

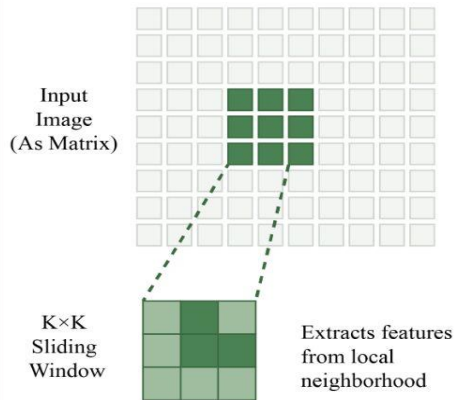
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S2M-Net: Spectral-Spatial Mixing with Morphology-Aware Adaptive Loss for Medical Image Segmentation

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Feature Interaction Paradigms in Medical Image Segmentation

CNN-Based



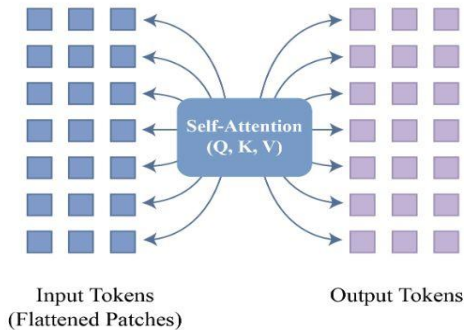
Strengths

- Effective local feature extraction
- Computationally efficient

Limitations

- Limited global context
- Misses long-range dependencies

Transformer-Based



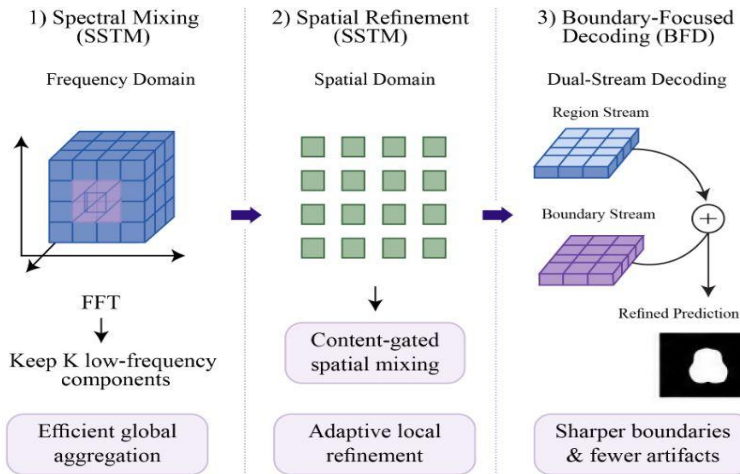
Strengths

- Captures global dependencies
- Powerful long-range context modeling

Limitations

- Quadratic complexity $O(n^2)$
- High memory and computation cost

Our Method (S2M-Net)



Strengths

- Efficient global context via spectral mixing $O(HW C \log(HW))$
- Boundary-aware refinement with dual-stream decoding
- Lower complexity with strong performance

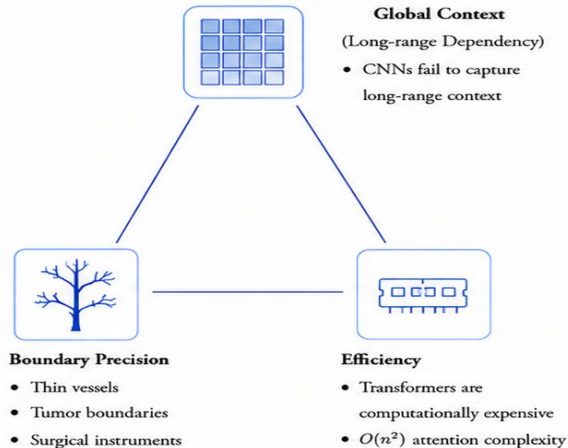
Outcome

Accurate edges, preserved details, and efficient computation

Comparison Aspect	Receptive Field	Context Modeling	Computational Complexity	Memory Usage	Boundary Accuracy	Artifacts
CNN-Based	Local	Local	$O(HW C K^2)$	Low	Coarse	More
Transformer-Based	Global	Global	$O((HW)^2 C)$	Very High	High	Moderate
Our Method (S2M-Net)	Global + Local (Adaptive)	Global + Local (Adaptive)	$O(HW C \log HW + HW C^2)$	Low	High	Fewer

