

REVIEW

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A survey on deep learning for polyp segmentation: techniques, challenges and future trends

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Abstract

Early detection and assessment of polyps play a crucial role in the prevention and treatment of colorectal cancer (CRC). Polyp segmentation provides an effective solution to assist clinicians in accurately locating and segmenting polyp regions. In the past, people often relied on manually extracted lower-level features such as color, texture, and shape, which often had problems capturing global context and lacked robustness to complex scenarios. With the advent of deep learning, more and more medical image segmentation algorithms based on deep learning networks have emerged, making significant progress in the field. This paper provides a comprehensive review of polyp segmentation algorithms. We first review some traditional algorithms based on manually extracted features and deep segmentation algorithms, and then describe benchmark datasets related to the topic. Specifically, we carry out a comprehensive evaluation of recent deep learning models and results based on polyp size, taking into account the focus of research topics and differences in network structures. Finally, we discuss the challenges of polyp segmentation and future trends in the field.

Keywords: Polyp segmentation, Deep learning, Comprehensive evaluation, Medical imaging

1 Introduction

Polyp segmentation aims to automatically identify and segment polyp regions within the colon. Its primary objective is to assist clinical doctors in efficiently and accurately locating and delineating these regions, providing vital support for early diagnosis and treatment of colorectal cancer (CRC) [1]. Polyps exhibit varying sizes and shapes at different stages of development [2, 3], and their precise segmentation poses challenges due to their strong adherence to adjacent organs or mucosa [4].

In the early stage, polyp segmentation primarily relied on manually extracted features [5, 6]. For example, Tajbakhsh et al. [5] proposed a method that utilized shape features

and surrounding environmental information to automatically detect polyps in colonoscopy videos. Iwahori et al. [6] utilized edge and color information to generate a likelihood map and extracted the directional gradient histogram features. However, relying on manually extracted low-level features for segmentation tasks makes it difficult to handle complex scenarios and does not effectively utilize global contextual information [7].

In recent years, deep learning-based polyp segmentation models have demonstrated impressive capabilities in locating and segmenting polyp regions. Based on the encoder-decoder architecture, some works focus on enhancing the output features of the encoder [8, 9]. In addition, the variation between datasets collected from different devices is also an issue [10]. After the emergence of the segment anything model (SAM) [11], fine-grained models based on universal segmentation networks have shown promising momentum in polyp segmentation [12]. To provide a

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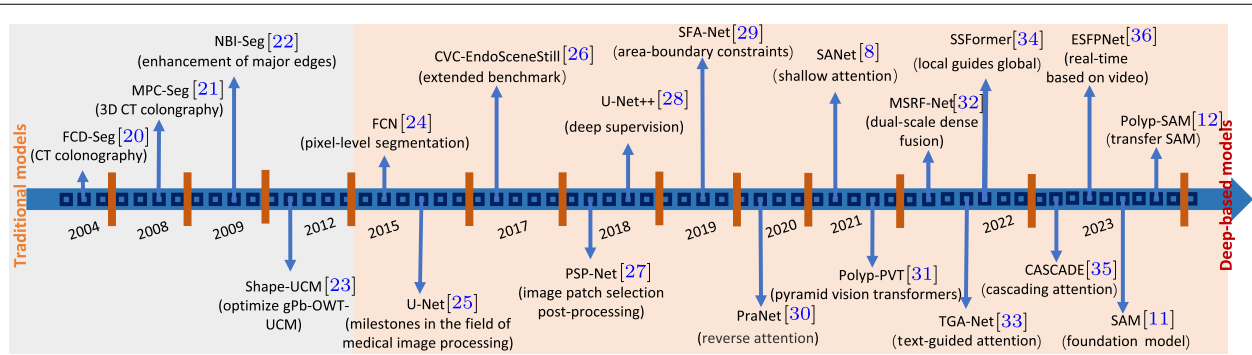


Figure 1 A brief chronology of polyp segmentation. Before 2015, methods relied on hand-crafted features combined with machine learning algorithms. Since 2015, U-Net [20] and FCN [21] have significantly advanced the development of deep learning techniques in polyp segmentation. More details can be found in Sect. 2

clearer depiction of the progress in polyp segmentation tasks, we show a concise timeline in Fig. 1.

Existing surveys typically provide systematic statistics on polyp segmentation, localization, and detection methods [13], or review medical image segmentation across different anatomical regions, such as the abdomen, heart, brain, and lungs [14–19]. In contrast to previous reviews on polyp segmentation or medical image segmentation, this paper aims to provide a comprehensive review of polyp segmentation methods. It covers both traditional algorithms and deep learning model-based approaches for polyp segmentation.

We discuss traditional methods and deep learning-based methods separately. Based on the unique design of model structures, we categorize deep models into boundary-aware models, attention-aware models, and feature fusion models. We discuss the advantages associated with each method and provide valuable insights into their respective applicability and performance characteristics. In Sect. 2, we review the existing polyp segmentation models from different aspects. In Sect. 3, we summarize and provide detailed information and usage of the current publicly available datasets used for polyp segmentation. Then, we conduct a comprehensive assessment of the segmentation performance for polyp sizes and an analysis of the advantages and disadvantages of several representative polyp segmentation models in Sect. 4. After that, in Sect. 5, we discuss the challenges and future trends for development in the field. Finally, we conclude the paper in Sect. 6.

2 Polyp segmentation models

Recent research in polyp segmentation has leveraged popular deep-learning methods to achieve remarkable results. In contrast, earlier approaches relied primarily on manually engineered features for polyp segmentation. A summary of these models can be found in Tables 1 and 2. To provide a comprehensive review of these polyp segmenta-

tion algorithms, we will introduce them from the following aspects.

- 1) *Traditional models*. They rely primarily on manually designed features such as color, texture, and shape information to formulate algorithms.
- 2) *Deep models*. Deep learning models automatically learn deep features, which enables them to handle unstructured and complex data and provides them with more powerful expressive capabilities.
- 3) *Boundary-aware models*. Edge information is crucial in providing boundary cues to boost the segmentation performance. Therefore, we will discuss the application of edge information in some existing models.
- 4) *Attention-aware models*. The analysis of the different attention strategies used in polyp segmentation research has provided insights for the potential design of attention modules in future work.
- 5) *Feature fusion models*. The integration and enhancement of multi-level features can significantly enhance model performance. Therefore, we investigate the effectiveness of feature fusion strategies in polyp segmentation models.

2.1 Traditional models

Early works primarily relied on manually designed features, such as color, texture, and shape, and then employed traditional machine learning techniques for heuristic modeling. For instance, Yao et al. [76] proposed an automatic polyp segmentation method that combines knowledge-guided intensity adjustment, fuzzy c-means clustering, and deformable models. Lu et al. [77] proposed a three-stage probabilistic binary classification method that integrates low-level and mid-level information to segment polyps in 3D CT colonography. Gross et al. [78] studied a segmentation algorithm that enhances primary edges through multiscale filtering. Ganz et al. [79] utilized

Table 1 Summary of polyp segmentation methods (published from 2019 to 2021)

#	Year	Method	Pub.	Backbone	Description	Code
1	2019	SFA [22]	MICCAI	light UNet	Boundary-sensitive loss; selective feature aggregation	N/A
2	2019	ResUNet++ [23]	ISM	ResUNet	Squeeze and excitation blocks; atrous spatial pyramid pooling (ASPP); attention blocks	https://github.com/DebeshJha/ResUNetPlusPlus
3	2020	PolypSeg [24]	MICCAI	U-Net	Improved attention mechanism; separable convolution	N/A
4	2020	ACSNet [25]	MICCAI	ResNet34	Adaptively select; aggregate context features through channel attention	https://github.com/ReaFly/ACSNet
5	2020	PraNet [26]	MICCAI	Res2Net	Parallel partial decoders; reverse attention	https://github.com/DengPingFan/PraNet
6	2021	ThresholdNet [1]	TMI	DeepLabv3+	Confidence-guided manifold mixup; threshold loss	https://github.com/Guo-Xiaoqing/ThresholdNet
7	2021	DDANet [28]	PR	ResUNet	Dual-decoder attention; out-of-training-set testing	https://github.com/nikhilroxtomar/DDANet
8	2021	MSRF-Net [29]	JBHI	N/A	Multi-scale residual fusion; dual-scale dense fusion	https://github.com/NoviceMAN-prog/MSRF-Net
9	2021	HarDNet-MSEG [30]	arxiv	HarDNet68	Cascaded partial decoder; dense aggregation	https://github.com/james128333/HarDNet-MSEG
10	2021	EU-Net [31]	CRV	ResNet34	Semantic feature; adaptive global context module	https://github.com/rucv/Enhanced-U-Net
11	2021	FANet [32]	arxiv	N/A	Feedback attention learning; iterative refining; embedded run-length encoding strategy	https://github.com/nikhilroxtomar/fanet
12	2021	Polyp-PVT [33]	arxiv	PVT	Cascaded fusion; camouflage identification; similarity aggregation	https://github.com/DengPingFan/Polyp-PVT
13	2021	UACANet [34]	ACM MM	Res2Net	Parallel axial attention; uncertainty augmented context attention	https://github.com/plemeri/UACANet
14	2021	C2FNet [35]	IJCAI	Res2Net-50	Context-aware cross-level fusion; dual-branch global context	https://github.com/thograce/C2FNet
15	2021	ResUNet++ TTA + CRF [36]	JBHI	ResUNet	conditional random fields; test-time augmentation	https://github.com/DebeshJha/ResUNet-with-CRF-and-TTA
16	2021	MPA-DA [10]	JBHI	ResNet-101	Inter-prototype adaptation network; progressive self-training; disentangled reconstruction	https://github.com/CityU-AIM-Group/MPA-DA
17	2021	TransFuse [37]	MICCAI	ResNet-34 + DeiT-S	self-attention; bilinear Hadamard product; gated skip-connection	https://github.com/Rayicer/TransFuse
18	2021	SANet [8]	MICCAI	Res2Net	Color exchange; shallow attention	https://github.com/weijun88/sanet
19	2021	STFT [38]	MICCAI	ResNet-50	Spatial-temporal feature transformation; deformable convolutions and channel-aware attention	https://github.com/lingyunwu14/STFT
20	2021	LOD-Net [39]	MICCAI	ResNet + FPN	Model the probability of each pixel being in the boundary region; adaptive thresholding policy	https://github.com/midsdsy/LOD-Net
21	2021	MSNet [9]	MICCAI	Res2Net-50	Multi-scale subtraction; training-free network	https://github.com/Xiaoqi-Zhao-DLUT/MSNet
22	2021	CCBANet [40]	MICCAI	ResNet34	Cascading context; balancing attention	https://github.com/ntcongyn/CCBANet
23	2021	HRENet [41]	MICCAI	ResNet34	Hard region enhancement; adaptive feature aggregation; edge and structure consistency aware loss	https://github.com/CathySH/HRENet
24	2022	GMSRF-Net [42]	ICPR	ResNet50	Cross-multi-scale attention; multi-scale feature selection	https://github.com/NoviceMAN-prog/GMSRFNet

