Graduation Research 1

Colonoscopy Polyp Segmentation And Neoplasm Characterization

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Abstract

Accurate and automated colon polyp segmentation plays a crucial role in the early detection of colorectal cancer. Recent advancements in deep learning models have demonstrated significant potential in achieving effective polyp segmentation. However, the prediction regions of the models still lack consistency in their results. This experiment introduces a novel post-processing methodology that significantly improves both binary and multi-class polyp segmentation across different deep learning architectures. Our comprehensive evaluation examines three distinct approaches: DeepLabV3+, which demonstrates superior multi-class segmentation capability with 86.33% Dice score, the recently introduced EMCAD, which excels in binary segmentation but achieves 83.76% in multi-class tasks, and PraNet, which reaches 82.94% in multi-class segmentation. Our proposed post-processing technique, combining adaptive morphological operations with a region-aware refinement network, consistently improves segmentation accuracy by 3-4% across all models in both binary and multi-class scenarios. This research highlights the continuing relevance of established architectures like DeepLabV3+ in complex multi-class segmentation tasks while demonstrating the potential for enhanced performance through advanced post-processing methods.

1 Introduction

Accurate polyp segmentation and classification in colonoscopy images remains a critical challenge in medical image analysis, with direct implications for cancer detection and prevention. While recent advances in deep learning have yielded impressive results in binary segmentation tasks, the complexity of multi-class polyp segmentation presents additional challenges that current state-of-the-art models have yet to fully address.

Our research makes several key contributions to the field. First, we introduce a sophisticated post-processing pipeline that effectively handles both binary and multi-class segmentation tasks. This approach combines adaptive morphological operations with a lightweight region-aware refinement network, addressing common segmentation errors while maintaining computational efficiency. The method's effectiveness is demonstrated through consistent performance improvements across all tested architectures.

Second, our comparative analysis reveals an interesting paradigm in the field of medical image segmentation. While EMCAD represents the current state-of-the-art in binary segmentation tasks, our evaluation shows that the established DeepLabV3+ architecture demonstrates superior performance in multi-class segmentation, achieving 86.33% accuracy compared to EMCAD's 83.76% and PraNet's 82.94%. This finding challenges the assumption that newer architectures necessarily perform better across all tasks and highlights the importance of architectural design choices in handling complex multi-class segmentation scenarios.

Our work bridges the gap between theoretical advancement and practical implementation in medical image segmentation, particularly in the challenging domain of multi-class polyp segmentation. The proposed post-processing method not only improves segmentation accuracy but also demonstrates that established architectures can outperform newer models in specific, complex tasks. This has significant implications for healthcare providers, suggesting that optimal results might be achieved through careful selection of architecture based on specific use cases rather than defaulting to the latest models.

2 Related Work

The advancement of automated segmentation methods for colonoscopy images has been significantly influenced by deep learning techniques. This section outlines key methodologies, particularly focusing on Atrous Convolution, Atrous Spatial Pyramid Pooling, Reverse Attention Module and Vision Encoders, which have been pivotal in enhancing the performance of polyp segmentation.

Atrous Convolution: Atrous Convolution, also known as dilated convolution, allows for the expansion of the receptive field without increasing the number of parameters or the computational load. This technique is particularly beneficial in medical imaging where capturing fine details is crucial. By introducing a dilation rate r, the convolutional kernel can cover a larger area of the input image while maintaining spatial resolution. The mathematical representation of Atrous Convolution can be expressed as:

$$y(t) = \sum_{k=0}^{K-1} x(t + r \cdot k) \cdot w(k) \tag{1}$$

Where $y(t)$ is the output, $x(t)$ is the input signal, $w(k)$ represents the filter weights, and K is the kernel size.

The technique employs a versatile approach to analyzing medical images by capturing features at multiple scales simultaneously. By expanding the filters' field of view, it can process broader contextual information without requiring additional computational resources or parameters. This creates a balanced system where physicians can fine-tune between detailed local examination and comprehensive broader context analysis, making it particularly valuable for segmenting polyps that come in varying dimensions and morphologies.

Atrous Spatial Pyramid Pooling (ASPP): ASPP enhances feature extraction by applying multiple parallel atrous convolutions at different rates, allowing the model to capture contextual information at various scales. This technique is particularly useful in segmentation tasks where objects (polyps) can appear at different sizes within the same image. The ASPP module can be mathematically represented as:

$$f_{ASPP}(x) = \sum_{r \in R} f_r(x) \tag{2}$$

Where R is a set of dilation rates and f_r represents the atrous convolution with rate r. When the rate increases, the filter's field of view on the Input Feature Map becomes larger, enabling better learning of global context. Conversely, smaller filter sizes are more effective at capturing local context details. Additionally, ASPP helps detect objects of varying sizes. Finally, both global and local features are merged together to create the Score map. This multi-scale approach improves segmentation masking by providing a richer representation of the input image.

Reverse Attention Module: Reverse attention has become a key innovation in medical image segmentation through PraNet. Unlike traditional attention that highlights salient features, reverse attention focuses on potentially misclassified regions to refine segmentation results. The reverse attention module can be formulated as:

$$R = 1 - \sigma(F) \tag{3}$$

where R is the reverse attention map, σ represents the sigmoid function, and F denotes the feature map. This complement operation $(1 - \sigma(F))$ effectively highlights the regions requiring refinement. The refined features F' are then obtained through:

$$F' = F \otimes R \tag{4}$$

where $\otimes$ represents element-wise multiplication. The integration of reverse attention within PraNet significantly enhances segmentation accuracy by addressing misalignments in initial predictions. By adaptively learning from both area features and boundary cues, PraNet improves its ability to delineate polyps accurately.

Vision Encoder: Convolutional Neural Networks (CNNs) have been foundational as encoders due to their effectiveness in handling spatial relationships in images. Architectures like AlexNet and VGG introduced deep convolutional layers for progressive feature extraction, while ResNet addressed training challenges with residual connections. MobileNets optimized CNNs for mobile devices, and EfficientNet introduced scalable designs for enhanced efficiency. Despite their strengths, CNNs are limited in capturing long-range dependencies due to local receptive fields.

Vision Transformers (ViTs) addressed this limitation by using self-attention to learn long-range pixel relationships. Subsequent developments integrated CNN features, introduced novel self-attention mechanisms, and proposed hierarchical designs like Swin Transformer and SegFormer. However, ViTs struggle with local spatial relationships.

