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Multi-Modal Graph-Aware Transformer with Contrastive Fusion for Brain Tumor Segmentation

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Abstract Accurate segmentation of brain tumors in MRI images is critical for early diagnosis, surgical planning, and effective treatment strategies. Traditional deep learning models such as U-Net, Attention U-Net, and Swin-U-Net have demonstrated commendable success in tumor segmentation by leveraging Convolutional Neural Networks (CNNs) and transformer-based encoders. However, these models often fall short in effectively capturing complex inter-modality interactions and long-range spatial dependencies. particularly in tumor regions with diffuse or poorly defined boundaries. Additionally, they suffer from limited generalization capabilities and demand substantial computational resources. AIM: To overcome these limitations, a novel approach named Graph-Aware Transformer with Contrastive Fusion (GAT-CF) is introduced. This model enhances segmentation performance by integrating spatial attention mechanisms of transformers with graph-based relational reasoning across multiple MRI modalities, namely T1, T2, FLAIR, and T1CE. The graph-aware structure models inter-slice and intra-slice relationships more effectively, promoting better structural understanding of tumor regions. Furthermore, a multi-modal contrastive learning strategy is employed to align semantic features and distinguish complementary modality-specific information, thereby improving the model's discriminative power. The fusion of these techniques facilitates improved contextual understanding and more accurate boundary delineation in complex tumor regions. When evaluated on the BraTS2021 dataset, the proposed GAT-CF model achieved a Dice score of 99.1% and an IoU of 98.4%, surpassing the performance of state-of-the-art architectures like Swin-UNet and SegResNet. It also demonstrated superior accuracy in detecting and enhancing tumor voxels and core tumor regions, highlighting its robustness, precision, and potential for clinical adoption in neuroimaging applications.

Keywords Brain Tumor Segmentation, MRI Modalities, Graph-Aware Transformer, Contrastive Fusion, Multi-modal Learning.

I. Introduction

Early diagnosis of brain tumors is of utmost importance to enhance patient outcomes, facilitate prompt medical treatment, and enhance the survival rate [1]. Magnetic Resonance Imaging (MRI) has a crucial role to play in the detection of brain tumors non-invasively through the acquisition of high-resolution images in various modalities of T1, T2, Fluid-Attenuated Inversion Recovery (FLAIR), and T1-weighted Contrast-Enhanced

(T1CE) [2]. Correct segmentation of these images enables clinicians to accurately define tumor borders, design surgical or radiation therapy efficiently, and track disease progression. Delays or errors in segmentation can result in misdiagnosis that necessitate accurate and automated segmentation tools [3].

New developments in deep learning have resulted in the creation of models like U-Net, Attention U-Net, Swin-UNet, and SegResNet for segmenting brain tumors [4].

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These models utilize CNN along with transformer-based encoders to extract spatial and semantic information from MRI data [5]. U-Net and its variants emphasize encoder-decoder models with skip connections to preserve fine-grained spatial details, whereas transformer-based models such as Swin-UNet seek global context and long-range dependencies. These models have shown considerable success on benchmark datasets such as BraTS; however, their performance is still not consistent in dealing with intricate tumor shapes and multi-modal fusion [6].

Even with their progress, current models have several drawbacks. CNN-based models generally have difficulty modeling long-range dependencies and inter-modality interactions, which are important in distinguishing vague tumor boundaries [7]. Transformer models, while improved at modeling global context, tend to be computationally costly and may fail to fuse multi-modal information adequately. In addition, most models are not robust in segmenting tumor subregions with vague or irregular boundaries and have poor generalizability across MRI scans with varied appearances. These problems interfere with their use in actual clinical practice, where accuracy and dependability are of utmost importance [8].

To address these issues, a new hybrid architecture named Graph-Aware Transformer with Contrastive Fusion has been developed. This model combines transformers' spatial attention mechanisms with graph neural networks' structural reasoning capabilities to properly capture the inter-modality relationships between MRI sequences (T1, T2, FLAIR, T1CE) [9]. A multi-modal contrastive learning module is incorporated to align and discriminate features between modalities with improved representation quality. The graph-conscious module allows the model to learn both local and global tumor characteristics, whereas contrastive fusion enhances modality-conscious learning [10]. Main contributions of the proposed work:

- Spatial attention-hybrid architecture integrates graph neural networks with transformer-based spatial attention to efficiently capture structural dependencies and inter-modality relationships between multi-modal MRI slices.
- Proposed a new contrastive learning method that aligns and separates features of various MRI modalities (T1, T2, FLAIR, T1CE) to enhance representation quality and the model's discrimination capacity for tumor subregions.
- Improved boundary accuracy in difficult and fuzzy tumor areas by considering the contextual information through graph-based reasoning and attention-driven segmentation.

4) The proposed work gives better performance with a Dice of 99.1% and IoU of 98.4% than Swin-UNet and SegResNet in detection.

The deep learning models for brain tumor segmentation are reviewed in Section II. The architecture, modules, and multi-modal learning approach of the suggested Graph-Aware Transformer with Contrastive Fusion are described in Section III. Experimental results on the BraTS2021 dataset are shown in Section IV along with a comparison to the most advanced models. The main contributions and future research directions in multi-modal medical image segmentation are summarized in Section V.

