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Brain Tumor Segmentation Based on Deep Learning Using Multimodal MRI Images

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Abstract

Accurate segmentation and localization of brain tumors from magnetic resonance imaging (MRI) scans remain one of the major and ongoing challenges in the field of medical image analysis. This task is critically important, as it directly impacts clinical diagnosis, surgical planning, and treatment strategies for patients. The heterogeneous nature of brain tumors, along with their varying sizes, shapes, and locations, makes automated segmentation particularly complex. To address this, recent advanced methodologies commonly incorporate multiple MRI modalities—such as T1-weighted, contrast-enhanced T1 (T1c), T2-weighted, and FLAIR images—each of which offers complementary information regarding different tissue characteristics. These multi-modal approaches have significantly improved segmentation performance by providing a more comprehensive understanding of the tumor's structure. However, despite the promising results achieved on benchmark datasets like BRATS 2018, many state-of-the-art methods rely on deep architectures with high computational complexity, which can hinder their deployment in real-time or resource-constrained clinical environments. To overcome these limitations, this study introduces a novel deep learning-based framework tailored specifically for brain tumor segmentation. Extensive experiments conducted on the BRATS 2018 dataset reveal that the proposed approach not only surpasses existing models in terms of accuracy but also shows strong generalization capability and robustness when segmenting complex and irregular tumor boundaries, making it a promising tool for real-world clinical applications.

Keywords: Brain Tumor Segmentation, Deep Learning, Multimodal MRI, Medical Image Analysis, BRATS 2018

1. Introduction

Accurate segmentation of brain tumors from Magnetic Resonance Imaging (MRI) scans is a critical step in the diagnosis and treatment of brain diseases. Precise identification of tumor boundaries assists clinicians in making informed decisions regarding treatment strategies and monitoring disease progression. Accurate segmentation enables precise estimation of tumor volume and identification of active and inactive tumor regions, which plays a crucial role in surgical planning and targeted therapies. Additionally, in research settings, analyzing tumor changes over time is not feasible without reliable segmentation [1-4].

Despite its importance, brain tumor segmentation faces several challenges. The brain's complex anatomy and diverse tissue structures make it difficult to accurately differentiate tumor tissue from healthy brain tissue. Tumor heterogeneity, meaning variability in cellular and imaging characteristics within tumor regions, results in variations in intensity and texture, complicating segmentation efforts. Furthermore, MRI images often contain noise and artifacts, and tumors themselves vary widely in shape, size, and location, limiting the accuracy of traditional segmentation techniques [5-8]. Distinguishing tumor subregions, such as the enhancing tumor, edema, and necrotic core, is also a significant challenge for algorithms.

In recent years, deep learning has emerged as a transformative force in the field of medical image processing, fundamentally changing how complex visual data is analyzed and interpreted. Among various deep learning architectures, convolutional neural networks (CNNs) have proven particularly effective due to their inherent ability to capture spatial hierarchies and local dependencies within images [9-13]. Unlike traditional image analysis techniques, which often depend on manually designed features such as texture, shape, or intensity histograms, CNNs learn to identify and extract relevant features directly from raw input data through multiple layers of nonlinear transformations. This hierarchical feature learning allows CNNs to automatically detect intricate and abstract patterns that might be difficult or impossible for human experts or conventional algorithms to explicitly define.

The adaptability of CNNs to diverse imaging modalities and their robustness to noise and variability in data have led to significant improvements in medical tasks, including tumor detection, classification, and segmentation. Particularly in brain tumor segmentation, CNN-based models can discern subtle differences between healthy tissue and various tumor subregions, resulting in more precise delineations than previously achievable. The capacity to learn end-to-end mappings—from raw MRI scans to segmentation masks—reduces reliance on domain-specific heuristics and manual intervention, enhancing both efficiency and reproducibility [14-18].

Moreover, CNNs benefit from large annotated datasets and advanced training techniques such as data augmentation, transfer learning, and regularization, which help overcome challenges related to limited data availability and overfitting. The remarkable performance of CNN-based methods has even, in some cases, surpassed that of experienced radiologists, indicating their potential as valuable clinical decision support tools. As a result, deep learning, with CNNs at its core, continues to drive innovation in medical imaging by enabling more accurate, reliable, and automated analyses that can ultimately improve patient outcomes [19-26].