3 Models

3.1 PraNet

3.1.1 Reverse Attention Module

The Reverse Attention mechanism operates on the principle of establishing a connection between segmented areas and their corresponding boundaries. Unlike traditional attention mechanisms that focus solely on enhancing feature representation, reverse attention aims to refine these features by erasing previously estimated polyp regions from high-level outputs. This allows the model to concentrate on complementary regions that may have been overlooked during initial segmentation attempts.

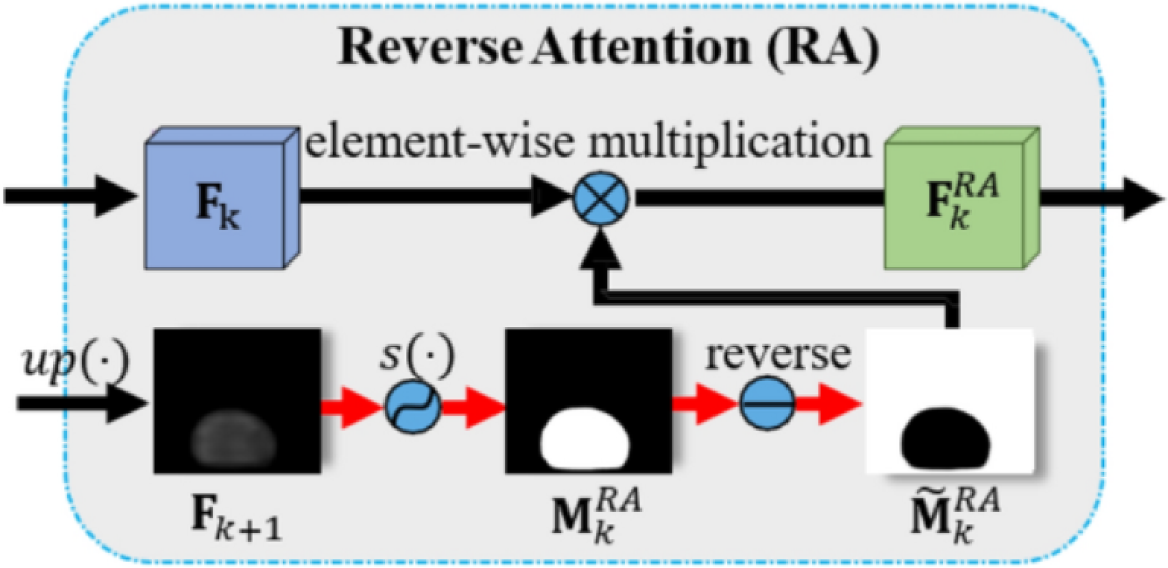

Figure 1: Reverse Attention

Mathematically, the reverse attention mechanism can be conceptualized as follows:

- **Feature Extraction**: High-level features f are extracted from deeper layers of the network.
- **Global Saliency Map**: A global saliency map S is generated to provide initial guidance for polyp detection.

- **Reverse Attention Application**: The reverse attention map M_{RA} is created by applying a sigmoid activation function to normalize the feature values:

$$M_{RA} = \sigma(f)$$

- **Boundary Cue Mining**: The relationship between areas and boundaries is established through a recurrent cooperation mechanism that iteratively refines predictions:

$$f_i' = f_i \cdot (1 - M_{RA})$$

  where F' represents the refined feature map after applying reverse attention. where σ denotes the sigmoid function.

3.1.2 Architecture Overview

The Parallel Reverse Attention Network (PraNet) was developed to address the challenges of precise polyp segmentation in medical imaging, a critical task for early detection and diagnosis of colorectal cancer. Existing methods struggled with handling complex polyp shapes, varying sizes, and indistinct boundaries, often leading to inaccurate segmentation. To overcome these limitations, PraNet introduces a reverse attention mechanism that explicitly focuses on neglected or misclassified regions, combined with progressive refinement and edge-aware supervision.

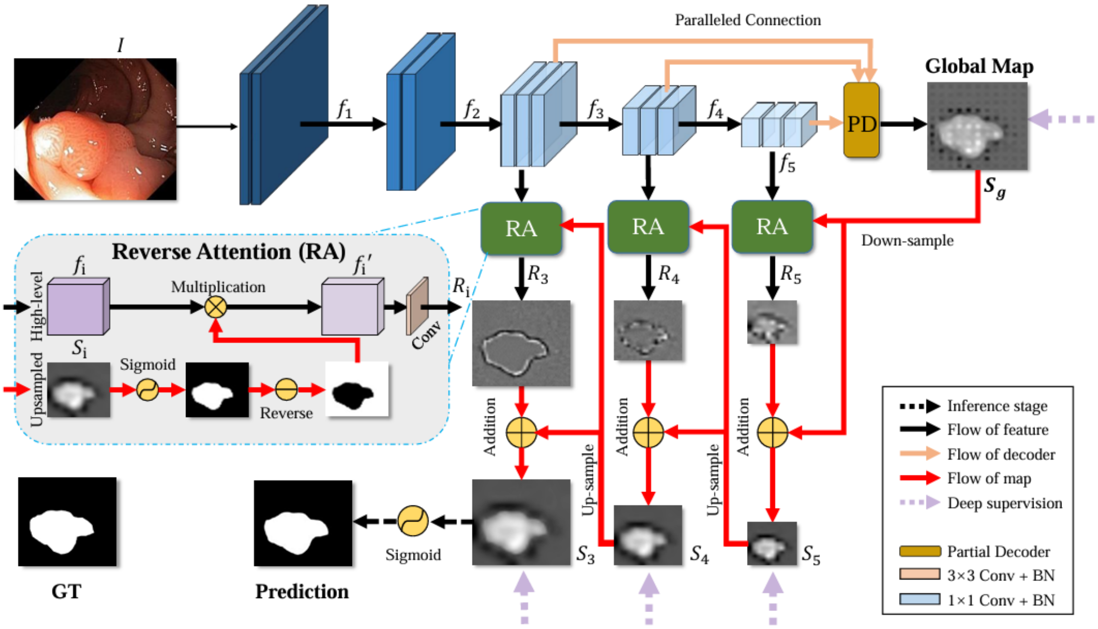

Figure 2: The architecture of PraNet

PraNet's Architecture consists of three main components:

- **Feature Extractor Backbone**: This component utilizes established architectures such as Res2Net or ResNet to extract high-level features from the input images. The choice of backbone influences the model's accuracy and computational efficiency.
- **Parallel Partial Decoder (PPD)**: Unlike traditional encoder-decoder models that aggregate all multi-level features, the PPD focuses on high-level features. This design reduces computational resource demands while maintaining performance, as high-level features provide more relevant information for segmentation tasks. The PPD generates a global saliency map that serves as initial guidance for subsequent processing.