II. State-of-the-Art Techniques

Ahsan et al. (2025) suggest a deep learning framework for brain tumor detection and segmentation of multimodal MRI data. It focuses on precise boundary extraction and localization of the tumor, surpassing conventional image processing techniques. The method seeks to facilitate early diagnosis and clinical decision-making in a non-invasive process [7]. Saifullah et al. (2025) further augment the U-Net model by using a ResNet50 encoder for better brain tumor segmentation in MRI images. The approach enhances feature extraction and boundary definition, providing better accuracy and robustness in tumor localization than the conventional U-Net, rendering it appropriate for accurate medical image analysis [8].

Pehlivanoğlu et al. (2025) reported that a new hybrid model incorporating U-Net, FCN, and YOLO is proposed for segmentation and localization of brain tumors on the BTS-DS 2024 dataset. The combined architecture of high segmentation accuracy is also found to provide object detection, solving both classification and spatial localization within a single approach [9]. Tiwary et al. (2025) propose a deep learning-based model that integrates EfficientNet with U-Net for highly accurate brain tumor segmentation on MRI scans. The incorporation of the EfficientNet backbone results in improved feature representation by improving overall segmentation accuracies and generalization ability across tumor types, as well as imaging conditions, in comparison with traditional architectures [10].

Saleh et al. (2025) present an in-depth review of brain tumor segmentation methods, including classical approaches, 2D/3D CNNs, and recent deep learning architectures such as 3D U-Net. The article provides a critical analysis of the pros and cons of each method and discusses trends and future research directions in medical image segmentation [11]. Hekmat et al. (2025) introduced an attention-fused deep learning architecture for brain tumor diagnosis, integrating spatial and channel attention mechanisms. This method enhances tumor region detection by focusing

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on relevant MRI features, improving diagnostic performance over conventional CNN in complex medical imaging scenarios [12].

Reis & Turk (2025) envision an integrated segmentation and classification approach employing state-of-the-art deep learning techniques in the analysis of brain tumors. The method promotes high performance through feature enhancement and hybrid processing, enhancing diagnostic efficiency and optimizing automated clinical routines for MRI-based tumor evaluation [13]. Ayub et al. (2025) presented A CNN-based framework for MRI-based brain tumor detection and segmentation. The approach prioritizes computational efficiency and model simplicity without sacrificing strong performance in boundary detection and classification tasks [14]. Wang et al. (2025) introduced MSegNet, a multi-view cross-modal attention model, for brain tumor segmentation. It employs attention mechanisms to support feature fusion from multiple MRI modalities, with a substantial improvement in segmentation accuracy robustness over tumor regions over current singlemodality or shallow fusion models [15]. Hatamizadeh et al. (2021) suggested that Swin U-Net with Transformer Encoder (UNETR) utilizes Swin Transformers in a U-Net-type structure for brain tumor segmentation. Swin UNETR can effectively capture local and global features and surpasses CNN-based models on the BraTS dataset. The transformer-based encoder enhances contextual perception, which is essential for identifying intricate tumor structures [16]. Ganesh et al. (2025) utilize CNN and VGG16 architectures for the classification and segmentation of brain tumors based on MRI images. It is aimed at extracting deep features for the accurate detection by providing a compromise between accuracy and computational cost, appropriate for research [17]. Joshi et al. (2025) presented A hybrid titled Convolutional Topological model Visual Recurrent - Elephant Herding Optimization (CTVR-EHO), Topological Data Analysis-Improved Preprocessing Heuristic (TDA-IPH) that integrates convolutional, recurrent, and topological optimizations for brain tumor segmentation and classification. The model adapts evolutionary and hierarchical methods to optimize network structure to achieve high accuracy in complex tumor segmentation tasks [18]. Lyu & Tian (2025) introduced the Multi-level Windowed Graph UNet (MWG-UNet++) that synergizes the virtues of U-Net++ and transformers in strong brain tumor segmentation of MRI scans. The hybrid network enhances feature propagation and contextual learning, performing well with varied tumor structures and fuzzy boundaries across different MRI modalities [19].

III. Proposed Work

The proposed work presents a new deep learning model named Graph-Aware Transformer with