A key factor in successful brain tumor segmentation is the simultaneous use of multiple MRI sequences. Each modality (e.g., T1-weighted, contrast-enhanced T1 [T1c], T2-weighted, and FLAIR) provides unique information about brain structures and tumor characteristics. For example, T1c images highlight active tumor regions, while FLAIR images are better suited for detecting edema. Combining these channels in a deep learning model allows for a more comprehensive understanding of the tumor, enabling more accurate identification of different tumor subregions. This multimodal approach significantly enhances segmentation accuracy and reduces errors.

Implementing deep learning models in clinical settings can greatly facilitate the diagnosis and treatment process. These systems provide fast and accurate results, reducing clinicians' workload and enabling frequent tumor monitoring without manual analysis. Moreover, they can serve as assistive tools during brain surgeries by precisely delineating tumor boundaries intraoperatively. With ongoing advancements in artificial intelligence and deep learning, fully automated and more sophisticated systems are expected to be developed for real-world clinical applications in the near future.

The remainder of the paper is organized as follows: Section 2 reviews the existing methods; Section 3 presents the proposed approach; Section 4 discusses the simulation results; and Section 5 concludes the paper.

2. Existing Methods

In [1], it was investigated whether pretraining state-of-the-art deep learning models on adult brain tumor data could enable knowledge transfer to pediatric data and improve segmentation performance. Multisequence MRI scans from 45 children diagnosed with diffuse midline glioma (DMG), totaling 82 scans at various timepoints, were retrospectively collected. Five-fold cross-validation was conducted on the DMG dataset using SegResNet and nnU-Net architectures, each evaluated with and without pretraining on the BraTS2021 dataset, which comprises 1,251 adult glioblastoma multiforme cases. These findings suggest that segmentation performance on pediatric brain tumors can be enhanced through knowledge transfer from adult tumor images. Additionally, faster convergence during training was observed when pretraining was applied. Brain tumor segmentation aims to distinguish tumor tissue from surrounding structures such as fat, edema, normal brain tissue, and cerebrospinal fluid. To address this challenge in [2], MRI images are initially enhanced using median filtering to preserve edge details. The segmentation process then involves applying a thresholding method, which is iteratively refined to isolate the largest connected region corresponding to the tumor. Brain region segmentation is carried out using the watershed algorithm by labeling brain and non-brain areas, followed by skull removal through cropping. In this study, a dataset of 14 brain tumor MRI images was utilized. The segmentation results were evaluated by comparing the extracted tumor regions with the brain tissue areas. The proposed system achieved an average tumor area estimation error of approximately 10%. The study presented in [3] introduces an automatic brain tumor segmentation algorithm for MRI images based on the U-Net architecture. Initially, by leveraging sample preprocessing techniques, an appropriate loss function, and an optimization algorithm, a U-Net baseline model with an optimal parameter configuration tailored for the segmentation task is developed. To enhance the model, a 1×1 convolutional layer—referred to as a feature recombination layer—is incorporated into the baseline. This addition enables linear recombination of high-level features, enriches the representational capacity of extracted features, reduces the number of network parameters, and ultimately improves segmentation performance. The proposed algorithm is validated on the Brain Tumor Segmentation (BraTS) 2015 challenge training dataset. Experimental results demonstrate that the method achieves competitive performance when compared to existing brain tumor segmentation approaches.

The article [4] provides an overview of various approaches for MRI-based image analysis and brain tumor segmentation. Given the intricate structure of the brain, accurate identification and delineation of tumor regions are critical for effective treatment. Key features such as shape, size, spatial configuration, and location within the image are extracted and analyzed. Based on these extracted features, tumor classification is subsequently carried out. The paper presents several techniques aimed at improving the accuracy and reliability of brain tumor prediction. Leveraging the effectiveness of convolutional neural networks (CNNs) in handling complex, high-dimensional data, this study applies fully convolutional networks (FCNs) combined with fully connected conditional random fields (DenseCRFs) for brain tumor segmentation. To enhance segmentation accuracy, K-means clustering is integrated with the FCN. The DenseCRF is then employed to refine the segmentation outputs of the FCN, followed by model fusion techniques to further improve the segmentation results [5]. Two significant modifications were integrated into the original U-Net architecture in [6]: a grid-based attention mechanism and a sharpening block. These enhancements effectively addressed the limitations of the standard U-Net while improving segmentation accuracy with minimal additional computational cost. Evaluation on the BraTS 2020 dataset, a recent widely used benchmark for brain tumor segmentation, demonstrated that the proposed model achieved improved performance, attaining a Dice score of

