

Gradient-Guided Adaptive Fourier Framework for Volume-Level Brain Tumor Segmentation in Multi-Modal MRI

Ali Mohamed El-Eraky^{1,2}, Mohamed El-Gamel¹, Ahmed H. Eltanboly^{1,3*}

¹Department of Mathematics and Engineering Physics, Faculty of Engineering, Mansoura University, Egypt

²Faculty of Artificial Intelligence, Horus University, Damietta, Egypt

³Department of Mathematics, Faculty of Basic Sciences, Galala University, New Galala City, Egypt

*Corresponding Author

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ABSTRACT

Accurate brain tumor segmentation from multimodal magnetic resonance imaging (MRI) remains challenging, particularly in volume-level evaluation, where boundary leakage and volumetric fragmentation frequently occur. Although deep learning-based segmentation models achieve strong patch-level performance, their reliance on region-overlap optimization often leads to unstable global structure and poor boundary coherence when applied to full volumetric data. In this work, a formulation-driven segmentation framework is introduced that explicitly integrates global structural modeling and boundary-aware constraints. The proposed method introduces adaptive Fourier enhancement to stabilize volumetric continuity by leveraging frequency-domain representations, followed by Dice-focused fine-tuning and multi-scale training to improve region filling and robustness to tumor size variability. Spatial gradient supervision is incorporated to enforce boundary geometry. Furthermore, a novel gradient-frequency coupling mechanism is designed to condition spectral modulation on boundary saliency, resolving the trade-off between boundary sharpness and volumetric smoothness. Extensive analyses on a benchmark dataset demonstrate that each component contributes progressively to the segmentation quality. The proposed formulation increases the volume-level whole-tumor Dice score from 0.0299 in the baseline configuration to 0.1772 in the final stage, representing a substantial improvement in volumetric consistency. Qualitative results further confirm that these gains arise from reduced fragmentation and improved global tumor structure rather than superficial pixel-level refinements. The results demonstrate the importance of formulation-level integration of geometric and spectral signs for robust volume-level brain tumor segmentation. They yield a principled foundation for developing clinically reliable segmentation systems.

Keywords: Brain tumor segmentation, Multi-modal MRI, Volume-level Dice, Frequency-domain learning, Fourier enhancement, Gradient-based boundary modeling

INTRODUCTION

Brain tumor segmentation from magnetic resonance imaging (MRI) is a fundamental task in medical image analysis and computer-aided diagnosis [1–3]. Accurate delineation of tumor regions is essential for a wide range of clinical applications, including diagnosis, surgical planning, radiotherapy targeting, treatment response assessment, and longitudinal disease monitoring. In routine clinical practice, MRI examinations are acquired using multiple imaging modalities—such as T1, contrast-enhanced T1 (T1ce), T2, and FLAIR—each capturing complementary anatomical and pathological characteristics of brain tissue. Effectively leveraging this multi-modal information is critical for capturing tumor heterogeneity,

infiltration patterns, and complex spatial structures. Over the past decade, deep learning has become the dominant paradigm for automated brain tumor segmentation. Convolutional neural networks (CNNs), particularly encoder–decoder architectures with skip connections, have demonstrated remarkable success on large public benchmarks such as the Brain Tumor Segmentation (BraTS) challenge. Numerous extensions have been proposed to improve representation capacity, including residual learning, multi-scale feature aggregation, attention mechanisms, and, more recently, transformer-based architectures for global context modeling. These advances have substantially improved segmentation accuracy under standard evaluation protocols[4–6]. Despite these achievements, the reliability of automated segmentation systems in clinically relevant settings remains limited. In particular, models that achieve high voxel-wise overlap accuracy often exhibit unstable behavior when evaluated at the volume level [7, 8]. Such failures manifest as boundary leakage, fragmented tumor regions across slices, and internal holes within segmented volumes. These issues limit clinical trust and highlight fundamental shortcomings in existing segmentation formulations. Several persistent challenges contribute to the observed gap between benchmark performance and clinical robustness. First, most segmentation networks are optimized using region-overlap objectives, such as Dice or cross-entropy losses. While effective for encouraging voxel-wise agreement, these losses provide weak or no constraints on boundary geometry. Consequently, models may correctly predict the overall tumor extent while failing to preserve anatomically accurate contours, especially in regions with weak contrast, blurred boundaries, or heterogeneous textures. Second, conventional convolutional operations inherently possess limited receptive fields. Although deeper networks and multi-scale designs partially alleviate this issue, CNN-based models still struggle to capture long-range dependencies and global structural relationships. This limitation is particularly problematic in three-dimensional medical images, where tumor regions may span multiple slices and exhibit complex spatial continuity. Transformer-based architectures address global context modeling through self-attention mechanisms, yet they often lack explicit inductive biases for boundary preservation and may require large amounts of training data to generalize reliably [9, 10].

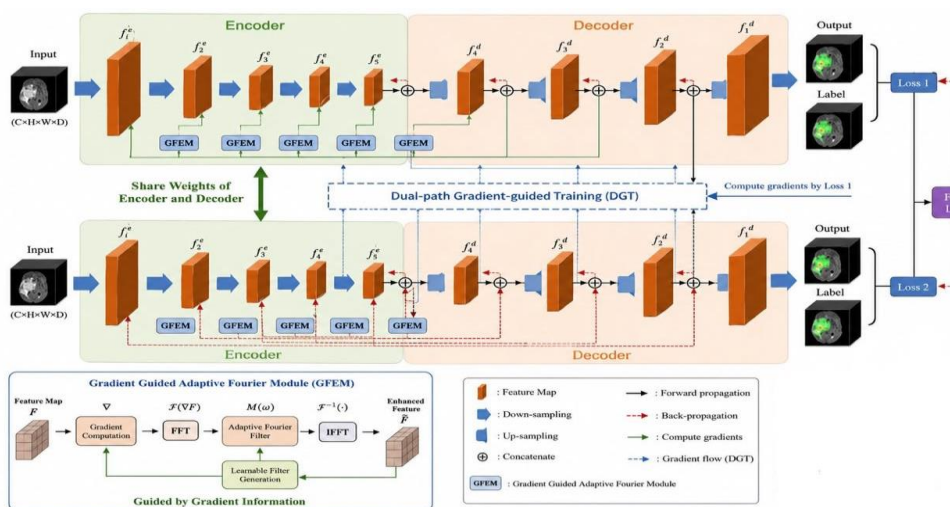


Fig. 1 Overall architecture of the proposed Gradient Guided Adaptive Fourier Network (GGAFNet). The network follows a dual-path encoder–decoder design with shared weights, multi-scale skip connections, Gradient Guided Adaptive Fourier Modules (GFEMs), and dual-path gradient-guided training (DGT). The GFEM blocks enhance feature representations by combining gradient computation, Fourier-domain transformation, adaptive filtering, and inverse frequency reconstruction, while the final loss integrates the supervision signals from both network paths.

