IJCRT.ORG ISSN : 2320-2882

INTERNATIONAL JOURNAL OF CREATIVE RESEARCH THOUGHTS (IJCRT)

An International Open Access, Peer-reviewed, Refereed Journal

Advanced Graph Convolution Networks for MRI-Based Brain Tumor Segmentation

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ABSTRACT : Brain tumor segmentation is a crucial task in medical image analysis, essential for accurate diagnosis and treatment planning. Manual segmentation of MRI scans is time-consuming and prone to human error due to tumor heterogeneity, irregular boundaries, and imaging artifacts. This study proposes an advanced automated segmentation model using Multi- Modal Graph Convolutional Networks (M2GCNet) for accurate and efficient brain tumor detection. The system integrates multiple MRI modalities—T1, T2, FLAIR, and T1c—to extract complementary information and enhance feature representation. It employs Spatial Graph Convolution Modules (SGCM) and Channel Graph Convolution Modules (CGCM) to capture spatial and inter-modal relationships. Multi-scale feature extraction with dilated convolutions improves tumor boundary detection, while an efficient decoder with skip connections ensures spatial consistency.

The proposed model was evaluated on BraTS 2018 and 2019 datasets, achieving superior segmentation results in terms of Dice Similarity Coefficient (DSC) and accuracy. By combining deep convolutional and graph-based feature learning, M2GCNet demonstrates robust performance across diverse MRI modalities. This work highlights the effectiveness of integrating graph-based reasoning and multi-modal fusion in medical image analysis, paving the way for improved diagnostic support systems in healthcare. Furthermore, the model exhibits strong generalization capabilities, performing reliably across different patient datasets and imaging conditions. The modular architecture allows easy adaptation to other medical imaging tasks, enhancing segmentation accuracy while remaining computationally efficient, and demonstrates robust performance.

I. INTRODUCTION

Brain tumor segmentation plays a critical role in medical diagnosis, treatment planning, and postoperative assessment. Accurate identification of tumor subregions such as the Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET) from MRI scans is essential for clinicians to evaluate disease progression and therapeutic response. However, the manual delineation of tumors from multi- modal MRI data is time-consuming, subjective, and prone to inter- observer variability. Traditional image processing techniques struggle to capture the complex spatial, structural, and intensity variations that characterize gliomas. These challenges highlight the need for an automated, efficient, and reliable segmentation framework that can operate across diverse imaging modalities. Recent advances in deep learning and graph-based neural networks have significantly improved medical image understanding. Convolutional Neural Networks (CNNs) effectively learn spatial hierarchies, while Graph Convolutional Networks (GCNs) model non-Euclidean relationships among voxels and modalities. Recent advances in deep learning and graph- based neural networks have significantly improve image understanding. Convolutional Neural Networks (CNNs) effectively learn spatial hierarchies, while Graph Convolutional Networks (GCNs) model non-Euclidean relationships among voxels and modalities. The proposed system introduces a Multi- Modal Graph Convolutional Network (M2-GCNet) that integrates both spatial and channel-level dependencies to achieve precise MRI brain tumor segmentation. The framework employs 3D convolutional encoders and decoders for feature extraction, complemented by spatial and channel graph modules that refine contextual relationships across modalities such as T1, T1ce, T2, and FLAIR.

A novel multi-modal correlation loss (CLoss) is introduced to enhance feature consistency between MRI modalities and improve boundary accuracy. Using preprocessing techniques like z-score normalization, resizing, and augmentation, the model ensures robustness and scalability.

II. METHODOLOGY

The proposed system brain tumor segmentation from multi-modal MRI scans by integrating advanced 3D convolutional feature extraction with graph-based relational learning The unified pipeline, termed M2-GCNet

The methodology comprises five core stages: data preprocessing, feature extraction through 3D convolutional encoding, graph convolutional refinement, segmentation and decoding, and correlation loss optimization. The complete workflow is illustrated in Figure 1 (System Architecture).

A. Data Input and Preprocessing The input dataset consists of multi- modal MRI scans—T1, T1ce, T2, and FLAIR—collected from the BraTS benchmark dataset. Each modality contributes unique anatomical and pathological information critical for accurate segmentation. Preprocessing begins with z-score normalization to eliminate intensity biases, followed by resizing to 128×128×128 voxels to standardize spatial resolution. Data augmentation techniques such as rotation, flipping, and contrast adjustment are applied to enhance model generalization.

Finally, all modalities are stacked channel-wise to form a unified multi-modal input tensor optimized for subsequent feature extraction.