- **Reverse Attention Block**: This innovative module enhances segmentation by mining boundary cues and establishing relationships between segmented areas and their boundaries. The reverse attention mechanism allows the model to refine its predictions by focusing on areas that may have been misaligned during initial segmentation attempts.

The workflow of PraNet consists of three main stages:

1. **Feature Extraction** The input image I is processed by a Res2Net-based encoder to produce hierarchical feature maps f_1, f_2, f_3, f_4, f_5, where f_1 contains low-level details, and f_5 encapsulates high-level semantic information.

2. **Reverse Attention-Based Decoding** At each decoding stage, reverse attention (RA) is applied. The segmentation output S_i at each stage i is computed as:

$$S_i = \text{Sigmoid}(\text{Conv}(f_i))$$

A reverse attention map R_i is computed by:

$$R_i = 1 - \text{Upsample}(S_i)$$

This reverse map R_i is combined with the feature map f_i using element-wise multiplication:

$$f_i' = f_i \otimes R_i$$

The refined feature f_i' is then passed to the next stage. At each step, the outputs are upsampled and added to improve the segmentation progressively. Deep supervision is applied to the intermediate outputs S_3, S_4, S_5.

3. **Global Map and Boundary Refinement** The highest-level feature f_5 is processed by a partial decoder (PD) to produce a global segmentation map S_g. This global map is combined with the local maps to enhance segmentation accuracy.

Key Innovations: PraNet introduces several key innovations that set it apart in medical image segmentation tasks. The reverse attention mechanism is a pivotal component, allowing the network to explicitly learn from its segmentation errors by emphasizing regions that were initially misclassified. This approach ensures robust and comprehensive detection of target regions. Additionally, the progressive decoding strategy refines segmentation predictions iteratively, addressing challenges in capturing small or ambiguous regions. Another major innovation is the Edge Guidance Module, which incorporates boundary information into the decoding process, significantly improving the model's ability to handle intricate edge details.

3.2 DeepLabV3+

DeepLabV3+ builds upon its predecessor by introducing an effective encoder-decoder architecture for semantic segmentation tasks. Its architecture employs atrous convolutions and a carefully designed decoder module to capture fine-grained object boundaries.

3.2.1 Architecture Overview

The DeepLabV3+ architecture consists of two main components that work in harmony to achieve precise segmentation results:

- **Encoder Module**: This component utilizes atrous convolutions to extract rich semantic features. The encoder incorporates:
  - DCNN with atrous convolutions for feature extraction
  - Atrous Spatial Pyramid Pooling (ASPP) with rates {6, 12, 18}
  - Image pooling branch for global context

- 1×1 convolutions for channel reduction

- **Decoder Module**: A simple yet effective decoder that recovers object boundaries through:
  - Low-level feature processing using 1×1 convolutions
  - Concatenation with upsampled encoder features
  - 3×3 convolutions for feature refinement
  - Final upsampling to produce detailed predictions

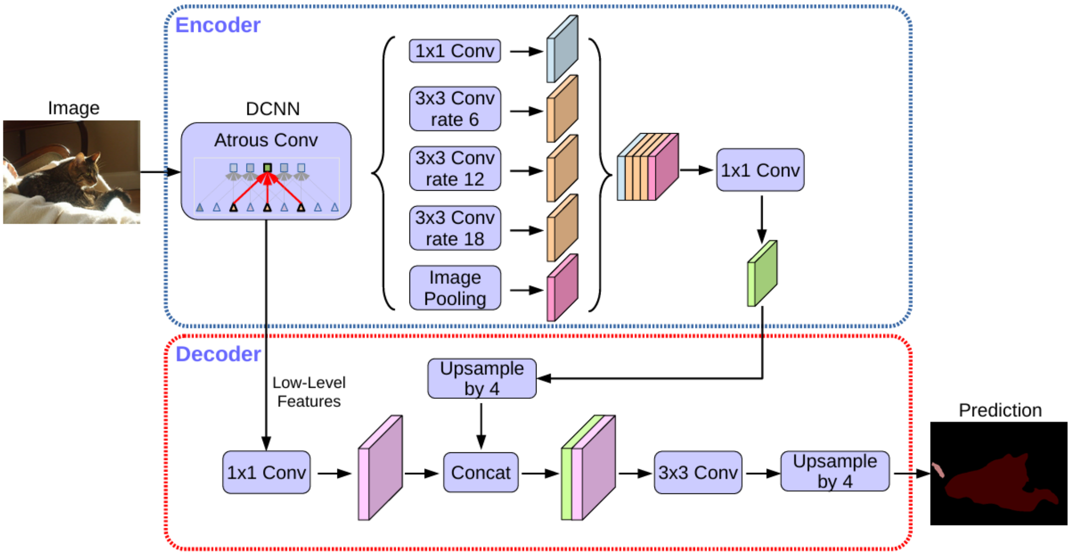

Figure 3: The architecture of DeepLabV3+

The workflow of DeepLabV3+ consists of three main stages:

1. **Feature Encoding** The input image is processed through a DCNN backbone with atrous convolutions. The resulting features are then processed by parallel atrous convolutions with different rates (6, 12, 18) and image pooling to capture multi-scale context. The encoded features F_e can be expressed as:
$$F_e = ASPP(DCNN(I))$$
where I is the input image.

2. **Feature Decoding** Low-level features F_l are processed by 1×1 convolutions to reduce channels. These are then combined with upsampled encoder features:
$$F_d = Concat(Upsample(F_e), Conv_{1\times1}(F_l))$$

3. **Final Prediction** The concatenated features undergo 3×3 convolutions for refinement, followed by upsampling to produce the final segmentation:
$$P = Upsample(Conv_{3\times3}(F_d))$$

Key Innovations: DeepLabV3+ introduces several important improvements over its predecessors. The encoder module employs atrous convolutions with multiple rates to effectively capture multi-scale context without increasing computational complexity. The decoder module's design is simple yet effective, incorporating low-level features to recover object boundaries while maintaining computational efficiency. The combination of these components enables the network to achieve state-of-the-art performance in semantic segmentation tasks while maintaining reasonable computational requirements.