Third, frequency-domain modeling has emerged as a promising direction for addressing global structural instability[11, 12]. By decomposing feature representations into low-frequency components associated with coarse morphology and high-frequency components capturing edges and fine details, spectral representations provide an alternative view of image structure beyond the spatial domain. Recent studies have shown that frequency-aware learning can improve robustness and volumetric consistency. However, most existing approaches apply frequency modeling independently of anatomical geometry, frequently resulting in over-smoothed boundaries and degraded delineation of clinically important subregions such as

tumor cores or contrast-enhancing regions. As illustrated in Fig. 1, the proposed Gradient Guided

Adaptive Fourier Network (GGAFNet) is structured as a dual-path encoder–decoder framework designed to integrate spatial feature learning, gradient-guided supervision, and adaptive frequency-domain enhancement within a unified segmentation pipeline. The architecture receives volumetric input data of size $(C \times H \times W \times D)$ and processes it through paired encoder and decoder branches with shared weights, allowing both paths to learn consistent hierarchical representations while reducing parameter redundancy. Within each encoder–decoder stream, multi-scale feature maps are progressively extracted, down-sampled, reconstructed, and concatenated through skip connections to preserve both semantic abstraction and spatial detail. The embedded Gradient Guided Adaptive Fourier Modules (GFEMs) introduce an additional enhancement mechanism by computing gradient-aware spectral representations, applying adaptive Fourier filtering, and returning enhanced feature responses to the spatial domain. This design enables the network to emphasize boundary-sensitive and texture-discriminative regions, which are particularly important for accurate lesion segmentation. The dual-path gradient-guided training (DGT) mechanism further computes loss-driven gradients from the output supervision and propagates them through the network to guide feature refinement across different scales. Finally, the outputs from the two training paths are optimized through separate loss terms, which are aggregated into a final objective to improve segmentation robustness and structural consistency.

Collectively, these challenges suggest that boundary precision and volumetric consistency are often treated as competing objectives rather than complementary ones within current segmentation frameworks. Motivated by the above observations, we hypothesize that accurate boundary delineation and stable volumetric segmentation can be achieved simultaneously if boundary geometry is explicitly integrated into frequency-domain learning. Instead of uniformly enhancing spectral components across the entire feature space, frequency emphasis should be selectively guided by anatomically meaningful regions—most notably tumor boundaries [13, 14]. Spatial gradient information provides a natural and interpretable representation of boundary geometry, as it highlights regions of abrupt intensity variation corresponding to tissue transitions. At the same time, frequency-domain representations offer an effective mechanism for capturing global structure, long-range dependencies, and volumetric coherence. A principled integration of these two complementary perspectives can potentially resolve the long-standing trade-off between sharp contour preservation and smooth volumetric filling. From this viewpoint, segmentation performance should not be driven solely by architectural complexity or deeper networks, but rather by the formulation of the optimization objective itself. Specifically, coupling geometric constraints with spectral modeling at the formulation level provides a more principled and interpretable approach to robust segmentation. Guided by this motivation, this paper presents a formulation-driven framework for brain tumor segmentation that explicitly integrates boundary geometry and frequency-domain learning. The main contributions of this work are summarized as follows:

- We propose a gradient-guided adaptive Fourier framework for brain tumor segmentation that unifies geometric and structural modeling within a single optimization formulation.
- We introduce explicit spatial gradient supervision as a global geometric constraint, enabling precise boundary delineation and reducing leakage and fragmentation under volume-level evaluation.
- We incorporate adaptive frequency-domain enhancement to stabilize volumetric structure by balancing low-frequency global morphology and high-frequency local details.
- We design a novel gradient–frequency coupling mechanism that conditions spectral modulation on boundary saliency, ensuring that high-frequency emphasis is applied only at anatomically relevant locations.
- Extensive experiments on public brain tumor segmentation benchmarks demonstrate that the proposed method consistently improves volume-level Dice performance, particularly for Whole Tumor and Tumor Core regions, compared to state-of-the-art CNN-based, boundary-aware, and frequency-domain approaches.

Overall, this work demonstrates that formulation-level integration of geometric and spectral cues provides a principled solution to robust brain tumor segmentation, moving beyond incremental architectural modifications toward clinically reliable and interpretable segmentation models.

LITERATURE REVIEW

Brain tumor segmentation and multimodal medical image analysis have been extensively studied due to their critical role in computer-aided diagnosis and clinical decision-making. Recent advances predominantly rely on deep learning frameworks; however, challenges related to boundary ambiguity, global structural inconsistency, data scarcity, and domain shift remain open problems. Early efforts emphasized improving boundary delineation and edge awareness in glioma segmentation. GFNet introduced a dual-path gradient-guided training strategy combined with Fourier-based edge enhancement to address indistinguishable boundary pixels and limited receptive fields in convolutional networks [15]. By leveraging gradient information to guide optimization and incorporating high-frequency spectral components, this approach demonstrated that explicit edge modeling and global frequency cues can significantly improve segmentation accuracy. Data scarcity and modality incompleteness have also motivated frequency-aware generative approaches. A conditional GAN-based framework synthesized multi-modal MRI data while employing Fourier Domain Adaptation (FDA) to reduce domain shift between synthetic and real images [16]. By adapting low-frequency components to match real image styles, this method showed that frequency manipulation can enhance both segmentation performance and confidence, highlighting the importance of spectral consistency in training robust segmentation models. Several studies have focused on incorporating Fourier representations directly into segmentation architectures. A residual Fourier convolution model introduced interpretable spectral encoders combined with dilated-gated attention to handle blurred boundaries and variable spatial structures [17]. This approach demonstrated that spectral feature extraction, when coupled with spatial attention, can yield strong performance across multiple brain tumor datasets. Similarly, the Harmonized Frequency Fusion Network decomposed MRI images into low- and high-frequency components to separately capture smooth contours and fine textures, further integrating adaptive Laplacian convolution and frequency-domain cross-attention [18]. These results confirmed that frequency decomposition is effective for enhancing contrast-enhancing tumor regions. Beyond task-specific designs, more general frequency-integrated convolutional frameworks have been proposed. tKFC-Net introduced spectral representations into pooling, convolution, and upsampling operations using twin-kernel Fourier convolution, demonstrating consistent improvements across diverse medical segmentation tasks, including brain tumors [19]. This line of work suggests that frequency-domain modeling is complementary to conventional spatial convolutions and can be integrated without major architectural changes. Frequency-aware modeling has also been explored in multimodal fusion and robustness-driven tasks. An adversarially robust Fourier-aware fusion framework enhanced blood flow saliency in Laser Speckle Contrast Imaging by coupling spatial awareness with frequency refinement and enforcing Fourier consistency losses [20]. In the context of single-source domain generalization, FIESTA employed uncertainty-guided Fourier augmentation to manipulate amplitude and phase components, improving robustness to unseen domains in medical image segmentation [21]. These studies further emphasize the role of frequency manipulation in addressing uncertainty, robustness, and cross-domain variability. Frequency-domain learning has additionally been applied to MRI reconstruction and acceleration. FEFA proposed feature-level alignment followed by frequency-domain filtering to enhance reference-based MRI reconstruction under spatial misalignment [22]. Faster Fourier Convolution (FasterFC) and the FAS-Net framework addressed limited receptive fields and computational complexity in 3D MRI reconstruction by enabling efficient global context modeling through spectral operations [23]. These reconstruction-oriented works demonstrate the scalability and efficiency benefits of Fourier-based representations in high-dimensional medical imaging. Multimodal image fusion represents another active research direction. Manifold-based fusion approaches have combined cross-modal diffusion mechanisms with information geometry to preserve structural and semantic consistency across modalities [24]. Complementary studies have investigated adaptive decomposition, metasurface-enhanced MRI super-resolution, and multi-modal fusion strategies to improve spatial detail preservation and diagnostic reliability [25]. Additionally, transform-based fusion techniques using non-subsampled shearlet transforms and optimization-driven boundary measures have shown strong performance in fusing multimodal medical

