Polyp-PVT: Polyp Segmentation with Pyramid Vision Transformers

Bo Dong, Wenhai Wang, Deng-Ping Fan, Jinpeng Li, Huazhu Fu, and Ling Shao

Abstract—Most polyp segmentation methods use CNNs as their backbone, leading to two key issues when exchanging information between the encoder and decoder: 1) taking into account the differences in contribution between different-level features and 2) designing an effective mechanism for fusing these features. Unlike existing CNN-based methods, we adopt a transformer encoder, which learns more powerful and robust representations. In addition, considering the image acquisition influence and elusive properties of polyps, we introduce three standard modules, including a cascaded fusion module (CFM), a camouflage identification module (CIM), and a similarity aggregation module (SAM). Among these, the CFM is used to collect the semantic and location information of polyps from high-level features; the CIM is applied to capture polyp information disguised in low-level features, and the SAM extends the pixel features of the polyp area with high-level semantic position information to the entire polyp area, thereby effectively fusing cross-level features. The proposed model, named Polyp-PVT, effectively suppresses noises in the features and significantly improves their expressive capabilities. Extensive experiments on five widely adopted datasets show that the proposed model is more robust to various challenging situations (e.g., appearance changes, small objects, rotation) than existing representative methods. The proposed model is available at https://github.com/DengPingFan/Polyp-PVT.

Index Terms—Polyp segmentation, pyramid vision transformer, colonoscopy, computer vision

I. INTRODUCTION

Colonoscopy is the gold standard for detecting colorectal lesions since it enables colorectal polyps to be identified and removed in time, thereby preventing further spread. As a fundamental task in medical image analysis, polyp segmentation (PS) aims to locate polyps accurately in the early stage, which is of great significance in the clinical prevention of rectal cancer. Traditional PS models mainly rely on low-level features, e.g., texture [1], geometric features [2], simple linear iterative clustering superpixels [3]. However, these methods yield low-quality results and suffer from poor generalization ability. With the development of deep learning, PS has achieved promising progress. In particular, the U-shaped [4] has attracted significant attention due to its ability to adopt multi-level features for reconstructing high-resolution results.

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Fig. 1. The segmentation examples of our model and SANet [7] with different challenge cases, e.g., camouflage (1st and 2nd rows) and image acquisition influence (3rd row). The images from top to bottom are from ClinicDB [8], ETIS [9], and ColonDB [10], which show that our model has better generalization ability.
collects polyps’ semantic and location information from the high-level features through progressive integration. Meanwhile, the camouflaged identification module (CIM) is applied to capture polyp cues disguised in low-level features, using an attention mechanism to pay more attention to potential polyps, reducing incorrect information in the lower features. We further introduce the similarity aggregation module (SAM) equipped with a non-local and convolutional graph layer to mine local pixels and global semantic cues from the polyp area.

- Finally, we conduct extensive experiments on five challenging benchmark datasets, including Kvasir-SEG [13], ClinicDB [8], ColonDB [10], Endoscopy [14], and ETIS [9], to evaluate the performance of the proposed Polyp-PVT. On ColonDB, our method achieves a mean Dice (mDice) of 0.808, which is 5.5% higher than the existing cutting-edge method SANet [7]. On the ETIS dataset, our model achieves a mean Dice (mDice) of 0.787, which is 3.7% higher than SANet [7].

II. RELATED WORKS

A. Polyp Segmentation

Traditional Methods. Computer-aided detection is an effective alternative to manual detection, and a detailed survey has been conducted on detecting ulcers, polyps, and tumors in wireless capsule endoscopy imaging [15]. Early solutions for polyp segmentation were mainly based on low-level features, such as texture [2], geometric features [2], or simple linear iterative clustering superpixels [3]. However, these methods have a high risk of missed or false detection due to the high similarity between polyps and surrounding tissues.

Deep Learning-Based Methods. Deep learning techniques [16]–[25] have greatly promoted the development of polyp segmentation tasks. Akbari et al. [26] proposed a polyp segmentation model using a fully convolutional neural network, whose segmentation results are significantly better than traditional solutions. Brandao et al. [27] used the shape from the shading strategy to restore depth, merging the result into an RGB model to provide richer feature representations. More recently, encoder-decoder-based models, such as U-Net [4], UNet++ [28], and ResUNet++ [29], have gradually come to dominate the field with excellent performance. Sun et al. [30] introduced a dilated convolution to extract and aggregate high-level semantic features with resolution retention to improve the encoder network. Psi-Net [31] introduced a multi-task segmentation model that combines contour and distance map estimation to assist segmentation mask prediction. Hemini et al. [32] first attempted to use a deeper feature extractor to perform polyp segmentation based on Mask R-CNN [33].

Different from the methods based on U-Net [4], [28], [34], PraNet [5] uses reverse attention modules to mine boundary information with a global feature map, which is generated by a parallel partial decoder from high-level features. PolypNet [35] proposed a dual-tree wavelet pooling CNN with a local gradient-weighted embedding level set, effectively avoiding erroneous information in high signal areas, thereby significantly reducing the false positive rate. Rahim et al. [36] proposed to use different convolution kernels for the same hidden layer for deeper feature extraction with MISH and rectified linear unit activation functions for deep feature propagation and smooth non-monotonicity. In addition, they adopted joint generalized intersections, which overcome scale invariance, rotation, and shape differences. Jha et al. [37] designed a real-time polyp segmentation method called ColonSNet. For the first time, Ahmed et al. [38] applied the generative adversarial network to the field of polyp segmentation. Another interesting idea proposed by Thambawita et al. [39] is introducing pyramid-based augmentation into the polyp segmentation task. Further, Tomar et al. [40] designed a dual decoder attention network based on ResUNet++ for polyp segmentation. More recently, MSEG [41] improved the PraNet and proposed a simple encoder-decoder structure. Specifically, they used Hardnet [42] to replace the original backbone network Res2Net50 backbone network and removed the attention mechanism to achieve faster and more accurate polyp segmentation. As an early attempt, Transfuse [43] was the first to employ a two-branch architecture combining CNNs and transformers in a parallel style. DCRNet [44] uses external and internal context relations modules to separately estimate the similarity between each location and all other locations in the same and different images. MSNet [45] introduced a multi-scale subtraction network to eliminate redundancy and complementary information between the multi-scale features. Providing a comprehensive review of polyp segmentation is beyond the scope of this paper. In Tab. I, however, we briefly survey representative works related to ours.

B. Vision Transformer

Transformers use multi-head self-attention (MHSA) layers to model long-term dependencies. Unlike the convolutional layer, the MHSA layer has dynamic weights and a global receptive field, making it more flexible and effective. The transformer [65] was first proposed by Vaswani et al. for the machine translation task and has since extensively influenced the natural language processing field. To apply transformers to computer vision tasks, Dosovitskiy et al. [66] proposed a vision transformer (ViT), which was the first pure transformer for image classification. ViT divides an image into multiple patches, which are sequentially sent to a transformer encoder after being encoded, and then an MLP is used to perform image classification. HVT [67] is based on a hierarchical progressive pooling method to compress the sequence length of a token and reduce the redundancy and number of calculations in ViT. The pooling-based vision transformer [68] draws on the principle of CNNs whereby, as the depth increases, the number of feature map channels increases, and the spatial dimension decreases. Yuan et al. [69] pointed out that the simple token structure in ViT cannot capture important local features, such as edges and lines, which reduces the training efficiency and leads to redundant attention mechanisms. T2T ViT was thus proposed to use layer-by-layer tokens-to-token transformation to gradually merge neighboring tokens and model local features while reducing the token’s length. TNT [70] employs a transformer suitable for fine-grained image tasks, which
divides the original image patch and conducts self-attention mechanism calculations in smaller units. Meanwhile, external and internal transformers are used to extract global and local features.

To adapt to dense prediction tasks such as semantic segmentation, several methods [71]–[77] have also introduced the pyramid structure of CNNs to the design of transformer counterparts, and performs better in detection and segmentation, several methods [71]–[77] have also introduced the pyramid structure of CNNs to the design of transformer
III. PROPOSED POLYP-PVT

A. Overall Architecture

As shown in Fig. 2, our Polyp-PVT consists of 4 key modules: namely, a pyramid vision transformer (PVT) encoder, cascaded fusion module (CFM), camouflage identification module (CIM), and similarity aggregation module (SAM). Specifically, the PVT extracts multi-scale long-range dependencies features from the input image. The CFM is employed to collect semantic cues and locate polyps by aggregating high-level features progressively. The CIM is designed to remove noise and enhance low-level representation information of polyps, including texture, color, and edges. The SAM is adopted to fuse the low- and high-level features provided by the CIM and CFM, effectively transmitting the information from the pixel-level polyp to the entire polyp.