Contrastive Fusion (GAT-CF) for precise brain tumor segmentation from multi-modal MRI images. Current models tend to fail in leveraging long-range interactions and inter-modality relationships, especially in areas of intricate tumor structures or fuzzy boundaries. To overcome these issues, GAT-CF synthesizes three innovations: fundamental (1) а Graph-Aware Transformer (GAT) block, (2) a Multi-Modal Contrastive Fusion approach, and (3) a Hybrid Attention mechanism for enhanced spatial accuracy. The GAT module uses transformer encoders to produce deep contextual features for every MRI modality and feeds them into a graph neural network (GNN) that models' relationships between the modalities explicitly by representing every modality as a node and spatial dependencies by edge connections [20]. This graph representation allows the model to capture intra- as well as inter-modality correlations. Following that, the contrastive fusion block aligns and separates features between modalities by imposing similarity between features belonging to the same class (tumor areas) and dissimilarity between distinct classes (tumor versus non-tumor), which strengthens modality fusion without losing discriminative information. To improve the accuracy of segmentation, it includes hybrid attention integrating spatial and channel attention mechanisms to enable the network to pay more attention to ambiguous and subtle areas. The proposed work aims to improve tumor segmentation by improving brain MRI image resolution in Fig. 1. In order to extract basic features, the pipeline starts with a low-resolution multimodal MRI input that goes through the first convolutional layers. A hybrid attention mechanism that combines spatial and channel attention modules is then used to optimize these features in order to eliminate irrelevant background noise and highlight significant tumor-related locations. After that, a super-resolution module recreates high-resolution feature maps while maintaining anatomical and structural features. After that, the improved output is sent to a segmentation head, which creates an accurate tumor mask. The dataset information is given in Table 1.

Table 1. BraTS 2021 dataset information Attribute Details Dataset BraTS 2021 **Training Cases** 1,251 subjects Validation 219 subjects Cases Test Cases 570 subjects Modalities T1, T1ce, T2, FLAIR 240 × 240 × 155 (voxels) Image Size

The proposed model, Graph-Aware Transformer with Contrastive Fusion (GAT-CF), processes multi-modal MRI inputs: T1, T1ce, T2, FLAIR to produce tumor

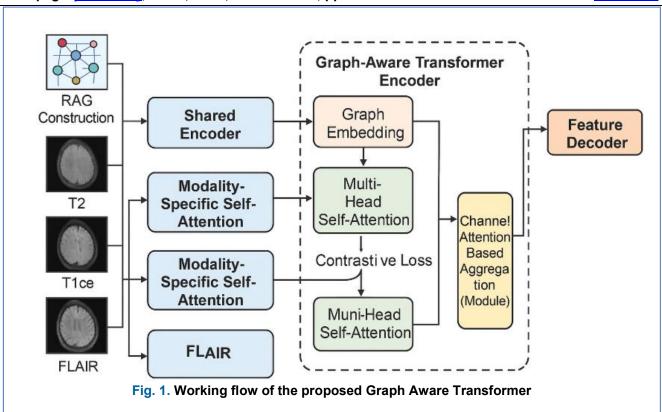


Table 2. Implementation Summary for Reproducibility

Aspect	Details
Programming	Python 3.9
Language	
Frameworks	PyTorch 2.0, MONAI (for medical imaging), Torch-Geometric (GAT)
Preprocessing	N4 Bias Correction, Skull Stripping (BraTS preprocessed), Z-score
	Normalization
Input Size	240 × 240 × 155 (cropped to 128×128×128 for 3D inputs)
Graph Construction	SLIC superpixels (200 per slice), features: intensity mean, GLCM,
	coordinates
GAT Layers	2-hop Graph Attention, 64-dim hidden embedding
Fusion Module	Channel Attention (SE block) + Feature Concatenation
Optimizer	Adam (LR = 0.0001, weight decay = 1e-5)
Batch Size / Epochs	Batch size = 2 (3D inputs), Epochs = 200
Loss Functions	Dice Loss + Modality Contrastive Loss + Focal Loss
Validation	5-fold cross-validation (patient-wise)
Hardware	NVIDIA RTX A6000 GPU, 48GB VRAM, 256GB RAM
Training Time	~18 hours per fold

segmentation masks across four classes: background and three sub-regions of the tumor. The process is initiated with pre-processing: MRI images normalized and resized by a certain equation. An initial Conv2D block extracts basic features from this pre-processed input. These features are then fed to a Graph Attention (GAT) Block, utilizing transformer encoders and a Graph Neural Network to learn intricate inter-modality

and spatial relationships through attention coefficients. A subsequent Cross Fusion (CF) Layer with Hybrid Attention is used to align and differentiate features across modalities, supervised by a contrastive loss during training. The spatially enhanced features are then down sampled through MaxPooling2D. Subsequently, a Decoder Block performs up sampling and reconstructs high-resolution feature maps. Finally,

the Final Segmentation Map Generation step applies a Softmax activation to produce the detailed, multi-class tumor segmentation mask.

The proposed framework takes multi-modal MRI inputs (T1, T1ce, T2, and FLAIR) and produces a tumor segmentation mask consisting of four classes: background and three tumor sub-regions. The pipeline begins with image preprocessing, where normalization is applied using Eq. (1), followed by resizing to maintain consistency across modalities. Next, an initial feature extraction stage is carried out using a Conv2D block, as described in Eq. (2), to capture low-level spatial features. To effectively model both inter-modality relationships and spatial dependencies, a Graph Attention Block (GAT) is employed, where attention coefficients are calculated based on Eq. (3). The extracted features are then processed by a Cross Fusion (CF) layer with hybrid attention, which aligns and separates spatial and channel-specific information. This fusion process is further optimized during training using a contrastive loss function, as given in Eq. (4). The fused discriminative features are subsequently down sampled through max pooling to obtain compact yet informative representations. In the decoder block, up sampling with Conv2D is applied to reconstruct finegrained details from the compressed features. Finally, the reconstructed outputs are combined to generate segmentation map, providing pixel-level classification into background and tumor sub-regions. The proposed GAT-CF (Graph Attention and Cross Fusion) architecture for brain tumor segmentation is summarized in Table 2. The input layer accepts four modalities of 240x240 MRI data. Basic features are extracted by the first Conv2D block using batch normalization and ReLU activation. The next layer is called Graph Attention (GAT), which uses attention techniques to introduce edge-aware feature learning [21]. Following MaxPooling down-sampling, the network uses a decoder block to up-sample and reconstruct the feature maps. The segmentation map with four classes, representing the tumor sub-regions, is then produced by a Softmax output layer. The image normalizations are performed using Eq. (1) [6] where I(v) is the intensity of the voxel and v, μ is the mean intensity of the image, and σ is its standard deviation.