0.9275 and a Jaccard index of 0.8684 compared to baseline methods.

A comprehensive review of research studies conducted between 1998 and 2020 on brain tumor segmentation from MRI images is presented in the article [7]. The core segmentation algorithms used in each study have been thoroughly examined. A broad perspective on the topic is provided to readers, and new insights into the application of various machine learning and image segmentation techniques for brain tumor identification are explored. Through comparative analysis of state-of-the-art and emerging approaches, deep learning methods have been identified as the most effective for tumor segmentation from brain MRI scans. The segmentation process is characterized by a high degree of consistency between anatomical structures and adjacent brain tissues. Extreme Learning Machine (ELM) is a learning algorithm composed of one or more layers of hidden nodes and is widely applied in tasks such as regression and classification [8]. In the context of brain MRI analysis, a probabilistic neural network classifier has been employed to train and evaluate the accuracy of tumor detection. Numerical results indicate that the proposed system achieves an accuracy of approximately 98.51% in distinguishing between abnormal and normal brain tissues, demonstrating its effectiveness.

A new Feature Alignment Module (FAM) has been introduced to adjust the feature distributions between monomodal normal brain images and multimodal tumor brain images, ensuring consistency in normal regions and discrepancy in tumor regions to enable effective feature comparison. The proposed framework in [9] has been evaluated using both the public BraTS2022 dataset and an internal tumor brain image dataset. Experimental results have shown that segmentation accuracy has been significantly improved on both datasets, with performance surpassing that of existing state-of-the-art methods. The study [10] proposes a morphology-based image processing method for tumor segmentation in brain MRI scans. Initially, the MRI images are preprocessed using an anisotropic diffusion filter (ADF) to remove high-frequency noise while preserving edge details. Subsequently, the filtered images undergo skull stripping to eliminate scalp tissue, skull, and dura mater. Afterward, characteristics of the skull-stripped images are analyzed to detect the presence of a tumor. If a tumor is detected, the morphology-based segmentation technique is applied to isolate the tumor region. The results indicate that the proposed system accurately identifies tumor-bearing images and effectively extracts features from the segmented tumor. An Aligned Cross-Modality Interaction Network (ACMINet) is proposed in [11] for segmenting brain tumor and tissue regions from MRI scans. This network first incorporates a cross-modality feature interaction module that adaptively and efficiently fuses and refines features from multiple imaging modalities. Additionally, a volumetric feature alignment module is introduced to dynamically align low-level and high-level features through a learnable volumetric feature deformation field.

3. Proposed Method

In this section, the architecture of the proposed deep learning-based method for segmentation is presented and explained in detail. The overall structure of the network, its main components, and the interactions between different layers are thoroughly described. Key modules and mechanisms designed to enhance feature extraction, improve segmentation accuracy, and effectively utilize spatial and contextual information in the images are introduced and analyzed. If this architecture, with a significantly low number of parameters, achieves accuracy comparable to or even better than more complex models, it represents a valuable innovation—particularly for real-time applications or deployment on embedded systems.

In this section, we present a comprehensive description of the architecture designed for the proposed deep learning-based segmentation model. The network follows an encoder-decoder paradigm, which has been widely used in semantic segmentation tasks due to its capacity to capture multi-scale contextual information while enabling pixel-level prediction. Each component of the network (Figure 1) is described in detail as follows:

1. Input Layer

The architecture begins with an imageInputLayer, which defines the size and format of the input images. This layer is configured using the predefined variable imageSize, ensuring consistency across training and inference phases. Notably, the normalization parameter is explicitly set to 'none', meaning that the network does not apply any internal normalization to the input data.