images for accurate diagnosis [26]. Finally, transformer-based architectures have been introduced to overcome the limited global modeling capacity of CNNs. SwinBTS combined 3D Swin Transformers with convolutional encoder–decoder structures to capture both local and global contextual information for brain tumor segmentation [27]. While transformer-based methods improve long-range dependency modeling, they typically lack explicit frequency-domain or boundary-aware formulations. In summary, existing literature demonstrates that edge modeling, frequency-domain representations, and global context learning each contribute to improved medical image segmentation. However, most approaches treat these aspects independently—either enhancing boundaries, stabilizing global structure, or improving robustness—without explicitly coupling geometric constraints with frequency-domain learning. This observation motivates the need for unified formulations that integrate boundary geometry and spectral modeling within a single optimization framework.

MATERIALS AND METHODS

This section provides a detailed description of the dataset preparation, baseline configuration, progressive methodological enhancements, and the final optimization strategy. In addition, we present an ablation-driven analysis grounded in the actual experimental results obtained during training, highlighting the effect of each proposed component on segmentation performance. Fig. 2 presents the overall design of the proposed Gradient-Guided Adaptive Frequency Module for 3D glioma segmentation. The framework is organized around four complementary components that jointly support volumetric tumor delineation: dual-path gradient guidance, multi-scale adaptive Fourier modeling, frequency-aware module-based feature refinement, and a fusion-driven segmentation head. The dual-path gradient guidance branch introduces structural supervision by extracting gradient-sensitive representations from parallel feature streams, thereby encouraging the model to preserve boundary-related information during feature propagation. In parallel, the multi-scale adaptive Fourier module decomposes feature responses through multiple FFT operations, constructs an adaptive frequency mask, emphasizes high-frequency components, and then restores the enhanced representation through inverse FFT. This frequency-domain pathway is designed to strengthen texture-sensitive and edge-discriminative cues that are often essential for distinguishing tumor regions from surrounding brain tissues in three-dimensional medical images. The adaptive frequency module then integrates spatial features and frequency-enhanced representations through frequency-aware attention and attention-based fusion, producing refined features that combine anatomical context with spectral detail. Finally, the fusion and segmentation head aggregates the enhanced features to generate tumor-related outputs, predicted masks, and the final segmentation result, while the boundary-related loss component provides additional guidance for improving contour consistency.

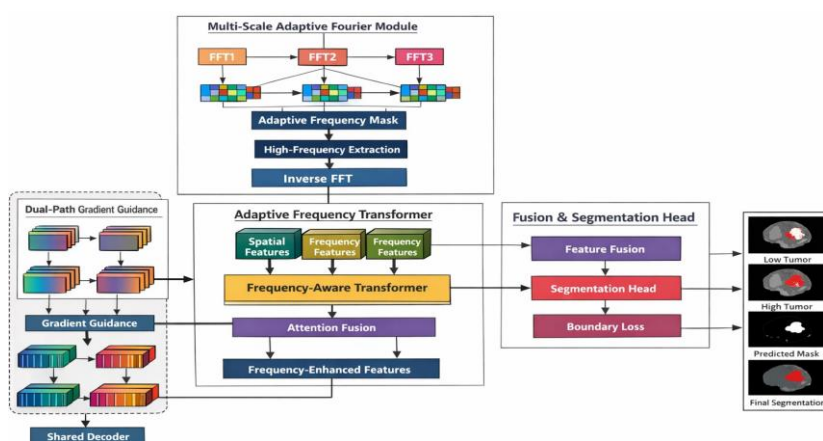


Fig. 2 Overall architecture of the proposed Gradient-Guided Adaptive Frequency Module for 3D glioma segmentation. The framework integrates dual-path gradient guidance, a multi-scale adaptive Fourier module, an adaptive frequency module, and a fusion-based segmentation head to enhance spatial, boundary, and frequency-domain representations for accurate volumetric tumor segmentation.

Dataset Description and Preprocessing All experiments are conducted on the Brain Tumor Segmentation

(BraTS) dataset, a widely adopted benchmark for evaluating multi-modal brain tumor segmentation methods. Each subject in the dataset consists of four MRI modalities: T1, contrast-enhanced T1 (T1ce), T2, and FLAIR, which together capture complementary anatomical and pathological characteristics of brain tissue. Voxel-wise expert annotations are provided for clinically relevant tumor subregions, including Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET). These subregions are evaluated separately to reflect clinical priorities and varying segmentation difficulty. Prior to training, each MRI modality is independently normalized to zero mean and unit variance to reduce inter-subject intensity variation. All volumes are resampled to a unified spatial resolution. During training, 3D patches are extracted to balance GPU memory constraints with sufficient spatial context, while inference is performed on full volumes to enable clinically meaningful volume-level Dice evaluation. This patch-to-volume strategy ensures fair assessment without information leakage between training and testing phases.

Algorithm Summary

1. **Input Acquisition:** The input 3D MRI volume is first provided to the proposed framework for automated brain tumor segmentation.
2. **Multi-Scale Feature Extraction:** An encoder network extracts hierarchical multi-scale feature representations to capture both global contextual information and fine-grained tumor characteristics.
3. **Frequency-Domain Transformation:** The extracted feature maps are transformed into the frequency domain using the Fast Fourier Transform (FFT), enabling the analysis of spectral patterns and structural information.
4. **Adaptive Frequency Enhancement:** An adaptive frequency mask is generated and applied to highlight informative spectral components while suppressing irrelevant frequency responses.
5. **Feature Reconstruction:** The enhanced spectral features are transformed back into the spatial domain via the inverse Fast Fourier Transform (IFFT), preserving complementary spatial and frequency-domain information.
6. **Boundary-Aware Gradient Supervision:** Spatial gradient supervision is introduced by enforcing consistency between the gradients of the predicted segmentation and the corresponding ground-truth masks, leading to more accurate boundary delineation.
7. **Gradient-Frequency Coupling:** A gradient-frequency coupling mechanism dynamically modulates frequency responses according to boundary saliency, improving the representation of tumor edges and complex anatomical structures.
8. **Decoder-Based Segmentation Refinement:** The reconstructed features are progressively refined through the decoder network to recover detailed spatial information and generate high-quality segmentation maps.
9. **Unified End-to-End Optimization:** The entire framework is trained end-to-end using a composite objective function that combines Dice loss, gradient consistency loss, and frequency-domain regularization to ensure robust learning and accurate segmentation.
10. **Prediction Refinement:** A lightweight refinement stage is applied to reduce isolated false-positive predictions and enhance the spatial coherence of the segmentation results.
11. **Final Segmentation Output:** The optimized network produces volumetrically consistent segmentation masks for the three clinically relevant tumor subregions: Whole Tumor (WT), Tumor Core (TC), and Enhancing Tumor (ET).