Table 2 Summary of polyp segmentation methods (published from 2022 to 2023)

#	Year	Method	Pub.	Backbone	Description	Code
25	2022	TGANet [43]	MICCAI	ResNet50	Text-guided attention; weights the text-based embeddings	https://github.com/nikhilroxtomar/tganet
26	2022	CaraNet [44]	SPIE MI	Res2Net	Context axial reverse attention	https://github.com/AngelouCN/CaraNet
27	2022	MSRAformer [45]	CBM	Swin Transformer	multi-scale spatial reverse attention	https://github.com/ChengLong1222/MSRAformer-main
28	2022	HSNet [46]	CBM	PVTv2	Cross-semantic attention; hybrid semantic complementary; multi-scale prediction	https://github.com/baiboat/HSNet
29	2022	FuzzyNet [47]	NeurIPS	Res2Net/ConvNext/ PVT	fuzzy attention; focus on the blurry pixels	https://github.com/krushi1992/FuzzyNet
30	2022	LDNet [48]	MICCAI	Res2Net	Lesion-aware dynamic kernel; self-attention	https://github.com/ReaFly/LDNet
31	2022	HarDNet-DFUS [49]	arxiv	HarDNetV2	Real-time model; enhanced backbone	https://github.com/YuWenLo/HarDNet-DFUS
32	2022	BDG-Net [50]	SPIE MI	EfficientNet-B5	Boundary distribution guided; boundary distribution generation	https://github.com/zihuanqiu/BDG-Net
33	2022	ColonFormer [51]	Access	MiT	Integrate a hierarchical Transformer and a hierarchical pyramid CNN; residual axial attention	https://github.com/ducnt9907/ColonFormer
34	2022	FCBFormer [52]	MIUA	PVTv2	Improved progressive locality decoder; fully convolutional branch + Transformer branch	https://github.com/ESandML/FCBFormer
35	2022	DCRNet [53]	ISBI	ResNet-34	Duplex contextual relation network; cross-image contextual relations	https://github.com/PRIS-CV/DCRNet
36	2022	SSFormer [54]	MICCAI	PVTv2	Aggregate local and global features stepwise	https://github.com/Qiming-Huang/ssformer
37	2022	LAPFormer [55]	arxiv	MiT-B1	Hierarchical Transformer encoder and CNN decoder; progressive feature fusion	N/A
38	2022	PPFormer [56]	MICCAI	CvT	Shallow CNN encoder; deep Transformer-based encoder	N/A
39	2022	BSCA-Net [57]	PR	Res2Net	Bit-plane slicing information; segmentation squeeze bottleneck union module; multi-path connection attention	N/A
40	2022	BoxPolyp [58]	MICCAI	Res2Net/ PVT	Box annotations; fusion filter sampling module	N/A
41	2022	ICBNet [59]	BIBM	PVT	Iterative feedback learning strategy; context and boundary-aware information	N/A
42	2022	CLD-Net [60]	BIBM	MiT	Small polyp segmentation; local edge feature extraction	N/A
43	2022	BANet [61]	PRCV	Res2Net-50	Attention-aware localization; residual pyramid convolution	N/A
44	2023	DuAT [62]	PRCV	PVT	Dual-aggregation Transformer; global-to-local spatial aggregation; selective boundary aggregation	https://github.com/Barrett-python/DuAT
45	2023	PolypSeg+ [63]	TCYB	ResNet50	Adaptive scale context module; lightweight attention mechanism	https://github.com/szuzzb/polypsegplus
46	2023	APCNet [64]	TIM	ResNet50	Attention-guided multi-level aggregation strategy; complementary information from different layers	N/A
47	2023	RA-DENet [65]	CBM	Res2Net	Improved reverse attention; distraction elimination	N/A
48	2023	EFB-Seg [66]	Neurocom-puting	ConvNet	Boundary Embedding; semantic offset field learned	N/A
49	2023	PPNet [67]	CBM	P2T	Channel attention; pyramid feature fusion	N/A
50	2023	Fu-TransHNet [68]	arxiv	HardNet68	CNN and Transformer; multi-view learning	N/A

Table 2 (Continued)

#	Year	Method	Pub.	Backbone	Description	Code
51	2023	DilatedSegNet [69]	MMM	ResNet50	Dilated convolution pooling block; convolutional attention	https://github.com/nikhilroxtomar/DilatedSegNet
52	2023	FEDNet [70]	BSPC	PVT	Decouple edge features and main body features	https://github.com/suoyanzhou626/FEDNet-BSPC
53	2023	PEFNet [71]	MMM	EfficientNet V2-L	Positional encoding and information fusion	https://github.com/huyquoctrinh/PEFNet
54	2023	Polyp-SAM [12]	arxiv	ViT	Fine-tuned SAM model for polyp segmentation [11].	https://github.com/ricklisz/Polyp-SAM
55	2023	ESFPNet [72]	SPIE MI	MiT	Efficient stage-wise feature pyramid decoder	N/A
56	2023	TransNetR [73]	MIDL	ResNet50	Transformer-based residual network; multi-center out-of-distribution testing	https://github.com/DebeshJha/TransNetR
57	2023	CASCADE [74]	WACV	PVTv2/TransUNet	Cascaded attention-based decoder; multi-stage loss optimization; feature aggregation	https://github.com/SLDGroup/CASCADE
58	2023	CFA-Net [75]	PR	Res2Net-50	Cross-level feature aggregated; boundary aggregated	https://github.com/taozh2017/CFANet

prior knowledge of polyp shapes using narrow band imaging (NBI) to optimize the inherent scale selection of gPb-OWT-UCM. This optimization aims to achieve better segmentation results by incorporating the shape information of polyps.

2.2 Deep models

However, the aforementioned methods are constrained by the limited information representation capabilities of manual features. They lack generalization capabilities and are not suitable for large-scale deployment. We will review some representative deep learning-based methods in the field of polyp segmentation.

CNN-based methods. Thanks to the development of convolutional neural network (CNN), especially with the introduction of U-Net [20], many models inspired by this architecture have demonstrated promising results. AC-SNet [25] modifies the skip connections in U-Net into local context extraction modules and adds a global information extraction module. The features are integrated and then adaptively selected based on a channel attention strategy. EU-Net [31] is an enhanced U-Net framework that enhances semantic information and introduces an adaptive global context module to extract key features. MSNet [9] designs a subtraction unit to generate difference features between adjacent layers and pyramidically equips it with different receptive fields to capture multi-scale information. In addition, it introduces LossNet to supervise the perceptual features at each layer. PEFNet [71] utilizes an improved U-Net in the merging phase and embeds new location feature information. Thanks to the rich knowledge of positional information and concatenated features, this model achieves higher accuracy and universality in polyp segmentation.

Transformer-based methods. CNNs have limitations in capturing long-range dependencies. However, the Transformer model, which first gained popularity in natural language processing, has been introduced to computer vision. Its advantage in capturing long-range dependencies has sparked a research trend in Vision Transformers. MSRAformer [45] adopts a Swin Transformer as the encoder with a pyramid structure to extract features at different stages and utilizes a multi-scale channel attention module to extract multi-scale feature information. DuAT [62] is a dual-aggregation Transformer network for polyp segmentation, which aggregates global and local spatial features and locates multi-scale objects. SSFormer [54] incorporates PVTv2 [80] and Segformer as the encoder while introducing a novel progressive local decoder. This decoder is specifically designed to complement the pyramid Transformer backbone by emphasizing local features and mitigating attention dispersion. ColonFormer [51] adopts a lightweight architecture based on the Transformer as the encoder and uses a hierarchical network structure for learning multi-level features in the decoder. TransNetR [73] is a Transformer-based residual network, comprising a pre-trained encoder, three decoder blocks, and an upsampling layer, demonstrating excellent real-time processing speed and multi-center generalization capability. Polyp-PVT [33] cascades to aggregate advanced semantic and positional information, employing a similarity aggregation module to extend high-level features to the entire region.

Hybrid methods. Furthermore, numerous models have combined the strengths of both CNN and Transformer, capturing both local context information and long-range dependencies to significantly enhance segmentation performance. TransFuse [37] combines the Transformer and

CNN branches in parallel. It employs a self-attention mechanism and a multi-modal fusion mechanism to integrate features from different branches, and uses spatial attention to enhance local details. LAPFormer [55] employs a hierarchical Transformer encoder with a CNN decoder. Additionally, it introduces a progressive feature fusion module to integrate multi-scale features and incorporates a feature refinement module and a feature selection module for feature handling. PPFormer [56] adopts a shallow CNN encoder and deep Transformer-based encoder to extract features. HSNet [46] utilizes a dual-branch structure composed of Transformer and CNN networks to capture both long-range dependencies and local appearance details. Fu-TransHNet [68] designs a novel feature fusion module to fully make use of the local and global features obtained from CNN and Transformer networks.

