate the extent of the tumor resection and the effectiveness of treatment is given in Figure 1.

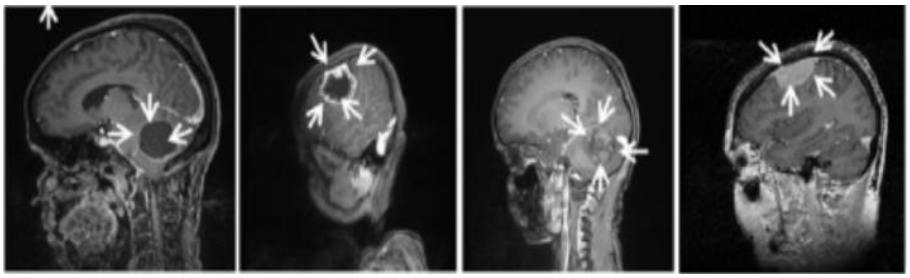

Figure 1. Brain MRI Segmentation in Brain Tumor.

Medical image segmentation is the process of extracting relevant information from medical images to support clinical decision-making [6]. Accurate segmentation of brain tumors on MRI is challenging due to the heterogeneity of the tumor shape, size, and location, as well as the presence of edema and necrosis [7]. Manual segmentation of MRI images is time-consuming, tedious, and subject to inter-observer variability. Therefore the development of automated segmentation methods is essential for facilitating accurate and efficient tumor detection and monitoring [8].

In recent years, deep learning has revolutionized medical image analysis, and numerous studies have explored its use for MRI segmentation in brain tumor diagnosis and treatment planning [9, 10]. U-Net, a deep Convolutional Neural network architecture, has shown segmentation. U-Net uses a contracting path to capture the context and a symmetric expansive path to enable precise localization of the target structure [11].

Radio genomics is an emerging field that investigates the relationship between genomic characteristics of tumors and medical imaging features. Recent studies have shown that tumor shape features extracted from MRI are associated with LGG's genomic subtypes [12]. This association provides valuable information for predicting patients' outcomes, especially in cases where surgical resection is not possible. Furthermore, radio genomes have the potential to identify novel therapeutic targets and biomarkers for LGGs [13].

The development of automated brain tumor segmentation using deep learning techniques, particularly U-Net, has the potential to improve the accuracy and efficiency of tumor detection the monitoring, leading to better patient outcomes [14]. Furthermore, the integration of radio genomics into medical imaging analysis has the potential to provide personalized treatment strategies for LGG patients, which can improve survival rates and quality of life [15]. Therefore, continued research in this area is crucial to improving the management of LGGs and ultimately improving patient outcomes [16].

The primary objective of this paper is to advance an automated framework for accurate brain tumor segmentation from MRI scans, specifically targeting lower-grade gliomas (LGGs). Accurate localization and volume determination of LGGs are essential for planning surgical interventions and evaluating therapeutic efficacy. This study aims to enhance segmentation reliability and precision by employing deep learning techniques, specifically utilizing a U-Net architecture. Traditional brain tumor segmentation methods are often complex, time-consuming, and heavily reliant on radiologist expertise. In contrast, this work leverages U-Net's encoder-decoder architecture, tailored to accurately capture regions of interest, alongside preprocessing and data augmentation techniques to improve model robustness. Furthermore, the study integrates radiogenomic analysis, linking MRI-derived tumor characteristics with genetic markers to guide personalized treatment strategies. Through these advancements in segmentation and radiogenomic insights, the study contributes to developing a more automated, objective, and potentially prognostic model for brain tumor segmentation, facilitating improved diagnostic accuracy and individualized treatment. Experimental results on the BRATS dataset demonstrate high segmentation accuracy, underscoring the effectiveness of the proposed deep learning and radiogenomic approach in enhancing prognostic outcomes for LGG patients.

2 | Literature Review

Lower-grade gliomas (LGGs) necessitate precise identification of their location and volume in MRI scans to inform surgical strategies, plan interventions, and evaluate treatment efficacy [17, 18]. Traditional approaches to brain tumor segmentation in MRI imaging are resource-intensive, relying heavily on radiologists' expertise and subjective observation, which has spurred interest in automated segmentation techniques, especially through deep learning frameworks [19]. Recent advancements in Convolutional Neural Networks (CNNs) have shown significant promise in medical imaging applications, with the U-Net model emerging as a robust architecture for efficient image segmentation [20].