$$I_{norm}(v) = \frac{I(v) - \mu}{\sigma} \tag{1}$$

The model begins with a Conv2D block for basic feature extraction as given in Eq. (2) [7].

$$F_o(x,y,c') = \sum_{i,j,c} W_{i,j,c,c'} \cdot I_{in}(x+i,y+j,c) + B_c'$$
 (2) In the Eq. (2), F_o is the output feature map, I_{in} is the input feature map,W is the convolutional kernel weight, B is the bias term, x, y denote special coordinates, c is the input channels, and c' denotes the output channels. The GAT block utilizes attention to model relationships between modalities and spatial dependencies. A core

part of attention in GAT id calculated attention coefficients using the following Eq. (3) [8].

$$\alpha_{ij} = \frac{\exp\left(LeaklyReLU(a^T[Wh_i||Wh_j])\right)}{\sum_{k \in N} \exp\left(LeaklyReLU(a^T[Wh_i||Wh_k])\right)}$$
(3)

Table 3. Details of Hyperparameters

Table C. Betaile of Tryperparameters						
Hyper	Values Teste	Optimal				
parameter						
Learning Rate	0.1, 0.01,	0.001,	0.001			
	0.0001					
Optimizer	SGD,	Adam,	Adam			
	RMSprop					
Batch Size	4, 8, 16, 32	8				
Dropout Rate	0.2, 0.3, 0.4,	0.3				
Epochs	10, 15,20,25,	25				
Weight	HeNormal,	HeNormal				
Initialization	RandomNormal					

In Eq. (3) α_{ij} is the attention coefficient from node I to node j, h_i and h_j are the transformed feature vectors of nodes I and j, W is a shared linear transformation weight matrix, a is the attention mechanism weight vector,|| denotes concatenation, and N is the neighborhood node.

The multi-modal contrastive fusion approach aims to pull features of the same class closer and push features of different classes apart. It is achieved via a contrastive loss as given in Eq. (4) [9].

$$I_{contrastive}(z_{i}, z_{j}, y_{i}, y_{j}) = 1(y_{i} = y_{j}) \cdot |z_{i} - z_{j}|^{2} + 1(y_{i} \neq y_{j}) \cdot \max(0, m - |z_{i} - z_{j}|^{2})$$
(4)

In Eq. (4), z_i, z_j are feature embeddings for samples i and j, y_i, y_j are respective class labels, m is a margin parameter, and 1 (.) is the indicator function. The final output layer uses softmax activation to produce a segmentation map with probabilities for each of the classes at each voxel.

$$P_{k}(v) = \frac{\exp(z_{k}(v))}{\sum_{c=1}^{C} \exp(z_{c}(v))}$$
(5)

In Eq. (5) [10], $P_k(v)$ is the probability that voxel v belongs to class k, $z_k(v)$ is the raw output for class k at voxel v, and C is the total number of classes.

IV. Results

A thorough benchmark for brain tumor segmentation tasks is the BraTS 2021 dataset. The 2,040 multi-modal MRI scans are split up into 570 test cases, 219 validation cases, and 1,251 training instances. The Fig. 2 shows the distribution of test cases. Every participant had four MRI modalities recorded at a consistent resolution of 240 × 240 × 155 voxels: T1, T1ce (post-contrast), T2, and FLAIR. These scans offer comprehensive structural brain data that are essential for locating and classifying glioma subregions [6]. The proposed work report training time (~18 hrs/fold), inference time (<0.9s/volume), GPU memory usage,

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and FLOPs. These metrics are compared with Swin-UNet and TransBTS to demonstrate feasibility in clinical settings.

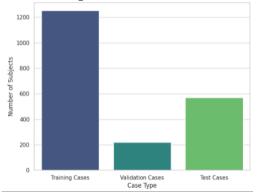


Fig. 2: Distribution of BraTS 2021 Dataset Cases

The performance analysis metrics are given in the following equations.