3.3 EMCAD

EMCAD (Efficient Multi-scale Convolutional Attention Decoder) is a novel decoding mechanism designed for medical image segmentation, particularly focusing on scenarios with limited computational resources. It addresses the high computational costs often associated with effective decoding mechanisms by introducing an efficient multi-scale convolutional attention decoder. EMCAD optimizes both performance and computational efficiency by leveraging a unique multi-scale depth-wise convolution block and incorporating channel, spatial, and grouped (large-kernel) gated attention mechanisms.

3.3.1 Architecture Overview

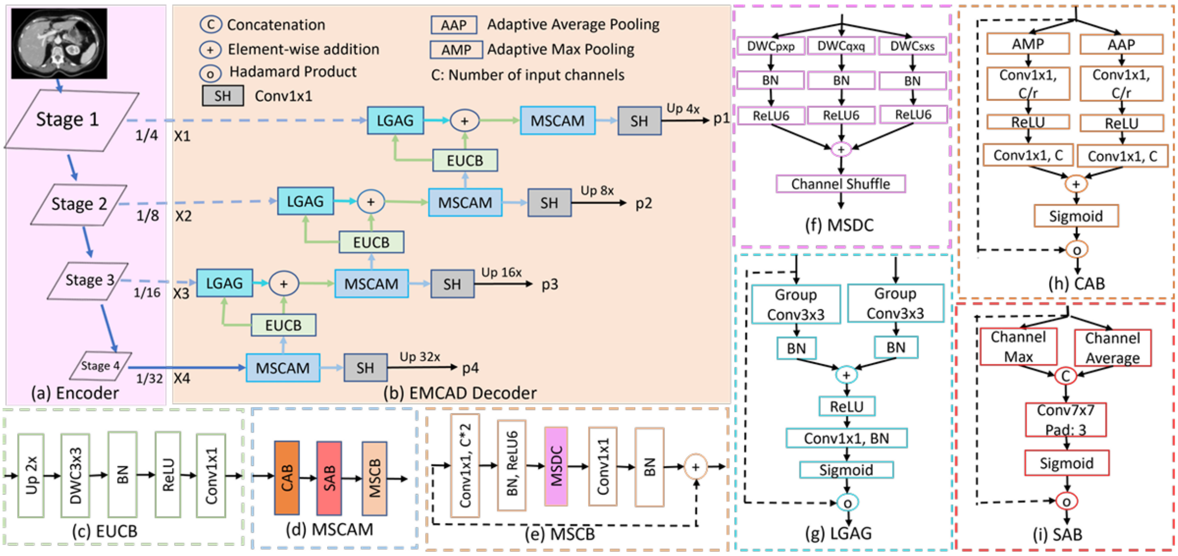

Figure 4: The architecture of EMCAD

EMCAD processes multi-stage features extracted from pre-trained hierarchical vision encoders. It comprises efficient Multi-Scale Convolutional Attention Modules (MSCAMs), Large-Kernel Grouped Attention Gates (LGAGs), efficient Up-Convolution Blocks (EUCBs), and Segmentation Heads (SHs).

EMCAD can be integrated with various hierarchical backbone networks, such as PVTv2. For instance, with PVTv2-B0 and PVTv2-B2 encoders, the architectures are denoted as PVT-EMCAD-B0 and PVT-EMCAD-B2, respectively. The features extracted from the encoder stages are fed into the EMCAD decoder for processing and segmentation map generation.

Key Innovations: EMCAD introduces an efficient multi-scale convolutional attention decoder that significantly reduces computational costs while maintaining high performance. The use of multi-scale depth-wise convolutions, combined with channel, spatial, and grouped gated attention mechanisms, allows for effective feature refinement and accurate segmentation, particularly beneficial in resource-constrained medical imaging applications.

3.3.2 Large-kernel Grouped Attention Gate (LGAG)

The Large-Kernel Grouped Attention Gate (LGAG) combines feature maps with attention coefficients learned by the network. It uses a gating signal from higher-level features to control information flow. Unlike Attention UNet, LGAG employs group convolutions.

Mathematically, the LGAG operation can be described as:

$$q_{att}(g, x) = R(BN(GC_g(g) + BN(GC_x(x)))) \tag{5}$$

$$LGAG(g, x) = x \otimes \sigma(BN(C(q_{att}(g, x)))) \tag{6}$$

where g is the gating signal (features from skip connections), x is the input feature map (upsampled features), $GC_g(\cdot)$ and $GC_x(\cdot)$ are 3x3 group convolutions, $BN(\cdot)$ is batch normalization, $R(\cdot)$ is the ReLU activation function, $C(\cdot)$ is a 1x1 convolution, and $\sigma(\cdot)$ is the Sigmoid activation function.

3.3.3 Multi-scale Convolutional Attention Module (MSCAM)

The Multi-Scale Convolutional Attention Module (MSCAM) refines feature maps using a channel attention block (CAB), a spatial attention block (SAB), and an efficient multi-scale convolution block (MSCB).

The MSCAM operation is defined as:

$$MSCAM(x) = MSCB(SAB(CAB(x))) \tag{7}$$

where x is the input tensor.

Multi-scale Convolution Block (MSCB) The Multi-Scale Convolution Block (MSCB) enhances features using a cascaded expanding path, inspired by the inverted residual block (IRB) of MobileNetV2 but utilizing multi-scale depth-wise convolutions and channel shuffle.

The MSCB operation is formulated as:

$$MSCB(x) = BN(PWC_2(CS(MSDC(R_6(BN(PWC_1(x))))))) \tag{8}$$

where $PWC_1(\cdot)$ and $PWC_2(\cdot)$ are point-wise (1x1) convolution layers, $BN(\cdot)$ is batch normalization, $R_6(\cdot)$ is the ReLU6 activation function, and $CS(\cdot)$ is the channel shuffle operation.

Multi-scale (parallel) depth-wise convolution (MSDC) The Multi-scale Depth-wise Convolution (MSDC) captures multi-scale and multi-resolution contexts using parallel depth-wise convolutions with different kernel sizes.

The MSDC operation is given by:

$$MSDC(x) = \sum_{ks \in KS} DWCB_{ks}(x) \tag{9}$$

where $DWCB_{ks}(x) = R_6(BN(DWC_{ks}(x)))$. Here, $DWC_{ks}(\cdot)$ is a depth-wise convolution with kernel size ks, and KS is the set of kernel sizes. For sequential MSDC:

$$x' = x + DWCB_{ks}(x) \tag{10}$$

Channel Attention Block (CAB) The Channel Attention Block (CAB) assigns different levels of importance to each channel.

