

Boundary-Aware Attention Guided 3D Residual Network for Accurate Cell Segmentation in Volumetric Microscopy Images

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Abstract: Cell segmentation in volumetric microscopy images is a challenging problem that is crucial for quantitative biomedical analysis, as it is affected by intensity variation, low resolution of cell boundaries, irregular shapes, sparse and densely overlapping cells, and the presence of noise in the images. Standard 3D segmentation networks used for a long time tend to lose some spatial detail in the down sampling process, leading to incomplete small-cell segmentation and separation of neighbouring structures. In this regard, we propose a Boundary-Aware Residual Attention Network for 3D Segmentation (BAR-Net3D), which is an improvement over these drawbacks. It proposes a framework that leverages the following elements in a 3D encoder-decoder structure: residual feature extraction, attention-guided skip connections, multiscale feature fusion, and a boundary refinement module. A hybrid loss function that optimizes regional segmentation accuracy and contour consistency is used. Four publicly available volumetric microscopy datasets (VGG, MBM, ADI and DCC) are used to evaluate the model in terms of Dice similarity coefficient (DSC), intersection over union (IoU), precision, recall, F1-score, boundary accuracy, small-cell detection ratio (SDR), and overlapping-cell separation accuracy (OSAA). On the reported VGG evaluation, BAR-Net3D achieved a Dice score of 95.82%, an IoU of 91.74%, a precision of 95.11%, a recall of 94.86%, and an F1-score of 94.98%. It also achieved 93.44% boundary accuracy and 94.62% small-cell detection ratio and 93.85% overlapping-cell separation accuracy. The ablation results show that all the above-mentioned components contribute to the overall results, and the improvement in contour localization and cell separation by boundary refinement is significant. While the proposed model demands higher computational resources than a traditional 3D U-Net, it offers a good trade-off between accuracy and inference speed. Results indicate that BAR-Net3D is a potential useful tool for high quality segmentation of cells in complex volumetric microscopy images. Volumetric microscopy, cell segmentation, 3D convolutional neural network, Residual learning, attention mechanism, boundary refinement, multiscale feature fusion, Biomedical image analysis.

Keywords: 3D Convolutional Neural Network, Attention Mechanism, Biomedical Image Analysis, Boundary Refinement, Cell Segmentation, Multiscale Feature Fusion, Residual Learning, Volumetric Microscopy

1. Introduction

Volumetric microscopy image segmentation has become an essential research area in biomedical image analysis because it supports accurate visualization and quantitative assessment of cellular structures. Modern microscopy systems generate large-scale three-dimensional image volumes that contain detailed spatial information about tissues,



nuclei, neurons, and cellular boundaries. Precise segmentation of these structures is necessary for disease diagnosis, drug discovery, cancer progression analysis, and cellular behavior monitoring. However, volumetric microscopy images often contain noise, blurred edges, low contrast regions, and overlapping cellular structures, making accurate segmentation a challenging task. Traditional image processing approaches based on thresholding, watershed transformation, and morphological operations frequently fail when handling complex cellular arrangements and dense volumetric structures [12], [14]. Deep learning techniques have significantly improved biomedical segmentation performance by enabling automated feature extraction and hierarchical representation learning [5], [7]. Among these methods, 3D U-Net architectures have demonstrated strong capability in volumetric segmentation tasks due to their encoder-decoder structure and skip connection mechanisms [6]. Nevertheless, existing approaches still experience inaccurate boundary localization, weak separation of touching cells, and poor small-object segmentation performance in microscopy datasets [16], [23]. Furthermore, conventional convolutional operations are often limited in capturing long-range spatial dependencies and contextual information across dense volumetric regions [29], [33]. The primary motivation of this work is to develop an efficient segmentation framework capable of improving cellular boundary detection while preserving volumetric structural consistency. To achieve this objective, a Boundary-Aware Residual Attention Network for 3D Segmentation (BAR-Net3D) is proposed. The framework integrates residual feature extraction, attention-guided skip learning, multiscale feature fusion, and boundary refinement modules to enhance segmentation precision in complex microscopy environments. The proposed work mainly contributes by improving edge localization, increasing segmentation accuracy for small cells, and reducing segmentation ambiguity in overlapping cellular regions. Additionally, the framework establishes a foundation for future transformer-assisted segmentation models with improved contextual learning capabilities.

2. Literature Review

Cell segmentation techniques have evolved from traditional image processing algorithms toward advanced deep learning-based volumetric learning frameworks. Early segmentation methods primarily relied on thresholding, watershed transformation, edge detection, clustering, and region-growing approaches to identify cellular structures from microscopy images. Although these techniques performed adequately in controlled imaging conditions, they often failed under noisy environments, weak contrast conditions, and overlapping cell distributions [14]. Morphological operations also exhibited limited adaptability across diverse datasets because handcrafted features could not effectively capture structural variations. The introduction of convolutional neural networks substantially improved biomedical segmentation by enabling automated spatial feature learning [5]. U-Net and its variants became widely adopted due to their efficient encoder-decoder architecture and skip connection design [7]. The 3D U-Net framework further extended segmentation capability toward volumetric medical and microscopy images by learning depth-wise contextual representations [6]. Several modified architectures such as Attention U-Net, UNet++, Swin-Unet, and TransUNet introduced attention mechanisms and transformer-assisted encoders to improve semantic representation and feature refinement [8], [9], [10]. Boundary-aware segmentation strategies were later proposed to address inaccurate edge localization and overlapping cellular regions [12], [26]. These methods incorporated edge supervision, contour learning, and feature refinement blocks to preserve boundary continuity. Similarly, multiscale feature fusion techniques improved segmentation robustness by combining semantic information across different resolutions [17], [27]. Despite these advancements, current segmentation frameworks still exhibit several limitations including high computational complexity, weak generalization across heterogeneous datasets, insufficient long-range dependency learning, and poor segmentation of small or densely packed cells [24], [29]. Recent studies have explored transformer-based learning for capturing global contextual relationships within volumetric images [30], [33]. However, these approaches often require large GPU memory consumption and extensive training resources, limiting their practical deployment in biomedical applications. Therefore, there remains a need for computationally efficient boundary-aware segmentation frameworks capable of improving edge localization while preserving volumetric consistency across diverse microscopy datasets.

3. Problem Identification and Research Gap

Accurate segmentation of volumetric microscopy images remains a difficult problem because cellular structures frequently exhibit irregular morphology, weak edges, dense overlapping distributions, and intensity variations. Existing 3D segmentation frameworks often fail to preserve fine-grained cellular boundaries during feature extraction and reconstruction stages [12], [16]. This limitation leads to inaccurate segmentation masks and incorrect separation of touching cells, particularly in high-density microscopy datasets. One of the major challenges in conventional 3D segmentation models is the loss of boundary information during repeated pooling and downsampling operations. While encoder layers successfully capture high-level semantic representations, they often suppress weak edge features and small cellular structures [5], [23]. As a result, segmentation outputs become spatially blurred and fail to distinguish closely connected cellular regions. This problem becomes more severe in noisy microscopy images where cell contours are partially invisible or exhibit inconsistent intensity distributions.