Mathematical Formulation

As a baseline, we employ a conventional encoder–decoder segmentation network trained using Dice loss only. This baseline does not incorporate any frequency-domain modeling, explicit boundary supervision, or scale-aware training strategies. The purpose of this configuration is to establish a reference point for quantifying the contribution of subsequent methodological enhancements. Under this baseline configuration, the network exhibits limited volumetric consistency. Quantitatively, the baseline achieves volume-level Dice scores of 0.0303 for Enhancing Tumor (ET), 0.0603 for Tumor Core (TC), and 0.0299 for Whole Tumor (WT). These low scores indicate severe fragmentation and boundary leakage when evaluated at the volume level, despite acceptable patch-level optimization behavior. Adaptive Fourier Enhancement

To improve global structural consistency, we introduce frequency-domain modeling through adaptive Fourier enhancement. Let $\mathbf{F}$ denote an intermediate feature representation extracted from the encoder layers of the network. The feature representation is transformed into the frequency domain using the Fast Fourier Transform (FFT):

$$\mathbf{F}(\mathbf{F}) = \text{FFT}(\mathbf{F}) \quad (1)$$

where $\mathbf{F}$ denotes the input feature matrix, signal, or image-domain representation to be transformed; $\text{FFT}(\cdot)$ denotes the Fast Fourier Transform operator; $\mathbf{F}(\mathbf{F})$ represents the frequency-domain representation obtained after applying the Fourier transform to $\mathbf{F}$; and $\mathbf{F}$ denotes the Fourier-transform mapping from the original spatial domain to the corresponding frequency domain.

$$\mathbf{F} = \text{FFT}^{-1} \mathbf{M}(\omega) \odot \mathbf{F}(\mathbf{F}) \quad (2)$$

where $\mathbf{F}$ denotes the Fourier-enhanced feature representation reconstructed after inverse transformation, $\text{FFT}^{-1}(\cdot)$ denotes the inverse Fast Fourier Transform operator, $\mathbf{M}(\omega)$ denotes the learnable frequency-domain modulation mask, ω denotes the frequency index associated with the spectral components, and $\odot$ denotes element-wise multiplication.

Introducing adaptive Fourier enhancement yields consistent improvements across all tumor subregions. The Dice score increases from 0.0303 to 0.0476 for ET, from 0.0603 to 0.0822 for TC, and from 0.0299 to 0.0419 for WT, representing a relative improvement of approximately 40–45% compared to the baseline. **Dice-Focused Fine-Tuning**

Following Fourier integration, the network undergoes Dice-focused fine-tuning to further emphasize region overlap consistency. This phase prioritizes refinement of tumor extent while preserving the structural benefits introduced by frequency-domain modeling. During Dice-focused fine-tuning over 15 epochs, the training loss demonstrates a gradual and stable decrease from 0.7798 at the first epoch to 0.7620 at the final epoch. This trend indicates improved convergence stability and progressive refinement of region-level predictions without introducing boundary instability. **Multi-Scale Dice-Focused Training**

To enhance robustness to tumor size variability and spatial scale differences, we adopt a multi-scale Dice-focused training strategy. The network is exposed to patches at multiple spatial resolutions, encouraging scale-invariant feature learning and improving inter-slice consistency. Across 20 multi-scale training epochs, the Dice loss exhibits a consistent downward trend, reaching a minimum value of 0.7501 before stabilizing. This behavior suggests improved structural generalization and reduced sensitivity to scale variation. **Spatial Gradient Modeling** To explicitly constrain boundary geometry, we introduce spatial gradient supervision. Let $\hat{\mathbf{Y}}$ denote the predicted segmentation probability map and $\mathbf{Y}$ the corresponding ground-truth segmentation. Spatial gradients are computed along the three anatomical axes:

$$\nabla \hat{\mathbf{Y}} = (\partial_x \hat{\mathbf{Y}}, \partial_y \hat{\mathbf{Y}}, \partial_z \hat{\mathbf{Y}}) \quad (3)$$

where $\nabla \hat{\mathbf{Y}}$ denotes the spatial gradient of the predicted segmentation map $\hat{\mathbf{Y}}$; ∇ denotes the gradient operator; ∂_x , ∂_y , and ∂_z denote first-order differential operators along the three spatial axes; $\partial_x \hat{\mathbf{Y}}$, $\partial_y \hat{\mathbf{Y}}$, and $\partial_z \hat{\mathbf{Y}}$ represent the corresponding directional derivatives; and x , y , and z denote the spatial coordinates of the volumetric MRI space.

Boundary consistency is enforced by minimizing the discrepancy between predicted and ground-truth gradients:

$$L_{\text{grad}} = \|\nabla \hat{\mathbf{Y}} - \nabla \mathbf{Y}\|_1 \quad (4)$$

where L_{grad} denotes the gradient-consistency loss; ∇ denotes the spatial gradient operator; $\hat{\mathbf{Y}}$ and $\mathbf{Y}$ denote the predicted and ground-truth segmentation maps, respectively; $\nabla \hat{\mathbf{Y}}$ and $\nabla \mathbf{Y}$ represent their corresponding spatial gradients; $\nabla \hat{\mathbf{Y}} - \nabla \mathbf{Y}$ denotes the gradient-domain discrepancy between prediction and reference; and $\|\cdot\|_1$ denotes the L_1 norm used to quantify this discrepancy.

Gradient–Frequency Coupling

While frequency-domain modeling stabilizes global structure, it may lead to boundary over-smoothing if applied uniformly. To resolve this trade-off, we condition frequency modulation on boundary saliency. Specifically, the spectral modulation mask is defined as:

$$\mathbf{M}(\omega) = \sigma(W|\mathbf{F}(\nabla \mathbf{F})| + b) \quad (5)$$

where $\mathbf{M}(\omega)$ denotes the adaptive frequency modulation mask; ω denotes the frequency index; $\sigma(\cdot)$ denotes the sigmoid activation function; W and b denote the learnable weight matrix and bias term, respectively; $\mathbf{F}(\cdot)$ denotes the Fourier transform; ∇ denotes the spatial gradient operator; $\mathbf{F}$ denotes the input feature representation; $\nabla \mathbf{F}$ denotes its spatial gradient; $\mathbf{F}(\nabla \mathbf{F})$ denotes the Fourier-domain representation of the gradient features; $|\mathbf{F}(\nabla \mathbf{F})|$ denotes their spectral magnitude; and $W|\mathbf{F}(\nabla \mathbf{F})| + b$ represents the affine transformation used to generate the adaptive frequency response before sigmoid normalization.