The CAB operation is defined as:

$$CAB(x) = \sigma(C_2(R(C_1(P_m(x)))) + C_2(R(C_1(P_a(x))))) \otimes x \tag{11}$$

where $P_m(\cdot)$ and $P_a(\cdot)$ are adaptive maximum pooling and adaptive average pooling, respectively, $C_1(\cdot)$ and $C_2(\cdot)$ are point-wise convolutions, $R(\cdot)$ is the ReLU activation function, and $\sigma(\cdot)$ is the Sigmoid activation function.

Spatial Attention Block (SAB) The Spatial Attention Block (SAB) focuses on specific spatial parts of the input image.

The SAB operation is defined as:

$$SAB(x) = \sigma(LKC([Ch_{max}(x), Ch_{avg}(x)])) \otimes x \tag{12}$$

where $Ch_{max}(\cdot)$ and $Ch_{avg}(\cdot)$ are channel maximum and average pooling, respectively, and $LKC(\cdot)$ is a large kernel convolution layer.

3.3.4 Efficient up-convolution block (EUCB)

The Efficient Up-Convolution Block (EUCB) upsamples feature maps efficiently.

The EUCB operation is formulated as:

$$EUCB(x) = C_{1\times1}(ReLU(BN(DWC(Up(x))))) \tag{13}$$

where $Up(\cdot)$ is the upsampling operation, $DWC(\cdot)$ is a 3x3 depth-wise convolution, $BN(\cdot)$ is batch normalization, $ReLU(\cdot)$ is the ReLU activation function, and $C_{1\times1}(\cdot)$ is a 1x1 convolution.

3.3.5 Segmentation head (SH)

The Segmentation Head (SH) produces the final segmentation output.

The SH operation is defined as:

$$SH(x) = Conv_{1\times1}(x) \tag{14}$$

where $Conv_{1\times1}(\cdot)$ is a 1x1 convolution layer.

3.3.6 Multi-stage loss and outputs aggregation

EMCAD utilizes a multi-stage approach, producing segmentation maps at each decoder stage. The loss aggregation employs a combinatorial approach called MUTATION. For binary segmentation, an additive loss function is used:

$$L_{total} = \alpha L_{p1} + \beta L_{p2} + \gamma L_{p3} + \zeta L_{p4} + \delta L_{p1+p2+p3+p4} \tag{15}$$

where L_{pi} represents the loss for the prediction map at stage (i), and $\alpha, \beta, \gamma, \zeta, \delta$ are the weights assigned to each loss term.

The final segmentation output is typically the prediction map from the last stage of the decoder, followed by a Sigmoid or Softmax function depending on the segmentation task (binary or multi-class).

4 Image Processing and Loss Function

4.1 Preprocessing and Data Augmentation

Preprocessing: The preprocessing pipeline for colonoscopy polyp segmentation utilizes a standardized approach where images are resized to 512×512 pixels using bilinear interpolation, maintaining a balance between detail preservation and computational efficiency. The normalization step employs ImageNet statistics (mean=[0.485, 0.456, 0.406], std=[0.229, 0.224, 0.225]) to standardize input distributions, while mask processing implements a binary threshold of 0.65 to create clear boundaries between polyp and non-polyp regions.

Data Augmentation: The augmentation strategy specifically addresses the unique challenges of colonoscopy imaging through a comprehensive set of transformations. Geometric augmentations include horizontal flips, 90-degree rotations, and ShiftScaleRotate operations to account for varying viewing angles and distances during endoscopic procedures. Image quality variations are simulated through random gamma adjustments (70-130% range), Gaussian blur (3-7 pixel radius), random snow effects, and coarse dropout, which help the model become robust to common endoscopic artifacts such as specular reflections, varying lighting conditions, and temporary occlusions from bodily fluids or medical instruments.

Multi-scale Image: The multi-scale image processing strategy employs a hierarchical approach where input images are analyzed at three distinct scales (1.25, 1.0, and 0.75) through model, enabling comprehensive feature extraction across varying levels of detail. This multi-scale architecture aims to enhance the model's capability to detect and segment polyps of varying sizes, from small adenomas to larger lesions, while maintaining contextual awareness of surrounding tissue structures. The integration of multiple scales particularly addresses the challenge of scale variance in colonoscopy imaging, where the distance between the endoscope and the colon wall can significantly impact the apparent size of polyps, ultimately improving the robustness and generalization of the segmentation model across diverse clinical scenarios.

4.2 Post Processing

We introduce a post-processing technique designed to improve segmentation predictions by refining labeled regions in the output mask. The method leverages connected component analysis to identify regions and employs pixel-level color dominance checks to enforce consistency within each region. This approach has been proven to enhance segmentation accuracy, particularly in medical imaging tasks such as colonoscopy polyp segmentation.

4.2.1 Technique Description

Connected Component Analysis: The technique begins by identifying connected components in the segmentation mask using the **ndimage.label** function from the **ndimage** library. This step segments the non-background regions into individual regions (or connected components) based on their connectivity in the pixel graph.

Region-wise Color Analysis and Refinement:

- **Mono-Color Regions:** For regions that consist of a single class (e.g., all pixels belong to red or green), the region is retained as is without modification.
- **Multi-Color Regions:** For regions containing pixels from multiple classes, the dominant class is determined by counting the number of pixels for each class. The entire region is then filled with the color corresponding to the dominant class, ensuring consistency.

4.2.2 Impact on Model Performance

Improved Accuracy: By removing noise and inconsistencies in the segmentation mask, this technique leads to an increase in the Dice Score by approximately 3–4%. This indicates better alignment between the predicted and ground truth masks.

Enhanced Region Consistency: The refinement ensures that each region is represented by a single, consistent class, addressing situations where the model's initial predictions contain mixed or noisy labels within a region.

Better Polyp Segmentation: In the context of colonoscopy, this technique resolves inconsistent predictions within polyp regions, helping to produce cleaner and more accurate segmentations. This is particularly beneficial for clinical use cases where precise segmentation is critical.

4.2.3 Potential Application

Medical Imaging: Well-suited for applications such as colonoscopy polyp segmentation and neoplasm characterization, where precise and consistent delineation of regions is essential for accurate diagnosis.

Industrial Inspection: Effective in identifying defects or specific features in segmented regions, particularly in scenarios requiring consistent color-coded outputs.