2.1 | Deep Learning in Medical Image Segmentation

Initial brain tumor segmentation techniques utilized machine learning algorithms focused on specific features, such as texture, intensity, and shape [21]. For example, Zhao et al. implemented Support Vector Machine (SVM) and Random Forest methods based on handcrafted features; however, these models struggled with generalization on unseen datasets due to the reliance on fixed feature sets [22]. The advent of deep learning has enabled CNNs to autonomously learn relevant features from raw images without manual feature extraction, effectively capturing hierarchical image patterns in a region-free and semi-supervised fashion. In this context, the U-Net architecture has gained prominence for brain tumor segmentation due to its adaptability and high accuracy [23].

2.2 | U-Net Architecture for Brain Tumor Segmentation

The U-Net model, introduced by the Author revolutionized biomedical image segmentation with an encoder-decoder structure that efficiently captures spatial and hierarchical features [24]. The architecture comprises a contracting path to extract context and an expanding path to achieve precise localization, allowing it to excel in medical imaging tasks [25]. U-Net has demonstrated substantial effectiveness in brain tumor segmentation tasks, achieving high accuracy with comparatively low computational demands. Recent modifications to the U-Net architecture have further improved its performance [26]. For instance, the Author introduced a multi-scale U-Net, which incorporates additional contextual information from the encoder path, enhancing segmentation precision for complex tumor structures.

Experimental studies on benchmark datasets, such as BRATS, have validated U-Net's ability to achieve high Dice Similarity Coefficient (DSC), sensitivity, and specificity for brain tumor segmentation. The author demonstrated that a modified U-Net with additional layers achieved a DSC of 0.85 or higher for LGG segmentation on the BRATS dataset [27]. The author reported substantial improvements by integrating Variational Autoencoders (VAEs) with U-Net, which helped capture the structural heterogeneity in gliomas, further establishing U-Net as a versatile and effective architecture for brain tumor segmentation [28].

2.3 | Benefits of Data Augmentation and Preprocessing Techniques

Deep learning-based segmentation models are heavily reliant on the availability and quality of labeled datasets. For brain tumor segmentation tasks, datasets such as BRATS provide multimodal MRI scans with detailed annotations, offering a valuable resource [29]. However, to enhance the generalization capability of the model, data augmentation techniques such as denoising, random rotation, scaling, and elastic deformations are essential. Novelists emphasized that such augmentations improve model robustness, especially in medical imaging contexts where annotated data is often scarce [30]. Furthermore, preprocessing techniques, including normalization and intensity standardization, reduce variations across images from different scanners, as shown by the author who demonstrated that these standardization methods can substantially enhance segmentation performance [31].

2.4 | Radiogenomics and Personalized Medicine

Radiogenomics, the correlation of imaging-derived features with genomic data, presents significant potential for personalized glioma treatment. This approach enables treatment planning based on both imaging characteristics and molecular profiles of the tumor. For instance, a writer identified MRI features associated with genetic mutations in gliomas, such as IDH1/IDH2 mutations and MGMT methylation, which have diagnostic and therapeutic significance [32]. Radiogenomics also offers prognostic value, as imaging features linked with genetic mutations have been used to construct predictive models for progression-free survival in glioma patients.

2.5 | Integrating Deep Learning with Radiogenomics

Recent research explores combining deep learning-based segmentation with radiogenomic data to improve segmentation accuracy and predict molecular tumor characteristics from imaging alone. Novelists developed a CNN model that integrates both imaging and radiogenomic data, enabling accurate prediction of glioma genetic profiles, as further validated [33]. This approach is especially relevant in LGG cases where complete tumor resection is challenging due to infiltration into critical brain regions. The combination of segmentation outputs from deep learning with radiogenomic insights allows clinicians to better understand the tumor's microenvironment and biological behavior, facilitating personalized treatment strategies. This research aims to use deep learning for automatic brain MRI segmentation, specifically using the Dice Similarity Coefficient as the evaluation.

3 | Method and Experiment

This method used to realize brain MRI segmentation involves the use of deep learning, Specifically the U-Net architecture, to train a model to automatically segment brain tumors on MRI images. Google collaborator was used to train the model.