Given an input image $I \in \mathbb{R}^{H \times W \times 3}$, we use the transformer-based backbone [71] to extract four pyramid features $X_i \in \mathbb{R}^{\frac{H}{2^i} \times \frac{W}{2^i} \times C_i}$, where $C_i \in \{64, 128, 320, 512\}$ and $i \in \{1, 2, 3, 4\}$. Then, we adjust the channel of three high-level features $X_2, X_3$ and $X_4$ to 32 through three convolutional units and feed them (i.e., $X_2', X_3',$ and $X_4'$) to CFM to fuse, leading a feature map $T_1 \in \mathbb{R}^{\frac{H}{2^i} \times \frac{W}{2^i} \times 32}$. Meanwhile, low-level features $X_1$ are converted to $T_2 \in \mathbb{R}^{\frac{H}{2^i} \times \frac{W}{2^i} \times 64}$ by the CIM. After that, the $T_1$ and $T_2$ are aligned and fused by SAM, yielding the final feature map $F \in \mathbb{R}^{\frac{H}{2^i} \times \frac{W}{2^i} \times 32}$. Finally, $F$ is fed into a $1 \times 1$ convolutional layer to predict the polyp segmentation result $P_2$. We use the sum of $P_1$ and $P_2$ as the final prediction. During training, we optimize the model with a main loss $\mathcal{L}_{main}$ and an auxiliary loss $\mathcal{L}_{aux}$. The main loss is calculated between the final segmentation result $P_2$ and the ground truth (GT), which is used to optimize the final polyp segmentation result. Similarly, the auxiliary loss is used to supervise the intermediate result $P_1$ generated by the CFM.

B. Transformer Encoder

Due to uncontrolled factors in their acquisition, polyp images tend to contain significant noise, such as motion blur, rotation, and reflection. Some recent works [78], [79] have found that the vision transformer [66], [71], [72] demonstrates stronger performance and better robustness to input disturbances than CNNs [16], [17]. Inspired by this, we use a vision transformer as our backbone network to extract more robust and powerful features for polyp segmentation. Different from [66], [73] that uses a fixed “columnar” structure or shifted windowing manner, the PVT [71] is a pyramid architecture whose representation is calculated with spatial-reduction attention operations; thus it enables to reduce the resource consumption. Note that the proposed model is backbone-independent; other famous transformer backbones are feasible in our framework. Specifically, we adopt the PVTv2 [72], which is the improved version of PVT with a more powerful feature extraction ability. To adapt PVTv2 to the polyp segmentation task, we remove the last classification layer and design a polyp segmentation head on top of four multi-scale feature maps (i.e., $X_1$, $X_2$, $X_3$, and $X_4$) generated by different stages. Among these feature maps, $X_1$ gives detailed appearance information of polyps, and $X_2$, $X_3$, and $X_4$ provide high-level features.

C. Cascaded Fusion Module

To balance the accuracy and computational resources, we follow recent popular practices [5], [80] to implement the cascaded fuse module (CFM). Specifically, we define $\mathcal{F}(\cdot)$ as a convolutional unit composed of a $3 \times 3$ convolutional layer with padding set to 1, batch normalization [81] and ReLU [82]. As shown in Fig. 2 (b), the CFM mainly consists of two cascaded parts, as follows:
(1) In part one, we up-sample the highest-level feature map $X'_4$ to the same size as $X'_3$ and then pass the result through two convolutional units $F_1(·)$ and $F_2(·)$, yields $X'_4$ and $X'_2$. Then, we multiply $X'_4$ and $X'_3$ and concatenate the result with $X'_2$. Finally, we use a convolution unit $F_3(·)$ to smooth the concatenated feature, yielding fused feature map $X'_{34} \in \mathbb{R}^{H/16 \times W/16 \times 16}$. The process can be summarized as Eqn. 1.

$$X'_{34} = F_3(\text{Concat}(F_1(X'_4) \odot X'_3, F_2(X'_4))),$$

(1) where “$\odot$” denotes the Hadamard product, and Concat($·$) is the concatenation operation along the channel dimension.

(2) As shown Eqn. 2, the second part follows a similar process to part one. Firstly, we up-sample $X'_4$, $X'_3$, $X'_{34}$ to the same size as $X'_2$, and then smooth them using convolutional units $F_4(·)$, $F_5(·)$, and $F_6(·)$, respectively. Then, we multiply the smoothed $X'_4$ and $X'_3$ with $X'_2$, and concatenate the resulting map with up-sampled and smoothed $X'_{34}$. Finally, we feed the concatenated feature map into two convolutional units (i.e., $F_7(·)$ and $F_8(·)$) to reduce the dimension, and obtain $T_1 \in \mathbb{R}^{H/16 \times W/16 \times 32}$, which is also the output of the CFM.

$$T_1 = F_8(F_7(\text{Concat}(F_4(X'_4) \odot F_5(X'_3) \odot X'_2, F_6(X'_{34}))),$$

(2) As shown in Fig. 2 (c), we introduce a camouflage identification module (CIM) to capture the details of polyps from different dimensions of the low-level feature map $X_1$. Specifically, the CIM consists of a channel attention operation [83] $\text{Att}_c(·)$ and a spatial attention operation [84] $\text{Att}_s(·)$, which can be formulated as:

$$T_2 = \text{Att}_s(\text{Att}_c(X_1)),$$

(3) The channel attention operation $\text{Att}_c(·)$ can be written as follow:

$$\text{Att}_c(x) = \sigma(\mathcal{H}_1(P_{\text{max}}(x)) + \mathcal{H}_2(P_{\text{avg}}(x))) \odot x,$$

(4) where $x$ is the input tensor and $\sigma(·)$ is the Softmax function. $P_{\text{max}}(·)$ and $P_{\text{avg}}(·)$ denote adaptive maximum pooling and adaptive average pooling functions, respectively. $\mathcal{H}_i(·), i \in \{1, 2\}$ shares parameters and consists of a convolutional layer with $1 \times 1$ kernel size to reduce the channel dimension 16 times, followed by a ReLU layer and another $1 \times 1$ convolutional layer to recover the original channel dimension. The spatial attention operation $\text{Att}_s(·)$ can be formulated as:

$$\text{Att}_s(x) = \sigma(\mathcal{G}(\text{Concat}(R_{\text{max}}(x), R_{\text{avg}}(x)))) \odot x,$$

(5) where $R_{\text{max}}(·)$ and $R_{\text{avg}}(·)$ represent the maximum and average values obtained along the channel dimension, respectively. $\mathcal{G}(·)$ is a $7 \times 7$ convolutional layer with padding set to 3.

D. Camouflage Identification Module

Low-level features often contain rich detail information, such as texture, color, and edges. However, polyps tend to be very similar in appearance to the background. Therefore, we need a powerful extractor to identify the polyp details.

As shown in Fig. 2 (c), we introduce a camouflage identification module (CIM) to capture the details of polyps from different dimensions of the low-level feature map $X_1$. Specifically, the CIM consists of a channel attention operation [83] $\text{Att}_c(·)$ and a spatial attention operation [84] $\text{Att}_s(·)$, which can be formulated as:

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$$\text{Att}_s(x) = \sigma(\mathcal{G}(\text{Concat}(R_{\text{max}}(x), R_{\text{avg}}(x)))) \odot x,$$

(5) where $R_{\text{max}}(·)$ and $R_{\text{avg}}(·)$ represent the maximum and average values obtained along the channel dimension, respectively. $\mathcal{G}(·)$ is a $7 \times 7$ convolutional layer with padding set to 3.

E. Similarity Aggregation Module

To explore high-order relations between the lower-level local features from CIM and higher-level cues from CFM. We introduce the non-local [85, 86] operation under graph convolution domain [87] to implement our similarity aggregation module (SAM). As a result, SAM can inject detailed appearance features into high-level semantic features using global attention.