This design choice is intentional and advantageous in scenarios where input data are pre-processed externally. Common preprocessing strategies include min-max normalization (scaling to the [0, 1] range) or z-score standardization (zero mean and unit variance). Disabling internal normalization allows for greater control over the preprocessing pipeline, particularly useful when the input images exhibit specific statistical properties that need to be preserved or manipulated explicitly.

2. Encoder: Feature Extraction Module

The encoder component is responsible for extracting hierarchical features from the input image. It consists of three convolutional blocks, each composed of a convolutional layer followed by batch normalization and a ReLU activation function:

- Block 1 (Conv1 → BN1 → ReLU1): Applies a 3×3 convolution with 16 filters. 'Same' padding is used to maintain spatial resolution. Batch normalization (BN) stabilizes training by normalizing the activations, and ReLU introduces non-linearity, enhancing the expressive power of the network.
- Block 2 (Conv2 → BN2 → ReLU2): Increases the depth of feature maps to 32 while reducing the spatial resolution by a factor of two using a stride of 2. This downsampling operation allows the network to extract more abstract representations and reduces computational complexity.
- Block 3 (Conv3 → BN3 → ReLU3): Further increases the channel depth to 64 and halves the spatial dimensions again. This block captures high-level semantic information and compresses the

spatial structure into a compact feature representation.

Together, these encoding layers progressively extract low-level to high-level features, forming a compressed latent representation suitable for subsequent decoding.

3. Decoder: Feature Reconstruction Module

The decoder component mirrors the encoder by gradually reconstructing the spatial dimensions of the input image. It consists of two transposed convolutional layers (also known as deconvolution layers), each followed by batch normalization and ReLU:

- Block 4 (TConv1 → BN4 → ReLU4): A 4×4 transposed convolution with stride 2 is used to upsample the feature maps, doubling the spatial dimensions. The number of channels is reduced to 32, balancing detail recovery with computational efficiency.
- Block 5 (TConv2 → BN5 → ReLU5): Performs another upsampling step with similar configuration, restoring the original spatial size of the image. The channel depth is reduced to 16, matching the structure of the first convolutional block in the encoder.

These upsampling operations are essential for generating fine-grained segmentation maps that align with the resolution of the input image. The decoder ensures that semantic information captured in the bottleneck layers is accurately projected back to the pixel level.

4. Output and Classification Layers

The final part of the network translates the decoded features into a pixel-wise segmentation output:

- ConvOut: A 1×1 convolutional layer maps the feature maps to numClasses output channels, where each channel corresponds to one semantic class. This layer produces a logit (unnormalized probability) for each class at each pixel location.
- Softmax Layer: Applies the softmax function across the class dimension, converting logits into normalized class probabilities for every pixel.
- Pixel Classification Layer: Computes the cross-entropy loss between predicted probabilities and ground-truth labels during training. This layer also handles class weighting and label management, enabling the model to learn effective decision boundaries, especially in the presence of class imbalance.

5. Summary of the Architecture

The proposed network adopts a symmetric encoder-decoder structure with a compact yet efficient design tailored for dense segmentation tasks. The downsampling operations in the encoder facilitate the extraction of robust and abstract features, while the decoder ensures accurate spatial reconstruction for pixel-wise prediction.

The consistent use of batch normalization across all convolutional and transposed convolutional layers contributes to improved gradient flow, accelerated convergence, and reduced sensitivity to initialization. The ReLU activation ensures non-linear transformation of features, enabling the network to learn complex mappings required for semantic segmentation.

This architecture is well-suited for a wide range of segmentation applications, including medical imaging (e.g., tumor boundary detection), satellite image analysis (e.g., land cover classification), and object-based segmentation in natural scenes. Its modular design also allows easy extension by incorporating additional components such as skip connections, attention modules, or multi-scale feature fusion layers in future work. Advantages of the Architecture are as follows:

1. Simplicity and High Efficiency for Real-Time or Embedded Applications

The architecture uses only three convolutional blocks in the encoder and two transposed convolutional layers in the decoder, resulting in a lightweight model with a low parameter count. This makes it highly suitable for deployment on resource-constrained devices such as embedded systems or real-time applications.