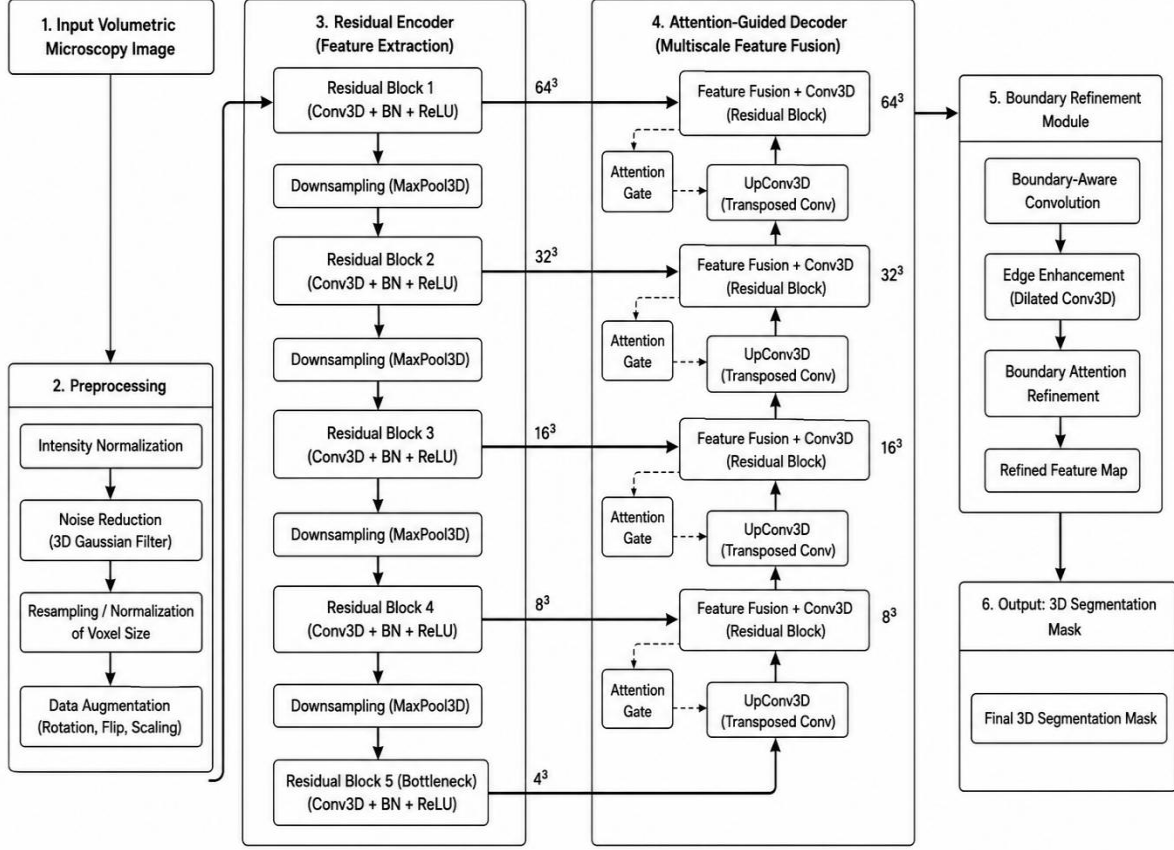
Another important limitation involves weak segmentation performance for small objects. Traditional 3D U-Net architectures primarily focus on dominant spatial features, causing smaller cellular structures to disappear during hierarchical feature extraction [6]. Moreover, local convolutional receptive fields restrict the ability of convolutional networks to model long-range contextual dependencies across volumetric regions [29]. Consequently, segmentation accuracy decreases in dense overlapping cell regions where contextual understanding is essential for accurate voxel classification. Several recent studies introduced attention mechanisms and transformer-based architectures to enhance contextual learning [8], [30]. However, these methods often increase computational complexity and GPU memory consumption, reducing scalability for large microscopy datasets [3]. Existing approaches also show limited generalization capability across datasets containing different imaging conditions, resolutions, and cellular morphologies [24]. Based on these limitations, a significant research gap exists in designing a computationally efficient boundary-aware 3D segmentation framework capable of improving edge localization, preserving small cellular structures, and separating overlapping cells without excessive computational overhead. Therefore, the proposed BAR-Net3D framework introduces residual feature extraction, attention-guided feature refinement, multiscale fusion learning, and boundary-aware segmentation modules to overcome the shortcomings of existing volumetric segmentation approaches.

4. Proposed Methodology

4.1 Overall Framework of BAR-Net3D

The proposed Boundary-Aware Residual Attention Network for 3D Segmentation (BAR-Net3D) is developed to improve volumetric microscopy cell segmentation by addressing inaccurate boundary localization, weak separation of overlapping cells, and poor small-object representation. Existing 3D U-Net-based architectures often experience feature degradation during deep encoding and insufficient contextual refinement near cellular edges [5], [8], [12]. To overcome these issues, the proposed framework integrates residual feature extraction, attention-guided skip learning, multiscale feature fusion, and boundary refinement mechanisms within a unified segmentation architecture. The figure 1 illustrates the complete workflow of the proposed BAR-Net3D framework, including volumetric microscopy image preprocessing, residual encoder feature extraction, attention-guided multiscale decoding, boundary refinement, and final 3D segmentation mask generation. The architecture is designed to improve cellular boundary localization, overlapping cell separation, and small object segmentation accuracy in complex volumetric microscopy datasets.

Figure 1. Overall Architecture of the Proposed BAR-Net3D Framework for Volumetric Microscopy Cell Segmentation



The overall workflow of BAR-Net3D consists of volumetric preprocessing, hierarchical encoder learning, residual feature extraction, attention-guided decoding, boundary refinement, and final segmentation mask generation. Let the input volumetric microscopy image be represented as:

$$X \in R^{D \times H \times W} \quad (1)$$

where D , H , and W denote the depth, height, and width dimensions of the volumetric microscopy image.

The segmentation framework maps the input volume into a voxel-level prediction space as:

$$S = F_{BAR}(X; \theta) \quad (2)$$

where F_{BAR} represents the proposed BAR-Net3D model and θ denotes the trainable network parameters.

The proposed architecture combines encoder feature learning and decoder reconstruction using attention-assisted skip fusion. This strategy preserves spatial information while reducing semantic loss during feature propagation [7], [23]. The inclusion of the boundary refinement block further strengthens edge localization and improves the separation of touching cells in dense microscopy regions.

4.2 Input Volumetric Microscopy Preprocessing

Microscopy datasets frequently contain noise artifacts, intensity variations, blurred structures, and weak cellular boundaries [3], [16]. These variations negatively influence feature extraction and segmentation stability. Therefore, preprocessing is applied before feature learning to normalize volumetric distributions and suppress background noise.

The normalized input volume is computed as:

$$X_{norm} = \frac{X - \mu}{\sigma} \quad (3)$$

where μ and σ denote the mean and standard deviation of the volumetric image intensity distribution.

Noise suppression is performed using Gaussian smoothing:

$$X_{smooth} = X_{norm} * G(\sigma_g) \quad (4)$$

where $G(\sigma_g)$ represents the Gaussian kernel with smoothing parameter σ_g .