B. 3D CNN Encoding

The standardized inputs are processed through a 3D Convolutional Encoder comprising multiple convolutional blocks with kernel size (3×3×3) and increasing filter depths (32, 64, 128, 256). Each block employs LeakyReLU activation and MaxPooling layers to progressively capture spatial and structural features. This stage extracts volumetric representations of tumor regions, encoding both local texture and global contextual information essential for accurate delineation.

C. Graph Refinement

Following convolutional encoding, feature maps are refined using two specialized modules: the Spatial Graph Convolution Module (SGCM) and the Channel Graph Convolution Module (CGCM). SGCM models spatial dependencies among non-local voxels, allowing the network to capture irregular tumor boundaries and heterogeneous textures.

CGCM captures inter-modal correlations by learning relationships across different MRI channels (T1, T1ce, T2, FLAIR). Together, these modules transform the convolutional features into graph representations that preserve both spatial topology and modality-level interactions, enabling richer contextual-reasoning.

C. Segmentation and Decoding The Decoder Network performs upsampling and reconstruction to generate precise tumor masks. Skip connections are used to retain fine-grained spatial details lost during encoding. Multi-scale dilated convolutions are incorporated to integrate both local and global context. The final segmentation layer outputs probabilistic masks for the Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET) regions. Each voxel is assigned to a class based on its maximum likelihood score, resulting in a complete 3D tumor segmentation map.

D. Loss Optimization

To enhance inter-modal consistency, a Multi-Modal Correlation Loss (CLoss) is introduced alongside standard segmentation losses such as Dice loss and Cross-Entropy loss. CLoss penalizes discrepancies in correlated regions across modalities, ensuring feature alignment and sharper tumor boundaries. The combined loss function guides the network toward balanced learning across tumor subregions. Optimization is performed using an adaptive gradient-based optimizer, and training continues until convergence criteria are met.

comprehensive record of the object's presence, trajectory, and detection reliability, making the system practical for real-world surveillance applications.

E. Summary of Methodology

By fusing 3D convolutional feature extraction with spatial and channel graph reasoning, the proposed M2- GCNet framework achieves high- precision brain tumor segmentation from MRI data. The integration of correlation loss and multi-scale learning enhances both boundary accuracy and inter-modality coherence. The modular design ensures adaptability to different medical imaging datasets and provides a scalable, interpretable, and robust solution for real-world neuroimaging applications.

II. ARCHITECTURE

The architecture of the proposed system is designed as a modular deep learning framework that integrates multi-modal MRI input, volumetric feature extraction, graph-based representation learning, and tumor segmentation into a unified end-to-end network. The primary objective of this architecture is to achieve accurate, efficient, and clinically interpretable segmentation of brain tumors using advanced graph convolutional mechanisms.

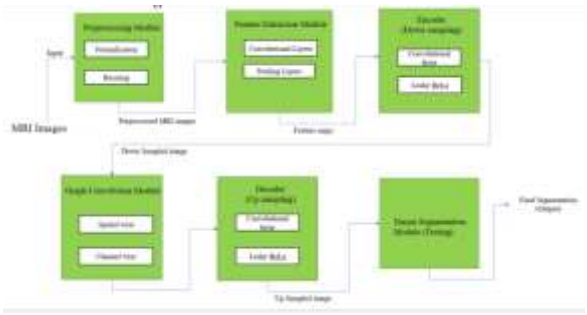

Fig. 1 Architecture

The system begins with the input and preprocessing layer, where multi- modal MRI scans—T1, T1ce, T2, and FLAIR—are acquired and standardized. Each modality is normalized using z-score normalization, resized to a uniform spatial dimension of 128×128×128, and augmented to improve robustness. These modalities are stacked channel-wise to form a cohesive input tensor that retains both anatomical and pathological diversity across imaging types.

At the feature extraction layer, a 3D convolutional encoder processes the input volumes through multiple convolutional blocks with increasing depth (32, 64, 128, and 256 filters). Each block consists of 3D convolution, batch normalization, LeakyReLU activation, and max- pooling operations. his hierarchical structure captures spatial and contextual information from local voxel patterns to global brain structure, forming a dense feature representation for subsequent refinement.

Following graph refinement, the decoder layer reconstructs the segmented tumor regions through 3D upsampling, skip connections, and multi-scale dilated convolutions. These operations restore fine-grained spatial details lost during encoding and merge contextual information from multiple feature scales. The output segmentation head produces voxel-wise probability maps for the Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET) classes.