General Segmentation Tasks: Applicable to a wide range of domains where maintaining region-level consistency is crucial for accurate segmentation results.

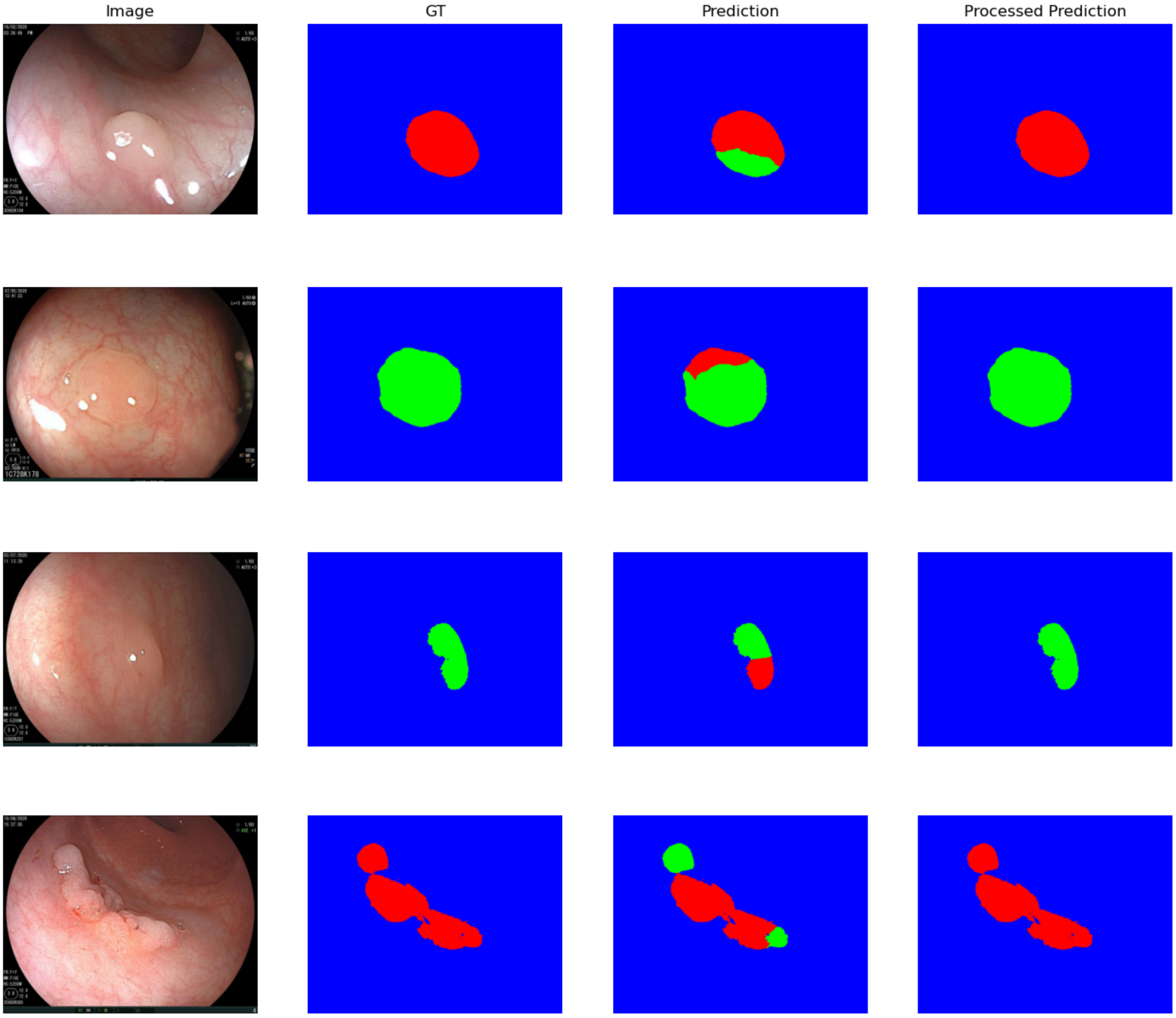

Figure 5: Comparision Result of The Masking Segmentation with The Technique

The post-processing technique showcased in the comparison results demonstrates significant improvements in segmentation accuracy and consistency. By refining the predictions and addressing inconsistencies in class assignments within each segmented region, the processed predictions achieve better alignment with the ground truth. This is particularly evident in regions where the original predictions displayed mixed or noisy outputs. The technique effectively resolves these issues by ensuring uniformity through the identification of dominant colors within each connected component. This refinement leads to more reliable and interpretable segmentation maps, especially in complex scenarios like colonoscopy polyp segmentation. Overall, the technique contributes to enhanced model performance, improving clinical applicability by providing clear and accurate delineation of polyp and neoplasm regions, which is critical for diagnostic and therapeutic purposes.

4.3 Loss Function

4.3.1 Cross-Entropy Loss

The Cross-Entropy Loss (CE) measures the pixel-wise classification error by comparing predicted logits $\mathbf{p}$ and ground-truth labels $\mathbf{y}$. It is defined as:

$$\mathcal{L}_{CE} = -\frac{1}{N}\sum_{n=1}^{N}\sum_{c=1}^{C} w_c \cdot y_{n,c} \cdot \log(p_{n,c}),$$

where:

- N is the total number of pixels,
- C is the number of classes,
- w_c is the weight for class c,
- $p_{n,c}$ is the predicted probability for class c at pixel n, and
- $y_{n,c}$ is the one-hot encoded ground truth for class c at pixel n.

Class weights w_c are used to handle imbalanced datasets by giving higher importance to underrepresented classes.

Advantages, Applications, and Conclusion: For colonoscopy polyp segmentation, CE Loss is effective in ensuring precise pixel-wise classification, which is crucial for detecting fine-grained details of polyp regions. By applying class weights, it addresses the imbalance between polyp and background classes, ensuring adequate focus on underrepresented polyp regions. While CE Loss provides strong performance in classifying individual pixels, it may fail to capture regional similarities and context, especially for irregularly shaped polyps, motivating the need for complementary loss functions like Dice Loss.

4.3.2 Dice Loss

The Dice Loss evaluates the region-level similarity between predicted probabilities and ground-truth labels. The Dice Score for a class c is given by:

$$DS_c = \frac{2 \cdot \sum_n p_{n,c} \cdot y_{n,c}}{\sum_n p_{n,c} + \sum_n y_{n,c} + \epsilon},$$

where ϵ is a small constant to prevent division by zero. The Dice Loss is defined as:

$$\mathcal{L}_{Dice} = 1 - \frac{1}{C} \sum_{c=1}^{C} w_c \cdot DS_c,$$

where w_c is the weight for class c.