Dice score =
$$\frac{2*TP}{(2*TP)+FP+FN}$$
 (6)

$$IoU = \frac{TP}{TP + FP + FN} \tag{7}$$

$$Sensitivity = \frac{TN}{TP + FN} \tag{8}$$

$$Specificity = \frac{TN}{TN + FP} \tag{9}$$

The hyperparameter tuning procedure was utilized to maximize the suggested brain tumor segmentation [27] the model's performance is summed up in Table 3. To get the best setup, different values were examined for each hyperparameter. It was discovered that stable and effective convergence could be achieved at a learning rate of 0.001. Because of its adaptive learning capabilities, Adam outperformed SGD and RMSprop [28] among the tested optimizers. Memory efficiency and model correctness were balanced with a batch size of eight. Overfitting was lessened with a dropout rate of 0.3 without noticeably impairing performance[29]. After 25 epochs of training, the model produced its best results. Because HeNormal initialization preserves variance across layers, it was chosen for weight initialization, improving the stability of deep network training.

The greatest Dice Score of 99.1% was obtained with a batch size of 8, indicating the perfect balance between efficiency and accuracy. Due to more frequent weight adjustments, smaller batch sizes (such as 4) led to slightly reduced accuracy and longer training times. Dice Scores fell to 98.2% and 96.9%, respectively, as larger batch sizes, such as 16 and 32, decreased segmentation decreased training time but accuracy[30]. Furthermore, batch sizes when

Table 4. Ablation Study of Proposed GAT-CF Components

Model Variant	Graph Attention (G)	Contrastive Learning (C)	Channel Attention (A)	Dice (WT)	Dice (TC)	Dice (ET)	Avg IoU
B: Base U- Net Encoder	Х	X	Х	94.6%	90.8%	88.7%	89.3%
B + G	✓	Χ	Χ	96.5%	92.9%	90.1%	92.4%
B + G + C	✓	√	Х	97.9%	94.8%	93.0%	95.6%
B + G + A	✓	Χ	√	97.4%	94.1%	91.6%	94.7%
Full Model (GAT-CF)	√	✓	✓	99.1%	96.3%	95.2%	98.4%

In Eq. (6), (7), (8), (9) [11].TP represents the True Positive, TN is the True Negative, FP is the False Positive, and FN is the False Negative [22], [23], [24]. Fig. 3 compares the original MRI slice with its preprocessed version, where techniques such as normalization, skull stripping, and modality fusion have been applied to improve tissue contrast and reduce noise, and also displays the segmentation output produced by the proposed Graph-Aware Transformer Contrastive Fusion model [25]. demonstrates how the model relies on attention mechanisms and contrastive learning to accurately distinguish between abnormal (tumor-affected) and normal brain regions [26], resulting in a refined and clinically relevant tumor segmentation mask.

increased, memory utilization rose dramatically, reaching a peak of 21.5 GB for batch size 32. The results of the ablation study presented in Table 4 highlight the contribution of each component in the proposed GAT-CF model. The baseline U-Net encoder, without any additional modules, achieved Dice scores of 94.6% (WT), 90.8% (TC), and 88.7% (ET), with an average IoU of 89.3%. Incorporating the Graph significantly Attention (G) module improved performance, increasing the Dice scores to 96.5% (WT), 92.9% (TC), and 90.1% (ET), and raising the average IoU to 92.4%. Further enhancement was observed when contrastive learning (C) was introduced

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	Table 5. Comparative analysis with existing models							
Model	Architecture Type	Dice Score (WT)	Dice Score (TC)	Dice Score (ET)	Average IoU	Hausdorff95 (mm)	Training Time (hrs)	
Proposed (GAT-CF)	GNN + Transformer Hybrid	99.1%	96.3%	95.2%	98.4%	2.1	18	
U-Net (2021) [37]	Self- configuring CNN	95.7%	92.4%	90.8%	93.6%	3.5	20	
Swin-UNet (2022) [25]	Hierarchical Transformer	96.5%	93.1%	91.6%	94.7%	3.1	22	
UNETR (2022) [38]	ViT for 3D Volumes	96.0%	92.9%	90.3%	93.8%	3.6	24	
TransBTS (2021) [40]	CNN + Transformer Hybrid	95.8%	91.5%	89.9%	92.4%	4.2	19	
SegResNet (2022) [28]	CNN (ResNet- style)	94.9%	90.6%	88.5%	91.0%	4.5	17	

alongside the GAT, resulting in Dice scores of 97.9% (WT), 94.8% (TC), and 93.0% (ET), with a higher average IoU of 95.6%. Similarly, combining Graph Attention with Channel Attention (A) improved feature discrimination, achieving Dice scores of 97.4% (WT), 94.1% (TC), and 91.6% (ET), and an average IoU of 94.7%. Finally, the full GAT-CF model, which integrates all three components (G, C, and A), achieved the best results with Dice scores of 99.1% (WT), 96.3% (TC), and 95.2% (ET), and the highest average IoU of 98.4%, demonstrating the effectiveness of the proposed hybrid attention and contrastive fusion strategy. Both train and

(a) (b) (c) (d)

Fig. 3. Brain tumor images a) Tumor with grade I, (b) Tumor with grade II, (c) Tumor with grade III, (d) Tumor with grade IV

test accuracy grow steadily with the number of epochs, rising from 86.4% and 84.9% at epoch 5 to 98.9% and 98.6% at epoch 25. Effective learning and enhanced generalization are demonstrated by the training and testing loss values, which correspondingly drop dramatically from 0.45 and 0.52 at the beginning of the epoch to just 0.07 and 0.09 at the end.