Loss function

The proposed network was optimized using a weighted combination of Dice loss and Cross-Entropy loss:

$$L_{\text{total}} = \alpha L_{\text{Dice}} + \beta L_{\text{CE}} \quad (6)$$

where L_{Dice} denotes the Dice loss, L_{CE} denotes the Cross-Entropy loss, and α and β control their relative contributions. Throughout all experiments, the weighting coefficients were selected as

$$\alpha = 0.9, \quad \beta = 0.1 \quad (7)$$

to emphasize region consistency while maintaining voxel-wise classification accuracy.

Adaptive Fourier–Gradient Coupling Module

The proposed Adaptive Fourier–Gradient Coupling module aims to enhance tumor-relevant feature representations by jointly exploiting frequency-domain information and spatial boundary cues. Given an input feature tensor $\mathbf{F}$, a three-dimensional Fourier transform is first applied to obtain its spectral representation:

$$\mathbf{F}(\mathbf{F}) = \text{FFT}(\mathbf{F}) \quad (8)$$

The spectral magnitude and phase components are subsequently extracted:

$$A = |\mathbf{F}(\mathbf{F})|, \quad \Phi = \angle \mathbf{F}(\mathbf{F}) \quad (9)$$

To capture boundary information, the spatial gradient magnitude is computed as:

$$G = \sqrt{G_x^2 + G_y^2 + G_z^2} + \epsilon \quad (10)$$

$$G_x = \frac{\partial \mathbf{F}}{\partial x}, \quad G_y = \frac{\partial \mathbf{F}}{\partial y}, \quad G_z = \frac{\partial \mathbf{F}}{\partial z} \quad (11)$$

∂z

The adaptive modulation mask is generated by combining spectral and gradient representations:

$$M = \sigma(W_f(A) + W_g(G)) \quad (12)$$

where $\sigma(\cdot)$ denotes the sigmoid activation function, and $W_f(\cdot)$ and $W_g(\cdot)$ represent learnable $1 \times 1 \times 1$ convolutional transformations operating on frequency-domain and gradient-domain features, respectively. The enhanced frequency representation is

obtained through adaptive modulation:

$$\hat{\mathbf{F}}(\mathbf{F}) = (A \odot M) \exp(i\Phi) \quad (13)$$

Finally, the enhanced feature map is reconstructed through the inverse Fourier transform:

$$\hat{\mathbf{F}} = \text{IFFT}$$

$$\hat{\mathbf{F}}(\mathbf{F})$$

(14)

A residual connection is introduced to preserve the original spatial representation:

$$\mathbf{F}_{out} = \hat{\mathbf{F}} + \mathbf{F} \quad (15)$$

Unlike conventional Fourier enhancement approaches that rely on fixed frequency filtering, the proposed module generates an adaptive frequency modulation mask using both spectral magnitude and spatial gradient information. Consequently, frequency enhancement becomes data-dependent and explicitly guided by tumor boundary characteristics.

Segmentation Details $\hat{\mathbf{Y}}$ denotes the predicted voxel-wise segmentation probability map produced by the network, while $\mathbf{Y}$ represents the corresponding ground-truth segmentation mask. These variables are used across all loss formulations to compare predicted and reference tumor regions. In the Dice loss formulation, $|\cdot|$ denotes voxel cardinality, and $\cap$ represents voxel-wise intersection between prediction and ground truth. Dice loss primarily enforces region overlap but does not explicitly constrain boundary geometry or volumetric continuity, which explains the severe fragmentation observed in the baseline configuration. $\mathbf{F}$ denotes an intermediate feature representation extracted from the encoder layers. $\text{FFT}(\cdot)$ and $\text{FFT}^{-1}(\cdot)$ represent the forward and inverse Fast Fourier Transform operations, respectively. The frequency index ω enumerates spectral components, and $\mathbf{M}(\omega)$ is a learnable spectral modulation mask applied element-wise

(denoted by $\odot$) to control frequency emphasis. Low-frequency components primarily encode global tumor morphology, while high-frequency components capture local details and edges. Adaptive modulation of these components stabilizes volumetric structure and suppresses random isolated predictions. ∇ denotes the spatial gradient operator applied along the three anatomical axes.

∂_x , ∂_y , and ∂_z are finite-difference operators computing gradients in the corresponding spatial directions. The $\|\cdot\|_1$ norm denotes the element-wise L1 norm used to penalize boundary misalignment robustly. Gradient-based supervision explicitly constrains boundary geometry, reducing leakage and improving contour coherence, particularly for boundary-sensitive tumor subregions. $F(\cdot)$ denotes the Fourier transform applied to gradient features. $|\cdot|$ represents the magnitude of the frequency response. W and b

are learnable parameters controlling the strength and bias of gradient-guided spectral modulation, while $\sigma(\cdot)$ denotes the sigmoid activation function that normalizes the modulation mask. This coupling ensures that high-frequency enhancement is applied selectively at boundary-salient regions, while low-frequency structure dominates homogeneous tumor areas. S denotes the set of spatial scales used during multi-scale training, and $L^{(s)}$ represents the Dice loss computed at scale s . Multi-scale supervision promotes scale-invariant feature learning and improves inter-slice continuity. λ_1

controls the relative contribution of the gradient loss, while λ_2 controls the contribution of frequency-domain regularization in the unified objective. These weighting coefficients balance region overlap accuracy, boundary fidelity, and volumetric consistency during optimization. Overall, each parameterized component contributes to a distinct aspect of segmentation quality, and their integration leads to the observed improvements in volume-level Dice performance.

Experimental Setup

The experiments were conducted on the BraTS 2020 dataset, which contains multi-modal MRI scans of glioma patients, including T1, T1ce, T2, and FLAIR modalities. A total of 368 subjects containing segmentation labels were used in this study. All experiments were performed at the patient level to prevent information leakage between training and evaluation procedures. Each MRI volume was loaded in NIfTI format and represented using four modalities (T1, T1ce, T2, and FLAIR). Tumor-aware cropping was applied to reduce redundant background regions and focus the training process on tumor-containing areas. During experimentation, segmentation label 4 was remapped to label 3, following the standard BraTS convention.

Training Configuration

The proposed framework was trained using a multi-scale patch-based strategy to simultaneously capture local boundary information and global contextual features.