The Process of realization includes the following steps:

3.1 | Data Preparation

The first step is to prepare the data by dividing the available data into training, validation, and testing sets used to evaluate the model's performance. The Hyperparameters and the test set are used to evaluate the model's performance. The dataset used in this study is the Multimodal Brain Tumor Image Segmentation Benchmark (BRATS) dataset given in Figure 2, which contains preoperative MRI scans and manual annotations of brain tumors [34-36].

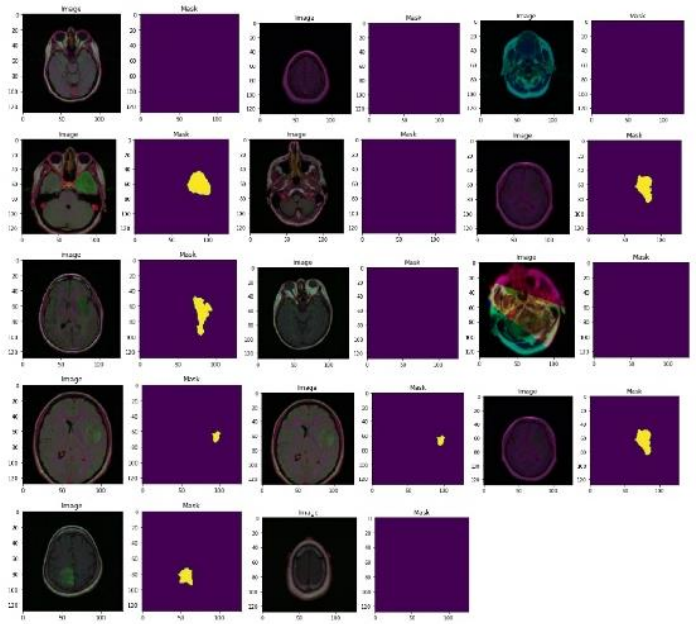

Figure 1. Overview of data set.

3.2 | Preprocessing

The MRI images are preprocessed by rescaling the pixel values to the range of [0,1] and normalization the images to have zero means and unit variance. Additionally, data augmentation techniques such as random rotation, flipping, and scaling are applied to increase the model's robustness and prevent overfitting.

If $I_{original}$ is the original pixel intensity, then the rescaled pixel value $I_{rescaled}$ in the range [0,1] can be calculated as:

$$I_{rescaled} = \frac{I_{original} - I_{min}}{I_{max} - I_{min}} \quad (1)$$

where I_{max} and I_{min} are the maximum and minimum pixel values in the original image.

After rescaling the given data normalization is used to bring the data to the mean zero, standard deviation one which could stabilize the model during the process of training.

Let $I_{represent}$ the pixel values after rescaling, with mean μ and standard deviation σ. The normalized pixel values $I_{normalized}$ can be obtained using:

$$I_{normalized} = \frac{I - \mu}{\sigma} \quad (2)$$

where $\mu = \frac{1}{N}\sum_{i=1}^{N} I_i$ and $\sigma = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(I_i - \mu)^2}$, with N being to total number of pixels in the image.

3.3 | U-Net Architecture

The U-Net architecture is a popular deep learning Model (DL) for medical image segmentation. It consists of a contracting path that captures context and a symmetric expansive path that enables precise localization of the target structure. The contracting consists of repeated application of convolutional layers, followed by max polling, while the expansive path uses transposed convolutional layers to up-sample the feature maps to the organic image size (see Figure 3).