2. Explicit Control over Input Normalization

By setting the input layer's normalization parameter to 'none', the architecture allows for external preprocessing of input data (e.g., min-max normalization or z-score standardization). This approach is beneficial in domains where preserving or explicitly controlling the statistical properties of the input images is critical—such as medical imaging.

3. Hierarchical Feature Extraction

The encoder progressively extracts features from low-level textures and edges to high-level semantic concepts. The use of strided convolution helps reduce spatial dimensions while deepening the feature space, enabling compact and abstract feature representations.

4. Effective Spatial Reconstruction via Decoder

The decoder uses transposed convolutions with appropriate strides to gradually upsample the feature maps, effectively restoring the spatial resolution of the input. This design ensures that the semantic information encoded in the latent space is accurately projected back to the pixel domain.

5. Pixel-Wise Output for Semantic Segmentation

The final 1×1 convolution layer maps the feature maps to the number of semantic classes, followed by a softmax activation that produces per-pixel class probabilities. The pixel classification layer further enables effective learning by incorporating loss functions and class balancing strategies.

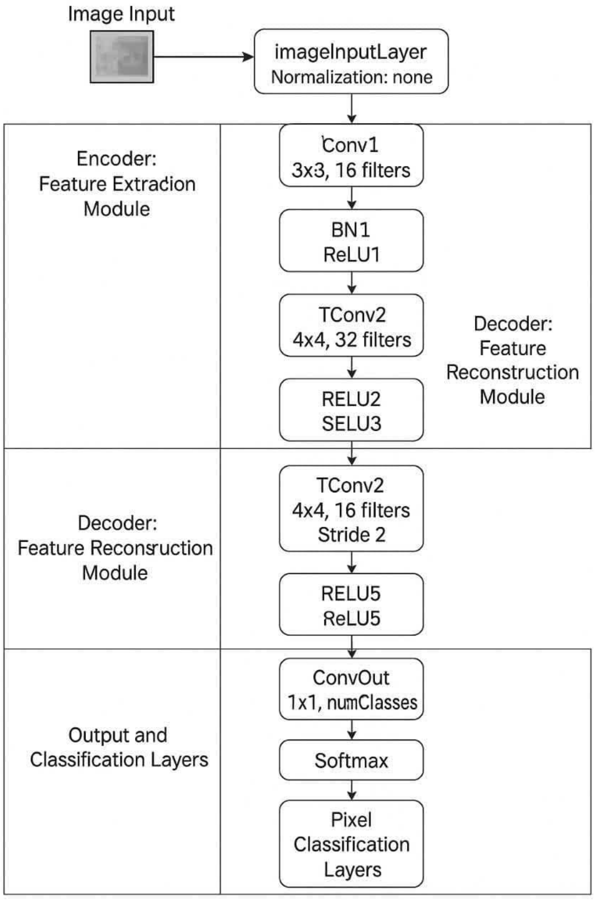

Figure 1. The architecture of the proposed method.

4. Simulation Results

The algorithms for both the proposed and baseline methods were executed in MATLAB R2025a (MathWorks) on a workstation powered by an Intel® Core™ i9-13900K processor and 64 GB of RAM.

Figure 2 presents a set of mid-slice brain MRI images across four common imaging modalities: T1-weighted, T1 with gadolinium contrast enhancement (T1-Gd), T2-weighted, and FLAIR. Each modality provides distinct and complementary diagnostic information: T1 highlights anatomical structures, T1-Gd enhances regions with abnormal blood-brain barrier permeability (such as tumors), T2 is effective for visualizing cerebrospinal fluid, and FLAIR suppresses fluid signals to reveal hidden lesions more clearly. Alongside these images, a corresponding ground truth mask is included, which delineates the region of interest—typically a lesion or specific anatomical area. This mask is essential for supervised learning tasks such as training deep learning models for segmentation. Together, these multimodal MRI images provide a rich and comprehensive dataset for accurate medical image analysis.