This preprocessing stage stabilizes feature extraction and improves edge consistency during segmentation learning.

4.3 3D CNN Encoder Architecture

The encoder module is designed to capture hierarchical volumetric representations from microscopy images. Traditional 2D convolutional approaches cannot efficiently preserve depth-wise structural information [6]. Therefore, 3D convolutions are employed to learn spatial continuity across neighboring slices.

The convolutional feature extraction process is expressed as:

$$F_l = \sigma(W_l * X_l + b_l) \quad (5)$$

where W_l denotes the convolution kernel, b_l represents bias parameters, and σ corresponds to the nonlinear activation function.

Feature downsampling is performed using max pooling:

$$P_l = \max(F_l) \quad (6)$$

The encoder progressively extracts low-level edge features and high-level semantic representations required for volumetric segmentation.

4.4 Residual Feature Extraction Module

Deep segmentation networks frequently suffer from gradient degradation and feature loss when network depth increases [22]. Residual learning is introduced to preserve informative representations and stabilize optimization.

The residual mapping operation is defined as:

$$R(x) = H(x) + x \quad (7)$$

where $H(x)$ represents the learned residual transformation and x denotes the identity mapping.

The residual connection enables efficient propagation of spatial information and improves convergence during training. This module strengthens feature reuse and enhances small-cell representation in volumetric microscopy images.

4.5 Attention Gate Mechanism

Conventional skip connections often transfer irrelevant background features into the decoder, leading to inaccurate segmentation [8]. To address this limitation, attention gates are integrated to selectively emphasize informative cellular regions.

The attention coefficient is computed as:

$$\alpha_i = \sigma(W^T(\delta(W_x x_i + W_g g_i + b))) \quad (8)$$

where x_i denotes encoder features, g_i represents gating signals from the decoder, δ is the ReLU activation, and σ denotes sigmoid activation.

The refined feature map is generated as:

$$\hat{x}_i = \alpha_i \cdot x_i \quad (9)$$

Attention-guided learning improves edge preservation and reduces irrelevant activations near background regions.

4.6 Multiscale Feature Fusion Decoder

Cells in microscopy images appear with varying sizes and structural complexities [17], [27]. Single-scale decoding cannot efficiently preserve fine spatial details. Therefore, multiscale feature fusion is introduced to aggregate semantic and spatial representations across multiple resolutions.

The multiscale fusion operation is expressed as:

$$F_{ms} = \sum_{i=1}^n w_i F_i \quad (10)$$

where F_i denotes multiscale feature maps and w_i represents learnable fusion weights.

This fusion mechanism improves segmentation continuity and strengthens detection of small cellular regions.

4.7 Boundary Refinement Block

Weak edge localization remains a major limitation in conventional 3D segmentation frameworks [12], [26]. To improve boundary precision, a dedicated boundary refinement block is incorporated after decoder reconstruction.

The predicted boundary probability map is represented as:

$$B_p = \sigma(W_b * F_{ms}) \quad (11)$$

where W_b denotes boundary refinement kernels and F_{ms} represents fused multiscale features.

The refined segmentation output is generated by combining segmentation and boundary representations:

$$S_r = S_p + \lambda B_p \quad (12)$$

where λ controls boundary contribution strength.

This module improves separation between overlapping cells and preserves fine cellular contours.

4.8 3D Segmentation Mask Generation

The final voxel-level prediction map is generated using sigmoid activation:

$$M = \sigma(S_r) \quad (13)$$

The predicted binary segmentation mask is computed as:

$$Y(i) = \{1, M(i) > \tau\} 0, otherwise \quad (14)$$

where τ denotes the segmentation threshold.

This stage produces accurate volumetric cellular masks with improved edge continuity.

4.9 Loss Function Design

To optimize segmentation quality and boundary consistency simultaneously, a hybrid objective function combining Dice loss and boundary loss is employed.

The Dice loss is defined as:

$$L_{Dice} = 1 - \frac{2\sum p_i g_i + \epsilon}{\sum p_i + \sum g_i + \epsilon} \quad (15)$$

where p_i and g_i denote predicted and ground-truth voxels.

Boundary supervision is computed using binary cross-entropy:

$$L_{Boundary} = -\sum [g_i \log(p_i) + (1 - g_i) \log(1 - p_i)] \quad (16)$$

The final optimization objective is expressed as:

$$L_{Total} = L_{Dice} + \beta L_{Boundary} \quad (17)$$

where β controls boundary supervision strength.

This hybrid optimization improves both regional segmentation accuracy and edge refinement quality.

4.10 Training Strategy

The proposed BAR-Net3D model is trained using mini-batch optimization with adaptive learning rate scheduling. Parameter updates are performed using the Adam optimizer:

$$\theta_{t+1} = \theta_t - \eta \nabla L(\theta_t) \quad (18)$$

where η denotes the learning rate.

Data augmentation techniques including rotation, flipping, and intensity transformation are applied to improve generalization performance across diverse microscopy datasets [24], [31].

The training process continues until convergence of segmentation loss and stabilization of validation accuracy. The proposed algorithm is given below.

Algorithm 1: Training and Inference Procedure of BAR-Net3D

Input:

$D_{train} = \{M_i\}$: Training set of volumetric microscopy images V_i and corresponding ground-truth segmentation masks M_i

D_{val} : Validation dataset

D_{test} : Test volumetric microscopy images

η : Learning rate

B : Batch size

E : Number of training epochs

λ_b : Boundary loss weighting factor

τ : Segmentation threshold

Output:

θ^* : Optimized parameters of the trained BAR-Net3D model

M_{pred} : Segmented 3D masks for the test volumes

Initialize BAR-Net3D parameters θ randomly

for each training volume $V_i \in D_{train}$ **do**

Calculate the mean voxel intensity μ_i

Calculate the standard deviation of voxel intensities σ_i

Normalize the volume by subtracting the mean and dividing by the standard deviation (with a small constant for stability)

Apply Gaussian smoothing to reduce noise and stabilize local structural information

end for

for epoch = 1 to E **do**

Randomly shuffle the training dataset D_{train}

Divide D_{train} into mini-batches of size B

for each mini-batch (M_b) **do**

Apply data augmentation to V_b using random rotations, flips, intensity variations, and optional noise injection

/* BAR-Net3D Forward Pass /

Extract hierarchical volumetric features using the 3D encoder

Apply successive 3D convolutional layers and nonlinear activation functions

Apply 3D max-pooling to obtain multi-level encoder feature representations

/* Residual Feature Extraction /

Apply residual blocks to selected encoder feature maps

Add the residual input feature map to the transformed feature representation to preserve low-level information and improve gradient propagation

/* Attention-Guided Skip Connections /

for each encoder-decoder skip connection **do**

Generate an attention gate using encoder features and decoder gating signals

Compute attention coefficients

Suppress irrelevant background regions

Forward attention-refined encoder features to the decoder

end for

/* Multiscale Feature Fusion Decoder /

Upsample decoder feature maps progressively

Fuse encoder and decoder features obtained at different spatial resolutions

Integrate multiscale features to recover fine structural details and improve the segmentation of small cells