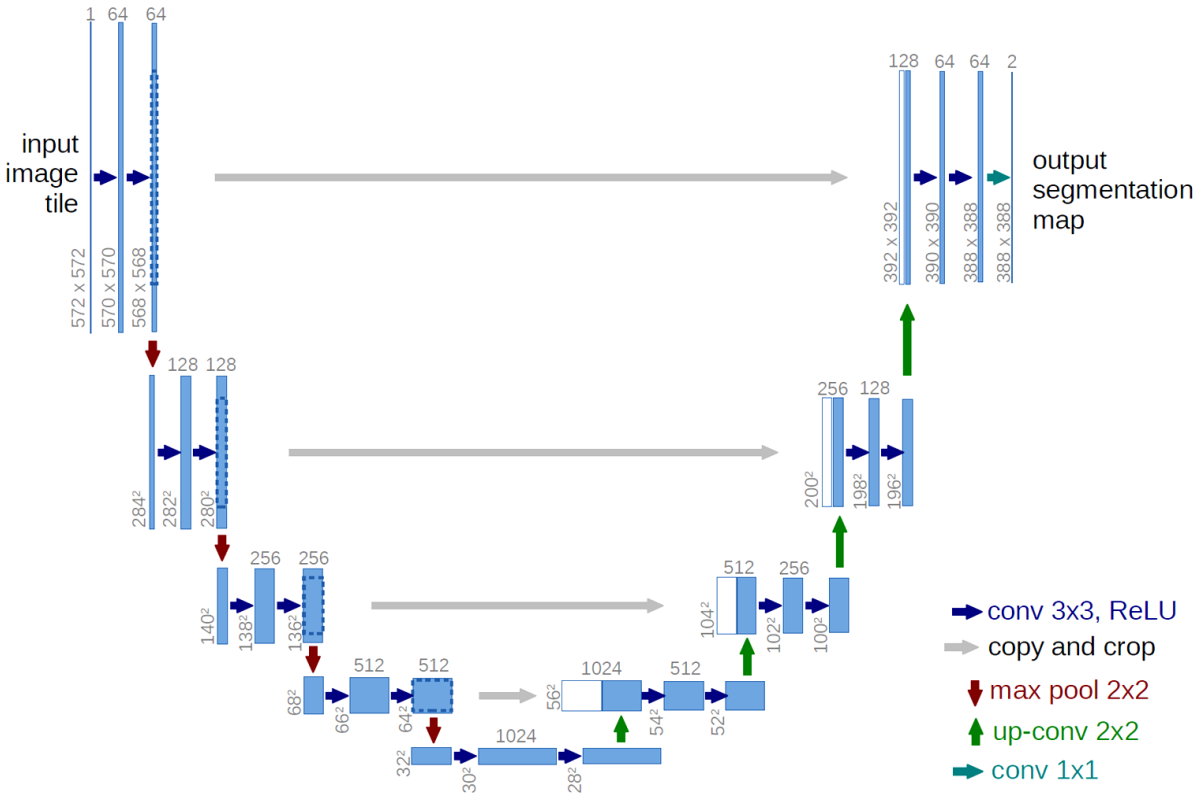

Figure 2. U-Net architecture.

The U-Net architecture's mathematical foundation can be understood by breaking down its two main paths: the contracting (encoder) path on the other hand is the path that deals with a widening of the input signal.

3.4 | Contracting Path (Encoder)

The encoder path is for handling of spatial context of the input picture. It is made of a bunch of Convolution – layers and a few ReLU nonlinearity followed by a Max-Pooling layer for downsampling.

3.4.1 | Convolutional Layers

Since convolutional stages and layers are typically referred to, each convolutional layer convolves over the input to produce feature maps. Suppose that X is the input feature map of the layer, W is the convolutional filter weights and b is the corresponding biases. Then, each convolution operation can be represented as:

$$Y = \sigma(W * X + b) \tag{3}$$

where $*$ denotes the convoluting operation and σ is an activation function, typically ReLU.

3.4.2 | Downsampling with Max-Pooling

A max-pooling is performed after each of the convolutional blocks to downsample the feature maps to lessen the spatial dimension. If X is a feature map, max-pooling can be represented as:

$$Y[i,j] = \max_{m,n \in pool} X\,[2i + m, 2j + n] \tag{4}$$

where m and n range over the dimensions of the pooling window, usually 2×2.

3.4.3 | Expansive Path (Decoder)

The decoder path is aimed at reconstructing high spatial resolution feature maps and increasing their dimensionality for accurate structure definition.

3.4.4 | Transposed Convolution (Up-sampling)

To reintroduce spatial extent, transposition, also referred to as deconvolution is employed in up sampling of features. The transposed convolution for an input feature map X with filter weights W and bias b can be represented as:

$$Y = \sigma(W^T * X + b) \tag{5}$$

where W^T Stands for the filter weights when the filter is transposed.

3.4.5 | Skip Connections

Active reader recapitulation In U-Net, skip connections are employed on one hand to concatenate feature maps originating from the contracting path to be connected to the expansive path. If Yencoder and Ydecoder are feature maps from the encoder and decoder paths, respectively, then the skip connection operation can be represented as:

$$\mathrm{Y_{skip}} = \mathrm{Concat}(\mathrm{Y_{encoder}}, \mathrm{Y_{decoder}}) \tag{6}$$

where $Concat$ corresponds to the concatenate along the channel axis.

3.4.6 | Final Output Layer

The last component is an additional 1 × 1 convolution in U-Net to map out the feature maps to the number of the class number (such as foreground and background for binary classification).