Given the feature map $T_1$, which contains high-level semantic information, and $T_2$ with rich appearance details, we fuse them through self-attention. First, two linear mapping functions $W_\theta(·)$ and $W_\phi(·)$ are applied on $T_1$ to reduce the dimension and obtain feature maps $Q \in \mathbb{R}^{H/16 \times W/16 \times 16}$ and $K \in \mathbb{R}^{H/16 \times W/16 \times 16}$. Here, we take a convolution operation with a kernel size of $1 \times 1$ as the linear mapping process. This process can be expressed as follows:

$$Q = W_\theta(T_1), K = W_\phi(T_1).$$

(6) For $T_2$, we use a convolutional unit $W_g(·)$ to reduce the channel dimension to 32 and interpolate it to the same size as $T_1$. Then, we apply a Softmax function on the channel dimension and choose the second channel as the attention map, leading to $T'_2 \in \mathbb{R}^{H/16 \times W/16 \times 1}$. These operations are represented as $F(·)$ in Fig. 3. Next, we calculate the Hadamard product between $K$ and $T'_2$. This operation assigns different weights to different pixels, increasing the weight of edge pixels. Then, we apply an adaptive pooling operation to reduce the displacement of features and apply a center crop on it to obtain the feature map $V \in \mathbb{R}^{4 \times 4 \times 16}$. In summary, the process can
be formulated as follows:

\[ V = AP(K \odot F(W_g(T_2))) , \]

where \( AP(\cdot) \) denotes the pooling and crop operations.

Then, we establish the correlation between each pixel in \( V \) and \( K \) through an inner product, which is written as follows:

\[ f = \sigma(V^T \otimes K), \]

where \( \otimes \) denotes the inner product operation, \( V^T \) is the transpose of \( V \) and \( f \) is the correlation attention map.

After obtaining the correlation attention map \( f \), we multiply it with the feature map \( Q \), and the result features are fed to the graph convolutional layer [86] GCN(\cdot), leading to \( G \in \mathbb{R}^{4 \times 4 \times 16} \). Same to [86], we calculate the inner product between \( f \) and \( G \) as Eqn. 9, reconstructing the graph domain features into the original structural features:

\[ Y' = f^T \odot GCN(f^T \otimes Q). \]

The reconstructed feature map \( Y' \) is adjusted to the same channel sizes with \( Y \) by a convolutional layer \( W_z(\cdot) \) with \( 1 \times 1 \) kernel size, and then combined with the feature \( T_1 \) to obtain the final output \( Z \in \mathbb{R}^{\frac{H}{16} \times \frac{W}{16} \times 32} \) of the SAM. Eqn. 10 summarizes the details of this process:

\[ Z = T_1 + W_z(Y'). \]

**F. Loss Function**

Our loss function can be formulated as Eqn. 11:

\[ \mathcal{L} = \mathcal{L}_{\text{main}} + \mathcal{L}_{\text{aux}}, \]

where \( \mathcal{L}_{\text{main}} \) and \( \mathcal{L}_{\text{aux}} \) are the main loss and auxiliary loss, respectively. The main loss \( \mathcal{L}_{\text{main}} \) is calculated between the final segmentation result \( P_2 \) and ground truth \( G \), which can be written as:

\[ \mathcal{L}_{\text{main}} = \mathcal{L}_{\text{IoU}}(P_2, G) + \mathcal{L}_{\text{BCE}}(P_2, G). \]

The auxiliary loss \( \mathcal{L}_{\text{aux}} \) is calculated between the intermediate result \( P_1 \) from the CFM and ground truth \( G \), which can be formulated as:

\[ \mathcal{L}_{\text{aux}} = \mathcal{L}_{\text{IoU}}(P_1, G) + \mathcal{L}_{\text{BCE}}(P_1, G). \]

\[ \mathcal{L}_{\text{IoU}}(\cdot) \] and \( \mathcal{L}_{\text{BCE}}(\cdot) \) are the weighted intersection over union (IoU) loss [88] and weighted binary cross entropy (BCE) loss [88], which restrict the prediction map in terms of the global structure (object-level) and local details (pixel-level) perspectives. Unlike the standard BCE loss function, which treats all pixels equally, \( \mathcal{L}_{\text{BCE}}(\cdot) \) considers the importance of each pixel and assigns higher weights to hard pixels. Furthermore, compared to the standard IoU loss, \( \mathcal{L}_{\text{IoU}}(\cdot) \) pays more attention to the hard pixels.

**G. Implementation Details**

We implement our Polyp-PVT with the PyTorch framework and use a Tesla P100 to accelerate the calculations. Considering the differences in the sizes of each polyp image, we adopt a multi-scale strategy [5], [41] in the training stage. The hyperparameter details are as follows. To update the network parameters, we use the AdamW [89] optimizer, which is widely used in transformer networks [71]–[73]. The learning rate is set to 1e-4 and the weight decay is adjusted to 1e-4. Further, we resize the input images to 352 × 352 with a mini-batch size of 16 for 100 epochs. More details about the training loss curves, parameter setting, and network parameters are shown in Fig. 4, Tab. II, and Tab. III, respectively. The total training time is nearly 3 hours to achieve the best (e.g., 30 epochs) performance. For testing, we only resize the images to 352 × 352 without any post-processing optimization strategies.

**IV. EXPERIMENTS**

**A. Evaluation Metrics**

We employ six widely-used evaluation metrics, including Dice [90], IoU, mean absolute error (MAE), weighted F-measure \( (F_w^\beta) \) [91], S-measure \( (S_\alpha) \) [92], and E-measure \( (E_\alpha) \) [93], [94] to evaluate the model performances. Among these metrics, Dice and IoU are similarity measures at the regional level, which mainly focus on the internal consistency of segmented objects. Here, we report the mean value of Dice and IoU, denoted as mDice and mIoU, respectively. MAE is a pixel-by-pixel comparison indicator that represents the average value of the absolute error between the predicted value and the true value. Weighted F-measure \( (F_w^\beta) \) comprehensively considers the recall and precision and eliminates the effect of considering each pixel equally in conventional indicators. S-measure \( (S_\alpha) \) focuses on the structural similarity of target prospects at the

| Optimizer | Learning Rate (lr) | Multi-scale | Clip | Decay rate | Weight decay | Epochs | Input Size |
|----------|--------------------|-------------|------|------------|--------------|-------|------------|
| AdamW    | 1e-4               | [0.75,1,1.25] | 0.5  | 1e-4       | 0.1          | 100   | 352 × 352  |

The auxiliary loss \( \mathcal{L}_{\text{aux}} \) is calculated between the intermediate result \( P_1 \) from the CFM and ground truth \( G \), which can be formulated as:

\[ \mathcal{L}_{\text{aux}} = \mathcal{L}_{\text{IoU}}(P_1, G) + \mathcal{L}_{\text{BCE}}(P_1, G). \]
TABLE III
NETWORK PARAMETERS OF EACH MODULE. NOTE THAT THE ENCODER PARAMETERS ARE THE SAME AS PVT WITHOUT ANY CHANGES.

| Encoder    | SAM          |
|------------|--------------|
| patch_size | AvgPool2d    |
| embed_dims | Conv2d [64, 128, 320, 512] |
| num_heads  | Conv2d [1, 2, 5, 8] |
| mlp_ratios | Conv2d [8, 4, 4] |
| depths     | GCN [3, 4, 18, 3] |
| sr_ratios  | BasicConv2d [8, 4, 2, 1] |
| drop_rate  | AvgPool2d [0] |
| drop_path_rate | BasicConv2d [64, 32, 1, 0] |

CFM

| BasicConv2d | [32,32,3,1] | BasicConv2d | [32,32,3,1] | BasicConv2d | [64,64,3,1] | BasicConv2d | [64,64,3,1] | BasicConv2d | [96,96,3,1] | BasicConv2d | [96,32,3,1] |
|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| AvgPool2d   | [1]         | AvgPool2d   | [1]         | Conv2d [64,4,1,0] | [1]         | Conv2d [4,6,1,0] | [1]         | Conv2d [2,1,7,3] | Sigmoid     | Sigmoid     |

dataset, the mDic score of our model is 2.1% higher than that of SANet and 3.8% higher than that of PraNet.

D. Analysis of Generalization Ability

Settings. To verify the generalization performance of the model, we test it on three unseen (i.e., Polycentric) datasets, namely ETIS, ColonDB, and EndoScene. There are 196 images in ETIS, 380 images in ColonDB, and 60 images in EndoScene. It is worth noting that the images in these datasets belong to different medical centers. In other words, the model has not seen their training data, which is different from the verification methods of ClinicDB and Kvasir-SEG.