2.3 Boundary-aware models

The utilization of edge information as a guiding strategy was initially prevalent in object detection and has been increasingly applied to polyp segmentation tasks. Precise edge-aware representation aids in improving segmentation accuracy. In the following sections, we will review several models that exhibit exceptional capability in perceiving and incorporating edge information. FeDNet [70] simultaneously optimizes the main body and edges to improve polyp segmentation performance. BSCA-Net [57] utilizes bit-plane slicing information to effectively extract boundary information. BoxPolyp [58] mitigates overfitting issues by using box annotations, iteratively enhancing the segmentation model to generate fine-grained polyp regions. BDG-Net [50] utilizes a boundary distribution generation module to aggregate high-level features, which are taken as supplementary spatial information and fed to the boundary distribution guided decoder for guiding polyp segmentation. ICBNet [59] enhances encoder features from preliminary segmentation and boundary prediction by incorporating context and boundary-aware information. CLD-Net [60] employs a progressive strategy to extract edge features and addresses the issue of feature loss during downsampling by combining a local edge feature extraction module with a local-global feature fusion module. BANet [61] identifies the main location of polyps through an attention-aware localization module. SFA [22] improves segmentation performance by constructing a selective feature aggregation network with regional and boundary constraints. FCBFormer [52] fully leverages the strengths of fully convolutional networks (FCNs) and Transformers for polyp segmentation.

2.4 Attention-aware models

Achieving superior performance in polyp segmentation requires the ability to prioritize relevant information. By incorporating an attention mechanism, this problem can

be effectively addressed. This allows the model to focus on the most important features, ultimately improving segmentation performance. CASCADE [74] takes advantage of the multi-scale features using a hierarchical vision Transformer architecture. APCNet [64] extracts multi-level features from a pyramid structure and leverages an attention-guided multi-level aggregation strategy to enhance each layer's context features. RA-DENet [65] enhances the representation of different regions through inverse attention, and then eliminates noise through distractor removal. TGANet [43] incorporates a text attention mechanism, which utilizes features related to the size and number of polyps to adapt to varying polyp sizes and effectively handle scenarios with multiple polyps. LDNet [48] extracts global context features from the input image and then updates them iteratively based on the lesion features predicted by the segmentation. SANet [8] eliminates the impact of colors through a color swap operation, and then filters out background noise from shallow features based on a shallow attention module.

2.5 Feature fusion models

It is crucial to incorporate multi-scale features to effectively handle variations in object size [81]. Moreover, integrating multi-level features through feature fusion and leveraging both high-level and low-level features can significantly enhance segmentation performance [82, 83]. In the context of polyp segmentation tasks, various feature fusion strategies have been utilized to achieve this goal. CFA-Net [75] is a novel cross-level feature aggregation network that adopts a hierarchical strategy to incorporate edge features into the dual-stream segmentation network. EFB-Seg [66] enhances multi-level feature fusion by introducing a feature fusion module that utilizes the learned semantic offset field to align multi-level feature maps, thereby addressing the issue of feature misalignment. MSRF-Net [29] innovatively uses a dual-scale dense fusion block to exchange multi-scale features with different receptive fields. DCRNet [53] captures both intra-image and inter-image context relationships. Within the image, a positional attention module is presented to capture pixel-level context information. PPNet [67] uses a channel attention scheme in the pyramid feature fusion module to learn global context features, thereby guiding the information transformation of the decoder branches. PraNet [26] aggregates high-level features using parallel partial decoders, uses a reverse attention module to mine boundary clues, and establishes the relationship between region and boundary cues. PolypSeg [24] aggregates multi-scale context information and focuses on the target area using an improved attention mechanism.

2.6 Video polyp segmentation

To facilitate the deployment of automated segmentation methods in clinical settings, a shift in focus has been ob-

served in some studies toward video-based polyp segmentation methods. By considering temporal information, these approaches aim to overcome the limitations of single-image segmentation and enable more precise and efficient segmentation in real-time scenarios within clinical requirements. ESFPNet [72] constructs a pre-trained mixed Transformer (MiT) encoder and an efficient stage-wise feature pyramid decoder, in which the MiT uses overlapping path merging modules and self-attention prediction. PNS+ [84] extracts long-term spatiotemporal representations using global encoders and local encoders and refines them gradually with normalized self-attention blocks. SSTAN [85] presents a semi-supervised video polyp segmentation task that only requires sparsely annotated frames for training. PNS-Net [86] leverages standard self-attention modules and CNN to efficiently learn representations from polyp videos in real time without the need for post-processing. NanoNet [87] has fewer parameters and can be integrated with mobile and embedded devices. It utilizes a pre-trained MobileNetV2 [88] as the encoder. In the architecture between the encoder and decoder, a modified residual block is incorporated to enhance the generalization capability of the decoder.

3 Polyp segmentation datasets

The rapid progress in the field of medical image segmentation has led to the construction of various public benchmark datasets specifically designed for polyp segmentation tasks. By utilizing these benchmark datasets, researchers can compare their methods against established baselines, facilitate reproducible research, and encourage further advances in the field of polyp segmentation. Table 3 summarizes eight popular image-level polyp segmentation datasets, and Fig. 2 shows examples of images (including edge maps, and annotations) from these datasets. Moreover, we provide some details about each dataset below. Please note that some video-level polyp segmenta-

tion datasets are summarized in Table 3, and some works [5, 7, 84, 89, 90] are based on them.

- 1) ETIS-LaribPolypDB [91] is a collection of early colorectal polyp images consisting of 196 polyp instances, each captured at a resolution of 966×1225 pixels.
- 2) CVC-ClinicDB [7] is a dataset collected from clinical cases at a hospital in Barcelona, Spain, and is developed from 23 colonoscopy video studies acquired with white light. This dataset contains 612 high-resolution color images with a resolution of 576×768 , all derived from clinical colonoscopy examinations. Each image comes with a corresponding manual annotation file that clearly delineates the location of the polyp.
- 3) CVC-ColonDB [5] is maintained by the Computer Vision Center (CVC) in Barcelona. It includes 380 colonoscopy images with a resolution of 500×574

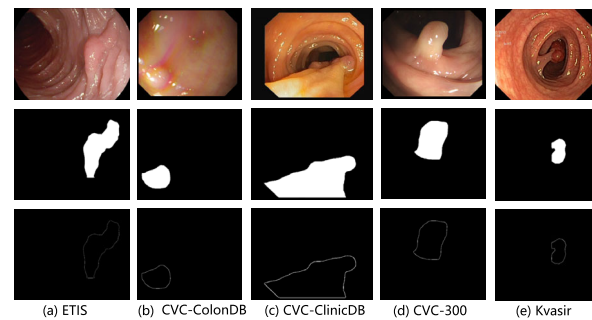


Figure 2 Examples of images, ground truth maps, and edges in five polyp segmentation datasets, including (a) ETIS-LaribPolypDB [91], (b) CVC-ColonDB [5], (c) CVC-ClinicDB [7], (d) CVC-300 [92], and (e) Kvasir-SEG [93]. In each dataset, the image, ground truth maps, and edges are shown from top to bottom

Table 3 Statistics on the datasets are made according to the year (Year), journal or conference publication (Pub.), the dataset size (Size), the number of objects in the images (Obj.), and the resolution (Resolution). More detailed information about each dataset can be found in Sect. 3

	#	Dataset	Year	Pub.	Size	Obj.	Resolution
Image-level	1	ETIS-LaribPolypDB [91]	2014	IJCARS	196	Multiple	966×1225
	2	CVC-ClinicDB [7]	2015	CMIG	612	Multiple	576×768
	3	CVC-ColonDB [5]	2016	TMI	380	One	500×574
	4	CVC-300 [92]	2017	JHE	60	One	500×574
	5	CVC-EndoSceneStill [92]	2017	JHE	912	Multiple	$[500 \sim 576] \times [574 \sim 768]$
	6	Kvasir-SEG [93]	2020	MMM	1000	Multiple	$[332 \sim 1920] \times [487 \sim 1072]$
	7	PICCOLO [94]	2020	AS	3433	Multiple	$[480 \sim 1080] \times [854 \sim 1920]$
	8	PolypGen [95]	2023	SD	8037	Multiple	$[288 \sim 1080] \times [384 \sim 1920]$
Video-level	9	ASU-Mayo Clinic [5]	2016	TMI	36,458	One	550×688
	10	CVC-ClinicVideoDB [96]	2017	GIANA	11,954	Multiple	N/A
	11	LDPolypVideo [89]	2021	MICCAI	40,266	Multiple	480×560
	12	SUN-SEG [84]	2022	MIR	158,690	One	$[1008 \sim 1080] \times [1158 \sim 1240]$

and segmentation masks manually annotated to precisely mark the location of polyps.

- 4) CVC-300 [92] includes 60 colonoscopy images with a resolution of 500×574 .
- 5) CVC-EndoSceneStill [92] includes CVC-ClinicDB and CVC-300, thereby containing 912 colonoscopy examination images along with corresponding annotations.
- 6) Kvasir-SEG [93] contains 1000 images of gastrointestinal polyps along with corresponding segmentation masks and bounding boxes. These were manually annotated by a doctor and validated by a gastroenterology expert.
- 7) PICCOLO [94] consists of 3433 clinical colonoscopy images from 48 patients, including white light and narrow-band images. It also provides annotations including the number and size of polyps detected during colonoscopy. The data are divided into a training set (2203), a validation set (897), and a test set (333).
- 8) PolypGen [95] originates from colonoscopy detection images of over 300 patients from six different centers. It includes both single-frame data and sequence data, containing 3762 annotated polyp labels. The delineation of polyp boundaries was validated by six senior experts in gastroenterology. Specifically, the dataset also contains 4275 negative samples.

4 Model evaluation and analysis

4.1 Evaluation metrics

We briefly review several popular metrics for polyp segmentation task, i.e., intersection over union (IoU), precision-recall (PR), specificity, dice coefficient (Dice), F -measure (F_β) [97], mean absolute error (MAE) [98], structural measure (S_α) [99], and enhanced-alignment measure (E_ϕ) [100].

In this survey, we focus on pixel-level performance within a single image (or video frame), with performance calculated at the frame level. TP denotes true positives, indicating the number of pixels accurately identified as foreground (or objects of interest) in the segmentation result, corresponding to actual foreground pixels in the true annotation. FP signifies false positives, representing the number of pixels incorrectly identified as foreground in the segmentation result, despite being background pixels in the true annotation. FN refers to false negatives, denoting the number of pixels inaccurately labeled as background in the segmentation result, while these pixels are foreground in the true annotation. TN stands for true negatives, signifying the number of pixels correctly recognized as background in the segmentation result, consistent with background pixels in the true annotation.