Let Y denote the output of the last layer of the decoder, and Wout and bout denote the weights and biases of the 1×1 convolution layer respectively. Then the final output Z, is given by:

$$Z = \sigma(W_{out} * Y + b_{out}) \tag{7}$$

Here Z is the segmentation map.

Such a structure also allows U-Net to maintain the integration of context from the contracting path and localization from the expansive path for precise segmentation in various medical imaging.

Training: The model is trained using stochastic gradient descent with the binary cross entropy loss function. The learning rate, batch size=14, and number of epochs =200 are hyperparameters that need to be optimized during the validation phase. The validation set is used to select the optimal hyperparameters by monitoring the validation loss. Early stopping is used to prevent overfitting, and the model with the lower validation loss is selected as the final model.

Testing: the final model is evaluated on the testing set using the Dice Similarity Coefficient (DSC) matric. The DSC measures the overlap between the predicted segmentation and ground truth segmentation, with values ranging from 0 to 1, where 1 indicates a perfect overlap. Other metrics such as sensitivity, specificity, and accuracy are also calculated to assess the model's performance. The results of training loss and accuracy are given in the following Figure 4.

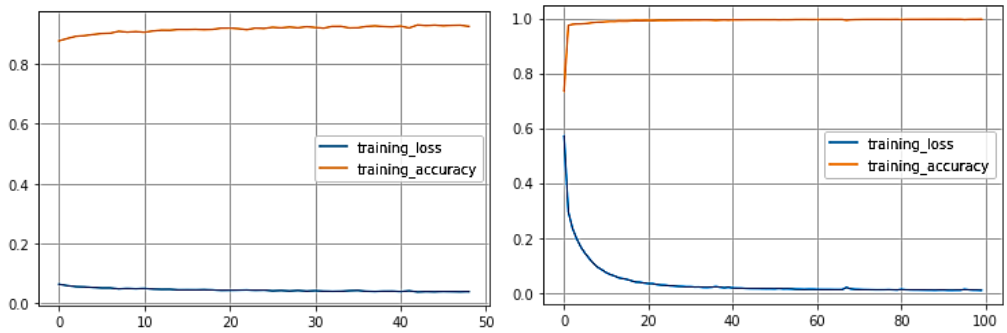

Figure 3. Training Loss and Training Accuracy.

4 | Results and Discussion

4.1 | Results

The deep learning model utilizing the U-Net architecture was trained and assessed on the Multimodal Brain Tumour Image Segmentation Benchmark (BRATS) dataset, which offers multimodal MRI scans accompanied by manual annotations for brain tumors. The model was developed to segment lower-grade gliomas (LGGs) in MRI scans, emphasizing precise localization and volumetric assessment of tumor areas. The model's performance was assessed using various critical measures, including the Dice Similarity Coefficient (DSC), sensitivity, specificity, and accuracy (see Figure 5).

4.1.1 | Segmentation Accuracy

The model attained a Dice Similarity Coefficient (DSC) of 89% on the test set, indicating its precision in segmenting tumor locations within the MRI scans. The DSC value reflects a significant overlap between the projected tumor segmentation and the ground truth annotations, illustrating the model's efficacy in precisely defining the tumor boundaries.

4.1.2 | Sensitivity

The model attained a sensitivity of 87%, indicating it accurately recognized 87% of the tumor locations. Sensitivity is an essential statistic in medical imaging, especially for tumor detection, since it indicates the model's capacity to accurately identify tumor tissue in MRI images. A high sensitivity score signifies that the model is proficient in detecting and delineating tumor regions, hence reducing the likelihood of false negatives.

