

SemiGDA: Generative Dual-distribution Alignment for Semi-Supervised Medical Image Segmentation

Supplementary Material

001 A. More Experiment

002 A.1. Experiments on Colonoscopy Datasets

003 **Dataset description:** In the endoscopic dataset, two
004 additional unseen datasets are included, namely CVC-
005 ColonDB [14] and ETIS [13]. Note that, consistent with the
006 previous settings [6], the weights used for testing here are
007 those trained on the two seen datasets (CVC-ClinicDB [1]
008 and Kvasir [7]) in the main text. The number of test samples
009 in these two datasets is 380 and 196, respectively.

010 **Quantitative and Qualitative Results:** Tab. 1 reports
011 the quantitative results on two unseen endoscopic datasets,
012 CVC-ColonDB and ETIS. As observed, with only 10%
013 of annotations, our method achieves increases of 10.18%
014 and 7.65% in the Dice and IoU metrics, respectively, com-
015 pared to the second-best method (UnCo). Similarly, on the
016 ETIS dataset, the advantage of our method becomes even
017 more pronounced with limited annotations. This demon-
018 strates that generative-based methods outperform discrimi-
019 native segmentation methods under low-annotation settings.
020 Additionally, although this advantage decreases at the 30%
021 annotation level, our method still achieves the best perfor-
022 mance across all metrics. As shown in Fig. 2, our method
023 effectively captures the full shape of the target, particularly
024 in small targets and along contour boundaries.

025 A.2. Experiments on Thyroid Datasets

026 **Dataset description:** The thyroid dataset is composed of
027 three subsets: TN3K [4], TG3K [17], and DDTI [12]. The
028 training and validation sets are derived from 2, 879 images
029 of TN3K and 3, 585 images of TG3K, comprising 6, 142
030 images for training and 322 images for validation. The test
031 dataset is constructed using images from TN3K and DDTI,
032 totaling 614 images.

033 **Comparison with State-of-the-Art Methods:** Tab. 2
034 presents the comparative results on the ultrasound task with
035 other semi-supervised medical image segmentation meth-
036 ods, where DDTI serves as the unseen test set. It can be
037 seen that our model achieves state-of-the-art performance
038 across all metrics. Notably, on the TN3K test set, our
039 method exhibits significantly superior performance com-
040 pared to others. For instance, with 30% labeled data on
041 the TN3k dataset, our method improves the Dice coeffi-
042 cient from 80.73% to 83.57% and the IoU from 71.41% to
043 72.21%, compared to the second-best method. Moreover,
044 Fig. 2 shows visual results of different semi-supervised
045 medical image segmentation methods. It can be observed

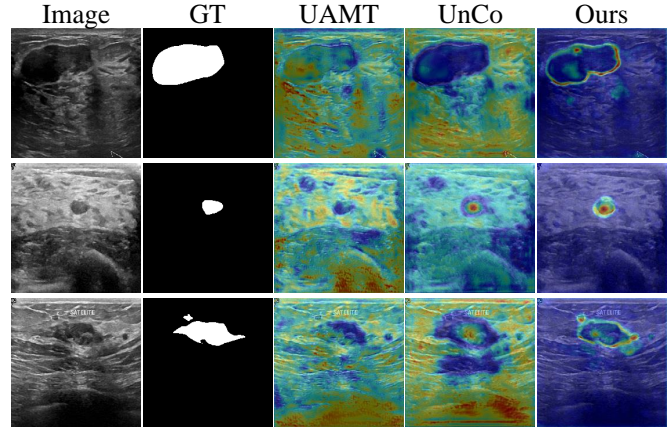


Figure 1. Heatmap comparison with other semi-supervised methods on the BUSI dataset.

that our model accurately identifies and segments the nod- 046
ule regions, while other methods frequently struggle with 047
inaccuracies in segmentation fragments. 048

049 B. More Model Analysis

050 As shown in the heatmap in Fig. 1, our method demon- 051
strates clear advantages in target region focusing and 052
boundary accuracy across large, small, and irregular targets. 053
This confirms that our generative-based semi-supervised 054
framework effectively captures fine-grained boundary fea- 055
tures, crucial for medical image segmentation and clinical 056
diagnosis. Additionally, its ability to reduce background 057
interference and learn feature distributions from unlabeled 058
data further supports the effectiveness of our method in fea- 059
ture alignment and consistency constraint design.