Results. The results are shown in Tab. VI and Tab. V. As can be seen, our Polyp-PVT achieves a good generalization performance compared with the existing models. And our model generalizes easily to multicentric (or unseen) data with different domains/distributions. On ColonDB, it is ahead of the second-best SANet and classical PraNet by 5.5% and 9.6%, respectively. On ETIS, we exceed the SANet and PraNet by 3.7% and 15.9%, respectively. In addition, on EndoScene, our model is better than SANet and PraNet by 1.2% and 2.9%, respectively. Moreover, to prove the generalization ability of Polyp-PVT, we present the max Dice results in Fig. 5, where our model shows a steady improvement on both ColonDB and ETIS. In addition, we show the standard deviation (SD) of the mean dice (mDic) between our model and others in Tab. VII. As seen, there is not much difference in SD between our model and the comparison model, and they are both stable and balanced.

E. Qualitative Analysis

Fig. 6 and Fig. 7 show the visualization results of our model and the compared models. We find that our results have two advantages.

- Our model is able to adapt to data under different conditions. That is, it maintains a stable recognition and segmentation ability under different acquisition environments (different lighting, contrast, reflection, motion blur, small objects, and rotation).
- The model segmentation results have internal consistency and predicted edges are closer to the ground-truth labels.

region and object level. E-measure ($E_{\xi}$) is used to evaluate the segmentation results at the pixel and image level. We report the mean and max value of E-measure, denoted as $mE_{\xi}$ and $max E_{\xi}$, respectively. The evaluation toolbox is derived from https://github.com/DengPingFan/PraNet.

B. Datasets and Compared Models

Datasets. Following the experimental setups in PraNet [5], we adopt five challenging public datasets, including Kvasir-SEG [13], ClinicDB [8], ColonDB [10], EndoScene [14] and ETIS [9] to verify the effectiveness of our framework.

Models. We collect several open source models from the field of polyp segmentation, for a total of nine comparative models, including U-Net [4], UNet++ [28], PraNet [5], SFA [95], MSEG [41], ACSNet [49], DCRNet [44], EU-Net [52] and SANet [7]. For a fair comparison, we use their open-source codes to evaluate the same training and testing sets. Note that the SFA results are generated using the released test model.

C. Analysis of Learning Ability

Settings. We use the ClinicDB and Kvasir-SEG datasets to evaluate the learning ability of the proposed model. ClinicDB contains 612 images, which are extracted from 31 colonoscopy videos. Kvasir-SEG is collected from the polyp class in the Kvasir dataset and includes 1,000 polyp images. Following PraNet, we adopt the same 900 and 548 images from ClinicDB and Kvasir-SEG datasets as the training set, and the remaining 64 and 100 images are employed as the respective test sets.

Results. As can be seen in Tab. IV, our model is superior to the current methods, demonstrating that it has a better learning ability. On the Kvasir-SEG dataset, the mDic score of our model is 1.3% higher than that of the second-best model, SANet, and 1.9% higher than that of PraNet. On the ClinicDB
### TABLE IV
QUANTITATIVE RESULTS OF THE TEST DATASETS, i.e., KVASIR-SEG AND CLINICDB.

| Model               | mDic | mIoU | F\text{\textsubscript{\beta}} | S\alpha | mE\xi | maxE\xi | MAE   | mDic | mIoU | F\text{\textsubscript{\beta}} | S\alpha | mE\xi | maxE\xi | MAE   |
|---------------------|------|------|-------------------------------|--------|-------|--------|-------|------|------|-------------------------------|--------|-------|--------|-------|------|
| MICCAI’15 U-Net     | 0.818 | 0.746 | 0.794 | 0.858 | 0.881 | 0.893 | 0.055 | 0.823 | 0.755 | 0.811 | 0.889 | 0.913 | 0.954 | 0.019 |
| DLMIA’18 UNet+++    | 0.821 | 0.743 | 0.808 | 0.862 | 0.886 | 0.909 | 0.048 | 0.794 | 0.729 | 0.785 | 0.873 | 0.891 | 0.931 | 0.022 |
| MICCAI’19 SFA       | 0.723 | 0.611 | 0.670 | 0.782 | 0.834 | 0.849 | 0.075 | 0.700 | 0.607 | 0.647 | 0.793 | 0.840 | 0.885 | 0.042 |
| arXiv’21 MSEG       | 0.897 | 0.839 | 0.885 | 0.912 | 0.942 | 0.948 | 0.028 | 0.909 | 0.864 | 0.907 | 0.938 | 0.961 | 0.969 | 0.007 |
| arXiv’21 DCRNet     | 0.886 | 0.825 | 0.868 | 0.911 | 0.933 | 0.941 | 0.035 | 0.896 | 0.844 | 0.890 | 0.933 | 0.964 | 0.978 | 0.010 |
| MICCAI’20 ACSNet    | 0.898 | 0.838 | 0.882 | 0.920 | 0.941 | 0.952 | 0.032 | 0.882 | 0.826 | 0.873 | 0.927 | 0.947 | 0.959 | 0.011 |
| MICCAI’20 PraNet    | 0.898 | 0.840 | 0.885 | 0.915 | 0.944 | 0.948 | 0.030 | 0.899 | 0.849 | 0.896 | 0.936 | 0.963 | 0.979 | 0.009 |
| CRV’21 EU-Net       | 0.908 | 0.854 | 0.893 | 0.917 | 0.951 | 0.954 | 0.028 | 0.902 | 0.846 | 0.891 | 0.936 | 0.959 | 0.965 | 0.011 |
| MICCAI’21 SANet     | 0.904 | 0.847 | 0.892 | 0.915 | 0.949 | 0.953 | 0.028 | 0.916 | 0.859 | 0.909 | 0.939 | 0.971 | 0.976 | 0.012 |
| Polyp-PVT (Ours)    | 0.917 | 0.864 | 0.911 | 0.925 | 0.956 | 0.962 | 0.023 | 0.937 | 0.889 | 0.936 | 0.949 | 0.985 | 0.989 | 0.006 |

### TABLE V
QUANTITATIVE RESULTS OF THE TEST DATASETS COLONDB AND ETIS. The SFA result is generated using the published code.

| Model               | mDic | mIoU | F\text{\textsubscript{\beta}} | S\alpha | mE\xi | maxE\xi | MAE   | mDic | mIoU | F\text{\textsubscript{\beta}} | S\alpha | mE\xi | maxE\xi | MAE   |
|---------------------|------|------|-------------------------------|--------|-------|--------|-------|------|------|-------------------------------|--------|-------|--------|-------|------|
| MICCAI’15 U-Net     | 0.512 | 0.444 | 0.498 | 0.712 | 0.696 | 0.776 | 0.061 | 0.398 | 0.335 | 0.366 | 0.684 | 0.643 | 0.740 | 0.036 |
| DLMIA’18 UNet+++    | 0.483 | 0.410 | 0.467 | 0.691 | 0.680 | 0.760 | 0.064 | 0.401 | 0.344 | 0.390 | 0.683 | 0.629 | 0.776 | 0.035 |
| MICCAI’19 SFA       | 0.469 | 0.347 | 0.379 | 0.634 | 0.675 | 0.764 | 0.094 | 0.297 | 0.217 | 0.231 | 0.557 | 0.531 | 0.632 | 0.109 |
| MICCAI’20 ACSNet    | 0.716 | 0.649 | 0.697 | 0.829 | 0.839 | 0.851 | 0.039 | 0.578 | 0.509 | 0.530 | 0.754 | 0.737 | 0.764 | 0.059 |
| arXiv’21 MSEG       | 0.735 | 0.666 | 0.724 | 0.834 | 0.859 | 0.875 | 0.038 | 0.700 | 0.630 | 0.671 | 0.828 | 0.854 | 0.890 | 0.015 |
| arXiv’21 DCRNet     | 0.704 | 0.631 | 0.684 | 0.821 | 0.840 | 0.848 | 0.052 | 0.556 | 0.496 | 0.506 | 0.736 | 0.742 | 0.773 | 0.096 |
| MICCAI’20 PraNet    | 0.712 | 0.640 | 0.699 | 0.820 | 0.847 | 0.872 | 0.043 | 0.628 | 0.567 | 0.600 | 0.794 | 0.808 | 0.841 | 0.031 |
| CRV’21 EU-Net       | 0.756 | 0.681 | 0.730 | 0.831 | 0.863 | 0.872 | 0.045 | 0.687 | 0.609 | 0.636 | 0.793 | 0.807 | 0.841 | 0.067 |
| MICCAI’21 SANet     | 0.753 | 0.670 | 0.726 | 0.837 | 0.869 | 0.878 | 0.043 | 0.750 | 0.654 | 0.685 | 0.849 | 0.881 | 0.897 | 0.015 |
| Polyp-PVT (Ours)    | 0.808 | 0.727 | 0.795 | 0.865 | 0.913 | 0.919 | 0.031 | 0.787 | 0.706 | 0.750 | 0.871 | 0.906 | 0.910 | 0.013 |