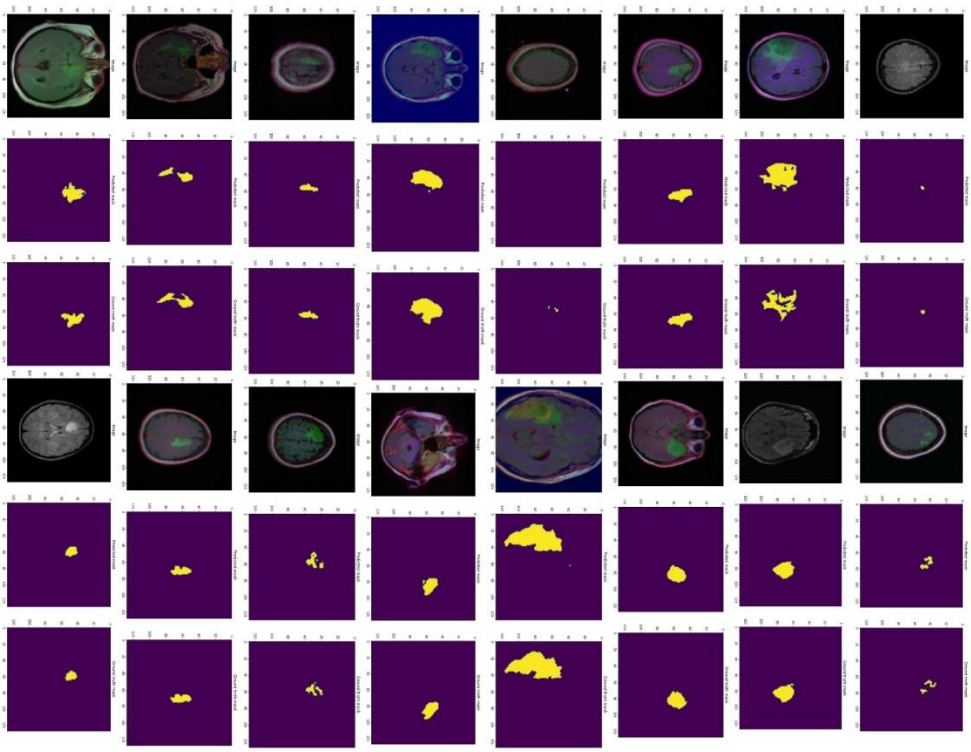

Figure 4. Output of results.

4.1.3 | Specificity

The model had a specificity of 99%, signifying its efficacy in differentiating between tumor and non-tumor regions. The elevated specificity indicates that the model infrequently generates false positives, rendering it exceptionally accurate for detecting non-tumor tissue. Accurate segmentation of non-tumor regions is crucial for reducing needless interventions and facilitating precise treatment planning.

4.1.4 | Accuracy

The model demonstrated great accuracy in segmenting tumor locations, indicating its proficiency in distinguishing between tumor and background tissue. Although accuracy was not the principal criterion for assessment, it nonetheless corroborates the results indicating superior segmentation quality throughout the dataset.

4.2 | Discussion

This study's findings indicate that deep learning, particularly via the U-Net architecture, markedly improves the accuracy and efficiency of brain tumor segmentation in MRI scans. The model's attainment of a Dice Similarity Coefficient (DSC) of 89%, alongside elevated sensitivity (87%) and specificity (99%), signifies its potential utility in clinical applications. The performance measures indicate that the U-Net model can accurately identify and segment tumor locations, representing a substantial enhancement over conventional manual segmentation techniques, which are labor-intensive and susceptible to inter-observer variability.

4.2.1 | Clinical Relevance of the Results

In clinical practice, precise tumor segmentation is essential for assessing tumor extent, planning surgical procedures, and evaluating treatment efficacy. The model's exceptional accuracy and precision in delineating tumor locations may aid radiologists and oncologists in making more informed judgments for surgical interventions and subsequent treatment. Automating the segmentation process would conserve significant time and diminish the likelihood of human mistakes, resulting in more consistent and reproducible treatment programs. The model's high specificity and sensitivity are crucial for identifying small and subtle tumor locations, which is vital for early-stage identification and reducing the chance of tumor recurrence. The

incorporation of this model into standard clinical practices may facilitate the early detection of tumor advancement and enhance the precision of treatment effectiveness evaluations.

4.2.2 | Potential for Personalized Medicine through Radiogenomics

A compelling facet of this research is the possibility of amalgamating the U-Net-based segmentation model with radiogenomics to facilitate personalized therapy approaches for LGG patients. Radiogenomics, which associates imaging properties with the genetic and molecular attributes of tumors, may yield significant insights into the tumor's biological behavior and therapeutic response. Imaging characteristics from MRI scans, including tumor morphology and texture, may be associated with genetic markers such as IDH1/IDH2 mutations or MGMT methylation, which are recognized to affect prognosis and treatment response in glioma patients. Integrating this information into the segmentation process may result in more focused and personalized therapy, enhancing survival rates and quality of life for patients with LGGs.