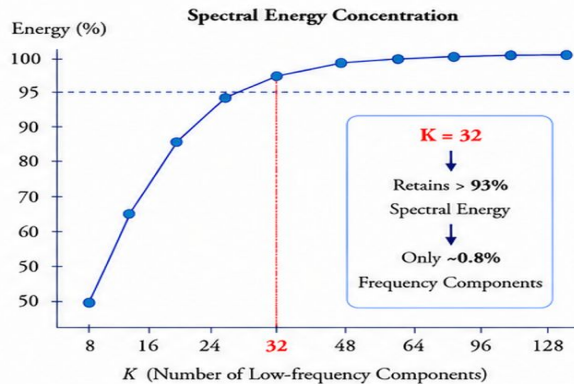
Motivation, Problem Formulation & Contributions

Motivation: The Clinical Trilemma



Current methods struggle to achieve all three simultaneously.

Core Insight: Spectral Concentration in Medical Images



Medical images contain highly concentrated low-frequency information. This enables efficient global context modeling without expensive self-attention.

Problem Formulation

We formulate medical image segmentation as:

$$(\theta^*, w^*) = \arg \min_{\theta, w} E_{(x, y) \sim \mathcal{D}} [\mathcal{L}_{MASL}(y, f_{\theta}(x); w)]$$

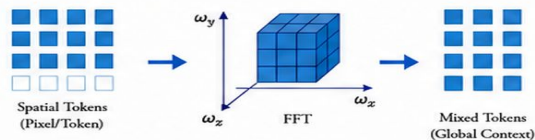
Where:

- x : Input image
- y : Ground-truth segmentation
- f_{θ} : S2M-Net with parameters θ
- w : Adaptive loss weights
- $\mathcal{L}_{MASL}$: Morphology-Aware Adaptive Loss
- $\mathcal{D}$: Data distribution

Goal: Learn optimal network parameters θ and adaptive loss weights w to minimize the MASL.

1) Efficient Global Context Modeling

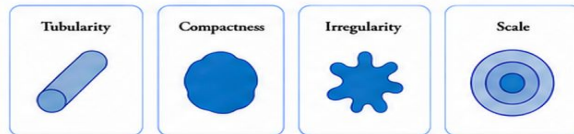
Spectral-Spatial Token Mixing (SSTM)



- FFT-based global aggregation in frequency domain
- $O(HWC \log(HW))$ complexity (vs. $O(n^2)$ attention)
- Captures long-range dependencies efficiently

2) Adaptive Morphology-Aware Supervision

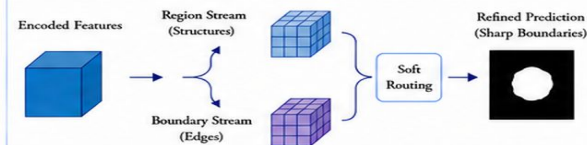
Morphology-Aware Adaptive Loss (MASL)



- Captures key morphological properties of medical structures
- Automatically balances multiple objectives via learnable weights
- Improves generalization across datasets and structures

3) Boundary-Focused Decoding

Boundary-Focused Decoding (BFD)



- Dual-stream decoding with soft routing mechanism
- Focuses on boundaries without extra annotations
- Produces sharper boundaries with fewer artifacts

Architecture Overview

MRF-SE Block (Local Feature Extraction):

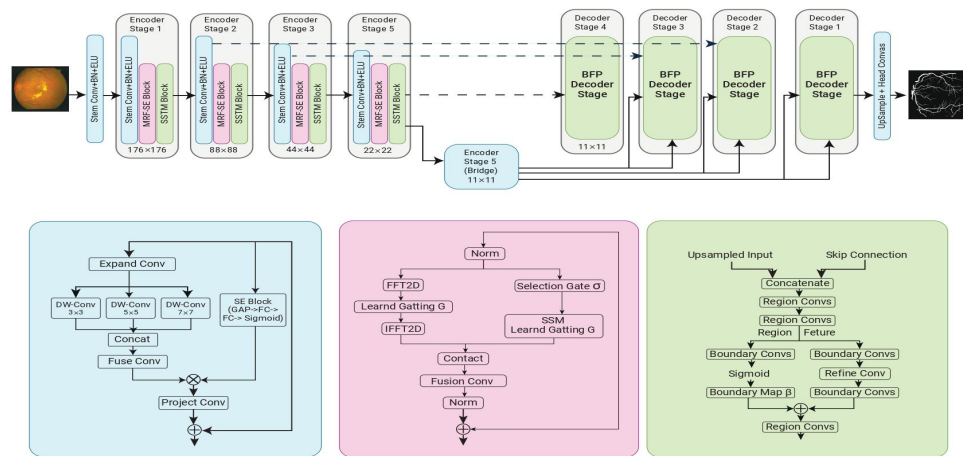
- Parallel DW-Conv with $k = \{3, 5, 7\}$ captures multi-scale local patterns.
- SE recalibration: $\text{GAP} \rightarrow \text{FC} \rightarrow \text{Sigmoid}$ for channel attention.
- Handles both tiny polyps (5 px) and large vessels (>20 px) simultaneously.
- Removing MRF-SE: -5.90% average Dice across 4 datasets.