Fig. 6. Visualization results with the current models. Green indicates a correct polyp. Yellow is the missed polyp. Red is the wrong prediction. As we can see, the proposed model can accurately locate and segment polyps, regardless of size.
TABLE VI
QUANTITATIVE RESULTS OF THE TEST DATASET ENSOENCE. THE SFA RESULT IS GENERATED USING THE PUBLISHED CODE.

| Model     | mDic | mIoU  | Fβ  | Sα  | mEξ  | maxEξ | MAE |
|-----------|------|-------|-----|-----|------|-------|-----|
| U-Net     | 0.710| 0.627 | 0.684| 0.843| 0.847| 0.875 | 0.022|
| UNet++    | 0.707| 0.624 | 0.687| 0.839| 0.834| 0.898 | 0.018|
| SFA       | 0.467| 0.329 | 0.341| 0.640| 0.644| 0.817 | 0.065|
| MSEG      | 0.874| 0.804 | 0.852| 0.924| 0.948| 0.957 | 0.009|
| ACSNet    | 0.863| 0.787 | 0.825| 0.923| 0.939| 0.968 | 0.013|
| DCRNet    | 0.856| 0.788 | 0.830| 0.921| 0.943| 0.960 | 0.010|
| PraNet    | 0.871| 0.797 | 0.843| 0.925| 0.950| 0.972 | 0.010|
| EU-Net    | 0.837| 0.765 | 0.805| 0.904| 0.919| 0.933 | 0.015|
| SANet     | 0.888| 0.815 | 0.859| 0.928| 0.962| 0.972 | 0.008|
| Polyp-PVT | 0.900| 0.833 | 0.884| 0.935| 0.973| 0.981 | 0.007|

We also provide FROC curves on ColonDB in Fig. 8, and our result is at the top, indicating that our effect achieves the best.

F. Ablation Study

We describe in detail the effectiveness of each component on the overall model. The training, testing, and hyperparameter settings are the same as mentioned in Sec. III-G. The results are shown in Tab. VIII.

Components. We use PVTv2 [72] as our baseline (Bas.) and evaluate module effectiveness by removing or replacing components from the complete Polyp-PVT and comparing the variants with the standard version. The standard version is denoted as “Polyp-PVT (PVT+CFM+CIM+SAM)”, where “CFM”, “CIM” and “SAM” indicate the usage of the CFM, CIM, and SAM, respectively.

Effectiveness of CFM. To analyze the effectiveness of the CFM, a version of “Polyp-PVT (w/o CFM)” is trained.
TABLE VII
THE STANDARD DEVIATION (SD) OF THE MEAN DICE (mDIC) OF OUR MODEL AND THE COMPARISON MODELS.

| Datasets | Kvasir-SEG | ClinicDB | ColonDB | ETIS | Endoscreen |
|----------|-----------|----------|---------|------|------------|
| Metrics  | mDic ± SD | mDic ± SD | mDic ± SD | mDic ± SD | mDic ± SD |
| MICCAI’15 U-Net | .818 ± .039 | .823 ± .047 | .483 ± .034 | .398 ± .033 | .710 ± .049 |
| DLMIA’18 UNet++ | .821 ± .040 | .794 ± .044 | .456 ± .037 | .401 ± .057 | .707 ± .053 |
| MICCAI’19 SFA | .723 ± .052 | .701 ± .054 | .444 ± .037 | .297 ± .025 | .468 ± .050 |
| arXiv’21 MSEG | .897 ± .041 | .910 ± .048 | .735 ± .039 | .700 ± .039 | .874 ± .051 |
| MICCAI’20 ACSNet | .898 ± .045 | .882 ± .048 | .716 ± .040 | .578 ± .035 | .863 ± .055 |
| arXiv’21 DCRNet | .886 ± .043 | .896 ± .049 | .704 ± .039 | .556 ± .039 | .857 ± .052 |
| MICCAI’20 PraNet | .898 ± .041 | .899 ± .048 | .712 ± .038 | .628 ± .036 | .871 ± .051 |
| CRV’21 EU-Net | .908 ± .042 | .902 ± .048 | .756 ± .040 | .687 ± .039 | .837 ± .049 |
| MICCAI’21 SANet | .904 ± .042 | .916 ± .049 | .752 ± .040 | .750 ± .047 | .888 ± .054 |
| Polyp-PVT (Ours) | .917 ± .042 | .937 ± .050 | .808 ± .043 | .787 ± .044 | .900 ± .052 |

TABLE VIII
QUANTITATIVE RESULTS FOR ABLATION STUDIES.

| Dataset       | Metric | Bas. | w/o CFM | w/o CIM | w/o SAM | Final  |
|---------------|--------|------|---------|---------|---------|--------|
| Endoscreen    | mDic   | 0.869| 0.892   | 0.882   | 0.874   | 0.900  |
|               | mIoU   | 0.792| 0.826   | 0.806   | 0.801   | 0.833  |
| ClinicDB      | mDic   | 0.903| 0.915   | 0.930   | 0.930   | 0.937  |
|               | mIoU   | 0.847| 0.865   | 0.881   | 0.877   | 0.889  |
| ColonDB       | mDic   | 0.796| 0.802   | 0.805   | 0.779   | 0.808  |
|               | mIoU   | 0.707| 0.721   | 0.724   | 0.696   | 0.727  |
| ETIS          | mDic   | 0.759| 0.771   | 0.785   | 0.778   | 0.787  |
|               | mIoU   | 0.668| 0.690   | 0.711   | 0.693   | 0.706  |
| Kvasir-SEG    | mDic   | 0.910| 0.922   | 0.910   | 0.910   | 0.917  |
|               | mIoU   | 0.856| 0.872   | 0.858   | 0.853   | 0.864  |

TABLE IX
ABLATION STUDY OF GCN IN THE SAM MODULE.

| Setting       | Endoscreen | ClinicDB | ColonDB | ETIS | Kvasir-SEG |
|---------------|------------|----------|---------|------|------------|
| w/o GCN       | 0.874      | 0.920    | 0.784   | 0.725 | 0.894      |
| w/ Conv       | 0.894      | 0.919    | 0.787   | 0.742 | 0.909      |
| w/ GCN        | **0.900**  | **0.937** | **0.808** | **0.787** | **0.917** |

Tab. VIII shows that the model without the CFM drops sharply on all five datasets compared to the standard Polyp-PVT. In particular, the mDic is reduced from 0.937 to 0.915 on ClinicDB.

Effectiveness of CIM. To demonstrate the ability of the CIM, we also remove it from Polyp-PVT, denoting this as “Polyp-PVT (w/o CIM)”. As shown in Tab. VIII, this variant performs worse than the overall Polyp-PVT. Specifically, removing the CIM causes the mDic to decrease by 1.8% on Endoscreen. Meanwhile, it is obvious that the lack of the CIM introduces significant noise (please refer to Fig. 10). In order to further explore the internal of CIM, the feature visualizations of the two main configurations inside the CIM are shown in Fig 9. It can be seen that the low-level features have a large amount of detailed information. Still, the differences between polyps and other normal tissues cannot be mined directly from this information. Thanks to the channel attention and spatial attention mechanism, information such as details and edges of polyps can be discerned from a large amount of redundant information.

Effectiveness of SAM. Similarly, we test the effectiveness of the SAM module by removing it from the overall Polyp-PVT and replacing it with an element-wise addition operation, which is denoted as “Polyp-PVT (w/o SAM)”. The performance of the complete Polyp-PVT shows an improvement of 2.9% and 3.1% in terms of mDic and mIoU, respectively, on ColonDB. Fig. 10 shows the benefits of SAM more intuitively. It is found that the lack of the SAM leads to more detailed errors or even missed inspections. As reported in Tab IX, we add more results on the GCN in the SAM module. The experimental results further illustrate that GCN plays a key role. The effect of the lack of GCN is significantly reduced, and the effect is improved after replacing it with convolution. Still, GCN can significantly exceed the capabilities of the convolution module. The experimental results also verified the importance of GCN’s large receptive field and rotation insensitivity to polyp segmentation. The rotational robustness of GCN is stronger than convolutions. As shown in Tab X, under the condition of large rotation (15 degrees), GCN has better adaptability to image rotation than convolutions. To further explore the role of SAM, we visualized P1 and P2, and the results of P1 and P2 are shown in Fig 11. Compared with P1, P2 has higher reliability in error recognition and identification of uncertain regions. This is mainly due to the large number of low-level details collected by CIM and mining local pixels and global semantic cues from the polyp area of SAM.