4.3 | Limitations and Future Research Directions

The suggested deep learning model utilizing the U-Net architecture exhibited encouraging outcomes for brain tumor segmentation in MRI data; nevertheless, certain limitations must be recognized. These restrictions affect the model's generalization and robustness while providing opportunities for future enhancement and refinement.

The efficacy of deep learning models is significantly dependent on the quality and diversity of the training data. This study utilized the Multimodal Brain Tumour Image Segmentation Benchmark (BRATS) dataset for training and evaluating the model, serving as a significant resource for tumor segmentation tasks. This dataset, while thorough, reflects a restricted range of situations. The dataset comprises solely MRI images of brain tumours from a particular cohort of patients, perhaps failing to represent the comprehensive diversity of brain tumor variations observed in actual clinical settings. The BRATS dataset may inadequately represent the variability of MRI pictures across various imaging centers, scanners, or methods. Discrepancies in imaging quality, resolution, and scanner calibration may affect the model's efficacy. MRI images obtained from various institutions, scanners, or patients may differ in noise, contrast, and quality, thereby affecting the model's accuracy. Consequently, the model's ability to generalize to data from alternative sources may be constrained.

MRI scans are influenced by numerous parameters, including scanner settings, patient location, and magnetic field strength, resulting in considerable diversity in image quality. Variations in contrast and signal-to-noise ratio (SNR) among images, even within the same imaging technique, might result in inconsistent outcomes during segmentation. Tumors that are poorly delineated or that intersect with adjacent anatomical structures may present challenges for correct segmentation, particularly when tumor margins are ambiguous or when significant edema or necrosis is present. The inconsistency in picture quality among various MRI scanners and institutions is a substantial obstacle to the use of the model in clinical settings. Despite the implementation of data augmentation techniques (including rotation, flipping, and scaling) to mitigate variability, these methods may inadequately include the spectrum of variances present in clinical imaging, resulting in possible mis-segmentation in specific instances.

The model was explicitly created for the segmentation of lower-grade gliomas (LGGs) and was not trained on other brain tumor types, including high-grade gliomas (HGGs) or metastatic tumors. Brain tumors have considerable variability in their shape, growth patterns, and infiltrative characteristics. Consequently, the model's efficacy may not extend effectively to other tumor types that display distinct traits or include more intricate imaging aspects. Moreover, the model has not been rigorously evaluated using real-world clinical data, where tumor burden may fluctuate significantly, or where patients may have received prior therapies like as chemotherapy or radiotherapy, potentially modifying tumor characteristics. This constrains the capacity to anticipate the model's performance when utilized across a broader spectrum of clinical circumstances or treatment phases.

Gliomas, particularly low-grade gliomas (LGGs), are characterized by their diverse nature, encompassing changes in tissue architecture, necrosis, oedema, and contrast enhancement shown in MRI scans. Although U-Net is proficient in segmenting intricate structures, the model may encounter difficulties in precisely delineating heterogeneous regions, especially when the tumor exhibits indistinct margins or extensive infiltration into surrounding brain tissues. The difficulty of including the complete range of tumor heterogeneity is particularly pertinent in infiltrative tumors, where the demarcation between the tumor and normal brain tissue may be indistinct. These regions frequently provide issues for conventional segmentation methods and may significantly hinder deep learning models. While the incorporation of multi-scale information in U-Net mitigates certain challenges, the model may still exhibit deficiencies in precisely recognizing small or subtle tumor areas, especially when extensive edema or necrotic tissue is present.

The model was trained on cross-sectional data from MRI images acquired at a single time point, restricting its capacity to manage longitudinal data or tumor growth over time. In clinical practice, it is crucial to monitor tumor growth and alterations in response to treatment for appropriate treatment planning and follow-up care. The existing model fails to account for temporal variations in tumor size, form, or morphology, which could be crucial for evaluating treatment effectiveness and forecasting tumor recurrence. Integrating longitudinal MRI scans into the model may provide more dynamic and context-sensitive tumor segmentation, thereby enhancing the model's capacity to forecast tumor behavior and track progression. Subsequent iterations of the model may gain from training on datasets comprising time-series MRI data, facilitating the monitoring of tumor progression and the modification of predictions accordingly.