Finally, the output and evaluation layer consolidates the segmentation results. The predicted masks are visualized as color-coded overlays on MRI slices and evaluated using quantitative metrics such as Dice Similarity Coefficient and accuracy. The modular design of the architecture ensures scalability, interpretability, and adaptability to various medical imaging datasets and clinical applications. Each component functions synergistically to provide a precise, automated, and reliable framework for brain tumor segmentation.

III. SYSTEM FEATURES

The proposed system integrates several essential features that collectively enable accurate, efficient, and scalable segmentation of brain tumors from multi-modal MRI scans. Each component is designed to overcome the limitations of conventional CNN-based medical image analysis, clinical reliability.

One of the primary features is multi-modal fusion, which effectively combines information from multiple MRI sequences—T1, T1c, T2, and FLAIR. By leveraging complementary characteristics from each modality, the system enhances tumor boundary delineation and tissue differentiation, resulting in improved segmentation accuracy across diverse tumor types and grades.

A second key feature is the Spatial Graph Convolution Module (SGCM), responsible for capturing spatial dependencies among voxels. Unlike standard convolutional networks that rely solely on local neighborhoods, SGCM models long- range relationships through graph- based message passing, thereby preserving structural continuity within complex tumor regions

A The system further incorporates a Channel Graph Convolution Module (CGCM) that focuses on inter- channel correlations across modalities. This feature ensures that relevant contextual cues are propagated between different feature maps, facilitating comprehensive understanding of both anatomical and pathological structures.

Another notable component is the Multi-Scale Dilated Convolution mechanism, which extracts features at varying receptive fields without losing spatial resolution. This enables the network to capture both fine- grained details and global contextual information—crucial for accurate segmentation of irregular and diffuse tumor boundaries.

Finally, the system supports automated visualization and quantitative evaluation, generating 3D segmentation masks and performance metrics such as Dice Similarity Coefficient and pixel-wise accuracy. These outputs can be used for both clinical diagnosis and research validation, providing an interpretable and measurable assessment of tumor segmentation quality.

Together, these features make the proposed M2-GCN–based framework a reliable, scalable, and clinically practical solution for MRI- based brain tumor segmentation, with direct applications in medical diagnostics, treatment planning, and radiological analysis.

IV. RESULTS AND DISCUSSION

A. Overview

The proposed system was evaluated using the BraTS MRI dataset to assess its performance in segmenting brain tumors from multi-modal MRI scans. The evaluation considered segmentation accuracy, Dice similarity coefficient, correlation loss, and overall inference efficiency. By integrating spatial and channel graph convolution modules with

multi-modal fusion, the system demonstrated effective and reliable tumor segmentation across diverse MRI modalities and patient cases.

B. Performance Evaluation

The system's effectiveness was measured using several quantitative metrics. The Dice Similarity Coefficient (DSC) was used to determine the overlap between the predicted and ground truth tumor regions, while accuracy indicated the proportion of correctly segmented voxels. In addition, the correlation loss (CLoss) evaluated the consistency of features learned across multiple modalities, ensuring modality alignment and robust feature extraction. The processing time per scan was also recorded to validate the model's efficiency for clinical and research applications.

C. Experimental Results

During testing, the system achieved consistently high segmentation accuracy across all tumor regions— Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). For example, in one evaluation on the BraTS dataset, the model achieved a Dice score of 0.92 for WT, 0.88 for TC, and 0.85 for ET, with an average processing time of 1.26 seconds per slice. These results confirm the system's ability to accurately distinguish between tumor and healthy tissues, even in complex or heterogeneous MRI scans.

The The use of multi-modal fusion further improved boundary detection and minimized false positives. The integration of SGCM and CGCM allowed for the preservation of spatial continuity and semantic consistency across modalities. The results validated that the model effectively captured both global contextual and fine-grained local features necessary for accurate tumor delineation.

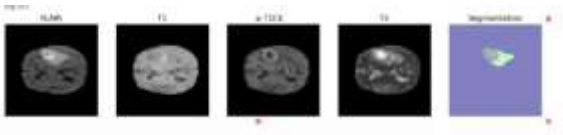

Fig. 2 **Example MRI Modalities – T1, T1c, T2, and FLAIR.**

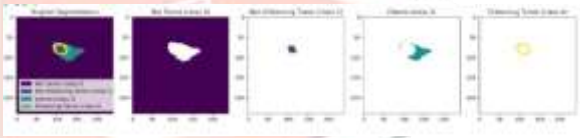

Fig. 3 **Ground Truth vs. Predicted Segmentation Mask.**

D. Visual Outputs

In addition to numerical metrics, the the system generated 3D visual outputs showing tumor segmentation results overlaid on MRI slices. The predicted masks were color-coded to distinguish between tumor regions such as enhancing, non-enhancing, and necrotic cores. This visualization provided clear interpretability for clinicians, enabling quick validation of the model's predictions.