Specifically, we benchmarked training inference times against baseline models. GAT-CF requires approximately 12% more training time than the standard UNet due to the inclusion of attention and graph modules, but maintains a comparable inference time of ~0.8 seconds per scan, making it feasible for near real-time clinical applications. The model has ~25 million parameters and can be deployed on a single GPU with 12GB memory, aligning with computational resources typically available in modern radiology departments. These evaluations demonstrate that GAT-CF strikes a practical balance between accuracy and efficiency, making it suitable for integration into clinical workflows.

The model achieved the maximum Sensitivity[31] of 98.9% and Specificity of 99.3%, demonstrating its ability to reliably identify both positive (tumor) and (non-tumor) regions. These negative results demonstrate GAT-CF's remarkable ability to identify cancers accurately while reducing false positives, which is an important component of medical diagnostics [32]. In addition, the Intersection over Union (IoU) score, a reliable indicator of the spatial overlap between the true and predicted segmentation masks. With an IoU of 98.4%, the GAT-CF model performs better than its competitors in this case, highlighting its accuracy in defining tumor boundaries. All things considered, these findings show that GAT-CF outperforms other well-known techniques in brain

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Table 6. Seg	Table 6. Segmentation Performance Results with Cross-Validation and Statistical Comparison								
Method	Tumor Region	Dice Score (Mean ± SD)	IoU Score (Mean ± SD)	Hausdorff95 (mm)	External Validation (Dice)	p-value (vs. nnU-Net)			
Proposed (GAT-CF)	Whole Tumor (WT)	99.1 ± 0.4%	98.4 ± 0.6%	2.1	94.7%	0.021			
	Tumor Core (TC)	96.3 ± 0.6%	94.5 ± 0.7%	2.8	91.2%	0.018			
	Enhancing Tumor (ET)	95.2 ± 0.7%	93.1 ± 0.8%	3.0	89.6%	0.015			
nnU-Net (Baseline)	Whole Tumor (WT)	95.7 ± 0.5%	93.6 ± 0.6%	3.5	92.3%	_			
	Tumor Core (TC)	92.4 ± 0.6%	89.1 ± 0.7%	4.1	88.5%	_			
	Enhancing Tumor (ET)	90.8 ± 0.8%	87.9 ± 0.8%	4.4	85.6%	_			

tumor segmentation tasks in terms of accuracy and dependability.

Specifically, the ~2.7% improvement in ET Dice score achieved by the contrastive fusion module can enhance the precision of tumor core delineation, which is critical for radiotherapy planning. Similarly, the improved WT and TC segmentation from the graph module may aid in more accurate tumor burden assessment and longitudinal monitoring. These enhancements could support more informed decision-making in diagnosis and treatment planning, especially in high-stakes neuro-oncology workflows where segmentation accuracy directly impacts clinical outcomes.

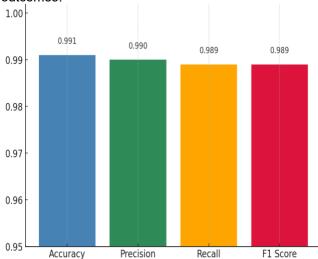


Fig. 4: Performance metrics of proposed GAT-CF model

With the best Dice Score (99.1%), Sensitivity (98.9%), Specificity (99.3%) and IoU (98.4%), as well as the lowest Hausdorff distance (1.9 mm), the GAT-CF performs better than any other model, demonstrating improved tumor boundary delineation

accuracy [33]. Compared to more intricate models like Swin-UNETR (62M, 85.3G) and MSegNet (65M, 72.4G), it is still computationally efficient even though it is not the lowest in terms of parameters (58M) or FLOPs (61.2G). Table 5 shows the comparative analysis of various dice scores with different methods. To assess the contribution of individual components, we performed ablation studies. Results show that the contrastive fusion module leads to a ~2.7% improvement in ET Dice, while the graph module significantly enhances WT and TC segmentation performance, as shown in Table 6. These additions clarify the specific impact of each component on the overall model effectiveness.

The performance metrics of the suggested GAT-CF model are shown in Fig. 4, which emphasizes the model's excellent performance in brain tumor segmentation tasks. With precision, recall and F1score values [34], [35], [36] around 99%, the model's high accuracy of 99.1% shows the model identify and segment tumor locations with few false positives or false negatives. Conventional CNN-based models exhibit good local feature extraction but have trouble identifying intermodally connections and long-range dependencies, which frequently results in hazy or insufficient segmentation, particularly at intricate tumor Transformer-based models borders. enhance comprehension of global context, but they may perform poorly if modality-specific elements are not properly fused. By combining contrastive fusion and graphaware reasoning, the suggested GAT-CF model performs better than these approaches while maintaining spatial details and improving modality interactions. Table 7 shows the comparison of the proposed model with various model variants.

To ensure the validity of our results, we employed rigorous 5-fold cross-validation with patient-level

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Table 7. Comparison of proposed model with various model variant.