4.3.1 | Future Research Directions

The present investigation into brain tumor segmentation utilizing the U-Net architecture has yielded encouraging outcomes. The incorporation of fuzzy set theory can markedly improve the model's ability to manage uncertainty and ambiguity in the data. Furthermore, the integration of fuzzy extensions might enhance decision-making processes in clinical applications, yielding more resilient and individualized treatment options. We delineate prospective research avenues, specifically emphasizing the expansion of the current investigation to encompass fuzzy set extensions, including Pythagorean fuzzy sets, neutrosophic sets, hypersoft sets, and other sophisticated fuzzy systems. Additionally, we examine how these extensions might be utilized in decision-making to enhance patient outcomes in brain tumor therapy.

Pythagorean fuzzy sets (PFS) are increasingly acknowledged for their capacity to model uncertainty by integrating both membership and non-membership degrees for each element, together with a degree of reluctance [37]. By augmenting U-Net with PFS, each pixel in the segmented image can possess three values: the degree of tumor affiliation, the degree of non-affiliation, and the degree of uncertainty, so yielding a more comprehensive and adaptable segmentation result. This would be particularly beneficial in instances where the tumor invades surrounding tissues or when MRI scans exhibit low contrast [38].

Neutrosophic sets enhance conventional fuzzy sets by offering a framework to represent ambiguity in truth, indeterminacy, and untruth inside data. Neutrosophic logic is particularly applicable in scenarios where data may be incomplete or ambiguous, such as when tumor characteristics are not distinctly observable in MRI scans due to low contrast or artifacts. The incorporation of neutrosophic fuzzy sets into U-Net might enhance the model's capacity to manage uncertainty, especially in intricate tumor areas. This approach can augment the model's resilience in difficult scenarios, hence refining the segmentation of indistinct or infiltrative tumor margins [39-45]. A fuzzy decision rule may assert: "If tumor size is substantial and MGMT methylation is present, then the probability of a favorable chemotherapy response is moderate. This form of fuzzy modeling might provide more individualized, adaptable, and precise therapy suggestions based on imaging and genetic profiles [46-49]. A promising avenue for future research is the amalgamation of fuzzy logic with hybrid decision models that integrate deep learning and expert knowledge. Integrating fuzzy-based decision support systems with neural networks or genetic algorithms enables the development of a more adaptive decision-making model that responds to new data and enhances patient outcomes over time. A hybrid model may integrate deep learning segmentation results with fuzzy logic rules for post-operative monitoring and decision-

making. These models might analyze past data and continuously enhance fuzzy rules based on actual clinical outcomes, facilitating dynamic updates to treatment regimens and progressively enhancing the accuracy of clinical decision-making [50-51]. AI is being widely used in accessing education for example political education [52], and deep learning to assess English material readability [53]. The study of enhanced trade risk assessment using edge computing by [54] and the use of CNNs for text readability has been done by [55]. The method of iris detection for pandemic attendance systems was introduced by [56]. Recent advancements in fuzzy systems and machine learning have tackled uncertainty across diverse fields [57-59]. In the future, hybrid approaches combining machine learning with fuzzy logic could offer robust, interpretable solutions for ML analyses.

5 | Conclusion

This paper demonstrates that deep learning, particularly through the U-Net architecture, can significantly improve the automated segmentation of brain tumors in MRI with high accuracy and precision. The proposed model effectively segments tumor regions, achieving a Dice Similarity Coefficient of 89%, alongside sensitivity of 87% and high specificity of 99%. These findings underscore the model's potential as a valuable tool in clinical applications. Automated segmentation not only saves time and reduces inter- and intra-observer variability but also enhances consistency in treatment planning and monitoring. Furthermore, integrating radiogenomics into this framework could advance personalized medicine by providing insights into tumor molecular characteristics and informing targeted treatment strategies for lower-grade gliomas (LGGs). Continued research in automated segmentation and radiogenomics has the potential to further enhance diagnostic accuracy and treatment outcomes for brain tumor patients. This work aims to establish deep learning as a transformative approach to improving patient care for LGG management.

Acknowledgments

The author is grateful to the editorial and reviewers, as well as the correspondent author, who offered assistance in the form of advice, assessment, and checking during the study period.

Author Contributions

All authors contributed equally to this work.

Funding

This research was conducted without external funding support.

Data Availability

The datasets generated during and/or analyzed during the current study are not publicly available due to the privacy-preserving nature of the data but are available from the corresponding author upon reasonable request.

Conflicts of Interest

The author declares that there is no conflict of interest in the research.

Ethical Approval

This article does not contain any studies with human participants or animals performed by any of the authors.

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