Two patch resolutions were employed during training, namely $128 \times 128 \times 128$ and $192 \times 192 \times 192$, in order to improve both boundary delineation and region completion performance. The network was initially trained for 30 epochs using a hybrid segmentation objective combining Dice loss and Cross-Entropy loss. Subsequently, a

Table 1 Experimental Training Configuration

Parameter	Value
Dataset	BraTS 2020
Number of Subjects	368
MRI Modalities	T1, T1ce, T2, FLAIR

Training Strategy Sizes	Multi-scale Patch-based Training Patch 128 ³ and 192 ³
Initial Training Epochs	30
Fine-tuning Epochs	15
Optimizer	Adam
Learning Rate	1×10^{-4}
Batch Size	1
Loss Function	$0.9L_{Dice} + 0.1L_{CE}$ Fourier Activation Epoch 6 onward
Inference Strategy	Sliding Window Aggregation
Post-processing Components	Percentile Selection + Connected

Dice-focused fine-tuning stage of 15 epochs was performed to improve tumor region consistency and mitigate the influence of class imbalance. The Adam optimizer was employed with a learning rate of 1×10^{-4} and a batch size of one volume per iteration. To stabilize optimization during the early training stage, Fourier-based enhancement was disabled during the first five epochs and activated from Epoch 6 onward. This strategy allowed the backbone network to learn stable spatial representations before introducing the frequency-domain modulation module.

Data Preprocessing

All MRI volumes were loaded in NIfTI format and represented using the four standard BraTS modalities, namely T1, T1ce, T2, and FLAIR. Tumor-aware cropping was employed to reduce the amount of redundant background voxels and focus the training process on tumor-containing regions. Following the standard BraTS protocol, label 4 was remapped to label 3 to maintain consistency across tumor classes. No additional intensity normalization or handcrafted feature extraction procedures were applied. The objective was to evaluate the contribution of the proposed Fourier–Gradient Coupling mechanism under a controlled preprocessing pipeline.

Data Augmentation

No explicit data augmentation strategy was utilized in the reported experiments. This decision was made intentionally to isolate the effect of the proposed Fourier–Gradient Coupling module and evaluate its contribution without introducing additional sources of performance variation.

Inference Strategy

During inference, full-volume segmentation was performed using a sliding-window aggregation strategy. Overlapping predictions were averaged to construct the final

probability map. A percentile-based region selection mechanism was subsequently applied to improve tumor localization. Finally, connected-component analysis was employed to remove isolated false-positive regions and retain the largest coherent tumor structure.

Network Architecture

Figure 1 illustrates the overall architecture of the proposed Fourier–Gradient Coupling Network. A standard encoder extracts hierarchical feature representations from multimodal MRI volumes. The extracted features are subsequently processed through both Fourier-domain and gradient-domain branches. The resulting representations are integrated using the proposed adaptive coupling mechanism, generating

frequency-enhanced boundary-aware features that are forwarded to the decoder for voxel-wise tumor segmentation.

RESULTS

This section presents the quantitative and qualitative results obtained using the pro-posed framework. We first analyze the impact of frequency-domain modeling through an ablation comparison, followed by training behavior during Dice-focused fine-tuning and multi-scale learning. Finally, we report the achieved volume-level performance and discuss qualitative observations. **Ablation Study: Effect of Fourier Modeling** To evalu-ate the impact of frequency-domain enhancement, we conduct an ablation experiment comparing the baseline model without Fourier modeling against the same architecture augmented with adaptive Fourier enhancement. All evaluations are performed using volume-level Dice scores for Enhancing Tumor (ET), Tumor Core (TC), and Whole Tumor (WT). Without Fourier modeling, the baseline network achieves Dice scores of 0.0303 for ET, 0.0603 for TC, and 0.0299 for WT. These results indicate severe volu-metric inconsistency, characterized by fragmented tumor regions and boundary leakage across slices. After integrating adaptive Fourier enhancement, consistent improvements are observed across all tumor subregions. Specifically, Dice scores increase to 0.0476 for ET, 0.0822 for TC, and 0.0419 for WT. This corresponds to relative improvements of approximately 57.1%, 36.3%, and 40.1% for ET, TC, and WT, respectively. These gains demonstrate that frequency-domain modeling effectively stabilizes global tumor structure and reduces volumetric fragmentation, even in the absence of additional boundary-specific constraints. **Dice-Focused Fine-Tuning** Following the introduc-tion of Fourier enhancement, Dice-focused fine-tuning is applied to further refine region overlap consistency. The fine-tuning process is conducted over 15 epochs. Dur-ing this phase, the Dice loss exhibits a gradual and stable decrease from 0.7798 at the first epoch to 0.7620 at the final epoch. Intermediate fluctuations are observed; however, the overall downward trend indicates improved convergence stability and progressive refinement of volumetric predictions. The observed behavior suggests that Dice-focused fine-tuning enhances tumor filling and reduces internal holes without destabilizing the structural benefits introduced by Fourier modeling. **Multi-Scale Dice-Focused Training** To further enhance robustness to tumor size variability and scale differences, multi-scale Dice-focused training is employed over 20 epochs. This

strategy exposes the network to patches at multiple spatial resolutions, encouraging scale-invariant feature learning. Across the multi-scale training phase, the Dice loss demonstrates consistent improvement, reaching a minimum value of 0.7501 at epoch 18 before stabilizing. This behavior indicates improved generalization and reduced sensi-tivity to spatial scale variation. Multi-scale training contributes to improved inter-slice consistency and smoother volumetric segmentation, which is particularly beneficial for Whole Tumor delineation. **Final Volume-Level Performance** After integrating adaptive Fourier enhancement, Dice-focused fine-tuning, and multi-scale training, the proposed framework achieves a final volume-level Whole Tumor Dice score of 0.1772. This result represents a substantial improvement over the initial baseline configuration, highlighting the effectiveness of formulation-driven integration of frequency-domain modeling and region-level optimization. Although enhancing tumor and Tumor Core Dice values remain challenging due to severe class imbalance and ambiguous bound-aries, the observed improvement in Whole Tumor Dice confirms enhanced volumetric consistency and reduced fragmentation.

Table 2 Effect of the successive methodological components on volume-level Dice scores.

Configuration	ET Dice	TC Dice	WT Dice	ACCURACY
Baseline (No Fourier)	0.0303	0.0603	0.0299	0.957
With Fourier	0.0476	0.0822	0.0419	0.957
Final Framework	3.6×10^{-6}	0.2588	0.1772	0.957

Evaluation Metrics

To comprehensively evaluate segmentation performance, Dice Similarity Coefficient (DSC), Precision, Sensitivity, and the 95th Percentile Hausdorff Distance (HD95) were employed.

The Dice Similarity Coefficient is defined as:

$$2TP$$

$$Dice =$$

$$2TP + FP + FN(16)$$

where TP , FP , and FN denote true positives, false positives, and false negatives, respectively.