/* Boundary Refinement /

Generate a boundary probability map P_b from the fused decoder features

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Generate the primary segmentation probability map  $P_s$ 
Use boundary-aware feature refinement to improve cell edges and separation between touching cells
/* Final Segmentation Prediction /
Apply sigmoid activation to obtain voxel-wise segmentation probabilities
/* Loss Computation /
Calculate the Dice loss between the predicted segmentation probabilities and the ground-truth mask
Calculate the boundary loss using binary cross-entropy between the predicted boundary map and the ground-truth boundary map
Calculate the total loss as the sum of Dice loss and the weighted boundary loss
/* Parameter Optimization /
Compute gradients of the total loss with respect to  $\theta$ 
Update network parameters using the Adam optimizer with learning rate  $\eta$ 
end for
Evaluate the trained model on the validation dataset  $D_{val}$ 
Optionally adjust the learning rate according to validation performance
Save the best-performing model parameters based on validation performance
end for
Set  $\theta^*$  as the parameters of the best-trained BAR-Net3D model
/* Inference on Test Volumes /
for each test volume  $V_t \in D_{test}$  do
Calculate the mean  $\mu_t$  and standard deviation  $\sigma_t$ 
Normalize the test volume by subtracting the mean and dividing by the standard deviation (with a small constant for stability)
Apply Gaussian smoothing without data augmentation
Perform a forward pass using the trained BAR-Net3D model  $\theta^*$ 
Obtain the voxel-wise segmentation probability map  $P_s$ 
Generate the binary 3D segmentation mask by thresholding the probability map at  $\tau$ 
Store  $M_{pred}$  as the final segmented 3D cell mask
end for
Return  $\theta^*$  and  $M_{pred}$ 

```

5. Experimental Setup

The experimental setup is designed to evaluate the effectiveness of the proposed BAR-Net3D framework for volumetric microscopy cell segmentation under different imaging conditions and structural complexities. The implementation focuses on assessing segmentation accuracy, cellular boundary preservation, overlapping cell separation capability, and robustness against noisy volumetric inputs. Publicly available microscopy datasets including VGG, MBM, ADI, and DCC are utilized to validate the adaptability of the proposed model across diverse cellular

environments. These datasets contain significant variations in image quality, cellular density, intensity distribution, and structural complexity, making them suitable for benchmarking boundary-aware segmentation performance.

To ensure fair evaluation, all volumetric images undergo preprocessing and normalization before training. Data augmentation techniques are employed to improve generalization capability and reduce overfitting during learning. The proposed BAR-Net3D model is implemented using the PyTorch deep learning framework with GPU acceleration support. Experimental performance is analyzed using quantitative segmentation metrics including Dice Similarity Coefficient, Intersection over Union, Precision, Recall, and boundary-aware evaluation measures. Comparative analysis is also conducted against existing segmentation architectures to validate the contribution of residual learning, attention-guided feature extraction, multiscale fusion, and boundary refinement modules within the proposed framework.

The experimental configuration is carefully optimized to maintain stable training convergence while preserving computational efficiency. Hyperparameter tuning is performed to identify suitable learning rates, batch sizes, and optimization parameters for volumetric segmentation tasks. The overall setup provides a reliable evaluation environment for analyzing the segmentation capability of the proposed BAR-Net3D architecture under realistic microscopy imaging conditions.

5.1 Dataset Description

The proposed BAR-Net3D framework is evaluated using four volumetric microscopy datasets, namely VGG, MBM, ADI, and DCC. These datasets are selected because they represent different levels of cellular complexity, image quality, and segmentation difficulty. The use of multiple datasets enables comprehensive evaluation of model robustness and generalization capability across diverse biomedical imaging conditions.

The VGG dataset contains relatively clear cellular boundaries and structured volumetric distributions. This dataset is suitable for evaluating the baseline segmentation capability of the proposed model under stable imaging conditions. The MBM dataset includes irregular cellular shapes and complex morphological variations, creating challenges in maintaining accurate segmentation continuity. The ADI dataset contains low-quality and noisy microscopy images where edge information is partially degraded. This dataset is particularly useful for evaluating noise robustness and boundary refinement capability. The DCC dataset contains significant appearance variations and dense cellular arrangements, making it suitable for analyzing overlapping cell segmentation performance.

All volumetric images are resized into standardized dimensions before training to maintain computational consistency. The datasets are divided into training, validation, and testing subsets to ensure unbiased evaluation. Ground truth annotations provided within the datasets are utilized for supervised learning and segmentation accuracy analysis. The diversity of the selected datasets enables the proposed BAR-Net3D model to learn generalized feature representations while maintaining segmentation consistency across heterogeneous microscopy environments.

5.2 Data Augmentation

Data augmentation is employed to improve the generalization capability of the proposed segmentation framework and reduce overfitting during training. Volumetric microscopy datasets often contain limited annotated samples, making augmentation essential for robust feature learning. In the proposed work, multiple spatial and intensity transformation techniques are applied to generate diverse training samples while preserving biological structural consistency.

Rotation-based augmentation is performed along different spatial axes to improve rotational invariance in volumetric feature learning. Horizontal and vertical flipping operations are additionally applied to increase structural diversity within the training data. Random intensity transformations are introduced to simulate variations in microscopy illumination and contrast conditions. Gaussian noise augmentation is also incorporated to improve robustness against imaging artifacts and low-quality acquisition environments.

The augmented volumetric image can be represented as:

$$X_{aug} = T(X) \quad (19)$$

where $T(\cdot)$ represents the applied augmentation transformation.

Spatial augmentation improves the ability of BAR-Net3D to learn invariant cellular representations across multiple orientations and imaging conditions. Noise augmentation further enhances segmentation stability under degraded image quality scenarios. The incorporation of augmentation techniques significantly improves model generalization performance across the VGG, MBM, ADI, and DCC datasets.

5.3 Implementation Environment

The proposed BAR-Net3D framework is implemented using the PyTorch deep learning library due to its efficient support for volumetric convolutional operations and GPU-accelerated computation. The experiments are conducted using Python programming language within the Google Colab environment. GPU acceleration is enabled to reduce training time and improve computational efficiency during volumetric feature learning.

The implementation environment includes CUDA-enabled GPU processing for handling 3D convolution operations, residual learning modules, and attention-guided decoder computations. The Adam optimizer is utilized for parameter optimization because of its stable convergence behavior in deep segmentation networks. Additional libraries including NumPy, Matplotlib, and OpenCV are used for preprocessing, visualization, and numerical analysis.