060 C. More Implementation Details

061 Our method employs a two-stage training paradigm. The 062
first stage is specifically designed to warm up the Dual- 063
distribution Alignment Module (DAM). Given that DAM 064
involves complex distribution-matching operations, direct 065
end-to-end training is prone to optimization oscillations due 066
to unstable initial parameters. In the second stage, pre- 067
trained weights are loaded for fine-tuning, which effectively 068
enhances the robustness of the generative model. For the 069
Consistency-Driven Skip Adapter strategy, the maximum 070
number of N_f is set to 5, considering the original model 071
architecture and avoiding excessive increases in the number 072
of learnable parameters. We adopt the PolyLR learning rate 073
scheduling strategy.

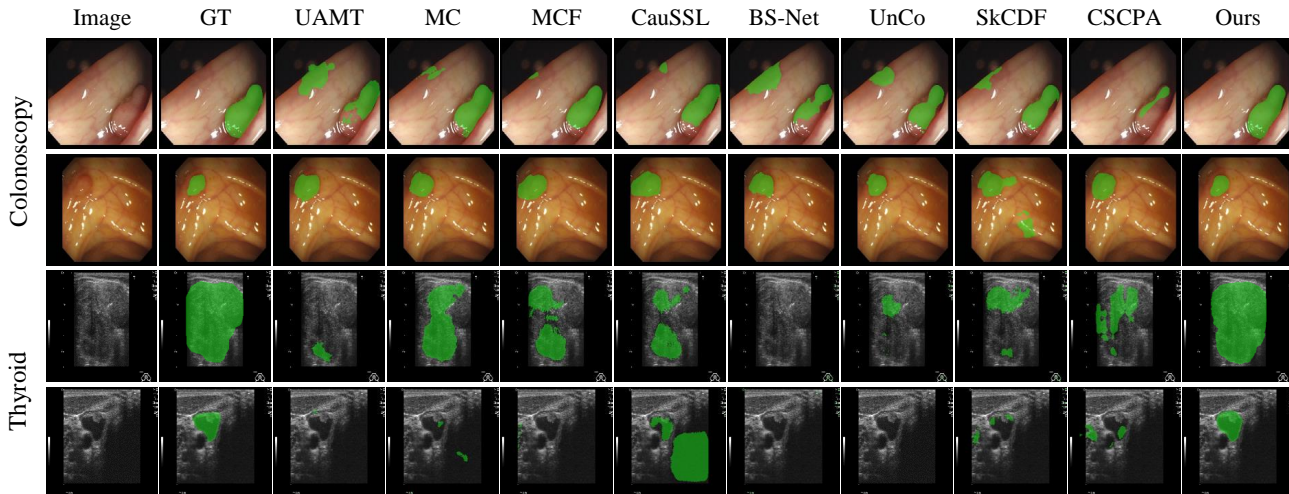


Figure 2. Visual comparisons of state-of-the-art medical segmentation methods on the colonoscopy and thyroid datasets.

Table 1. Quantitative results on the ETLs and CVC-ColonDB datasets.

Methods	10% labeled			30% labeled			10% labeled			30% labeled		
	Dice (%)	IoU (%)	95HD	Dice (%)	IoU (%)	95HD	Dice (%)	IoU (%)	95HD	Dice (%)	IoU (%)	95HD
UA-MT [18] [MICCAI'19]	41.34	33.49	5.72	59.43	51.30	4.74	31.84	25.59	4.96	41.18	34.80	4.64
DTC [9] [AAAI'21]	35.35	27.17	6.10	54.75	46.18	5.05	26.74	20.48	6.05	44.83	37.72	4.40
MC-Net [16] [MICCAI'21]	55.69	46.53	5.24	63.65	55.38	4.71	39.88	33.15	4.81	49.51	41.69	4.74
URPC [10] [MIA'22]	46.84	38.98	5.55	60.00	51.89	4.78	38.98	32.92	4.78	45.00	36.75	4.89
MCF [15] [CVPR'23]	48.72	40.60	5.25	63.24	55.05	4.64	31.13	25.81	4.84	48.46	41.28	4.33
CauSSL [11] [ICCV'23]	48.51	40.89	5.24	57.84	49.36	4.95	30.93	24.96	5.18	32.97	27.41	5.42
CDMA [21] [MICCAI'23]	44.88	35.72	5.77	59.39	49.10	5.20	37.23	28.85	4.87	38.29	29.37	6.07
BS-Net [5] [TMI'24]	43.88	36.57	5.43	55.89	48.15	4.87	31.77	26.26	5.28	38.08	31.65	4.91
PMT [3] [ECCV'24]	47.21	39.47	4.74	58.63	51.12	4.53	29.09	23.90	4.90	39.34	32.90	4.67
VCLIPSeg [8] [MICCAI'24]	50.19	42.19	4.79	62.02	54.34	4.67	37.92	31.14	4.83	45.89	38.99	4.46
UnCo [19] [TMI'25]	57.62	50.64	4.64	62.18	55.04	4.45	37.73	32.92	4.61	42.04	36.34	4.27
SKCDF [20] [CVPR'25]	45.82	37.51	4.55	58.02	47.58	4.79	35.02	28.34	4.82	36.50	30.14	5.15
CSCPA [2] [CVPR'25]	55.66	46.80	4.50	68.70	60.22	4.06	38.86	32.08	4.68	52.58	44.72	4.25
Ours	67.80	58.29	4.47	71.81	63.38	4.02	56.77	48.26	4.52	59.86	53.10	4.11