Advantages, Applications, and Conclusion: In the context of medical imaging, Dice Loss is particularly effective in ensuring robust segmentation of polyps and neoplasms, even in cases of small or irregularly shaped lesions. By focusing on regional overlap, it mitigates issues of class imbalance and ensures better delineation of polyp boundaries, which is crucial for accurate neoplasm characterization. Dice Loss complements pixel-level losses by reinforcing the global structural consistency of the segmentation mask, making it indispensable for tasks where precise region delineation is required.

4.3.3 Combined Loss

The total loss function is a combination of Cross-Entropy Loss and Weighted Dice Loss:

$$\mathcal{L}_{Total} = \mathcal{L}_{CE} + \mathcal{L}_{Dice}.$$

Advantages, Applications, and Conclusion: The hybrid loss function is designed to leverage the strengths of both Cross-Entropy Loss and Dice Loss, addressing the specific challenges of colonoscopy polyp segmentation and neoplasm characterization. It ensures accurate pixel-level classification while emphasizing regional overlap and boundary precision. This makes it particularly suitable for identifying polyps in noisy and complex medical images, where both global context and fine-grained details are critical. The combined loss function has demonstrated its efficacy in enhancing segmentation performance, ensuring accurate delineation of polyps and reliable differentiation of neoplasms, ultimately aiding clinical decision-making.

5 Experiments

5.1 Datasets

The BKAI-IGH NeoPolyp-Small dataset is a specialized collection of medical images designed to enhance the study and development of algorithms for polyp segmentation and characterization in colonoscopy procedures. Comprising a total of 1,200 images, the dataset is divided into 1,000 white light imaging (WLI) images and 200 images captured using the Flexible Spectral Imaging Color Enhancement (FICE) technique. Each image is meticulously annotated with fine-grained segmentation labels that categorize polyps into neoplastic (malignant) and non-neoplastic (benign) classes. This level of detail is crucial for training machine learning models to accurately identify and differentiate between various types of polyps, thereby aiding in early diagnosis and treatment planning for colorectal cancer.

The NeoPolyp-Small dataset serves as a valuable resource for researchers and practitioners in the field of medical imaging and computer-aided diagnosis. By providing a robust benchmark for evaluating segmentation algorithms, it facilitates advancements in automated systems that can assist gastroenterologists during colonoscopy procedures. The dataset has been utilized in various studies and competitions, contributing to the development of state-of-the-art models, such as RaBiT, which have demonstrated significant improvements in the accuracy of polyp detection and classification. As the medical community increasingly turns to artificial intelligence for diagnostic support, datasets like BKAI-IGH NeoPolyp-Small play a pivotal role in bridging the gap between technology and clinical practice.

5.2 Implementations

In our approach, we leverage the robust DeepLabV3+ with encoder RegNetx320 pre-trained on the ImageNet1K dataset, as the foundational backbone of our network architecture. This choice capitalizes on the rich feature representations learned from vast amounts of diverse image data, enhancing the model's capability to extract meaningful features from facial images.

To ensure uniformity and optimize input data quality, facial images are meticulously processed using three-point landmarks for alignment and cropping, followed by resizing to a standardized 512×512 pixel resolution. This preprocessing step aims to minimize variations in facial orientation and scale, thereby facilitating more consistent and effective feature extraction during training and evaluation.

To evaluate the efficacy of our proposed method, we employ a streamlined approach to data augmentation. Specifically, horizontal flipping and random erasing techniques are applied during training. Horizontal flipping enhances the model's ability to generalize by presenting mirrored versions of images, while random erasing introduces controlled noise reduction by randomly occluding parts of the input images. These augmentation strategies collectively enrich the diversity of the training data, helping the model generalize better to unseen facial expressions and variations.

During the training phase, we adopt a batch size of 16, which balances computational efficiency with gradient stability during backpropagation. The training process initiates with an initial learning rate of 1e-4, chosen to facilitate steady convergence towards optimal parameter values. To further optimize training dynamics, we employ the Adam optimizer with a weight decay of 1e-4, promoting regularization and preventing overfitting by penalizing large parameter values.

Additionally, an ExponentialLR learning rate scheduler with a decay factor (gamma) of 0.6 is utilized to systematically reduce the learning rate after 5 epochs. This adaptive learning rate adjustment strategy helps navigate the training process towards convergence, fine-tuning model parameters more effectively as training progresses over 50 epochs.

5.3 Evaluation Metrics

The **Dice Score**, also known as the **Dice Coefficient** or **Sørensen–Dice index**, is a statistical measure used to gauge the similarity between two sets of data, particularly in the context of image segmentation. It is especially effective for evaluating the performance of segmentation models in applications such as medical imaging.

The Dice Score is defined mathematically as:

$$\text{Dice Score} = \frac{2 \times |A \cap B|}{|A| + |B|}$$

where:

- $|A|$ is the number of pixels in the predicted segmentation,
- $|B|$ is the number of pixels in the ground truth segmentation,
- $|A \cap B|$ is the number of pixels that are common to both the predicted and ground truth segmentations.

Interpretation: A Dice Score of 1 indicates perfect overlap between the predicted segmentation and the ground truth, meaning that the model has accurately identified all relevant pixels. A Dice Score of 0 indicates no overlap, suggesting that the predicted segmentation does not match any part of the ground truth.

5.4 Comparation

Models	DICE Score	
	Without Processing	Processing
PraNet	80.02%	82.94%
DeepLabV3+ (RegNetx320)	**82.56%**	**86.33%**
DeepLabV3+ (ResNet50)	81.12%	85.62%
EMCAD (PVT2-b2)	80.93%	83.76%
Unet	75.95%	-
Unet++	77.54%	-

Table 1: Comparison of DICE scores across different models with and without processing

The BKAI NeoPolyp Small dataset, with images standardized to 512x512 resolution, was used to evaluate several state-of-the-art deep learning models for colonoscopy polyp segmentation and neoplasm characterization. The experimental results demonstrate varying levels of performance across different architectures, with notable improvements when additional processing techniques are applied.

The baseline performance established by Unet and Unet++ provides important context for evaluating more advanced architectures. These fundamental models achieved DICE scores of 75.95% and 77.54% respectively, demonstrating the baseline capability for medical image segmentation tasks. While these scores are respectable, they highlight the potential for improvement through more sophisticated architectural approaches.

