One Polyp Identifies All: One-Shot Polyp Segmentation with SAM via Cascaded Priors and Iterative Prompt Evolution

Supplementary Material

1. Extended Experimental Results

Due to page limitations, only experimental results from the first three centers from PolypGen were presented in the main text. The experimental results from Centers 4 and 5 are included in the supplementary materials Tab. 1. The results demonstrate that OP-SAM consistently outperforms state-of-the-art (SOTA) methods across these two additional centers. Notably, in Center 4, the proposed method achieved an 11.89 improvement in IoU compared to SOTA methods. Furthermore, the proposed method exhibits superior robustness, achieving optimal performance across both centers.

	PolypGen				
Method	Center 4		Center 5		
	IoU	Dice	IoU	Dice	
PerSAM	23.30	27.30	42.26	49.45	
PerSAM-f	24.36	27.94	26.75	32.99	
Matcher	26.31	33.94	38.78	47.71	
ProtoSAM	27.16	36.28	30.91	41.19	
OP-SAM(ours)	39.05	44.76	48.63	56.77	

Table 1. Continued quantitative performance comparison of the proposed method against state-of-the-art methods on PolypGen Dataset.

2. Feature Selection Ablations

Throughout all experiments presented in the main text, value embeddings from the final attention module of the DI-NOv2 model were extracted for cross-correlation computation. Here, we investigate the impact of different feature embeddings on the final segmentation results, see Tab. 2. The query, key, and value embeddings from the final attention module, as well as the feature embeddings output, are extracted and evaluated separately. The experimental results indicate that utilizing value embeddings for cross-correlation yields the highest accuracy. This finding aligns with previous literature suggesting that value embeddings most effectively capture the semantic features of each patch.

3. Self-refinement Ablations

Additional ablation experiments are conducted to investigate the impact of self-correlation in prior refinement. In the main text, the number of self-refinement iterations (ρ)

Method	Modules			IoU	Dice	
	Q	K	V	Feats	100	Dice
OP-SAM	~				70.61	79.16
		/			68.47	77.27
			1		76.93	84.53
				~	74.00	82.15

Table 2. Ablation studies of feature selections, Q, K, V, Feats denote query, key, value features and the final features output from the image encoder.

was set to 2. The effect of varying iteration numbers from 1 to 4 on the final segmentation results is subsequently evaluated Tab. 3. The experimental results demonstrate that segmentation accuracy initially increases and then decreases as the number of self-refinement iterations increases, reaching peak performance at 2 iterations. This phenomenon can be attributed to the fact that increasing the number of self-refinement iterations inevitably introduces erroneous relationships from self-correlation.

Method	Iter_num	IoU	Dice
OP-SAM	1	75.08	82.86
	2	76.93	84.53
	3	71.89	80.14
	4	54.96	65.71

Table 3. Ablation studies of self-refinement iterations.

4. Inference Time Comparison

Finally, a comparative analysis of inference time is conducted between OP-SAM and SOTA methods Tab. 4. The results indicate that OP-SAM achieves the fastest inference speed among all methods except PerSAM, while PerSAM exhibits significantly lower inference accuracy than other methods. By constraining the iteration number in the prompting module, OP-SAM achieves a superior balance between accuracy and inference speed.

Meth	od	PerSAM	Matcher	ProtoSAM	Ours
Tim	e/s	0.236	0.717	0.866	0.466

Table 4. Inference time comparison.

5. More Visual Results

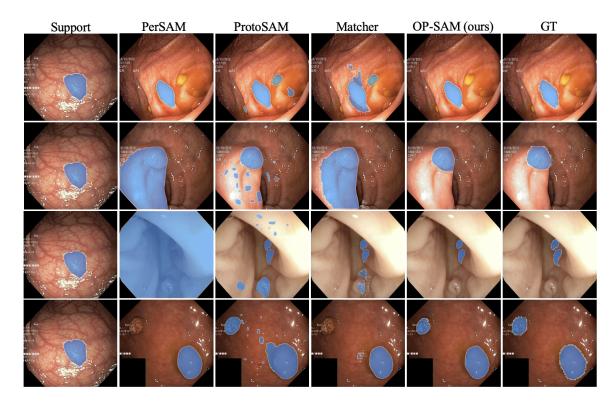


Figure 1. Qualitative comparison of OP-SAM against state-of-the-art methods. OP-SAM demonstrates enhanced discriminative capability, effectively reducing both false negative and false positive.

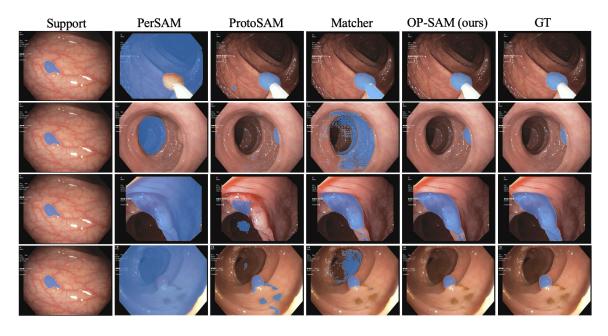


Figure 2. Qualitative comparison of OP-SAM against state-of-the-art methods. OP-SAM demonstrates superior robustness, maintaining accurate segmentation performance for polyps across various sizes.