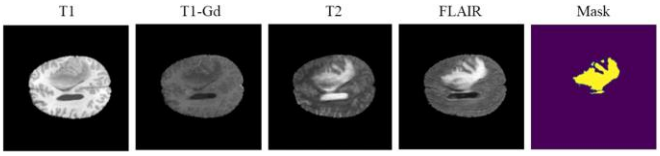

Figure 2. It shows mid-slice brain MRI images across four different modalities, including T1, T1-Gd, T2, and FLAIR, along with the corresponding region-of-interest (ROI) mask [27].

The proposed network was trained using the Adam optimizer with an initial learning rate of 1×10^{-3}, which is the standard default configuration in MATLAB. A mini-batch size of 4 and 100 training epochs were employed, aligned with common practices in multimodal brain tumor segmentation tasks. To enhance generalization and mitigate overfitting, the training data were shuffled at every epoch, and standard data-augmentation operations — including random rotation, translation, and horizontal/vertical flipping — were applied. All experiments were conducted using MATLAB's Deep Learning Toolbox, and the full training parameters are reported to ensure reproducibility.

The dataset was randomly partitioned into three subsets to enable robust training and fair performance evaluation. Specifically, 70% of the data was used for training, 15% for validation to fine-tune model hyperparameters and prevent overfitting, and the remaining 15% was reserved for testing to assess the model performance on unseen subjects. This splitting strategy is commonly adopted in brain tumor segmentation studies and ensures a reliable evaluation of the proposed method.

During the training process, the model's performance was monitored using the loss and accuracy curves, as depicted in Figures 3 and 4. The gradual decrease in loss values across successive epochs, accompanied by a steady increase in accuracy, indicates that the model is effectively learning from the data and successfully converging. These trends demonstrate the model's ability to capture both basic and complex patterns present in tumor images. Such learning behavior reflects the effectiveness of the network architecture as well as the quality and representativeness of the training dataset.

After the training phase was completed, the model was tested on the same input image to evaluate its performance in segmenting different tumor tissue regions. The prediction was carried out using the semanticseg function, and the results were overlaid on the fourth channel (FLAIR) as the background image. As shown in Figure 5, the results indicate that the model was able to approximately identify the main abnormal tissue regions, including edema, necrosis, and the enhancing tumor area, and distinguish them from healthy tissue. The predicted edema region (class 1) was well dispersed around the tumor margins, while the more central parts were accurately segmented and represented with colors corresponding to necrosis and the enhancing tumor core.

Subsequently, the results obtained from the proposed method are compared with those reported in existing studies. In these works, the authors also utilized the BRATS 2018 dataset [27] to evaluate their methods, allowing for a direct and fair comparison. Figure 6-9 illustrates the comparison between the proposed approach and the state-of-the-art techniques.

Convolutional Neural Networks (CNNs) are specifically optimized for image data and possess several key advantages that make them particularly effective in medical image segmentation tasks such as brain tumor delineation:

1. Local and spatial feature extraction: Convolutional layers employ small filters to detect local patterns and features in images, such as edges, textures, and complex structures. This capability enables the model to be sensitive to fine details.
2. Weight sharing: Unlike fully connected networks, convolutional layers share weights across the spatial dimensions of the image, reducing the number of

parameters and enhancing the model's generalization ability.

3. Preservation of spatial structure: CNNs maintain the two-dimensional (and, when necessary, three-dimensional) spatial relationships within images, which is critical for accurate tumor detection and segmentation.
4. Reduced need for manual preprocessing: Unlike traditional methods that rely on handcrafted feature extraction, CNNs automatically learn the most relevant features from raw data, leading to improvements in both accuracy and computational efficiency.
5. Hierarchical feature learning: Deeper layers in CNNs can extract increasingly complex and abstract features, which is essential for recognizing tumors with diverse and heterogeneous structures.

For these reasons, convolutional architectures generally outperform classical methods in medical image classification and segmentation tasks, including brain tumor analysis.

The proposed method achieved the highest performance among the compared techniques, with a positive predictive value (precision) of 98.4%, sensitivity (recall) of 98.8%, and an F1-score of 98.6%. These results indicate that the model not only excels at correctly identifying positive tumor samples (high sensitivity) but also effectively reduces false positive detections (high precision). Consequently, the harmonic mean of these two metrics, reflected in the F1-score, strongly confirms the superior overall performance of the proposed model.