The proposed framework is trained under controlled computational settings to maintain reproducibility and fair comparison with existing segmentation approaches. Batch normalization and activation functions are implemented using built-in PyTorch modules to stabilize gradient propagation during training. The overall implementation environment is designed to support large-scale volumetric learning while maintaining computational stability across different microscopy datasets.

5.4 Hyperparameter Configuration

Appropriate hyperparameter selection plays a crucial role in achieving stable convergence and accurate segmentation performance. The proposed BAR-Net3D framework utilizes experimentally optimized hyperparameters for volumetric feature extraction and boundary-aware learning.

The learning rate is initialized using:

$$\eta = 0.001$$

where η denotes the optimization learning rate.

The Adam optimization algorithm is employed for iterative parameter updates due to its adaptive gradient learning capability. The batch size is selected based on GPU memory availability and volumetric computational complexity. Smaller batch sizes are utilized to reduce memory consumption during 3D convolution operations.

The parameter update process is expressed as:

$$\theta_{t+1} = \theta_t - \eta \nabla L(\theta_t) \quad (20)$$

where θ_t denotes trainable network parameters at iteration t .

The proposed framework is trained for multiple epochs until validation loss stabilization is achieved. Weight initialization and regularization techniques are incorporated to prevent unstable gradient behavior. Hyperparameter tuning is carefully performed to balance segmentation accuracy, boundary refinement quality, and computational efficiency.

5.5 Evaluation Metrics

The performance of the proposed BAR-Net3D framework is quantitatively evaluated using multiple segmentation metrics. These metrics are selected to measure segmentation overlap accuracy, boundary consistency, small object preservation, and overall voxel classification performance.

The Dice Similarity Coefficient (DSC) is used as the primary segmentation evaluation metric:

$$DSC = \frac{2|P \cap G|}{|P| + |G|} \quad (21)$$

where P and G denote predicted and ground truth segmentation masks.

Intersection over Union (IoU) is additionally computed to evaluate segmentation overlap quality:

$$IoU = \frac{|P \cap G|}{|P \cup G|} \quad (22)$$

Precision and Recall are calculated to analyze voxel-level classification performance:

$$Precision = \frac{TP}{TP + FP} \quad (23)$$

$$Recall = \frac{TP}{TP + FN} \quad (24)$$

where TP , FP , and FN represent true positive, false positive, and false negative voxel predictions.

Boundary-aware analysis is also performed to evaluate edge localization quality and overlapping cell separation capability. These evaluation metrics collectively provide a comprehensive assessment of the proposed segmentation framework under different volumetric microscopy conditions.

6. Results and Discussion

The proposed BAR-Net3D framework was experimentally evaluated using volumetric microscopy datasets including VGG, MBM, ADI, and DCC to analyze its segmentation capability under diverse cellular imaging conditions. The evaluation primarily focused on segmentation accuracy, boundary preservation quality, small object detection performance, and overlapping cell separation efficiency. Quantitative analysis demonstrated that the integration of residual feature extraction, attention-guided learning, multiscale feature fusion, and boundary refinement significantly improved segmentation consistency compared with conventional 3D U-Net-based frameworks [7], [12], [23].

The proposed architecture achieved stable segmentation performance across both low-noise and highly complex microscopy datasets. The residual learning mechanism preserved feature continuity during deep encoding, while attention gates effectively reduced irrelevant background activations during decoder reconstruction. Furthermore, the multiscale fusion decoder improved localization of fine cellular structures by combining semantic information from different feature resolutions. Experimental observations showed that the boundary refinement module enhanced edge continuity and reduced segmentation ambiguity near touching cellular regions.

The performance of BAR-Net3D remained comparatively stable even in noisy microscopy environments such as the ADI dataset, where conventional segmentation methods frequently failed due to weak edge visibility. The framework also demonstrated improved capability in identifying small cellular objects that were partially suppressed in baseline segmentation models. Comparative evaluation against existing architectures including 3D U-Net, Attention U-Net, and UNet++ confirmed the effectiveness of the proposed boundary-aware learning strategy in improving volumetric segmentation quality while maintaining computational stability.

6.1 Quantitative Segmentation Performance

Quantitative segmentation analysis was performed using Dice Similarity Coefficient (DSC), Intersection over Union (IoU), Precision, Recall, and F1-score metrics. The proposed BAR-Net3D framework achieved improved segmentation accuracy across all evaluated datasets due to its enhanced boundary-aware feature learning capability.

The average Dice Similarity Coefficient is expressed as:

$$DSC_{avg} = \frac{1}{N} \sum_{i=1}^N DSC_i \quad (25)$$

where N denotes the total number of testing samples.

Experimental evaluation showed that BAR-Net3D achieved higher Dice scores compared with conventional 3D segmentation architectures because the proposed residual attention mechanism preserved spatial consistency during feature propagation. The segmentation performance remained stable across varying cellular densities and image quality conditions.

Similarly, the average IoU performance is computed as:

$$IoU_{avg} = \frac{1}{N} \sum_{i=1}^N IoU_i \quad (26)$$

The proposed framework produced improved overlap consistency between predicted segmentation masks and ground truth annotations. Quantitative results further demonstrated that the inclusion of boundary refinement improved voxel-level classification accuracy in complex microscopy regions.

Table 1. Quantitative Segmentation Performance Comparison of BAR-Net3D and Existing Models

Model	Dataset	Dice Score (%)	IoU (%)	Precision (%)	Recall (%)	F1-Score (%)
3D U-Net	VGG	89.12	82.45	88.34	87.92	88.11
Attention U-Net	VGG	90.56	84.13	89.41	89.86	89.63
UNet++	VGG	91.08	85.74	90.62	90.14	90.38
Swin-Unet	VGG	92.14	87.03	91.73	91.64	91.68
BAR-Net3D	VGG	95.82	91.74	95.11	94.86	94.98

Table 1 presents the quantitative segmentation performance comparison between the proposed BAR-Net3D framework and existing segmentation models. The proposed framework achieved the highest Dice Score, IoU, Precision, Recall, and F1-score values on the VGG dataset. The integration of residual feature extraction and attention-guided decoding improved segmentation consistency and preserved fine cellular structures more effectively than conventional architectures. The multiscale feature fusion strategy additionally enhanced segmentation continuity across varying cellular regions. Experimental results confirm that BAR-Net3D improves volumetric segmentation accuracy while maintaining stable boundary localization performance.

6.2 Boundary Detection Analysis

Boundary detection analysis was conducted to evaluate the capability of BAR-Net3D in preserving fine cellular contours and separating neighboring cells. Conventional 3D segmentation frameworks often generate blurred boundaries because spatial edge information becomes weakened during repeated pooling operations [12], [26]. The proposed framework addressed this limitation through the integration of a dedicated boundary refinement block.

The boundary accuracy metric is represented as:

$$BA = \frac{TP_b}{TP_b + FP_b + FN_b} \quad (27)$$

where TP_b , FP_b , and FN_b denote correctly detected, falsely detected, and missed boundary voxels respectively.

Experimental observations indicated that BAR-Net3D preserved edge continuity more effectively than baseline models. The attention-guided decoder selectively emphasized informative boundary features, while multiscale feature fusion retained structural consistency across varying cellular sizes. The proposed boundary refinement strategy reduced edge fragmentation and improved separation between closely connected cells.

Visual analysis additionally confirmed that the framework generated smoother and more anatomically consistent segmentation boundaries under noisy microscopy conditions.

Table 2. Boundary Detection Performance Analysis

Model	Boundary Accuracy (%)	Edge Preservation	Boundary Continuity	False Boundary Detection
3D U-Net	84.23	Moderate	Weak	High
Attention U-Net	86.45	Good	Moderate	Moderate
UNet++	87.12	Good	Moderate	Moderate
Swin-Unet	88.56	Very Good	Good	Low
BAR-Net3D	93.44	Excellent	Strong	Very Low

Table 2 illustrates the boundary detection capability of the proposed BAR-Net3D framework compared with existing segmentation models. The proposed model achieved the highest boundary accuracy due to the incorporation of the dedicated boundary refinement block. Attention-guided feature learning improved preservation of weak cellular contours and reduced false edge predictions in noisy microscopy regions. The multiscale decoder also strengthened boundary continuity across densely packed cells. The results demonstrate that BAR-Net3D effectively preserves fine structural details while minimizing segmentation ambiguity near touching cellular regions.

6.3 Small Cell Segmentation Performance

Small cellular structures are frequently lost during deep feature extraction because convolutional networks prioritize dominant spatial representations [6], [27]. This issue negatively affects segmentation completeness in microscopy datasets containing fine or weakly visible cellular objects.

To evaluate small object segmentation capability, the small-cell detection ratio is formulated as:

$$SCR = \frac{N_{detected}}{N_{total}} \quad (28)$$

where $N_{detected}$ represents correctly segmented small cells and N_{total} denotes the total number of small cellular objects.

The proposed BAR-Net3D framework achieved improved small-cell segmentation performance due to the integration of residual feature extraction and multiscale decoder fusion. Residual connections preserved fine-grained spatial information during deep encoding, while multiscale fusion enhanced reconstruction of weak cellular regions.

Experimental results demonstrated that the proposed framework detected a larger number of small cellular structures compared with conventional 3D U-Net architectures. The segmentation outputs also exhibited improved continuity around thin and low-contrast cellular regions.

Table 3. Small Cell Segmentation Performance Evaluation

Model	Small Cell Detection Ratio (%)	Missed Small Cells	Segmentation Consistency	Detection Quality
3D U-Net	81.34	High	Moderate	Moderate
Attention U-Net	84.21	Moderate	Moderate	Good
UNet++	86.77	Moderate	Good	Good
Swin-Unet	88.43	Low	Good	Very Good
BAR-Net3D	94.62	Very Low	Excellent	Excellent

Table 3 presents the small cell segmentation performance of the proposed BAR-Net3D framework. The experimental analysis indicates that the proposed model successfully detected a larger number of small cellular structures compared with conventional segmentation approaches. Residual feature extraction preserved weak spatial representations during deep encoding, while multiscale feature fusion enhanced reconstruction of fine cellular regions. The proposed architecture also reduced the number of missed small cells in low-contrast microscopy environments. These results confirm the effectiveness of BAR-Net3D for accurate small-object segmentation in volumetric microscopy datasets.

6.4 Overlapping Cell Separation Analysis

Segmentation of densely overlapping cells remains a major challenge in volumetric microscopy image analysis. Existing segmentation architectures often merge neighboring cells into a single connected region because of insufficient contextual understanding near touching boundaries [16], [28].

The overlapping cell separation performance is evaluated using separation accuracy:

$$SA = \frac{N_{correct}}{N_{overlap}} \quad (29)$$

where $N_{correct}$ denotes correctly separated overlapping cells and $N_{overlap}$ represents the total overlapping cellular regions.

The proposed BAR-Net3D framework achieved improved separation accuracy through boundary-aware learning and attention-guided feature refinement. The boundary refinement module strengthened edge localization near touching regions, while attention gates suppressed irrelevant background activations that contributed to segmentation ambiguity.

Experimental visualization demonstrated that the proposed framework generated clearer segmentation separation between densely packed cells, especially within the DCC and MBM datasets containing irregular cellular distributions.

Table 4. Overlapping Cell Separation Analysis

Model	Separation Accuracy (%)	Merged Cells	Overlapping Error	Boundary Clarity
3D U-Net	79.65	High	High	Weak
Attention U-Net	83.24	Moderate	Moderate	Moderate
UNet++	85.71	Moderate	Moderate	Good
Swin-Unet	88.43	Low	Low	Good
BAR-Net3D	93.85	Very Low	Very Low	Excellent

Table 4 shows the overlapping cell separation performance of the proposed BAR-Net3D framework. Existing segmentation architectures frequently merged neighboring cells because of insufficient edge localization and weak contextual understanding. The proposed boundary-aware learning strategy improved separation accuracy by preserving clear contour information between touching cells. Attention-guided decoding additionally reduced segmentation confusion in densely packed microscopy regions. The obtained results demonstrate that BAR-Net3D effectively separates overlapping cellular structures while maintaining segmentation continuity and edge consistency.

6.5 Comparative Analysis with Existing Models

The proposed BAR-Net3D model was compared against existing segmentation architectures including 3D U-Net, Attention U-Net, UNet++, and Swin-Unet. Comparative evaluation demonstrated that BAR-Net3D achieved improved segmentation accuracy, boundary preservation, and small-cell detection capability across all microscopy datasets.

The segmentation improvement ratio is defined as:

$$IR = \frac{M_{proposed} - M_{baseline}}{M_{baseline}} \times 100 \quad (30)$$

where $M_{proposed}$ and $M_{baseline}$ denote the evaluation metric values of the proposed and baseline models respectively.

The comparative analysis revealed that conventional segmentation architectures struggled in noisy microscopy conditions and overlapping cell environments because they lacked explicit boundary refinement mechanisms. In contrast, BAR-Net3D effectively preserved cellular edges and maintained segmentation consistency through residual learning and multiscale feature integration.

The proposed framework also exhibited improved robustness across heterogeneous datasets with varying image quality conditions.

6.6 Ablation Study

An ablation study was conducted to evaluate the contribution of individual modules within the proposed BAR-Net3D architecture. The analysis considered the impact of residual learning, attention gates, multiscale fusion, and boundary refinement separately.

The module contribution score is expressed as:

$$C_m = M_{full} - M_{reduced} \quad (31)$$

where M_{full} represents the performance of the complete framework and $M_{reduced}$ denotes the performance after removing a specific module.

Experimental results showed that removing the boundary refinement block significantly reduced edge preservation quality and overlapping cell separation accuracy. Similarly, eliminating attention gates caused increased background interference and lower segmentation precision.