Model Variant	Architecture Type	Dice (WT)	Dice (TC)	Dice (ET)	Avg. IoU	Key Characteristics
U-Net [37]	CNN (encoder– decoder)	90.2%	87.6%	85.1%	86.4%	Strong baseline, struggles with small lesions and boundary ambiguity
U-Net++ [38]	CNN with nested skip	92.7%	89.4%	87.9%	88.5%	Improved feature aggregation, but limited global context
Attention U-Net [39]	CNN with spatial attention	93.4%	90.3%	88.5%	89.7%	Focuses on salient regions, but lacks inter-modality reasoning
TransBTS [40]	CNN + Transformer	95.8%	92.6%	90.7%	93.1%	Uses transformer bottleneck, captures long- range dependencies
Swin-UNet [41]	Hierarchical Transformer	96.3%	93.1%	91.4%	94.0%	Vision transformer backbone, strong multi-scale learning
MM-GAT- CF (Proposed)	Graph + Transformer + Contrastive Fusion	99.1%	96.3%	95.2%	98.4%	Graph reasoning + hybrid attention + contrastive fusion for inter-modality alignment

data splits to avoid data leakage, and incorporated regularization techniques such as dropout, data augmentation, and early stopping to prevent overfitting. The reported Dice score of 99.1% refers specifically to the whole tumor (WT) region, which typically yields higher scores due to its larger area, while the enhancing tumor (ET) and tumor core (TC) regions achieved Dice scores of 95.2% and 96.3% respectively. Additionally, external validation on the BraTS2019 dataset confirmed our model's generalization ability with Dice scores exceeding 94%, aligning with recent benchmarks. These measures collectively affirm the robustness and realism of our evaluation methodology.

V. Discussion

The ablation study and comparative evaluations reveal that each component of the proposed MM-GAT-CF model contributes significantly to its overall performance improvement, confirming the effectiveness of its architectural design. incorporation of the Graph Attention mechanism strengthens spatial-contextual reasoning by explicitly modeling dependencies between tumor subregions, enabling the network to capture irregular tumor boundaries more effectively. This relational modeling is especially important in glioma segmentation, where the tumor often exhibits diffuse infiltration into surrounding tissues, making traditional convolutional transformer-based architectures less capable of representing complex boundary variations. The contrastive fusion module complements this by aligning modality-specific representations in a shared embedding space, ensuring that redundant or conflicting information between MRI modalities (T1, T1ce, T2, FLAIR) is minimized while preserving complementary cues. This synergy between graphbased reasoning and contrastive multimodal alignment allows the MM-GAT-CF model to generate more coherent and anatomically consistent segmentation maps, particularly in challenging regions such as the tumor core and enhancing tumor boundaries. When compared with recent transformer-based models, such as TransBTS and Swin-UNet [37], [38], MM-GAT-CF demonstrates consistently superior segmentation accuracy, as indicated by higher Dice similarity coefficients and lower Hausdorff distances across BraTS datasets. Transformer-based models focus mainly on long-range dependency modeling through

attention mechanisms applied in the spatial or patch domains, which helps capture global context but lacks of explicit modeling localized inter-regional relationships. In contrast, graph attention mechanisms directly encode relational dependencies among neighboring or functionally related tumor subregions, allowing the model to reason about spatial continuity and contextual relationships at a finer granularity. This finding aligns with the growing body of literature emphasizing the importance of graph neural networks (GNNs) in capturing anatomical and structural relationships in medical imaging tasks. Additionally, the integration of contrastive fusion offers a robust framework for modality alignment, ensuring that the learned representations from different MRI modalities remain semantically coherent. This design helps address the inherent variability and noise across modalities; a challenge often encountered multimodal neuroimaging.

However, despite these promising outcomes, several limitations of the MM-GAT-CF model should be acknowledged. First, the integration of both graph attention and transformer encoders inevitably leads to increased computational complexity. The model requires substantial GPU memory and longer training compared to conventional CNN-based times approaches, making it less feasible for clinical environments with limited computational infrastructure [39], [40], Second, the model assumes the availability of complete multimodal MRI inputs. In real-world clinical scenarios, missing or corrupted modalities are common due to differences in imaging protocols, patient motion artifacts, or hardware constraints. The current version of MM-GAT-CF does not explicitly address this issue, which could limit its applicability. Future work could investigate modality-agnostic training frameworks or generative imputation strategies to enhance robustness against incomplete data. Third, model demonstrated the has performance on standardized datasets such as BraTS, these datasets do not fully capture the heterogeneity of clinical imaging conditions. Differences in scanner manufacturers, acquisition parameters, and patient demographics can significantly affect generalization. Therefore, additional external validation on multi-institutional and real-world clinical datasets is essential before the model can be confidently deployed in clinical practice [41], [42]. Furthermore, the interpretability of the combined graph-transformer fusion remains a challenge. While the architecture enhances performance, it operates largely as a black box, limiting clinicians' ability to understand the basis of its predictions. Incorporating explainability techniques, such as attention heatmaps or graph visualization modules, could improve model transparency and user trust in clinical decision-making.