PR. Precision represents the proportion of correctly predicted positive samples by the model. Recall (also known

as sensitivity) represents the proportion of true positive samples successfully detected by the model out of all actual positive samples. PR curve can be plotted by taking recall as the x -axis and precision as the y -axis.

$$\text{Precision} = \frac{TP}{TP + FP}, \text{ Recall} = \frac{TP}{TP + FN}. \quad (1)$$

IoU. Intersection over union, also known as the Jaccard coefficient, is used to measure the overlap between the predicted result and the ground truth target. It is commonly used in handling imbalanced datasets.

$$\text{IoU} = \frac{TP}{TP + FP + FN}. \quad (2)$$

F -measure (F_β). The F -measure, also known as the $F1$ -score, combines precision and recall by considering their harmonic mean. It allows adjusting the weights of precision and recall to address specific problems and is effective in handling imbalanced datasets.

$$F_\beta = (1 + \beta^2) \frac{\text{Precision} \cdot \text{Recall}}{\beta^2 \cdot \text{Precision} + \text{Recall}}. \quad (3)$$

Dice. Dice coefficient is a commonly used evaluation metric for measuring the similarity between predicted segmentation results and the ground truth segmentation targets. It provides a score ranging from 0 to 1, where 1 indicates a perfect match and 0 indicates no match at all.

$$\text{Dice} = \frac{2 \times TP}{2 \times TP + FP + FN}. \quad (4)$$

S -measure (S_α). Structure measure [99] evaluates the structural similarity of segmentation results.

$$S_\alpha = \alpha \cdot S_O + (1 - \alpha) \cdot S_R, \quad (5)$$

where S_O represents the object similarity, which measures the overlap between the segmentation result and the ground truth target. S_R represents the region similarity, which assesses the structural similarity between the segmentation result and the ground truth target. The parameter α is used to balance the weights between these two measures.

E -measure (E_ϕ). Enhanced-measure [100] is used to evaluate region coverage.

$$E_\phi = \frac{(1 + \phi^2) \cdot S_O \cdot S_R}{\phi^2 \cdot S_O + S_R}, \quad (6)$$

where the parameter ϕ is a balancing parameter that adjusts the weight ratio between accuracy and region coverage.

Table 4 Benchmark results of 24 representative polyp segmentation models (18 CNN-based and 6 Transformer-based models) on five commonly used datasets in terms of SPE and SEN. The top three results are displayed in bold, italic, and underlined fonts

Method	Pub.	ETIS-Larib		CVC-ColonDB		CVC-ClinicDB		CVC-300		Kvasir	
		SPE	SEN	SPE	SEN	SPE	SEN	SPE	SEN	SPE	SEN
U-Net [20]	MICCAI 2015	0.703	0.484	0.798	0.525	0.947	0.835	0.965	0.768	0.949	0.857
UNet++ [101]	MICCAI 2018	0.727	0.415	0.828	0.497	0.927	0.795	0.957	0.738	<i>0.986</i>	0.807
SFA [22]	MICCAI 2018	0.781	0.633	0.861	0.703	0.919	0.802	0.934	0.889	0.965	0.799
PraNet [26]	MICCAI 2020	0.805	0.688	0.874	0.740	<u>0.990</u>	0.911	0.988	0.941	0.978	0.912
ACSNet [25]	MICCAI 2020	0.775	0.738	0.873	0.760	0.956	0.909	0.984	0.959	0.973	0.907
MSEG [30]	arxiv 2021	0.844	0.740	0.912	0.753	0.992	0.924	0.989	0.934	<u>0.985</u>	0.900
EU-Net [31]	CRV 2021	0.871	0.872	0.939	<i>0.851</i>	0.986	0.960	0.982	<i>0.969</i>	0.974	0.934
SANet [8]	MICCAI 2021	0.943	<i>0.904</i>	0.952	0.811	0.989	0.952	0.989	0.971	<i>0.986</i>	0.915
MSNet [9]	MICCAI 2021	0.893	0.796	0.931	0.775	0.975	0.933	0.988	0.931	0.981	0.911
UACANet-S [34]	ACM MM 2021	0.887	0.833	0.958	0.801	<i>0.991</i>	0.942	<i>0.992</i>	0.959	0.976	0.911
UACANet-L [34]	ACM MM 2021	0.932	0.813	0.953	0.754	0.992	0.943	0.993	0.940	0.983	0.923
C2FNet [35]	IJCAI 2021	0.902	0.745	0.894	0.752	0.973	0.941	0.988	0.952	0.974	0.904
DCRNet [53]	ISBI 2022	0.756	0.747	0.884	0.777	0.959	0.913	0.972	0.945	0.973	0.903
BDG-Net [50]	SPIE MI 2022	0.879	0.820	0.949	0.827	<u>0.990</u>	0.942	<i>0.992</i>	0.957	0.984	0.918
CaraNet [44]	SPIE MI 2022	0.910	0.812	0.947	0.858	<i>0.991</i>	0.955	0.976	0.927	0.982	0.912
EFA-Net [102]	arxiv 2023	0.918	0.866	0.940	0.820	0.975	0.934	0.988	0.950	0.987	0.914
CFANet [75]	PR 2023	0.910	0.804	0.953	0.761	<i>0.991</i>	0.960	0.990	0.952	<u>0.985</u>	0.926
M2SNet [103]	arxiv 2023	0.893	0.796	0.931	0.775	0.975	0.933	0.988	0.931	0.981	0.911
Polyp-PVT [33]	arxiv 2021	0.962	<u>0.902</u>	<i>0.965</i>	0.829	0.992	<i>0.959</i>	0.993	0.943	0.987	<u>0.928</u>
HSNet [46]	CBM 2022	<u>0.955</u>	0.868	<i>0.965</i>	0.821	0.992	0.949	<u>0.991</u>	0.947	<i>0.986</i>	0.913
DuAT [62]	PRCV 2023	0.941	0.891	<u>0.962</u>	0.841	0.992	<u>0.956</u>	<u>0.991</u>	0.956	0.984	0.933
ESFPNet [72]	MI 2023	<i>0.961</i>	0.917	0.961	0.837	0.992	0.940	<u>0.991</u>	<u>0.967</u>	<u>0.985</u>	0.910
FeDNet [70]	BSPC 2023	0.945	0.893	0.966	<u>0.845</u>	<i>0.991</i>	0.954	<i>0.992</i>	0.950	0.987	0.924
SAM-B [104]	arxiv 2023	0.717	0.415	0.621	0.246	0.681	0.309	0.730	0.412	0.904	0.510
SAM-H [104]	arxiv 2023	0.768	0.525	0.811	0.480	0.877	0.547	0.873	0.685	0.934	0.769
SAM-L [104]	arxiv 2023	0.810	0.567	0.813	0.500	0.834	0.623	0.904	0.756	0.935	0.774

MAE. Mean absolute error (MAE) is commonly used for evaluating regression tasks.

$$\text{MAE} = \frac{1}{W \times H} \sum_{i=1}^W \sum_{j=1}^H |S_{ij} - G_{ij}|, \quad (7)$$

where W and H denote the width and height of the map, S represents the predicted segmentation map, and G represents the ground truth segmentation map.

Specificity. Specificity measures the model's ability to recognize negative samples. Specifically, specificity can be calculated using Eq. (8):

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}}. \quad (8)$$

The value of specificity ranges between 0 and 1, with a higher value indicating a stronger ability of the model to recognize negative samples.

4.2 Performance comparison and analysis

4.2.1 Overall evaluation

To quantify the performance of different models, we conducted a comprehensive evaluation of 24 representative polyp segmentation models, including 1) 18 CNN-based

models: U-Net [20], UNet++ [101], SFA [22], PraNet [26], ACSNet [25], MSEG [30], EU-Net [31], SANet [8], MSNet [9], UACANet-S [34], UACANet-L [34], C2FNet [35], DCRNet [53], BDG-Net [50], CaraNet [44], EFA-Net [102], CFA-Net [75], and M2SNet [103], and 2) six Transformer-based methods: Polyp-PVT [33], HSNet [46], DuAT [62], ESFPNet [72], FeDNet [70], and SAM-based poly segmentation model (with three different backbones, i.e., SAM-B, SAM-H, and SAM-L [104]). First, we individually evaluated the performance of the aforementioned 24 models on SPE, SEN, Dice, IoU, S_α , F_β , E_ϕ , and MAE metrics across five public datasets (ETIS-LaribPolypDB [91], CVC-ColonDB [5], CVC-ClinicDB [7], CVC-300 [92], and Kvasir-SEG [93]). The evaluation results are presented in Table 4, Table 5 and Table 6. Note that the results of all evaluated methods have been sourced from their respective code repositories or original papers. Second, we also report the mean values of Dice and MAE across the five datasets for each model in Fig. 3. It is worth noting that better models are shown in the upper left corner (i.e., with a larger Dice and smaller MAE). From the results shown in Fig. 3, we have the following observations.