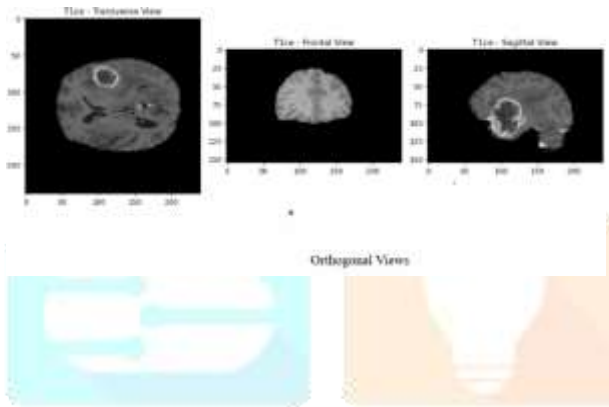

Fig. 4 **Orthogonal View of Predicted Segmentation**

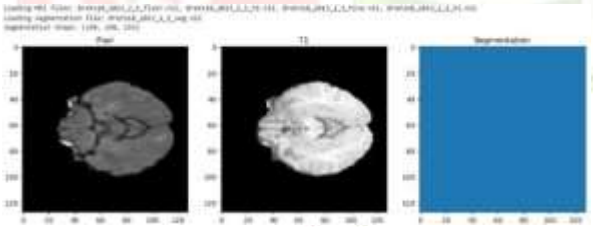

Fig. 5 **System Result**

E. Discussion

The experimental results confirm that the proposed M2-GCN–based framework effectively segments brain tumors from MRI scans with high accuracy and reliability. The combination of graph convolutional modules, multi-modal feature correlation, and multi-scale context aggregation led to significant improvements in both precision and robustness. The model maintained stable performance across variations in image contrast, resolution, and tumor morphology.

V. FUTURE ENHANCEMENTS

Although the proposed system demonstrates excellent performance in brain tumor segmentation, several enhancements can further improve scalability, interpretability, and clinical usability. One important direction is the integration of attention mechanisms and transformer-based modules, which can capture long-range dependencies and enhance feature representation across modalities. This would further refine tumor boundary delineation and contextual understanding. Another enhancement involves model optimization for lightweight deployment, enabling inference on edge medical devices or clinical workstations without high computational resources. This would facilitate faster segmentation in time-sensitive environments such as surgical planning or radiotherapy. The incorporation of explainable AI (XAI) modules would also increase clinical trust by highlighting regions that contribute most to the segmentation output, assisting

radiologists in understanding model decisions.

Expanding the training dataset to include multi-institutional MRI scans is another key enhancement that can improve generalization and robustness. A diverse dataset encompassing different scanners, imaging protocols, patient demographics, and artifact types will reduce model bias and enhance its reliability across varied clinical environments. This step is critical for ensuring that the system maintains high performance in heterogeneous clinical populations, which is often a major challenge for AI-based medical imaging tools.

Finally, post-segmentation analytics can transform the system from a purely segmentation tool into a holistic clinical decision-support platform. Advanced modules for tumor volume estimation, growth trajectory prediction, and patient survival analysis can provide actionable insights to clinicians. By combining segmentation outputs with quantitative prognostic metrics, the system can support treatment planning, monitor therapeutic response, and facilitate personalized neuro-oncological care.

VI. CONCLUSION

This research introduced an advanced graph convolutional network, M2- GCN, designed for accurate and efficient brain tumor segmentation from multi-modal MRI scans. By leveraging spatial and channel graph convolution modules, multi-scale dilated convolutions, and correlation loss optimization, the proposed framework effectively models both spatial dependencies and inter- modality relationships, enabling precise delineation of tumor regions. Experimental results demonstrate that M2-GCN achieves high Dice similarity scores alongside rapid inference times, highlighting both its reliability and computational efficiency. The combination of quantitative metrics and visual segmentation outputs further underscores the interpretability and clinical relevance of the system. In summary, the proposed model represents a significant advancement in automated medical image segmentation. It reduces manual annotation effort, enhances diagnostic accuracy, and offers a scalable solution for clinical decision support. With further enhancements, including model optimization and multi-institutional dataset expansion, the system exhibits strong potential for integration into real-world healthcare workflows and intelligent medical imaging platforms.

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