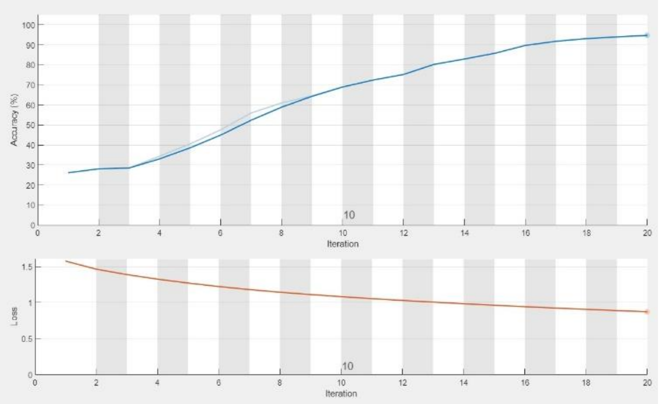

Figure 3. Training progress of the network over 20 epochs.

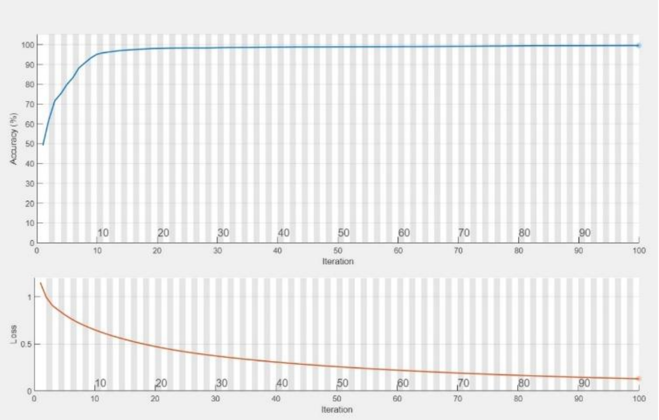

Figure 4. Training progress of the network over 100 epochs.

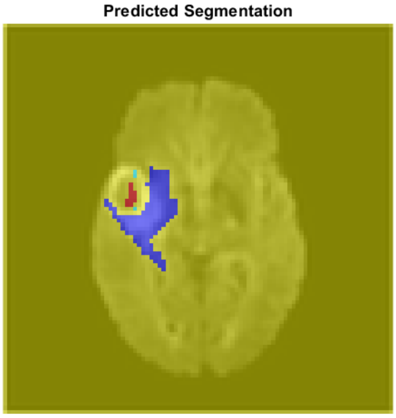

Figure 5. Segmentation results of the model overlaid on the FLAIR channel showing the predicted tumor regions including edema (class 1), necrosis, and enhancing tumor core.

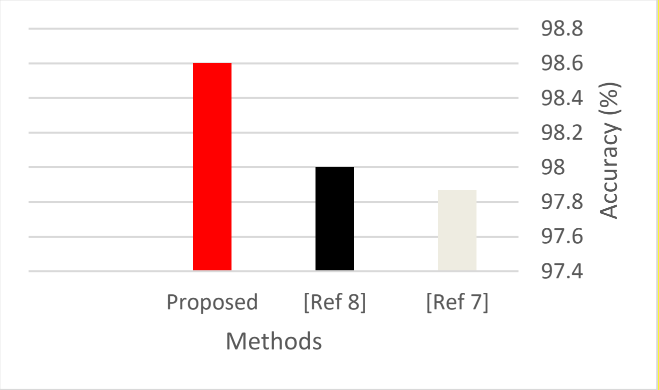

Figure 6. Comparison of accuracy between the proposed method and existing approaches.