G. Video Polypl Segmentation

To validate the superiority of the proposed model, we conduct experiments on the video polyp segmentation datasets. For a fair comparison, we re-train our model with the same training datasets and use the same testing set as PNS-Net [64], [97]. We compare our model on three standard benchmarks (i.e., CVC-300-TV [96], CVC-612-T [8], and CVC-612-V [8]) against six cutting-edge approaches, including U-Net [4],
Fig. 10. Visualization of the ablation study results, which are converted from the output into heat maps. As can be seen, removing any module leads to missed or incorrectly detected results.

Table XI

| Model               | CVC-612-T [8] | CVC-612-V [8] |
|---------------------|---------------|---------------|
|                     | mDic mIoU Fβ Sα mEξ maxEξ MAE | mDic mIoU Fβ Sα mEξ maxEξ MAE |
| MICCAI’15 U-Net     | 0.711 0.618 0.694 0.810 0.836 0.853 0.058 | 0.709 0.597 0.680 0.826 0.855 0.872 0.023 |
| TMI’19 UNet++       | 0.697 0.603 0.688 0.800 0.817 0.865 0.059 | 0.668 0.557 0.642 0.805 0.830 0.846 0.025 |
| ISM’19 ResUNet++    | 0.616 0.512 0.604 0.727 0.758 0.760 0.084 | 0.750 0.646 0.717 0.829 0.877 0.879 0.023 |
| MICCAI’20 ACSNet    | 0.780 0.697 0.772 0.838 0.864 0.866 0.053 | 0.801 0.710 0.765 0.847 0.887 0.890 0.054 |
| MICCAI’20 PraNet    | 0.833 0.767 0.834 0.886 0.904 0.926 0.038 | 0.857 0.793 0.855 0.915 0.936 0.965 0.013 |
| MICCAI’21 PNS-Net   | 0.837 0.765 0.838 0.903 0.903 0.923 0.038 | 0.851 0.769 0.836 0.923 0.944 0.962 0.012 |
| Polyp-PVT (Ours)    | 0.846 0.776 0.850 0.895 0.908 0.926 0.037 | 0.882 0.810 0.874 0.924 0.963 0.967 0.012 |

Fig. 11. Visualization of the P1 and P2 predictions.

Table XII

| Model             | CVC-300-TV [96] |
|-------------------|------------------|
|                   | mDic mIoU Fβ Sα mEξ maxEξ MAE |
| U-Net             | 0.631 0.516 0.567 0.793 0.826 0.849 0.027 |
| UNet++            | 0.638 0.527 0.581 0.796 0.831 0.847 0.024 |
| ResUNet++         | 0.533 0.410 0.469 0.703 0.718 0.720 0.052 |
| ACSNet            | 0.732 0.627 0.703 0.837 0.871 0.875 0.016 |
| PraNet            | 0.716 0.624 0.700 0.833 0.852 0.904 0.016 |
| PNS-Net           | 0.813 0.710 0.778 0.909 0.921 0.942 0.013 |
| Ours              | 0.880 0.802 0.869 0.915 0.961 0.965 0.011 |

Fig. 12. Visualization of the failure cases.

H. Limitations

Although the proposed Polyp-PVT model surpasses existing algorithms, it still performs poorly in certain cases. We present some failure cases in Fig. 12. As can be seen, one major existing model, PNS-Net, by 3.1% and 6.7% on CVC-612-V and CVC-300-TV, respectively, in terms of mDice.
limitation is the inability to detect accurate polyp boundaries with overlapping light and shadow (1\textsuperscript{st} row). Our model can identify the location information of polyps (green mask in 1\textsuperscript{st} row), but it regards the light and shadow part of the edge as the polyp (red mask in 1\textsuperscript{st} row). More deadly, our model incorrectly predicts the reflective point as a polyp (red mask in 2\textsuperscript{nd} and 3\textsuperscript{rd} rows). We notice that the reflective points are very salient in the image. Therefore, we speculate that the prediction may be based on only these points. More importantly, we believe that a simple way is to convert the input image into a gray image, which can eliminate the reflection and overlap of light and shadow to assist the model in judgment.

V. Conclusion

In this paper, we propose a new image polyp segmentation framework, named Polyp-PVT, which utilizes a pyramid vision transformer backbone as the encoder to explicitly extract more powerful and robust features. Extensive experiments show that Polyp-PVT consistently outperforms all current cutting-edge models on five challenging datasets without any pre-/post-processing. In particular, for the unseen ColonDB dataset, the proposed model reaches a mean Dice score of above 0.8 for the first time. Interestingly, we also surpass the current cutting-edge PNS-Net in terms of the video polyp segmentation task, demonstrating excellent learning ability. Specifically, we obtain the above-mention achievements by introducing three simple components, i.e., a cascaded fusion module (CFM), a camouflage identification module (CIM), and a similarity aggregation module (SAM), which effectively extract high and low-level cues separately, and effectively fuse them for the final output. We hope this research will stimulate more novel ideas for solving the polyp segmentation task.

REFERENCES

[1] M. Fiori, P. Musé, and G. Sapiro, “A complete system for candidate polyps detection in virtual colonoscopy,” IJPRAI, vol. 28, no. 07, p. 1460014, 2014.
[2] A. V. Mamonov, I. N. Figueiredo, P. N. Figueiredo, and Y.-H. R. Tsai, “Automated polyp detection in colon capsule endoscopy,” IEEE TMI, vol. 33, no. 7, pp. 1488–1502, 2014.
[3] O. H. Maghsoudi, “Superpixel based segmentation and classification of polyps in wireless capsule endoscopy,” in IEEE SPMB, 2017.
[4] O. Ronneberger, P. Fischer, and T. Brox, “U-net: Convolutional networks for biomedical image segmentation,” in MICCAI, 2015.
[5] D.-P. Fan, G.-P. Ji, T. Zhou, G. Chen, H. Fu, J. Shen, and L. Shao, “Pranet: Parallel reverse attention network for polyp segmentation,” in MICCAI, 2020.
[6] X. Guo, C. Yang, Y. Liu, and Y. Yuan, “Learn to threshold: Thresholdnet with confidence-guided manifold mixup for polyp segmentation,” IEEE TMI, vol. 40, no. 4, pp. 1134–1146, 2020.
[7] J. Wei, Y. Hu, R. Zhang, Z. Li, S. K. Zhou, and S. Cui, “Shallow attention network for polyp segmentation,” in MICCAI, 2021.
[8] J. Bernal, F. J. Sánchez, G. Fernández-Esparrach, D. Gil, C. Rodríguez, and F. Vilariño, “Wm-dova maps for accurate polyp highlighting in colonoscopy: Validation vs. saliency maps from physicians,” CMIG, vol. 43, pp. 99–111, 2015.
[9] J. Silva, A. Histace, O. Romain, X. Dray, and B. Granado, “Toward embedded detection of polyps in wce images for early diagnosis of colorectal cancer,” IJCARS, vol. 9, no. 2, pp. 283–293, 2014.
[10] N. Tajbakhsh, S. R. Gurudu, and J. Liang, “Automated polyp detection in colonoscopy videos using shape and context information,” IEEE TMI, vol. 35, no. 2, pp. 630–644, 2015.
[11] D.-P. Fan, G.-P. Ji, M.-M. Cheng, and L. Shao, “Concealed object detection,” IEEE TPAMI, 2021.
[12] D.-P. Fan, G.-P. Ji, G. Sun, M.-M. Cheng, J. Shen, and L. Shao, “Camouflaged object detection,” in CVPR, 2020.
[13] D. Jha, P. H. Smedsrud, M. A. Riegler, P. Halvorsen, T. de Lange, D. Johansen, and H. D. Johansen, “Kvasir-seg: A segmented polyp dataset,” in *MMM*, 2020.

[14] D. Vázquez, J. Bernal, F. J. Sánchez, G. Fernández-Esparrrach, A. M. López, A. Romero, M. Drozdzal, and A. Courville, “A benchmark for endoluminal scene segmentation of colonoscopy images,” *JHE*, vol. 2012, 2017.

[15] T. Rahim, M. A. Usman, and S. Y. Shin, “A survey on contemporary computer-aided tumor, polyp, and ulcer detection methods in wireless capsule endoscopy imaging,” *CMIG*, p. 101767, 2020.