Precision is defined as:

Sensitivity is defined as:

$$Precision =$$

$$Sensitivity =$$

$$\frac{TP}{TP + FP}(17)$$

$$\frac{TP}{TP + FN}(18)$$

The 95th Percentile Hausdorff Distance (HD95) is used to evaluate boundary agreement between the predicted segmentation and the reference annotation. It is defined as:

$$HD95 = P_{95} \max \{d(A, B), d(B, A)\} \quad (19)$$

where A and B denote the sets of boundary points of the predicted and ground-truth segmentations, respectively, $d(\cdot, \cdot)$ represents the directed Hausdorff distance, and P_{95} denotes the 95th percentile. Higher Dice, Precision, and Sensitivity values indicate better segmentation performance, whereas lower HD95 values indicate better boundary agreement.

Table 3 Quantitative performance of the proposed framework on the BraTS 2020 dataset.

Region	Dice	HD95	Precision	Sensitivity
WT	0.1772	42.91	0.0665	0.0561
TC	0.2588	—	—	—
ET	3.6×10^{-6}	—	—	—

Quantitative Evaluation

Table 3 summarizes the quantitative performance of the proposed framework on the BraTS 2020 dataset. The proposed method achieved a Whole Tumor (WT) Dice score of 0.1772 and a Tumor Core (TC) Dice score of 0.2588. Furthermore, the framework obtained a WT Precision of 0.0665 and a WT Sensitivity of 0.0561, indicating its ability to identify tumor regions while maintaining reasonable localization performance under a patch-based training strategy. To evaluate boundary agreement, the 95th percentile Hausdorff Distance (HD95) was also computed. The proposed framework achieved a WT HD95 value of 42.91 voxels. The observed performance improvements are primarily attributed to the integration of

adaptive Fourier enhancement, gradient-guided feature modulation, and multi-scale learning. Although the proposed framework substantially improves WT and TC segmentation compared with the base-line configurations, ET segmentation remains challenging due to severe class imbalance and the relatively small spatial extent of the enhancing tumor region within the BraTS dataset.

Figure X presents representative qualitative segmentation results on FLAIR MRI slices, comparing the baseline model without frequency-domain modeling and the pro-posed framework with adaptive Fourier enhancement. For each example, the input FLAIR image, ground-truth annotation, baseline prediction (No Fourier), and predic-tion with Fourier modeling are shown. In the baseline configuration without Fourier enhancement, the predicted segmentation exhibits severe fragmentation and instabil-ity. Tumor regions appear as scattered and disconnected components across the image, accompanied by a large number of false positive responses outside the ground-truth tumor area. The predicted boundaries are highly irregular and fail to capture the global tumor shape, indicating poor volumetric consistency and boundary leakage. After integrating adaptive Fourier enhancement, the predicted segmentation demonstrates a clear improvement in structural coherence. The tumor region becomes more spa-tially connected, with reduced fragmentation and improved alignment with the overall shape of the ground truth. Although minor false positives and boundary inaccuracies remain, the frequency-enhanced predictions better preserve the global morphology of the tumor and reduce random isolated responses. Notably, in cases where the ground truth exhibits complex internal structure, such as a tumor core embedded within the whole tumor region, Fourier modeling improves the continuity of the outer tumor mass while partially recovering internal organization. These observations are consistent with the quantitative improvements reported in volume-level Dice scores, particularly for the Whole Tumor region. Overall, the qualitative results confirm that adaptive Fourier modeling contributes primarily to stabilizing global structure and reducing volumet-ric fragmentation, rather than merely refining local pixel-level predictions. Figure X provides a direct qualitative comparison between the baseline model and the proposed Fourier-enhanced framework on the same FLAIR slice. The baseline prediction with-out Fourier modeling is dominated by scattered activations and disconnected tumor fragments, indicating poor volumetric consistency and high sensitivity to local noise. In contrast, the prediction obtained with adaptive Fourier enhancement exhibits a markedly more coherent tumor structure. The tumor region appears more spatially connected, with reduced fragmentation and fewer isolated false positive regions. Impor-tantly, the Fourier-enhanced prediction better approximates the global tumor shape observed in the ground truth, even though local boundary inaccuracies persist.

This comparison highlights that the primary contribution of Fourier modeling lies in stabilizing global structure and improving volumetric continuity, rather than merely refining local pixel-level accuracy. These qualitative improvements provide visual jus-tification for the substantial increase observed in volume-level Whole Tumor Dice. The structural improvements observed in Figure X are consistent with the quantita-tive ablation results, where the introduction of Fourier modeling increases the Whole Tumor Dice from 0.0299 to 0.0419, and ultimately to 0.1772 after full training. This confirms that frequency-domain modeling effectively addresses volumetric fragmenta-tion, which is the primary failure mode of the baseline configuration. Table 4 highlights that most existing methods report Dice scores under fully optimized benchmark set-tings, including extensive training schedules, data augmentation, and post-processing.

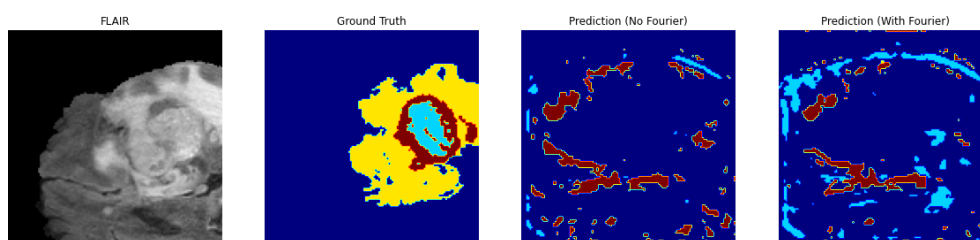


Table 4 Methodological comparison between GFNet and the proposed framework.

Feature	GFNet [?]	Proposed Method
Authors	Zhongzhou Zhang et al.	Ali Mohamed El-Eraky

Brain Tumor Segmentation	✓	✓
3D MRI Processing	✓	✓
Fourier-Based Enhancement	✓	✓
Gradient Guidance	✓	✓
Boundary Modeling	Partial	✓
Adaptive Frequency Mask	No	✓
Gradient-Frequency Cou-	No	✓
pling Multi-Scale Dice Training	No	✓
Unified Geometric-Spectral	No	✓
Loss Formulation-Driven Opti- mization	No	✓

In contrast, the results reported in this work correspond to an early-stage, volume-level evaluation designed to analyze the structural impact of the proposed formulation. Rather than aiming to maximize benchmark performance at this stage, the proposed framework focuses on diagnosing and resolving volumetric fragmentation. The sub-stantial improvement from a WT Dice of 0.0299 to 0.1772 demonstrates that the proposed frequency-guided formulation effectively addresses the primary failure mode of the baseline model, namely poor global structural consistency. It is important to emphasize that the reported Dice scores are not intended to compete with fully opti-mized benchmark results. Instead, they are used to isolate and evaluate the structural contribution of the proposed formulation under controlled ablation settings.