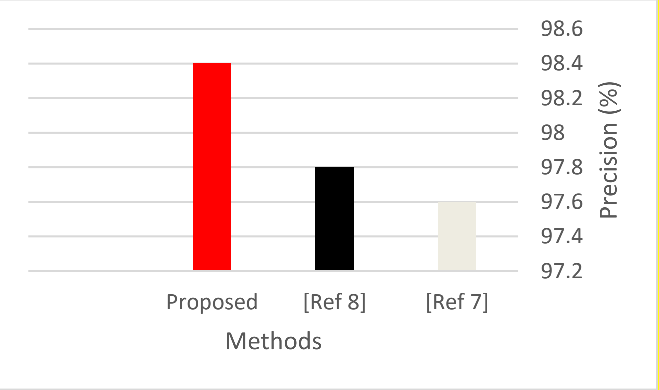

Figure 7. Precision values of the proposed method and existing methods.

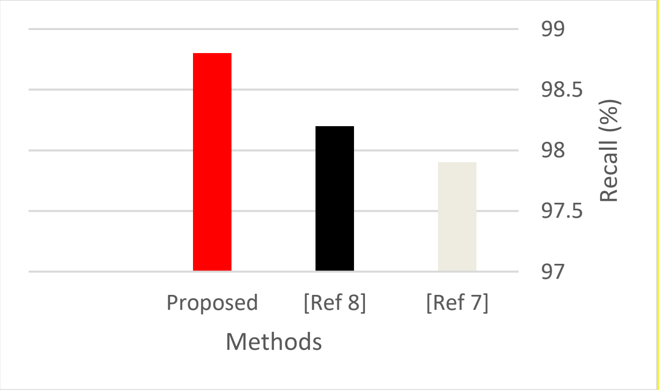

Figure 8. Recall values of the proposed method and existing approaches.

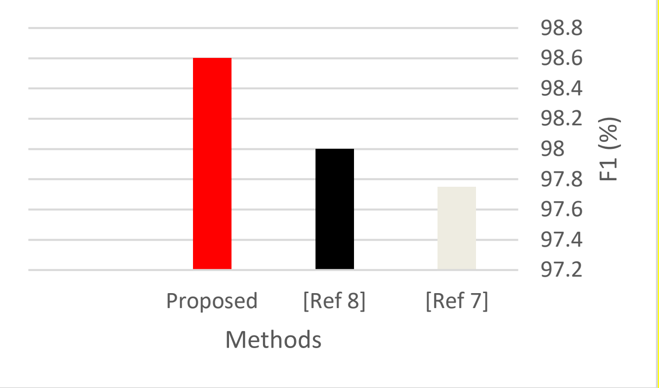

Figure 9. F1-score values of the proposed method and existing methods.

5. Conclusions

In this study, a comprehensive and well-structured convolutional neural network (CNN) architecture was proposed specifically for the task of segmenting brain MRI images and accurately identifying various tumor regions. The network employs a carefully designed encoder–decoder framework, where the encoder utilizes multiple convolutional layers in conjunction with batch normalization and ReLU activation functions to hierarchically extract both low-level spatial features and high-level semantic representations from the input multi-modal MRI data. This hierarchical feature extraction plays a crucial role in capturing the intricate patterns and structures associated with different tumor subregions.

The decoder component of the network leverages transposed convolutional layers (also known as deconvolution layers) to upsample the encoded features and reconstruct fine-grained segmentation maps that preserve anatomical details. To produce accurate and interpretable outputs, a softmax layer is applied at the final stage, converting the network outputs into pixel-wise probability maps across multiple classes. This enables precise classification of each pixel, even under conditions of class imbalance, which is common in medical imaging datasets. Experimental evaluations conducted on the BRATS 2018 benchmark dataset demonstrate the strong performance of the proposed model. The model achieves a high precision of 98.4%, a sensitivity of 98.8%, and an F1-score of 98.6%, outperforming several state-of-the-art methods. These results indicate the model's robust capability in distinguishing abnormal tumor tissues—such as enhancing tumor cores, necrotic cores, and peritumoral edema—from healthy brain regions. The success of this framework is attributed to the synergy between CNN-based architectural advantages (such as local receptive fields, spatial invariance, and weight sharing) and rigorous training on diverse data. Furthermore, the network's ability to automatically learn complex image patterns without requiring handcrafted features makes it highly suitable for clinical deployment. This study thus highlights the promise of the proposed approach for reliable, accurate, and scalable brain tumor segmentation and broader computer-aided diagnosis applications.

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