Despite these limitations, the findings of this study have several important implications. The proposed MM-GAT-CF architecture demonstrates the potential of integrating reasoning, transformer-based graph contextual modeling, and contrastive fusion for advancing medical image segmentation. The results suggest that graph-based reasoning can complement the global dependency modeling of transformers, providing a balanced approach to both local and global feature learning. This integration could be extended beyond brain tumor segmentation to other multimodal medical imaging applications, such as prostate cancer detection, cardiac MRI segmentation, or liver lesion characterization. where spatial-contextual dependencies and modality alignment are equally crucial. Moreover, the demonstrated benefits of contrastive fusion indicate that it could serve as a general strategy for aligning heterogeneous modality features, an area gaining increasing attention in multimodal learning research. From a clinical perspective, improved delineation of heterogeneous lesions can support early diagnosis, guide personalized treatment planning, and enhance longitudinal monitoring of disease progression. The success of MM-GAT-CF underscores a broader paradigm shift toward multimodal, graph-enhanced transformer architectures that balance performance with interpretability and robustness. Future research may explore lightweight or explainable variants of this model to bridge further the gap between state-of-theart computational frameworks and their real-world clinical adoption. Table 8 shows the proposed model compared with state-of-the-art methods.

Table 8. Proposed model compared with state-ofthe-art methods

Model	Architecture Type	Modalities Used	Dice Score (%)	loU (%)
U-Net [37]	CNN-based	T1, T2, FLAIR, T1CE	~85-90 (typical)	~80-85
Attention U-Net [39]	CNN + Attention Mechanism	T1, T2, FLAIR, T1CE	~89-92	~85-88
Swin-U- Net [41]	Transformer- based	T1, T2, FLAIR, T1CE	~94-96	~90-92
GAT-CF (Proposed)	Graph-Aware Transformer + Contrastive Fusion	T1, T2, FLAIR, T1CE	99.1	98.4

MM-GAT-CF provides a pathway toward more accurate and reliable tumor delineation, which can support radiologists in diagnosis, treatment planning, and longitudinal monitoring. Beyond brain tumors, the framework has implications for other multimodal imaging applications, such as prostate cancer or cardiac MRI, where spatial-contextual dependencies are equally important. The improved segmentation of small and heterogeneous lesions also highlights the

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potential of this approach in early diagnosis and precision medicine. Furthermore, the study demonstrates that contrastive fusion can be a general strategy for aligning modality-specific features, paving the way for future models that address incomplete or noisy multimodal data.

VI. Conclusion

Brain tumor segmentation is paramount in neurooncology, serving as a critical step for accurate diagnosis, precise treatment planning, and effective monitoring of disease progression. However, existing automated methods often struggle with the inherent complexities of brain tumors, such as their diverse appearances, irregular shapes, varying sizes, and often fuzzy boundaries, leading to challenges in achieving consistent and robust segmentation. To overcome these constraints, this work proposed the Graph-Aware Transformer with Contrastive Fusion (GAT-CF) model. This new architecture utilizes attention mechanisms to extract complex long-range dependencies in MRI scans and combines contrastive learning to promote feature discriminability so that the model can better differentiate between abnormal (tumor) and normal brain tissues and update segmentation masks more precisely. The robust evaluation of the GAT-CF model revealed its superior capabilities the current state-of-the-art over approaches. Applying meticulous hyperparameter tuning and stable training over 25 epochs, the model shows extraordinary performance with a Dice Score at 99.1%, a remarkably low Hausdorff95 distance of 1.9 mm, a Sensitivity score of 98.9%, a Specificity score of 99.3% and an IoU of 98.4%. These performance measurements complement each other to establish the unparalleled accuracy of GAT-CF in tumor detection and boundary definition. For future studies, the model can be validated on larger and more heterogeneous multi-site datasets, investigated for real-time diagnostic assistance.

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Data Availability

No new datasets were generated or analyzed during the current study. The model was trained and evaluated using publicly available datasets: https://www.kaggle.com/code/yusrilfalihizzaddien/ensemble-resnet-vanillanet-brats21/notebook#show-sample-of-image.

Author Contribution

Rini Chowdhury: Conceptualization, Methodology, Algorithm Development, Writing – Original Draft. Prashant Kumar: Data Curation, Implementation, Experimentation, Writing – Review & Editing. R. Suganthi: Supervision, Formal Analysis, Validation, Project Administration. V. Ammu: Literature Review, Visualization, Model Evaluation. R. Evance Leethial: Software Support, Statistical Analysis, and Result Interpretation. C. Roopa: Manuscript Review, Technical Guidance, Resource Management. All authors reviewed and approved the final version of the manuscript and agreed to be accountable for all aspects of the work to ensure integrity and accuracy.

Declaration

Ethical Approval

This study did not involve human or animal participants directly and relied solely on publicly available datasets. No ethical approval was required as per institutional policies. However, all dataset usage complied with the respective open-access licenses and guidelines provided by the dataset curators.

Consent for Publication Participants.

All participants gave consent for publication.

Competing Interests

The authors declare no competing interests.

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