CNN vs. Transformer. Compared with CNN-based models, Transformer-based methods achieve significantly better performance. Due to its feature extraction network

Table 5 Benchmark results of 24 representative polyp segmentation models (18 CNN-based and 6 Transformer-based models) on five commonly used datasets in terms of Dice, IoU, and S_α

Method	Pub.	ETIS-Larib			CVC-ColonDB			CVC-ClinicDB			CVC-300			Kvasir		
		Dice	IoU	S_α	Dice	IoU	S_α	Dice	IoU	S_α	Dice	IoU	S_α	Dice	IoU	S_α
U-Net [20]	MICCAI 2015	0.398	0.335	0.684	0.504	0.436	0.710	0.823	0.755	0.889	0.710	0.627	0.843	0.818	0.746	0.858
UNet++ [101]	MICCAI 2018	0.401	0.344	0.683	0.482	0.408	0.692	0.794	0.729	0.873	0.707	0.624	0.839	0.821	0.743	0.862
SFA [22]	MICCAI 2018	0.297	0.217	0.557	0.456	0.337	0.628	0.700	0.607	0.793	0.467	0.329	0.640	0.723	0.611	0.782
PraNet [26]	MICCAI 2020	0.628	0.567	0.794	0.712	0.640	0.820	0.899	0.849	0.936	0.871	0.797	0.925	0.898	0.840	0.915
ACSNet [25]	MICCAI 2020	0.578	0.509	0.754	0.716	0.649	0.829	0.882	0.826	0.927	0.863	0.787	0.923	0.898	0.838	0.920
MSEG [30]	arxiv 2021	0.700	0.630	0.828	0.735	0.666	0.834	0.909	0.864	0.938	0.874	0.804	0.924	0.897	0.839	0.912
EU-Net [31]	CRV 2021	0.687	0.609	0.793	0.756	0.681	0.831	0.902	0.846	0.936	0.837	0.765	0.904	0.908	0.854	0.917
SANet [8]	MICCAI 2021	0.750	0.654	0.849	0.753	0.670	0.837	0.916	0.859	0.939	0.888	0.815	0.928	0.904	0.847	0.915
MSNet [9]	MICCAI 2021	0.723	0.652	0.845	0.751	0.671	0.838	0.918	0.869	0.946	0.865	0.799	0.926	0.905	0.849	0.923
UACANet-S [34]	ACM MM 2021	0.694	0.615	0.815	0.783	0.704	0.847	0.916	0.870	0.939	0.902	0.837	0.934	0.905	0.852	0.914
UACANet-L [34]	ACM MM 2021	0.766	0.689	0.859	0.751	0.678	0.835	0.926	0.880	0.942	0.910	0.849	0.938	0.912	0.859	0.917
C2FNet [35]	IJCAI 2021	0.699	0.624	0.827	0.724	0.650	0.826	0.919	0.872	0.941	0.874	0.801	0.927	0.886	0.831	0.905
DCRNet [53]	ISBI 2022	0.556	0.496	0.736	0.704	0.631	0.821	0.896	0.844	0.933	0.856	0.788	0.921	0.886	0.825	0.911
BDG-Net [50]	SPIE MI 2022	0.752	0.681	0.860	0.797	0.723	0.870	0.905	0.857	0.936	0.902	0.837	<u>0.940</u>	0.915	0.863	0.920
CaraNet [44]	SPIE MI 2022	0.747	0.672	0.868	0.773	0.689	0.853	0.936	0.887	<u>0.954</u>	0.900	0.838	<u>0.940</u>	0.916	0.865	<i>0.929</i>
EFA-Net [102]	arxiv 2023	0.749	0.670	0.858	0.774	0.696	0.855	0.919	0.871	0.943	0.894	0.830	<i>0.941</i>	0.914	0.861	<i>0.929</i>
CFANet [75]	PR 2023	0.732	0.655	0.845	0.743	0.665	0.835	0.932	0.883	0.950	0.893	0.827	0.938	0.915	0.861	0.924
M2SNet [103]	arxiv 2023	0.723	0.652	0.845	0.751	0.671	0.838	0.918	0.869	0.946	0.865	0.799	0.926	0.905	0.849	0.923
Polyp-PVT [33]	arXiv 2021	0.787	0.706	0.871	0.808	0.727	0.865	<i>0.937</i>	<u>0.889</u>	0.949	0.900	0.833	0.935	<u>0.917</u>	<u>0.864</u>	0.925
HSNet [46]	CBM 2022	0.808	<u>0.734</u>	0.882	0.810	<u>0.735</u>	<u>0.868</u>	0.948	0.905	<u>0.953</u>	<u>0.903</u>	0.839	0.937	0.926	0.877	<u>0.927</u>
DuAT [62]	PRCV 2023	0.822	0.746	<u>0.889</u>	0.819	0.737	<i>0.873</i>	0.948	0.906	0.956	0.901	<u>0.840</u>	<u>0.940</u>	0.924	<i>0.876</i>	<i>0.929</i>
ESFPNet [72]	MI 2023	0.823	0.748	<i>0.891</i>	<u>0.811</u>	0.730	0.864	0.928	0.883	0.943	0.902	0.836	0.934	<u>0.917</u>	0.866	0.923
FeDNet [70]	BSPC 2023	<u>0.810</u>	0.733	0.892	0.823	0.744	0.878	<u>0.930</u>	0.885	0.949	0.911	<i>0.848</i>	0.946	0.924	<i>0.876</i>	0.933
SAM-B [104]	arxiv 2023	0.406	0.370	0.672	0.215	0.188	0.553	0.268	0.231	0.572	0.371	0.339	0.650	0.515	0.459	0.682
SAM-H [104]	arxiv 2023	0.517	0.477	0.730	0.441	0.396	0.676	0.547	0.500	0.738	0.651	0.606	0.812	0.778	0.707	0.829
SAM-L [104]	arxiv 2023	0.551	0.507	0.751	0.468	0.422	0.690	0.578	0.526	0.744	0.726	0.676	0.849	0.782	0.710	0.832

structure based on the self-attention mechanism, the Transformer can effectively capture global context information.

Comparison of deep models. Among the deep learning-based models, DuAT [62], FeDNet [70], ESFPNet [72], Polyp-PVT [33], HSNet [46], and BDG-Net [50] achieve much better performance.

Moreover, Fig. 4 shows the PR and F -measure curves for the 23 representative polyp segmentation models on five datasets (ETIS-LaribPolypDB [91], CVC-ColonDB [5], CVC-ClinicDB [7], CVC-300 [92], and Kvasir-SEG [93]).

To provide a deeper understanding of the better-performing models, we will discuss the main characteristics of the following six models in the sections below.

- DuAT [62]. Dual-aggregation Transformer network uses a Transformer architecture based on a pyramid structure as an encoder, and the decoder adopts a dual-stream design, building local spatial attention modules and global spatial attention modules to enhance the segmentation performance of polyps of different sizes.

- FeDNet [70] decouples the input features into high-frequency edge features and low-frequency main body features through a feature decoupling operator, and then predicts by fusing the optimized features through a feature fusion operator.

- ESFPNet [72] utilizes a pre-trained mixed Transformer encoder and an efficient stage-wise feature pyramid decoder structure, which fuses features from deep to shallow layers and also performs linear fusion of features from global to local, and connects them with intermediate aggregated features to obtain the final segmentation result.

- Polyp-PVT [33] introduces a pyramid vision Transformer encoder to extract multi-scale features with long-range dependencies, utilizes high-level features for side output supervision, incorporates attention mechanisms to enhance low-level features and eliminate noise, and finally fuses multi-level features.

- HSNet [46] is also based on a PVT encoder and suppresses noise information in low-level features by modeling the semantic spatial relationships and channel dependencies of lower-layer features. It bridges feature disparities through a semantic interaction mechanism and captures long-range dependencies and local appearance details via a dual-branch structure.

- BDG-Net [50] aggregates high-level features to generate a boundary distribution map, which is fed into a boundary distribution-guided decoder and employs a multi-scale feature interaction strategy to enhance segmentation precision.

Table 6 Benchmark results of 24 representative polyp segmentation models (18 CNN-based and 6 Transformer-based models) on five commonly used datasets in terms of F_β , E_ϕ , and MAE