Table 2. Quantitative results on the thyroid datasets.

Methods	10% labeled			30% labeled			10% labeled			30% labeled		
	Dice (%)	IoU (%)	95HD	Dice (%)	IoU (%)	95HD	Dice (%)	IoU (%)	95HD	Dice (%)	IoU (%)	95HD
UA-MT [18] [MICCAI'19]	34.96	27.31	6.73	49.76	39.85	6.07	74.73	64.23	4.83	78.42	69.16	4.53
DTC [9] [AAAI'21]	27.13	19.67	7.35	38.53	28.05	6.87	62.67	50.50	5.61	64.48	51.66	5.74
MC-Net [16] [MICCAI'21]	29.42	23.12	7.15	45.36	36.60	6.20	71.45	60.72	5.28	78.04	68.72	4.65
URPC [10] [MIA'22]	31.37	24.23	6.88	56.01	45.26	5.92	74.42	64.17	4.88	79.19	70.00	4.56
MCF [15] [CVPR'23]	57.69	46.84	5.71	55.09	44.08	5.97	74.50	64.46	4.79	78.04	68.79	4.43
CauSSL [11] [ICCV'23]	41.88	32.76	6.52	46.12	36.51	6.22	70.89	60.22	5.17	73.93	63.63	4.97
CDMA [21] [MICCAI'23]	46.42	36.17	6.28	54.68	42.48	6.34	72.97	61.54	5.12	76.24	65.60	4.81
BS-Net [5] [TMI'24]	31.41	24.82	6.74	40.55	32.42	6.33	73.70	64.22	4.77	79.25	70.60	4.39
PMT [3] [ICCV'24]	33.84	26.83	5.35	34.68	27.60	5.90	71.81	62.12	4.54	71.56	62.06	4.41
VCLIPSeg [8] [MICCAI'24]	37.80	29.99	6.25	49.74	40.77	5.92	71.31	61.56	4.48	77.65	68.24	4.31
UnCo [19] [TMI'25]	26.04	20.42	7.02	43.23	34.82	6.24	72.36	63.03	4.58	74.93	65.64	4.32
SKCDF [20] [CVPR'25]	53.66	42.08	6.22	52.37	40.89	6.58	72.44	62.02	4.82	75.89	65.75	4.74
CSCPA [2] [CVPR'25]	52.70	42.73	6.21	57.92	47.61	5.83	78.28	68.81	4.45	80.73	71.41	4.30
Ours	56.07	45.37	6.20	61.49	50.85	5.71	80.25	68.94	4.44	83.57	72.21	4.18

074 **D. Model Complexity**

075 Tab. 3 details the efficiency comparison. The parameter in-
076 crease is inherent to the generative paradigm. While heavier
077 than BSNet (86.49M vs 23.6M), SemiGDA gains +12.56%
078 Dice (75.57% vs 63.01%). Crucially, the 7.90 GB foot-
079 print enables effortless single-GPU deployment, while 32
080 FPS satisfies real-time requirements.

Table 3. Efficiency comparison on BUSI at 224×224 resolution.

Method	Params (M)	Memory (GB)	FPS	Dice (10%)
BSNet	23.6	4.2	164	63.01
CSCPA	46.5	4.7	121	65.16
Ours	86.4	7.9	32	75.57

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