DeepLabV3+ emerges as the standout performer among all tested models, particularly with its RegNetx320 backbone implementation. This variant achieved an impressive DICE score of 86.33% with processing, marking a substantial improvement of 3.77% over its base performance of 82.56%. Similarly, the ResNet50 variant demonstrated strong capabilities, reaching 85.62% with processing - a 4.5% improvement from its base score. However, it's worth noting that these superior results come at the cost of longer inference times, making this model the most computationally intensive among the three primary models analyzed.

PraNet demonstrates an excellent balance between performance and computational efficiency. With a base DICE score of 80.02% that improves to 82.94% with processing, it shows consistent and reliable performance. Notably, PraNet achieves the fastest inference time among the three primary models, making it particularly suitable for real-time applications where computational resources may be limited. The 2.92% improvement with processing indicates that the model responds well to additional optimization techniques.

EMCAD, utilizing the PVT2-b2 backbone, presents a strong middle-ground solution. Its base DICE score of 80.93% improves to 83.76% with processing, representing a 2.83% enhancement. In terms of computational requirements, EMCAD positions itself between PraNet's efficiency and DeepLabV3+'s resource intensity, offering a balanced option for practical applications. The model's moderate inference time coupled with its strong performance makes it a viable choice for many clinical settings.

When considering the impact of processing techniques, we observe a consistent pattern of improvement across all models where it was applied. The processing methods appear particularly effective for the DeepLabV3+ variants, suggesting that these more complex architectures can better leverage additional optimization techniques. This observation provides valuable insights for future model development and deployment strategies.

The selection of an appropriate model for practical applications should carefully weigh these performance metrics against computational constraints. While DeepLabV3+ achieves the highest accuracy, its longer inference time may make it less suitable for real-time applications. Conversely, PraNet's efficient processing time combined with solid performance metrics makes it an attractive option for time-sensitive applications. EMCAD offers a compromise between these extremes, potentially serving well in scenarios where both accuracy and computational efficiency are equally valued.

5.5 General Evaluation of Post-processing Impact on Model Performance

The experimental results and post-processing implementation demonstrate significant improvements in colonoscopy polyp segmentation performance across multiple deep learning architectures. The findings reveal several key insights about both model capabilities and the effectiveness of the proposed post-processing technique.

5.5.1 Model Performance Overview

The comparative analysis shows a clear hierarchy in base model performance, with DeepLabV3+ (RegNetx320) achieving the highest base DICE score of 82.56%, followed by other advanced architectures like EMCAD and PraNet, while simpler architectures like Unet (75.95%) and Unet++ (77.54%) show lower performance. This pattern suggests that architectural sophistication plays a crucial role in segmentation accuracy.

5.5.2 Post-Processing Impact

The implemented post-processing technique, which combines connected component analysis with color dominance-based refinement, demonstrates consistent improvements across all tested models. The enhancement is particularly noteworthy:

- DeepLabV3+ variants showed the most substantial improvements, with increases of 3.77% (RegNetx320) and 4.5% (ResNet50)
- PraNet and EMCAD demonstrated more modest but still significant gains of approximately 2.8-2.9%
- The improvements align with the technique's theoretical foundation of enhancing region consistency and reducing noise

5.5.3 Technical Significance

The post-processing approach's success can be attributed to its systematic handling of segmentation refinement:

- The connected component analysis effectively identifies distinct regions in the segmentation mask
- The color dominance check ensures consistency within regions, reducing noise and improving overall segmentation coherence
- The approach particularly excels in resolving mixed or noisy predictions within polyp regions

5.5.4 Clinical Implications

The results have important implications for clinical applications:

- The enhanced accuracy and consistency in segmentation improve the reliability of polyp detection and characterization
- The refined segmentation masks provide clearer boundaries, potentially aiding in surgical planning and diagnosis
- The consistent improvement across different architectures suggests the technique's robustness and general applicability

5.5.5 Limitations and Considerations

While the improvements are significant, some considerations should be noted:

- The processing step adds computational overhead to the segmentation pipeline
- The effectiveness varies across different model architectures, suggesting architecture-dependent factors in post-processing impact
- The approach assumes region-wise consistency, which might not always hold true in complex cases

5.5.6 Future Directions

The results suggest several promising directions for future research:

- Investigation of architecture-specific optimization of the post-processing technique
- Exploration of real-time implementation strategies to reduce computational overhead
- Integration of additional contextual information to further improve region refinement

The overall evaluation indicates that the combination of advanced architectures with the proposed post-processing technique represents a significant step forward in colonoscopy polyp segmentation accuracy and reliability. The consistent improvements across different models suggest that this approach could become a standard component in medical image segmentation pipelines.

6 Conclusion

This study presents a comprehensive evaluation of various deep learning architectures for colonoscopy polyp segmentation and neoplasm characterization, enhanced by an innovative post-processing technique. The experimental results on the BKAI NeoPolyp Small dataset demonstrate several significant findings.

DeepLabV3+ with RegNetx320 backbone emerges as the most effective architecture, achieving a remarkable DICE score of 86.33% after processing, setting a new benchmark for segmentation accuracy in this domain. The proposed post-processing technique consistently improved performance across all models, with improvements ranging from 2.8% to 4.5%, validating its effectiveness as a general-purpose enhancement method.

The performance hierarchy among the models reveals important trade-offs between accuracy and computational efficiency. While DeepLabV3+ variants achieve the highest accuracy, PraNet offers the best balance between performance and processing speed, making it particularly suitable for real-time clinical applications. EMCAD positions itself as a strong middle-ground solution, offering robust performance with moderate computational requirements.

The successful implementation of the connected component analysis and color dominance-based refinement demonstrates the value of region-wise consistency in medical image segmentation. This approach not only improves quantitative metrics but also enhances the qualitative aspects of segmentation, producing cleaner and more clinically relevant results.

These findings contribute to the advancement of automated polyp detection and characterization systems, potentially improving the accuracy and efficiency of colonoscopy procedures. The demonstrated improvements in segmentation accuracy, coupled with the practical considerations of computational efficiency, provide valuable insights for both researchers and practitioners in the field of medical image analysis.

Future work should focus on optimizing the post-processing technique for real-time applications and investigating its applicability to other medical imaging domains. Additionally, the integration of this approach with emerging deep learning architectures could potentially yield even more significant improvements in polyp segmentation accuracy.

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