Method	Pub.	ETIS-Larib			CVC-ColonDB			CVC-ClinicDB			CVC-300			Kvasir		
		F_β	E_ϕ	MAE	F_β	E_ϕ	MAE	F_β	E_ϕ	MAE	F_β	E_ϕ	MAE	F_β	E_ϕ	MAE
U-Net [20]	MICCAI 2015	0.366	0.643	0.036	0.491	0.692	0.059	0.811	0.913	0.019	0.684	0.848	0.022	0.794	0.881	0.055
UNet++ [101]	MICCAI 2018	0.390	0.629	0.035	0.467	0.680	0.061	0.785	0.891	0.022	0.687	0.834	0.018	0.808	0.886	0.048
SFA [22]	MICCAI 2018	0.231	0.531	0.109	0.366	0.661	0.094	0.647	0.840	0.042	0.341	0.644	0.065	0.670	0.834	0.075
PraNet [26]	MICCAI 2020	0.600	0.808	0.031	0.699	0.847	0.043	0.896	0.963	0.009	0.843	0.950	0.010	0.885	0.944	0.030
ACSNet [25]	MICCAI 2020	0.530	0.737	0.059	0.697	0.839	0.039	0.873	0.947	0.011	0.825	0.939	0.013	0.882	0.941	0.032
MSEG [30]	arxiv 2021	0.671	0.855	0.015	0.724	0.859	0.038	0.907	0.961	0.007	0.852	0.948	0.009	0.885	0.942	0.028
EU-Net [31]	CRV 2021	0.636	0.807	0.067	0.730	0.863	0.045	0.891	0.959	0.011	0.805	0.918	0.015	0.893	0.951	0.028
SANet [8]	MICCAI 2021	0.685	0.881	0.015	0.726	0.869	0.043	0.909	0.971	0.012	0.859	0.962	0.008	0.892	0.949	0.028
MSNet [9]	MICCAI 2021	0.677	0.875	0.020	0.736	0.872	0.041	0.913	0.973	<u>0.008</u>	0.848	0.945	0.010	0.892	0.947	0.028
UACANet-S [34]	ACM MM 2021	0.650	0.848	0.023	0.772	0.894	0.034	0.917	0.965	<u>0.008</u>	0.886	<u>0.974</u>	<u>0.006</u>	0.897	0.948	0.026
UACANet-L [34]	ACM MM 2021	0.740	0.903	0.012	0.746	0.875	0.039	0.928	0.974	0.006	0.901	0.977	0.005	0.902	0.955	0.025
C2FNet [35]	IJCAI 2021	0.668	0.860	0.022	0.705	0.854	0.044	0.906	0.969	0.009	0.844	0.949	0.009	0.869	0.929	0.036
DCRNet [53]	ISBI 2022	0.506	0.742	0.096	0.684	0.840	0.052	0.890	0.964	0.010	0.830	0.943	0.010	0.868	0.933	0.035
BDG-Net [50]	SPIE MI 2022	0.719	0.901	<u>0.014</u>	0.781	0.901	0.028	0.898	0.959	<u>0.008</u>	0.883	0.969	0.005	0.906	0.959	0.025
CaraNet [44]	SPIE MI 2022	0.709	0.875	0.017	0.729	0.880	0.042	0.931	0.985	<u>0.007</u>	0.887	0.977	<u>0.007</u>	0.909	0.962	<u>0.023</u>
EFA-Net [102]	arxiv 2023	0.698	0.872	0.018	0.753	0.884	0.036	0.916	0.972	0.009	0.878	0.961	0.009	0.906	0.955	<u>0.024</u>
CFANet [75]	PR 2023	0.693	0.881	<u>0.014</u>	0.728	0.869	0.039	0.924	<u>0.981</u>	0.007	0.875	0.962	0.008	0.903	0.956	<u>0.023</u>
M2SNet [103]	arxiv 2023	0.677	0.875	0.020	0.736	0.872	0.041	0.913	0.973	<u>0.008</u>	0.848	0.945	0.010	0.892	0.947	0.028
Polyp-PVT [33]	arxiv 2021	0.750	0.906	<u>0.013</u>	0.795	<u>0.913</u>	0.031	<u>0.936</u>	<u>0.985</u>	0.006	0.884	0.973	<u>0.007</u>	0.911	0.956	<u>0.023</u>
HSNet [46]	CBM 2022	<u>0.777</u>	0.904	0.021	0.796	0.912	0.032	0.951	0.990	0.006	0.887	0.970	<u>0.007</u>	0.918	<u>0.961</u>	<u>0.023</u>
DuAT [62]	PRCV 2023	0.789	<u>0.917</u>	<u>0.013</u>	<u>0.805</u>	0.922	0.026	<u>0.950</u>	0.990	0.006	<u>0.890</u>	0.965	0.005	<u>0.916</u>	0.960	<u>0.023</u>
ESFPNet [72]	MI 2023	<u>0.786</u>	<u>0.930</u>	0.012	<u>0.798</u>	0.908	<u>0.030</u>	0.930	0.976	<u>0.007</u>	0.882	0.970	<u>0.006</u>	<u>0.913</u>	0.957	<u>0.024</u>
FeDNet [70]	BSPC 2023	0.773	0.931	0.016	0.809	<u>0.918</u>	<u>0.029</u>	0.928	0.978	<u>0.007</u>	<u>0.897</u>	<u>0.976</u>	<u>0.006</u>	0.918	0.963	0.021
SAM-B [104]	arxiv 2023	0.404	0.574	0.035	0.210	0.412	0.077	0.259	0.431	0.092	0.374	0.563	0.058	0.509	0.624	0.104
SAM-H [104]	arxiv 2023	0.513	0.658	0.029	0.434	0.585	0.056	0.546	0.676	0.040	0.653	0.765	0.020	0.769	0.828	0.062
SAM-L [104]	arxiv 2023	0.544	0.686	0.030	0.463	0.607	0.054	0.563	0.683	0.057	0.729	0.824	0.020	0.773	0.834	0.061

4.2.2 Scale-based evaluation

To investigate the influence of scale variations, we carry out evaluations on several representative polyp segmentation models. We compute the ratio (r) of the size of the polyp body area in a given ground truth image, which is used to characterize the size of the polyp. For this purpose, three types of polyp scales are defined: 1) when r is less than 2.5%, the polyp is considered “small”; 2) when r is more than 20%, it is considered “large”; 3) when the ratio is within the range [2.5%, 20%], we call it “medium”. In addition, we mix and classify the five colonoscopy datasets and derive a newly constructed dataset containing 212, 334, and 77 images of “small”, “medium”, and “large” types, respectively. Figure 5 presents the comparison results in relation to scale variations. Segmentation performance is represented by three metrics (i.e., IoU, F_β , and E_ϕ).

Some sample images with different scales of polyps are shown in Fig. 6. Visual comparison results of the scale variation evaluation are shown in Table 7. According to the results, we can draw the following conclusions: (1) In terms of overall performance, DuAT [62] and FeDNet [70] perform better across all types, and (2) vertical analysis reveals that most models achieve better performance in segmenting “medium” polyps while they exhibit relatively lower performance in segmenting other types.

5 Challenges and future trends

5.1 Effective network structure

Edge feature extraction. The diverse shapes of polyps and the complex background of endoscopic images, combined with blurred edges and adherences of polyps often pose challenges for accurate segmentation. To further improve accuracy and robustness, and to leverage richer and more complex image features, some models introduce edge feature extraction modules ([22, 52, 59, 61]) to utilize low-level features to assist in polyp segmentation. Most polyp segmentation models capture the edge information by utilizing low-level features extracted by backbone networks, which are then aggregated with high-level features to accomplish segmentation. However, after operations like convolution, the extracted image features, including edge and body features, become intertwined, making decoupling extremely challenging. Additionally, as the tasks of feature extraction and segmentation are not orthogonal, incorrect edge estimation can lead to error propagation. Therefore, an optional choice is to decouple the original images using traditional image processing methods. There has already been some work in the fields of object detection and other semantic segmentation domains. Shan et al. [105] utilized Fourier Transform to derive high and low-frequency components from images. These components

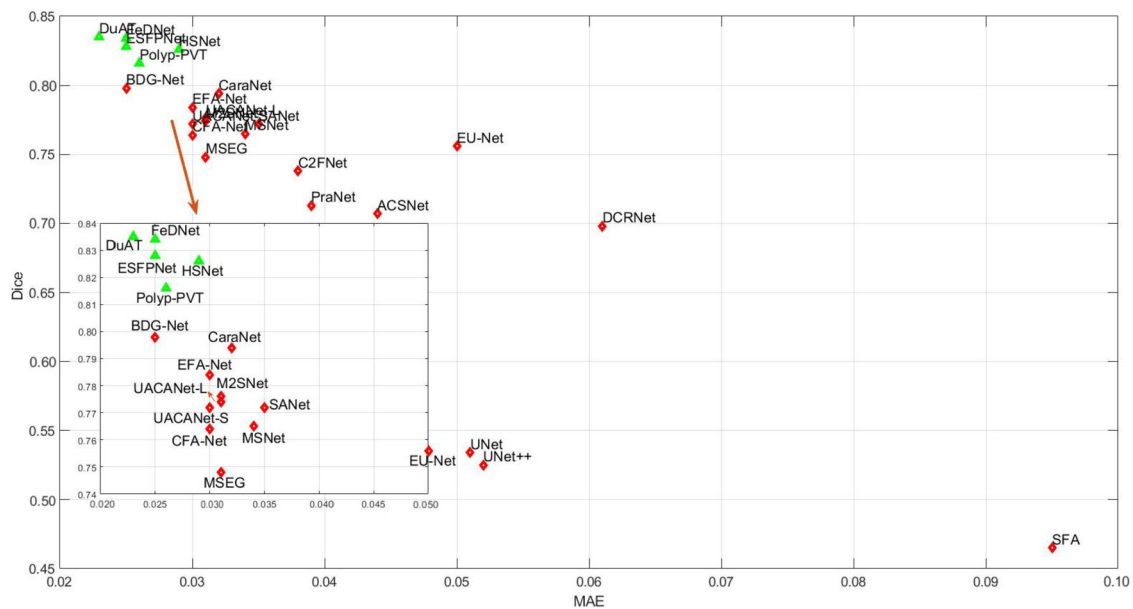


Figure 3 A comprehensive evaluation is conducted on 23 representative deep-learning models, including U-Net [20], UNet++ [101], SFA [22], PraNet [26], ACSNet [25], MSEG [30], EU-Net [31], SANet [8], MSNet [9], UACANet-S [34], UACANet-L [34], C2FNet [35], DCRNet [53], BDG-Net [50], CaraNet [44], EFA-Net [102], CFA-Net [75], M2SNet [103], Polyp-PVT [33], HSNet [46], DuAT [62], ESFPNet [72], and FeDNet [70], with SAM [104] excluded. We report the average Dice and MAE values for each model across five datasets (i.e., ETIS-LaribPolypDB [91], CVC-ColonDB [5], CVC-ClinicDB [7], CVC-300 [92], and Kvasir-SEG [93]). Please note that the models represented in the top left corner are better, i.e., they have larger Dice scores and smaller MAE values. In this context, the green triangles represent Transformer-based models, while the red diamonds signify CNN-based models

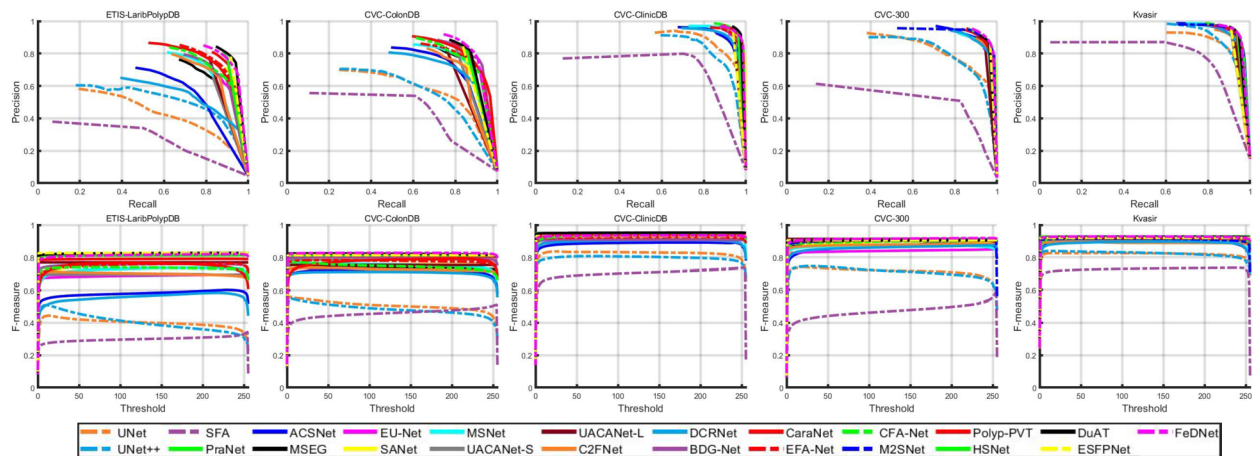


Figure 4 The PR curves and F -measures at different thresholds for 23 deep polyp segmentation models on five datasets from ETIS-LaribPolypDB [91], CVC-ColonDB [5], CVC-ClinicDB [7], CVC-300 [92], and Kvasir-SEG [93]

are then input into two parallel branches to obtain edge and body features, which are subsequently merged to perform semantic segmentation. Cong et al. [106] designed a full-frequency perception module based on Octave convolution. This module can automatically learn low and high-frequency features for coarse positioning, providing auxiliary information for segmentation. FeDNet [70]

employs Laplacian pyramid decomposition to decouple the input features into high-frequency edge features and low-frequency body features. Following this, these two types of features undergo deep supervised optimization. The accuracy of polyp boundary annotations is contingent upon the quality of the image. In instances of sub-standard image quality, like blurriness or inadequate light-