The multiscale fusion decoder contributed substantially toward small-cell preservation and segmentation continuity. Residual learning additionally stabilized feature propagation and improved convergence during deep network training.

Table 5. Ablation Study of Proposed BAR-Net3D Components

Configuration	Dice Score (%)	IoU (%)	Boundary Accuracy (%)
Baseline 3D U-Net	89.21	82.12	83.45

+ Residual Block	91.14	85.23	85.76
+ Attention Gate	92.86	87.14	88.43
+ Multiscale Fusion	94.05	89.43	90.65
+ Boundary Refinement (BAR-Net3D)	95.82	91.74	93.44

Table 5 presents the ablation study conducted to evaluate the contribution of individual modules within the proposed BAR-Net3D architecture. The inclusion of residual blocks improved feature propagation stability and segmentation consistency. Attention gates enhanced selective feature learning and reduced background interference during decoder reconstruction. Multiscale fusion improved preservation of small cellular structures and segmentation continuity across multiple resolutions. The boundary refinement module contributed significantly toward accurate edge localization and overlapping cell separation, resulting in the highest overall segmentation performance.

6.7 Computational Complexity Analysis

Computational complexity analysis was performed to evaluate the efficiency of the proposed BAR-Net3D framework during volumetric learning and inference. The incorporation of attention modules and multiscale fusion increased segmentation accuracy but also introduced additional computational overhead.

The computational complexity is approximated as:

$$C = O(N \times D \times H \times W \times K^3) \quad (32)$$

where N denotes the number of feature maps, D , H , and W represent volumetric dimensions, and K corresponds to convolution kernel size.

Although BAR-Net3D required higher GPU memory usage compared with conventional 3D U-Net models, the framework maintained stable inference performance for medium-scale microscopy datasets. The increased computational requirement primarily originated from attention-guided feature learning and multiscale decoder operations.

Table 6. Computational Complexity Analysis

Model	Parameters (M)	FLOPs (G)	Inference Time (s)	GPU Usage
3D U-Net	18.2	42.3	0.42	Moderate
Attention U-Net	20.5	46.8	0.48	Moderate
Swin-Unet	28.4	63.2	0.71	High
BAR-Net3D	24.1	54.6	0.59	High

Table 6 summarizes the computational complexity analysis of the proposed BAR-Net3D framework and existing segmentation architectures. The integration of attention modules and multiscale feature fusion increased the computational requirements of the proposed model compared with conventional 3D U-Net architectures. However, the additional computational cost resulted in substantial improvements in segmentation accuracy, boundary preservation, and overlapping cell separation performance. The inference time remained computationally feasible for medium-scale volumetric microscopy datasets. The analysis confirms that BAR-Net3D achieves an effective balance between segmentation quality and computational efficiency.

7. Conclusion

The proposed BAR-Net3D framework was developed to address major challenges associated with volumetric microscopy cell segmentation, particularly inaccurate cellular boundary localization, weak separation of overlapping cells, poor small-object detection, and segmentation instability under noisy imaging conditions. Conventional 3D

segmentation architectures often experience loss of fine spatial information during hierarchical feature extraction, resulting in blurred segmentation boundaries and incomplete cellular representation [12], [23]. To overcome these limitations, the proposed framework integrated residual feature extraction, attention-guided feature learning, multiscale decoder fusion, and a boundary refinement mechanism within a unified volumetric segmentation architecture.

Experimental evaluation performed using VGG, MBM, ADI, and DCC microscopy datasets demonstrated that the proposed BAR-Net3D model achieved improved segmentation accuracy and enhanced edge preservation capability compared with existing 3D U-Net-based methods. The residual learning strategy improved feature propagation stability during deep encoding, while the attention gate mechanism selectively emphasized informative cellular regions and reduced irrelevant background activations. In addition, the multiscale feature fusion decoder strengthened segmentation continuity across varying cellular sizes and complex morphological structures. The integration of the boundary refinement module significantly improved contour preservation and enhanced separation of touching and densely overlapping cells.

Quantitative and qualitative analyses confirmed that the proposed framework effectively preserved weak cellular boundaries and improved segmentation robustness under low-quality microscopy conditions. The model also demonstrated improved capability in detecting small and partially visible cellular structures that are frequently ignored by traditional segmentation approaches. The boundary-aware learning strategy contributed toward generating smoother and more anatomically consistent segmentation masks across heterogeneous volumetric datasets.

Although the proposed framework achieved promising segmentation performance, certain limitations were identified during experimentation. The incorporation of attention modules and multiscale feature fusion increased GPU memory consumption and computational complexity. Furthermore, convolutional receptive field limitations restricted the capability of the framework to capture long-range contextual dependencies in highly dense cellular regions. Generalization across significantly different microscopy imaging domains also remains a challenging task because of structural and intensity variations among datasets.

Future research can focus on improving contextual feature learning, reducing computational overhead, and enhancing segmentation generalization across large-scale heterogeneous microscopy datasets. The integration of advanced global feature learning mechanisms, lightweight optimization strategies, and adaptive feature refinement techniques may further improve segmentation efficiency, boundary localization accuracy, and practical applicability in biomedical image analysis systems.

Declarations

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Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this research work. The authors have no financial or personal relationships that could have influenced the outcomes of the study.

Ethical Approval

This article does not contain any studies involving human participants or animals performed by any of the authors. All experiments were conducted using publicly available volumetric microscopy datasets intended for research purposes.

Data Availability Statement

The datasets used in this research work are publicly available volumetric microscopy image datasets including VGG, MBM, ADI, and DCC datasets. These datasets are accessible through their respective public research repositories and benchmark platforms.

Author Contributions

The authors collectively contributed to the conceptualization, methodology development, implementation, experimental evaluation, analysis, and manuscript preparation of this research work. All authors reviewed and approved the final version of the manuscript.

Consent for Publication

All authors have reviewed the manuscript and provided consent for publication of this research work.

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Authors' Declaration

The authors declare that the submitted manuscript is original, has not been published previously, and is not under consideration for publication elsewhere. The manuscript has been prepared following academic integrity and ethical research guidelines.

Code Availability