[16] K. He, X. Zhang, S. Ren, and J. Sun, “Deep residual learning for image recognition,” in *CVPR*, 2016.

[17] K. Simonyan and A. Zisserman, “Very deep convolutional networks for large-scale image recognition,” in *ICLR*, 2015.

[18] X. Li, W. Wang, X. Hu, and J. Yang, “Selective kernel networks,” in *CVPR*, 2019.

[19] W. Wang, X. Li, T. Lu, and J. Yang, “Mixed link networks,” in *IJCAI*, 2018.

[20] J. Long, E. Shelhamer, and T. Darrell, “Fully convolutional networks for semantic segmentation,” in *CVPR*, 2015.

[21] L. Cui, M. Wu, L. Chen, W. Bai, M. Yang, S. Lyu, and Q. Zhao, “Using guide maps to self-attentive local information for polyp segmentation,” in *MICCAI*. Springer, 2022.

[22] N. K. Tomar, D. Jha, U. Bagci, and S. Ali, “Tganet: Text-guided attention with local information for polyp segmentation,” in *MICCAI*. Springer, 2022.

[23] R. Zhang, P. Lai, X. Wan, D.-J. Fan, F. Gao, X.-J. Wu, and G. Li, “Lesion-aware dynamic kernel for polyp segmentation,” in *MICCAI*. Springer, 2022.

[24] J.-H. Shi, Q. Zhang, Y.-H. Tang, and Z.-Q. Zhang, “Polyp-mixer: An efficient context-aware mlp-based paradigm for polyp segmentation,” *IEEE TCSVT*, 2022.

[25] X. Zhao, Z. Wu, S. Tan, D.-J. Fan, Z. Li, X. Wan, and G. Li, “Semi-supervised spatial temporal attention network for video polyp segmentation,” in *MICCAI*. Springer, 2022.

[26] M. Akbari, M. Mohrekesh, E. Nasr-Esfahani, S. R. Soroumshehr, N. Karimi, S. Samavi, and K. Najarian, “Polyp segmentation in colonoscopy images using fully convolutional network,” in *IEEE EMBC*, 2018.

[27] P. Brandao, O. Zisimopoulos, E. Mazomenos, G. Ciuti, J. Bernal, M. Visentini-Scarzanella, A. Mencassi, P. Dario, A. Kouloaizidis, A. Arezzo et al., “Towards a computer-aided diagnosis system in colonoscopy: automatic polyp segmentation using convolution neural networks,” *JMBR*, vol. 3, no. 02, p. 1840002, 2018.

[28] Z. Zhou, M. M. R. Siddiquee, N. Tajbakhsh, and J. Liang, “Unet+-: A nested u-net architecture for medical image segmentation,” in *DLMIA*, 2018.

[29] D. Jha, P. H. Smedsrud, M. A. Riegler, D. Johansen, T. de Lange, P. Halvorsen, and H. D. Johansen, “Resunet+-: An advanced architecture for medical image segmentation,” in *IEEE ISM*, 2019.

[30] X. Sun, F. Zhang, D. Wang, Y. Cao, and B. Liu, “Colorectal polyp segmentation by u-net with dilation convolution,” in *IEEE ICMLA*, 2019.

[31] B. Murugesan, K. Sarveswaran, S. M. Shankaranarayana, K. Ram, J. Joseph, and M. Sivaprakasam, “Psi-network: Shape and boundary aware joint multi-task deep network for medical image segmentation,” in *IEEE EMBC*, 2019.

[32] H. A. Qadir, Y. Shin, J. Solhusvik, J. Bergsland, S. Aabakken, and I. Balasingham, “Polyp detection and segmentation using mask r-cnn: Does a deeper feature extractor cnn always perform better?” in *ISMICT*, 2019.

[33] K. He, G. Gkioxari, P. Dollár, and R. Girshick, “Mask r-cnn,” in *ICCV*, 2017.

[34] S. Alam, N. K. Tomar, A. Thakur, D. Jha, and A. Rauniyar, “Automatic polyp segmentation using u-net-resnet50,” in *MediEval*, 2020.

[35] D. Banik, K. Roy, D. Bhattacharjee, M. Nasipuri, and O. Krejcar, “Polyp-net: A multimodal fusion network for polyp segmentation,” *IEEE TMM*, vol. 70, pp. 1–12, 2020.

[36] T. Rahim, S. A. Hassan, and S. Y. Shin, “A deep convolutional neural network for the detection of polyps in colonoscopy images,” *BSPC*, vol. 68, p. 102654, 2021.

[37] D. Jha, S. Ali, N. K. Tomar, H. D. Johansen, D. Johansen, J. Rittscher, M. A. Riegler, and P. Halvorsen, “Real-time polyp detection, localization and segmentation in colonoscopy using deep learning,” *IEEE Access*, vol. 9, pp. 40,496–40,510, 2021.

[38] A. M. A. Ahmed, “Generative adversarial networks for automatic polyp segmentation,” in *MediEval*, 2020.
“An image is worth 16x16 words: Transformers for image recognition at scale,” in *ICLR*, 2021.

[67] Z. Pan, B. Zhuang, J. Liu, H. He, and J. Cai, “Scalable visual transformers with hierarchical pooling,” in *ICCV*, 2021.

[68] B. Heo, S. Yun, D. Han, S. Chun, J. Choe, and S. J. Oh, “Rethinking spatial dimensions of vision transformers,” in *ICCV*, 2021.

[69] L. Yuan, Y. Chen, T. Wang, W. Yu, Y. Shi, Z. Jiang, F. E. Tay, J. Feng, and S. Yan, “Tokens-to-token vit: Training vision transformers from scratch on imagenet,” in *ICCV*, 2021.

[70] K. Han, A. Xiao, E. Wu, J. Guo, C. Xu, and Y. Wang, “Transformer in transformer,” *Advances in Neural Information Processing Systems*, vol. 34, pp. 15908–15919, 2021.

[71] W. Wang, E. Xie, X. Li, D.-P. Fan, K. Song, D. Liang, T. Lu, P. Luo, and L. Shao, “Pyramid vision transformer: A versatile backbone for dense prediction without convolutions,” in *ICCV*, 2021.

[72] W. Wang, E. Xie, X. Li, D.-P. Fan, K. Song, D. Liang, T. Lu, P. Luo, and L. Shao, “Pvt v2: Improved baselines with pyramid vision transformer,” *CVMJ*, vol. 8, no. 3, pp. 415–424, 2022.

[73] Z. Liu, Y. Lin, Y. Cao, H. Hu, Y. Wei, Z. Zhang, S. Lin, and B. Guo, “Swin transformer: Hierarchical vision transformer using shifted windows,” in *ICCV*, 2021.

[74] H. Wu, B. Xiao, N. Codella, M. Liu, X. Dai, L. Yuan, and L. Zhang, “Cvt: Introducing convolutions to vision transformers,” in *ICCV*, 2021.

[75] W. Xu, Y. Xu, T. Chang, and Z. Tu, “Co-scale conv-attentional image transformers,” in *ICCV*, 2021.

[76] X. Chu, Z. Tian, Y. Wang, B. Zhang, H. Ren, X. Wei, H. Xia, and C. Shen, “Twins: Revisiting the design of spatial attention in vision transformers,” *Advances in Neural Information Processing Systems*, vol. 34, pp. 9355–9366, 2021.

[77] B. Graham, A. El-Nouby, H. Touvron, P. Stock, A. Joulin, H. Jégou, F. Milletari, N. Navab, and S.-A. Ahmadi, “V-net: Fully convolutional neural networks for volumetric medical image segmentation,” in *3DV*, 2016.

[78] S. Ioffe and C. Szegedy, “Batch normalization: Accelerating deep network training by reducing internal covariate shift,” in *ICML*, 2015.

[79] X. Glorot, A. Bordes, and Y. Bengio, “Deep sparse rectifier neural networks,” in *AISTATS*, 2011.

[80] Z. Wu, L. Su, and Q. Huang, “Cascaded partial decoder for fast and accurate salient object detection,” in *CVPR*, 2019.

[81] S. Bhojanapalli, A. Chakrabarti, D. Glasner, D. Li, T. Unterthiner, and A. Veit, “Understanding robustness of transformers for image classification,” in *ICCV*, 2021.

[82] E. Xie, W. Wang, Z. Yu, A. Anandkumar, J. M. Alvarez, and P. Luo, “Segformer: Simple and efficient design for semantic segmentation with transformers,” *Advances in Neural Information Processing Systems*, vol. 34, pp. 12077–12090, 2021.