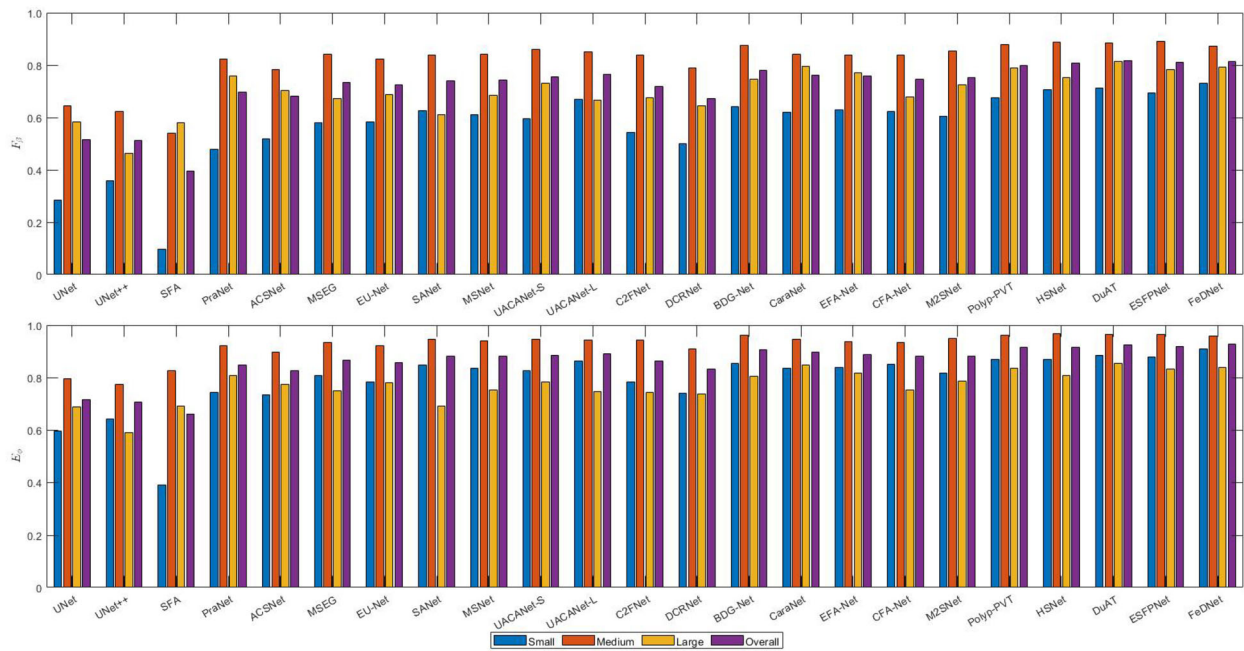


Figure 5 Comparison results for 23 representative polyp segmentation models are shown in terms of F_β (top) and E_ϕ (bottom)

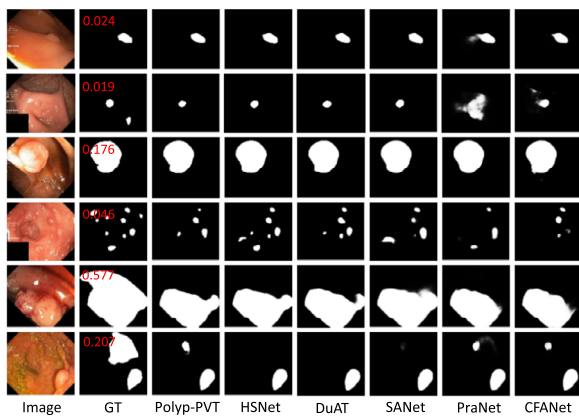


Figure 6 Some images of polyps in large, medium, and small sizes, along with the segmentation maps of six typical models, including three CNN-based models: PraNet [26], SANet [8], and CFA-Net [75], and three Transformer-based models: Polyp-PVT [33], HSNet [46], and DuAT [62]. The numbers on the GT map represent the proportion of polyp pixels to the total number of pixels in the image. The images are sourced from the Kvasir-SEG [93] dataset

ing, the boundary annotations may lack precision. In such scenarios, models dependent on clear boundary information could yield excessive or insufficient segmentation, resulting in reduced diagnostic accuracy. Furthermore, inaccurate boundary annotations may elevate the boundary loss function, potentially steering the model towards erro-

neous optimization paths, thus diminishing its generalization capacity and effectiveness.

Dual-stream structure. CNNs exhibit a powerful capability to extract local features, such as texture and shape. However, CNNs are relatively weaker in capturing long-distance global dependencies. In this context, the Transformer can serve as a supplement. Due to its self-attention mechanism, it possesses an excellent ability to capture global information. Therefore, introducing a dual-stream structure in existing polyp segmentation models can integrate local information captured by CNNs and global information captured by the Transformer, enhancing the performance of polyp segmentation. In addition, this structure may improve the model's capabilities to handle complex, uneven backgrounds and noise interference, thereby increasing the robustness of the model [37, 46, 55, 56, 68]. It is important to note that how to effectively merge the outputs from the two networks and balance their weights remains a problem. However, the tremendous potential and possibilities undoubtedly justify further exploration and research.

5.2 Different supervision strategies

Existing polyp segmentation models typically use fully-supervised strategies to learn features and produce segmentation results. However, annotating colonoscopy data is time-consuming and labor-intensive, especially for video data. To alleviate this problem, attention has been focused on weakly-supervised and semi-supervised learning and

Table 7 Performance studies based on polyp size. Comparison results for 24 representative polyp segmentation models (18 CNN-based models and 6 Transformer-based models, in this context, SAM [104] refers to SAM-L) are provided in terms of MAE, specificity (SPE), sensitivity (SEN) and S_α

	Scale	CNN-based models											
		U-Net [20]	UNet++ [101]	SFA [22]	PraNet [26]	ACNet [25]	MSEG [30]	EU-Net [31]	SANet [8]	MSNet [9]	UACANet -S [34]	UACANet -L [34]	C2FNet [35]
MAE	Small	0.026	0.015	0.109	0.037	0.034	<u>0.014</u>	0.041	<u>0.014</u>	0.019	0.020	<i>0.012</i>	0.026
	Medium	0.040	0.038	0.062	0.021	0.030	<u>0.016</u>	0.035	0.018	0.019	<u>0.016</u>	0.017	0.019
	Large	0.173	0.215	0.201	0.120	0.135	0.138	0.140	0.164	0.139	0.120	0.142	0.150
	Overall	0.051	0.052	0.095	0.039	0.044	0.031	0.050	0.035	0.034	<u>0.030</u>	0.031	0.038
SPE	Small	0.618	0.667	0.662	0.699	0.746	0.785	0.875	0.912	0.847	0.873	0.912	0.793
	Medium	0.888	0.911	0.940	0.955	0.915	0.964	0.954	0.980	0.975	0.975	0.974	0.974
	Large	0.856	0.869	0.966	0.937	0.942	0.946	0.919	0.941	0.918	<i>0.971</i>	0.953	0.899
	Overall	0.792	0.823	0.848	0.865	0.861	0.901	0.923	0.952	0.924	0.940	0.950	0.903
SEN	Small	0.377	0.402	0.575	0.569	0.680	0.660	0.806	<i>0.850</i>	0.720	0.743	0.743	0.642
	Medium	0.701	0.649	0.799	0.857	0.850	0.865	0.937	<u>0.906</u>	0.880	0.901	0.856	0.874
	Large	0.567	0.409	0.487	0.739	0.699	0.653	0.718	0.577	0.662	0.698	0.651	0.676
	Overall	0.574	0.535	0.684	0.744	0.773	0.769	<i>0.866</i>	0.846	0.799	0.822	0.792	0.770
S_α	Small	0.641	0.679	0.493	0.732	0.756	0.786	0.778	0.826	0.804	0.780	0.824	0.769
	Medium	0.800	0.784	0.736	0.893	0.876	0.904	0.885	0.902	0.907	0.907	0.897	0.903
	Large	0.684	0.590	0.639	0.791	0.772	0.743	0.745	0.698	0.751	0.768	0.735	0.741
	Overall	0.731	0.724	0.642	0.826	0.822	0.844	0.831	0.851	0.853	0.846	0.852	0.837