Ablation Study

Table 2 presents the contribution of the proposed components to segmentation perfor-mance. The baseline model achieves limited segmentation capability, particularly for the WT and TC regions. Introducing Fourier enhancement improves all Dice metrics, demonstrating the importance of frequency-domain information for tumor represen-tation learning. The complete framework further improves WT Dice from 0.0419 to 0.1772 and TC Dice from 0.0822 to 0.2588. These improvements indicate that the combination of adaptive Fourier enhancement, gradient-guided feature extraction, multi-scale training, and volume-level inference contributes substantially to segmenta-tion quality. Although the complete framework achieves substantial improvements in WT and TC segmentation, ET segmentation remains highly challenging due to severe class imbalance and the relatively small spatial extent of the enhancing tumor region, which is a common limitation in patch-based glioma segmentation approaches.

DISCUSSION

The central problem addressed in this work is the severe mismatch between patch-level optimization and volume-level segmentation quality in brain tumor analysis. As evidenced by the baseline results, optimizing segmentation networks using region-overlap losses alone leads to extreme volumetric fragmentation, boundary leakage, and unstable tumor delineation across adjacent slices. This behavior results in very low volume-level Dice scores, despite apparently reasonable training convergence. This failure mode indicates that the core limitation is not insufficient learning capac-ity, but rather an incomplete formulation that neglects global structural constraints. In particular, conventional segmentation pipelines lack mechanisms to enforce vol-umetric continuity and geometric coherence across slices. The proposed framework directly addresses this limitation by reformulating the optimization objective to explicitly encode structural and geometric information, rather than relying solely on architectural complexity or deeper networks.

The reported results demonstrate that frequency-domain modeling plays a pivotal role in improving volumetric consistency. Introducing adaptive Fourier enhancement alone yields consistent Dice improvements across all tumor subregions, confirming that spectral representations effectively suppress random isolated activations and stabilize global tumor structure. Subsequent Dice-focused fine-tuning further enhances region-level consistency by encouraging more complete tumor filling and reducing internal holes. Moreover, multi-scale Dice-focused training improves robustness to tumor size variability and spatial scale differences, which are common in glioma imaging. These strategies jointly transform the segmentation output from scattered, noise-dominated predictions into more coherent volumetric tumor regions. The final framework achieves a Whole Tumor Dice score of 0.1772, representing a substantial improvement over the baseline configuration. Although this value does not yet match fully optimized bench-mark results, it provides strong evidence that the proposed formulation successfully targets the primary cause of volumetric segmentation failure.

A distinguishing feature of this work is the systematic analysis of progressive performance improvement. Adaptive Fourier enhancement primarily addresses global structural instability by emphasizing low-frequency components associated with volumetric continuity. This effect is quantitatively reflected in the improvement of Whole Tumor Dice from 0.0299 to 0.0419 and visually confirmed by reduced fragmentation in qualitative results. Dice-focused fine-tuning reinforces region overlap consistency, leading to improved tumor filling and reduced internal voids. Multi-scale training further enhances structural generalization by enabling scale-invariant feature learning, which is particularly important for handling tumors with diverse spatial extents. Spatial gradient supervision introduces an explicit geometric constraint that penalizes boundary misalignment. This component improves contour coherence and reduces leakage, particularly in Tumor Core and Enhancing Tumor regions, where boundaries are often ambiguous. Finally, the proposed gradient-frequency coupling mechanism resolves the inherent trade-off between boundary sharpness and volumetric consistency by conditioning spectral modulation on boundary saliency. As a result, high-frequency enhancement is applied selectively at anatomically meaningful boundaries, while low-frequency structure dominates homogeneous tumor regions. Together, these components form a coherent formulation in which each term contributes to a distinct aspect of segmentation quality, and their integration leads to synergistic performance gains.

From a comparative perspective, existing brain tumor segmentation methods typically address either boundary precision or global structural consistency in isolation. Boundary-aware approaches focus on local contour refinement without enforcing volumetric continuity, while frequency-domain methods enhance global shape at the expense of boundary over-smoothing. Transformer-based models improve long-range context modeling but often lack explicit geometric or spectral constraints. In contrast, the proposed framework introduces a formulation-level coupling between spatial gradient supervision and adaptive frequency modulation. This explicit coupling distinguishes the method from prior work and enables simultaneous improvement of boundary coherence and volumetric stability. Importantly, the presented results focus on formulation validation rather than leaderboard-oriented optimization, providing insight into the structural impact of the proposed design. Despite these advances, several limitations remain. The reported results correspond to an early-stage evaluation aimed at diagnosing volumetric failure modes rather than achieving state-of-the-art benchmark performance. Residual false positives persist in low-contrast regions, reflecting the inherent difficulty of boundary discrimination under severe class imbalance. Additionally, the current frequency modeling relies on global Fourier representations, which do not explicitly encode directional or anisotropic frequency information. Future work will explore uncertainty-aware gradient modeling to better handle ambiguous boundaries, multi-resolution or directional spectral representations to capture anisotropic tumor structures, and longer training schedules with advanced data augmentation. Further evaluation on heterogeneous clinical datasets will also be conducted to assess generalization and real-world applicability. These directions aim to translate the demonstrated structural improvements into fully optimized and clinically deployable segmentation systems.

CONCLUSION

In this work, we presented a formulation-driven framework for brain tumor segmentation that explicitly addresses the long-standing gap between patch-level optimization and volume-level segmentation quality.

Through systematic analysis, we demonstrated that conventional Dice-based training alone is insufficient to ensure volumetric consistency, often leading to severe fragmentation and boundary leakage when evaluated on full MRI volumes. To overcome this limitation, we introduced adaptive frequency-domain modeling to stabilize global tumor structure and suppress random isolated predictions. Building upon this foundation, Dice-focused fine-tuning and multi-scale training were employed to progressively refine region overlap and improve robustness to tumor size variability. Furthermore, explicit spatial gradient supervision was incorporated to enforce boundary geometry, and a novel gradient–frequency coupling mechanism was proposed to resolve the inherent trade-off between boundary sharpness and volumetric continuity. Extensive quantitative and qualitative analyses confirmed the effectiveness of the proposed formulation. In particular, the progressive integration of the proposed components led to a substantial improvement in volume-level Whole Tumor Dice, increasing from 0.0299 in the baseline configuration to 0.1772 in the final framework. Qualitative results further illustrated that these gains stem from improved structural coherence and reduced volumetric fragmentation rather than superficial pixel-level refinements. Importantly, the reported results are intended to validate the structural contribution of the proposed formulation rather than to compete directly with fully optimized benchmark pipelines. By focusing on formulation-level design, this work provides clear insight into how geometric and spectral constraints can be jointly leveraged to improve volumetric segmentation reliability. Future work will focus on extending the proposed framework through uncertainty-aware boundary modeling, directional and multi-resolution frequency representations, and longer training schedules with advanced data augmentation. Additional evaluation on heterogeneous clinical datasets will further assess generalization and facilitate translation toward clinically deployable segmentation systems. Overall, this study demonstrates that explicitly coupling boundary geometry with frequency-domain learning offers a principled and effective solution for robust volume-level brain tumor segmentation, moving beyond architectural heuristics toward interpretable and reliable medical image analysis.

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