[83] J. Hu, L. Shen, and G. Sun, “Squeeze-and-excitation networks,” in *ICLR*, 2018.

[84] J. Hu, L. Shen, and G. Sun, “Squeeze-and-excitation networks,” in *ICLR*, 2018.

[85] X. Wang, R. Girshick, A. Gupta, and K. He, “Non-local neural networks,” in *CVPR*, 2018.

[86] J. Hu, L. Shen, and G. Sun, “Squeeze-and-excitation networks,” in *CVPR*, 2018.

[87] J. Hu, L. Shen, and G. Sun, “Squeeze-and-excitation networks,” in *CVPR*, 2018.

[88] J. Hu, L. Shen, S. Wang, and K.-y. Tong, “Selective feature aggregation network with area-boundary constraints for polyp segmentation,” in *MICCAI*, 2019.

[89] J. Bernal, J. Sánchez, and F. Vilarino, “Towards automatic polyp detection with a polyp appearance model,” *PR*, vol. 45, no. 9, pp. 3166–3182, 2012.

[90] F. Milletari, N. Navab, and S.-A. Ahmadi, “V-net: Fully convolutional neural networks for volumetric medical image segmentation,” in *3DV*, 2016.

[91] R. Margolin, L. Zelnik-Manor, and A. Tal, “How to evaluate foreground maps?” in *CVPR*, 2014.

[92] R. Margolin, L. Zelnik-Manor, and A. Tal, “How to evaluate foreground maps?” in *CVPR*, 2014.

[93] D.-P. Fan, G.-P. Ji, X. Qin, and M.-M. Cheng, “Cognitive vision inspired object segmentation metric and loss function,” *SSV*, 2021.
This is your template for Nordic Machine Intelligence

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Abstract
We present our solutions to the MedAI: Transparency in Medical Image Segmentation, for all the three tasks: polyp segmentation task, instrument segmentation task, transparency task. We use the same pipeline to process the two segmentation tasks of polyps and surgery, and use the same pre-processing and post-processing operations. The key improvement over last year is newer state-of-the-art vision architectures, especially transformers which significantly outperform ConvNets for the medical image segmentation task. Our solution consists of multi-model fusion, and each model uses a transformer as the backbone network. We finished the all the tasks and get the best score of 0.91 in instrument segmentation task and 0.83 in polyp segmentation task. Meanwhile, we provide complete solutions in https://github.com/dongbo811/MedAI-2021.

Keywords: artificial intelligence; machine learning; deep learning; robotics

Introduction
Colorectal cancer is one of the deadly cancers in the world. Colonoscopy is the standard treatment to check, locate and remove colorectal polyps. However, it has been shown that the missed diagnosis rate of colorectal polyps during colonoscopy is between 6% and 27%. The use of automatic, accurate and real-time polyp segmentation during colonoscopy can help clinicians eliminate missing lesions and prevent the further development of colorectal cancer.

In recent years, significant progress has been seen in robot-assisted surgery and computer-assisted surgery. The segmentation of surgical instruments can accurately locate robotic instruments and estimate their posture, which is essential for the navigation of surgical robots. In addition, the segmentation results can be used to predict dangerous operations and reduce surgical risks. At the same time, it can provide a variety of automated solutions for postoperative work, such as objective skill evaluation, surgical report generation, and surgical process optimization, which are of great significance to clinical work.

Model
The method in this paper integrates three models for fusion, namely Polyp-PVT, Sinv2-PVT, and Transfuse-PVT. The official Polyp-PVT [dong2021PolypPVT] is designed for polyp segmentation and achieves SOTA segmentation capabilities and generalization performance. It uses transformer as the backbone network to extract richer features and solves the impact of colorectal image acquisition. Here, we adopt the standard structure without any modification. For the Transfuse [zhang2021transfuse], which is also adopted in the polyp segmentation, we improve it by replacing the transformer part with the PVT [wang2021pyramid, wang2021pvtv2] to enhance its performance. The official Sinv2 [fan2021concealed] proposes an end-to-end network for search and recognition the concealed Object, which obtains considerable segmentation performance. This task is similar to the polyp segmentation and surgical instrument segmentation, so we adopt. Here we employ a stronger PVT transformer [wang2021pyramid, wang2021pvtv2] to replace the original res2net [gao2019res2net] backbone to extract more powerful features.

Hyperparameter settings
We use the PyTorch framework to implement our model, and use Tesla V100 to accelerate the calculation. Taking into account the difference in the size of each polyp image, we adopted a multi-scale strategy in the training phase. The hyperparameter details are as follows. To update the network parameters, we use the AdamW optimizer, which is widely used in transformer networks. The learning rate is set to 1e-4, and the weight attenuation is also
Table 1: 5-fold cross-validation results of surgical instrument segmentation. Intersection-Over-Union (Jaccard index), Dice coefficient, and the pixel accuracy are abbreviated as IoU, Dice, PA respectively.

| models       | Metrics | Flod-1     | Flod-2     | Flod-3     | Flod-4     | Flod-5     | Mean     |
|--------------|---------|------------|------------|------------|------------|------------|----------|
| Polyp-PVT    | IoU     | 0.9012     | 0.8744     | 0.9310     | 0.9529     | 0.9522     | 0.9224   |
|              | Dice    | 0.9427     | 0.9226     | 0.9616     | 0.9754     | 0.9748     | 0.9554   |
|              | PA      | 0.9915     | 0.9900     | 0.9939     | 0.9937     | 0.9934     | 0.9925   |
| Sinv2-PVT    | IoU     | 0.8971     | 0.8760     | 0.9315     | 0.9521     | 0.9519     | 0.9217   |
|              | Dice    | 0.9392     | 0.9237     | 0.9622     | 0.9751     | 0.9745     | 0.9549   |
|              | PA      | 0.9908     | 0.9897     | 0.9940     | 0.9936     | 0.9934     | 0.9923   |
| Transfuse-PVT| IoU     | 0.9034     | 0.8691     | 0.9313     | 0.9497     | 0.9511     | 0.9209   |
|              | Dice    | 0.9443     | 0.9207     | 0.9611     | 0.9734     | 0.9742     | 0.9547   |
|              | PA      | 0.9917     | 0.9891     | 0.9931     | 0.9925     | 0.9930     | 0.9919   |

Training stage:
We use the same training strategy to train Polyp-PVT, Sinv2-PVT, and Transfuse-PVT. Specifically, we first divide the dataset into 5 groups (folds). At each time, we use 4 groups of dataset as the training set and the remaining one as the validation set. During training, we keep the model weights with the best IoU on the validation set. After 5-fold training, all of Polyp-PVT, Sinv2-PVT, and Transfuse-PVT have 5 model weights, and a total of 15 different model weights are obtained.

Inference stage
In the inference stage, for the input images, we only resize the images to 352 × 352 without any data enhancement. For the output, we upsample it to the original feature size. So, we can obtain 15 different prediction results of test dataset without any data enhancement.

In order to obtain a more stable prediction, we merge the 15 prediction results with a minority voting method. Because the voting strategy will produce many independent noise pixels on the edge of polyps or surgical instruments. We use open operation and counting to remove. First, the open operation is used to remove independent noise points, and then the area of the block in the prediction image is counted to remove relatively small noise blocks in the prediction image, so as to obtain the final prediction result.

Result
We show the qualitative results in Fig. 1, and give the results of the evaluations in Tab. 1. At the same time, we shared our failure cases in Fig. 2.

Discussion
It can be found that both of our improved algorithms Sinv2-PVT and Transfuse-PVT have the same performance as polyp-pvt. In the 5-fold cross-validation, the three results are relatively stable. There are results above 0.92 on the IoU, and we give some visual results in 1. However, there are certain shortcomings shown in 2. Our results almost correctly segment the equipment, but introduce some noise. One characteristic of these noises is that they are biased towards black. This is mainly due to the fact that there are more black instruments in the entire data set. Therefore, small black areas (food residuals, etc.) in the colonoscope will be identified as surgical instruments. These noises can be filtered by the
size of the area to achieve the purpose of noise removal.

**Conclusion**
In this paper, we propose a robust generalized medical image segmentation framework, which is composed of multiple models, and uses the pyramid vision transformer backbone as an encoder to explicitly extract more powerful and powerful features.

**Acknowledgments**
I would first like to thank the researcher Dengping Fan in IIAI, whose expertise was invaluable in formulating the research questions and methodology.

**Conflict of interest**
Authors state no conflict of interest. (Either keep this sentence or describe any conflict of interest.)