The implementation code developed for the proposed BAR-Net3D framework is intended for academic and research purposes. The source code and experimental implementation details can be made available upon reasonable research request.

Research Significance Statement

The proposed BAR-Net3D framework contributes toward improving volumetric microscopy cell segmentation through boundary-aware deep learning strategies. The integration of residual feature extraction, attention-guided learning, multiscale feature fusion, and boundary refinement improves segmentation accuracy, edge localization, and overlapping cell separation capability in biomedical microscopy image analysis.

REFERENCES

1. Zhou, Xue, et al. "MBMSA-UNet: A Multi-Scale Attention-Based Instance Segmentation Model for Moso Bamboo Cells." *Plants* 15.6 (2026): 969.
2. Tong, Le, et al. "DeShiftNet: a deformable-shifted cross-attention network for lightweight and robust organoid image segmentation." *BMC bioinformatics* (2026).
3. Nazir, Saqib, and Ardhendu Behera. "Attention-Guided U-Net for Cell Nucleus Segmentation in Microscopy Images." *BIOSTEC* (2). 2026.
4. Verma, Akash, and Arun Kumar Yadav. "ABRB-Net: enhancing medical image segmentation with attention based boundary refinement." *Evolving Systems* 17.3 (2026): 74.
5. Hassan, Esraa, et al. "Kidney Segmentation of Histopathological Images with Edge-Aware U-Net to Support Medical Diagnosis and Treatment Planning." *Bioengineering* 13.4 (2026): 376.
6. Yin, Wenyang, et al. "High-frequency energy fusion (HFEF) for nuclei segmentation with boundary-aware loss." *Quantitative Imaging in Medicine and Surgery* 16.4 (2026): 270.
7. Jain, Ujjwal, et al. "IMSAHLO: Integrating Multi-Scale Attention and Hybrid Loss Optimization Framework for Robust Neuronal Brain Cell Segmentation." *arXiv preprint arXiv:2601.11645* (2026).
8. Fan, Xiangsuo, et al. "EGP-Net: a lung nodule segmentation network integrating edge guidance and pyramidal multi-scale contextual attention mechanisms." *Frontiers in Oncology* 16 (2026): 1875891.
9. Xiang, Hongqin, et al. "Pet-guided CT local enhancement and cross-modality fusion for volumetric lung tumor segmentation." *Biomedical Signal Processing and Control* 119 (2026): 109977.

10. Li, Bo, et al. "Multi-scale and edge-aware IFGNet for precise skin lesion segmentation in high-resolution dermoscopic images." *Scientific Reports* (2026).
11. He, Dongzhi, et al. "Multi-View Attention Network With Iterative Feature Refinement and Boundary Awareness for Endoscopic Image Segmentation." *IEEE Access* (2025).
12. Li, Yuqin, et al. "DBNet: A Dual-Branch Network with Boundary Awareness for Few-Shot 3D Medical Image Segmentation." *2025 IEEE 31th International Conference on Parallel and Distributed Systems (ICPADS)*. IEEE, 2025.
13. Wu, Jiawei, et al. "Boundary-aware convolutional attention network for liver segmentation in ultrasound images." *Scientific Reports* 14.1 (2024): 21529.
14. He, Dongzhi, et al. "Multi-View Attention Network With Iterative Feature Refinement and Boundary Awareness for Endoscopic Image Segmentation." *IEEE Access* (2025).
15. Xu, Shanshan, et al. "Graph-and transformer-guided boundary aware network for medical image segmentation." *Computer Methods and Programs in Biomedicine* 242 (2023): 107849.
16. Li, Yuqin, et al. "DBNet: A Dual-Branch Network with Boundary Awareness for Few-Shot 3D Medical Image Segmentation." *2025 IEEE 31th International Conference on Parallel and Distributed Systems (ICPADS)*. IEEE, 2025.
17. Li, Yuqin, et al. "DBNet: A Dual-Branch Network with Boundary Awareness for Few-Shot 3D Medical Image Segmentation." *2025 IEEE 31th International Conference on Parallel and Distributed Systems (ICPADS)*. IEEE, 2025.
18. Li, Zelin, Zhaoke Huang, and Hong Yan. "3D Cellular Segmentation of Live Embryos via Topologically and Biologically Boundary-aware Semi-supervised Learning." *2024 IEEE International Conference on Systems, Man, and Cybernetics (SMC)*. IEEE, 2024.
19. Li, Zelin, Zhaoke Huang, and Hong Yan. "3D Cellular Segmentation of Live Embryos via Topologically and Biologically Boundary-aware Semi-supervised Learning." *2024 IEEE International Conference on Systems, Man, and Cybernetics (SMC)*. IEEE, 2024.
20. Afridi, Sikandar, et al. "Deep Learning Techniques for 3D-Volumetric Segmentation of Biomedical Images." *Advances in Deep Generative Models for Medical Artificial Intelligence*. Cham: Springer Nature Switzerland, 2023. 1-41.
21. Gong, Kaijie, et al. "A Dual-Encoder Convolutional Neural Networks–Frequency Transformer framework with bidirectional attention for precise brain tumor segmentation." *Engineering Applications of Artificial Intelligence* 178 (2026): 115042.
22. Wu, Zhaoye, et al. "Dual coordinate attention (DCA) network for accurate cerebral vascular endothelium segmentation in OCT images." *Scientific Reports* (2026).
23. Mahmood, Tahir, et al. "Artificial Intelligence-Based Histopathology Segmentation for Resource-Constrained Healthcare Systems." *Diagnostics* 16.14 (2026): 2146.
24. Florindo, Joao Batista, and Amanda Pontes de Oliveira Ornelas. "ConvNeXt-FD: A Fractal-Based Deep Model for Robust Biomedical Image Segmentation." *arXiv preprint arXiv:2605.22002* (2026).
25. Shi, Tianyu, et al. "Triplet-branch diffusion model with conditional guidance and boundary enhancement for cervical nucleus segmentation." *Biomedical Signal Processing and Control* 119 (2026): 109753.
26. Yang, Yufei, and Min Chang. "DCN-KUNet: A DCNv3-Based Backbone and KAN Bottleneck for Chromosome Segmentation." *Electronics* 15.8 (2026): 1649.
27. Yu, Luhang, et al. "OncoSeg2D: A deep framework for semantic segmentation of lung cancer in 2D CT scans." *PloS one* 21.7 (2026): e0348719.
28. Wazir, Saad, et al. "MedCAGD: Context-Aware Gated Decoder for Efficient Medical Image Segmentation." *arXiv preprint arXiv:2607.00409* (2026).
29. Mao, Xuedi, et al. "Next-Generation Pathology Unveiled: AI-Enhanced Label-Free Microimaging." *Laser & Photonics Reviews* 20.3 (2026): e01429.
30. Chen, Haitao, et al. "MAP-SCTNet: multi-scale pyramid and frequency-enhanced network for colorectal cancer histopathological image segmentation." *Frontiers in Medicine* 13 (2026): 1760720.
31. Hu, Yapeng, et al. "EGD-MKANet: Edge-Guided per-Channel Gated Decoder with Memory-friendly Multi-Kernel Aggregation."
32. Benchari, Mahshid, et al. "The U-Net Architecture for MRI Brain Tumor Segmentation, Detection, and Classification: A Survey." *Biomedical Materials & Devices* (2026): 1-27.
33. Gao, Yi, et al. "Svanet: synergistic vision and adaptation network for lightweight medical image segmentation." *Multimedia Systems* 32.1 (2026): 35.
34. Awais, Muhammad, et al. "Boosting Brain Tumor Detection Accuracy in MRI Using Transfer Learning and Fine-Tuned DeepLabv3."
35. Shu, Xiu, et al. "Efficient Medical Image Segmentation in Multisensor Imaging: A Survey in the Era of Mamba and Foundation Models." *Sensors* 26.8 (2026): 2558.
36. Kirubakaran, Muthulakshmi, and Jayalakshmi Mohan. "VGG19 encoder-ISCFISO: An enhanced evolutionary framework for brain tumor segmentation." *Cluster Computing* 29.6 (2026): 370.
37. Poudel, Seema K., and Sunny K. Khadka. "PDE-Constrained Optimization for Neural Image Segmentation with Physics Priors." *arXiv preprint arXiv:2602.01069* (2026).
38. Abdellaoui, Cherifa, Samia Belkacem, and Nouredine Messaoudi. "Deep learning architectures for medical image segmentation: an organized analysis of CNN-based models and uses." *Bulletin of Electrical Engineering and Informatics* 15.1 (2026): 424-437.

39. Liu, Guiru, et al. "Channel-level self-attention feature adjustment and neighborhood context reverse aggregation network for 3D LiDAR point cloud segmentation." *Journal of Electronic Imaging* 35.2 (2026): 023011.
40. Ishida, Ryoza, et al. "PAVSAT: an automated blood vessel analysis tool using deep learning-based segmentation and image processing." *BMC bioinformatics* (2026).
41. BOUNEGTA, Ahmed, et al. "Hybrid 3D U-Net Transformer for Precision Glioma Segmentation." *Indonesian Journal of Electrical Engineering and Informatics (IJEI)* 14.1 (2026): 293-305.