	Scale	CNN-based models						Transformer-based models					
		DCRNet [53]	BDG-Net [50]	CaraNet [44]	EFA-Net [102]	CFA-Net [75]	M2SNet [103]	Polyp-PVT [33]	HSNet [46]	DuAT [62]	ESFPNet [72]	FeDNet [70]	SAM [104]
MAE	Small	0.068	0.011	0.022	0.017	0.011	0.021	0.017	0.023	<i>0.012</i>	<u>0.014</u>	<i>0.012</i>	0.020
	Medium	0.035	0.013	0.021	0.019	0.017	<u>0.016</u>	<i>0.014</i>	0.013	0.013	0.012	<u>0.016</u>	0.038
	Large	0.152	0.114	0.106	0.112	0.138	0.122	<u>0.101</u>	0.112	0.094	0.107	<i>0.099</i>	0.199
	Overall	0.061	<i>0.025</i>	0.032	<u>0.030</u>	<u>0.030</u>	0.031	0.026	0.029	0.023	<i>0.025</i>	<i>0.025</i>	0.051
SPE	Small	0.783	0.846	0.889	0.875	0.884	0.876	<u>0.929</u>	0.915	<i>0.940</i>	0.924	0.944	0.732
	Medium	0.921	0.986	0.973	0.971	0.979	<u>0.984</u>	0.983	0.983	<u>0.984</u>	<i>0.985</i>	0.976	0.905
	Large	0.840	0.925	0.937	0.955	0.963	0.975	0.966	0.959	0.966	<i>0.971</i>	<u>0.968</u>	0.745
	Overall	0.864	0.931	0.940	0.937	0.945	0.946	<u>0.963</u>	0.957	0.967	<u>0.963</u>	<i>0.964</i>	0.827
SEN	Small	0.735	0.758	0.772	0.791	0.706	0.720	0.794	0.840	0.832	<u>0.844</u>	0.862	0.547
	Medium	0.853	0.899	0.909	0.894	0.879	0.889	0.894	<i>0.908</i>	0.902	0.903	0.896	0.563
	Large	0.654	0.735	<i>0.805</i>	0.736	0.663	0.702	0.776	0.742	<u>0.786</u>	0.758	<i>0.776</i>	0.836
	Overall	0.788	0.831	0.849	0.840	0.793	0.808	0.845	0.864	0.864	<u>0.865</u>	0.870	0.591
S_α	Small	0.747	0.824	0.827	0.825	0.809	0.807	0.833	<u>0.849</u>	<i>0.854</i>	0.842	0.871	0.737
	Medium	0.878	0.922	0.912	0.905	0.902	0.909	0.916	0.922	<i>0.921</i>	0.922	<u>0.918</u>	0.747
	Large	0.731	0.790	0.824	0.801	0.745	0.768	0.806	0.782	<i>0.823</i>	0.796	<u>0.813</u>	0.696
	Overall	0.815	0.873	0.872	0.865	0.851	0.857	0.874	<u>0.880</u>	<i>0.886</i>	0.879	0.889	0.737

applying them to polyp segmentation tasks [62, 107]. Actually, semi-supervised or weakly supervised methods have been widely applied in the field of medical image segmentation. For example, Cho et al. [108] proposed a novel data augmentation approach for medical image segmentation that does not lose essential semantic information of the key objects. Judge et al. [109] redefined the traditional per-pixel segmentation task as a contour regression problem and modeled the position uncertainty. Wei et al. [110] introduced a semi-supervised medical image segmentation technique that first trains the segmentation model on a

small number of unlabeled images, generates initial labels for them, and then introduces a consistency-based pseudo-label enhancement scheme to improve the quality of the model's predictions. Therefore, in the future, semi/weakly supervised methods can be used for image-level labeling and pseudo-annotation to improve the accuracy of polyp segmentation.

5.3 Clinical requirements

Clinical application prospects. Advanced computer-aided diagnostic systems can greatly enhance the interpretability

of medical images, assisting clinicians in making more precise diagnoses and treatment decisions. The integration of artificial intelligence (AI) into neoadjuvant chemoradiotherapy also improves the treatment outcomes and efficacy assessment in colorectal cancer. AI offers tremendous opportunities in the era of precision medicine [111]. However, the utilization of AI in healthcare is subject to stringent regulations [112], with only a few AI-based medical devices having received regulatory approval [113]. In comparison to traditional systems, the final stage of innovation in medical AI confronts numerous challenges, with deep learning models often criticized for their “black box” issues. User skepticism also poses a barrier to the clinical implementation of AI models. Deep learning models rely heavily on ample labeled training data, highlighting the importance of engaging users consistently in algorithm enhancement and enhancing data quality as a potential new communication paradigm.

Dataset collection. The shape, texture, and color of polyps can vary depending on the time and stage of the disease. Colonoscopy data from multiple centers often exhibit different morphologies. Existing polyp segmentation datasets mostly consist of images containing a single polyp, and there are not many specialized datasets with a large number of images. Only 23 out of the 623 images in the aforementioned five datasets (ETIS-LaribPolypDB [91], CVC-ColonDB [5], CVC-ClinicDB [7], CVC-300 [92], and Kvasir-SEG [93]) contain multiple polyps. Therefore, models trained on these datasets often perform poorly on tasks involving multiple polyps. Although there are multiple public datasets available for polyp segmentation, their scale is quite limited. For instance, the largest dataset we present is PolypGen [95], which contains 3762 images. Therefore, it is necessary to develop a new large-scale polyp segmentation dataset to serve as a baseline for future research. In addition, collecting datasets for complex specialized scenarios is also a potential direction. For example, constructing multi-center datasets, multi-target datasets, and specialized datasets for small or large polyps could enhance the model’s performance in different scenarios. In medical diagnostics, various imaging techniques such as computed tomography, ultrasound, and endoscopy are commonly used. However, data utilized in polyp segmentation methods often stem from a single modality [114]. Aggregation of multi-modal and multi-center datasets plays a critical role in overcoming the challenges associated with polyp detection and segmentation during colonoscopy examinations, making this a key area for future research.

Cross-domain segmentation. Deep learning-based polyp segmentation methods have achieved promising performance, but they often suffer from performance degradation when applied to unseen target domain datasets collected from different imaging devices. Therefore, it remains a challenge to apply existing polyp segmentation

methods to unseen datasets. More importantly, manual annotation of new target datasets is tedious and labor-intensive, and leveraging the knowledge learned from the labeled source domains to boost the performance in the unlabeled target domain is highly demanded in clinical practice. To achieve this, Yang et al. [10] proposed a mutual-prototype adaptation network for cross-domain polyp segmentation, which significantly reduces the gap between the two domains to improve the segmentation performance on the target domain datasets. Thus, this direction deserves further exploration to develop more cross-domain segmentation models.

Real-time polyp segmentation. Real-time segmentation is important for the polyp segmentation task, as it is anticipated that the segmented results can be immediately presented to the physician during the colonoscopy procedure for further decisions and treatment. However, the current deep learning-based models often require huge computation complexity, making them challenging to apply for real-time segmentation. Several real-time polyp segmentation models have been developed [24, 63, 87, 115–119]. Indeed, the development of efficient lightweight networks for polyp segmentation without sacrificing performance is of utmost importance. However, it poses a significant challenge due to the inherent trade-off between model complexity and efficiency. Efficient lightweight networks can enable real-time segmentation, reduce computational costs, and facilitate deployment in resource-constrained clinical settings. Thus, overcoming this challenge involves finding innovative solutions that strike a balance between model complexity and performance, ultimately enhancing the practical applicability of polyp segmentation algorithms in clinical practice.

5.4 Ethical issues

The specificity of medical issues often raises concerns about privacy. Moreover, there are inherent differences between data obtained from different centers. Models trained on data from a single center tend to perform poorly when applied to unseen data acquired from different scanners or other centers. Thus, it becomes crucial to leverage the knowledge gained from labeled source domains to enhance the performance in unlabeled target domains. The aim is to reduce the domain shift observed in colonoscopy images obtained from multiple centers and devices. Federated learning emerges as a promising approach in this context, enabling multiple centers to collaboratively learn a shared prediction model while ensuring privacy protection. For instance, Liu et al. [120] presented a novel method of incidental learning in continuous frequency space, enabling diverse endpoints to utilize multi-source data distributions while addressing challenging constraints associated with data dispersion.

The widespread application of computer-assisted diagnostic systems has raised concerns regarding the potential

for unintended bias in AI systems [121]. Specifically, AI-based segmentation methods heavily depend on training data, resulting in various errors within AI models [122]. The utilization of AI technologies in healthcare is subject to stringent regulations in the United States and the European Union [113, 123], with accountability emerging as a significant issue warranting further exploration. Five primary themes influencing the credibility of medical AI include data quality, algorithmic biases, opacity, security considerations, and accountability [124]. Therefore, it is crucial not only to develop highly accurate and powerful segmentation models, but also to develop strategies to promote public acceptance of AI-assisted healthcare and to effectively manage and allocate responsibilities in the field of medical AI.

6 Conclusion

In this paper, to the best of our knowledge, we provide the first comprehensive review of the development and evaluation in the field of polyp segmentation. We first categorize models into traditional and deep, and then focus on reviewing existing deep models from various perspectives, followed by a summary of popular polyp segmentation datasets and detailed information for each dataset. Following that, we perform a comprehensive polyp size-based evaluation of 26 representative deep learning-based polyp segmentation models. To this end, we constructed a new dataset for 26 representative polyp segmentation models. Furthermore, we discuss some challenges and highlight open directions for future research. We hope this survey will spark more interest and understanding in this field.

Abbreviations

CNN, convolutional neural network; CRC, colorectal cancer; CVC, computer vision center; DGH, directional gradient histogram; FCN, fully convolutional network; MAE, mean absolute error; NBI, narrow band imaging; PR, precision-recall; SAM, segment anything model; ViTs, vision Transformers.

Author contributions

All authors contributed to the literature search and data analysis. JM and TZ drafted the original manuscript, after which all authors participated in reviewing and revising the paper. The final manuscript was read and approved by all authors.

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Data availability

The models, benchmark datasets, and source code links we collected are all published at <https://github.com/taozh2017/Awesome-Polyp-Segmentation>. The datasets used in this study are publicly available at: ETIS-LaribPolypDB: <https://www.kaggle.com/datasets/nguyenquoquocduong/etis-laribpolypdb>; CVC-ColonDB: <http://vi.cvc.uab.es/colon-qa/cvccolondb/>; CVC-ClinicDB: <https://polyp.grand-challenge.org/CVCClinicDB/>; CVC-300: <https://pages.cvc.uab.es/CVC-Colon/index.php/databases/cvc-endoscenestill/>; Kvasir-SEG: <https://datasets.simula.no/kvasir-seg/>.

Declarations

Competing interests

Huazhu Fu is an Associate Editor at Visual Intelligence and was not involved in the editorial review of this article or the decision to publish it. The authors declare that they have no other competing interests.

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