SSTM Block (Efficient Global Context):

- 2D FFT $\rightarrow$ retain only $K = 32$ low-frequency components, just 0.8% of the spectrum.
- Captures $>93\%$ spectral energy across all 8 modalities.
- Sub-quadratic complexity: $O(\text{HWC} \log(\text{HW}) + \text{HWC}^2)$ vs. $O((\text{HW})^2 \text{C})$ self-attention.
- Content-gated spatial branch with bottleneck $d = 16$.
- Removing SSTM: -6.70% average Dice across 4 datasets

BFD Decoder (Boundary Specialization):

- Dual-stream: region path for smooth interiors + boundary path for edge sharpness.
- Soft routing: $z = r \odot (1 - \beta) + b \odot \beta$.
- β is learned via backpropagation from MASL, with no edge annotations needed.
- Removing BFD: -5.06% average Dice across 4 datasets.



Morphology-Aware Adaptive Loss

- Automatically weights five objectives per sample: region, boundary, structure, focal, and texture.
- Uses four geometric descriptors: tubularity τ , compactness c , irregularity ι , and size s .
- Generalizes across 15 datasets using a single loss formulation, without manual tuning.
- Learned weights $w_i \in [0.1, 10]$ adapt to target structures, e.g., polyps $\rightarrow$ boundary, vessels $\rightarrow$ structure.

Results

Table 1. Architectural comparison under a unified training pipeline. All methods are retrained with identical optimization and preprocessing; MASL is applied to all to isolate architectural effects under a common supervision signal. For transparency, Table 2 evaluates S2M-Net and top baselines under standard Dice+CE loss to confirm that architectural gains are independent of MASL. Mean Dice (%) $\pm$ std over 5 runs. $\dagger$: statistically significant ($p < 0.0033$, Bonferroni-corrected). S2M-Net uses 4.7M parameters ($12.8\times$ fewer than TransUNet). FNet and GFNet are excluded as they lack decoders and skip connections required for dense prediction; see Section 2 for discussion. RAPUNet(Lee & Yoo, 2024) results follow the DuckNet data split; see footnote. †

Dataset	U-Net	U-Net++	PraNet	Swin-Unet	TransUNet	UMamba	DuckNet	RAPUNet	S2M-Net	Model Params
Polyp Segmentation (Endoscopy)										
Kvasir-SEG	90.64 $\pm$ 0.41	91.81 $\pm$ 0.53	93.03 $\pm$ 0.38	93.22 $\pm$ 0.44	93.75 $\pm$ 0.36	92.40 $\pm$ 0.47	94.11 $\pm$ 0.33	93.12 $\pm$ 0.45	96.05 $\pm$ 0.28 †	4.7M
CVC-ClinicDB	92.18 $\pm$ 0.38	92.70 $\pm$ 0.42	92.65 $\pm$ 0.44	92.52 $\pm$ 0.61	87.28 $\pm$ 0.52	90.09 $\pm$ 0.48	93.89 $\pm$ 0.54	95.10 $\pm$ 0.38	95.65 $\pm$ 0.31 †	4.7M
CVC-ColonDB	88.12 $\pm$ 0.56	88.98 $\pm$ 0.49	92.78 $\pm$ 0.37	91.45 $\pm$ 0.43	90.33 $\pm$ 0.47	86.62 $\pm$ 0.58	92.69 $\pm$ 0.39	91.85 $\pm$ 0.52 †	90.69 $\pm$ 0.52	4.7M
ETIS-LaribDB	91.22 $\pm$ 0.44	89.80 $\pm$ 0.51	93.46 $\pm$ 0.35	94.10 $\pm$ 0.33	94.43 $\pm$ 0.31	91.23 $\pm$ 0.46	94.98 $\pm$ 0.29	94.23 $\pm$ 0.41	96.12 $\pm$ 0.30	4.7M
Dermoscopy (Skin Lesions)										
ISIC-2018	86.93 $\pm$ 0.48	87.51 $\pm$ 0.45	89.05 $\pm$ 0.39	89.43 $\pm$ 0.42	87.12 $\pm$ 0.47	89.23 $\pm$ 0.38	90.10 $\pm$ 0.43	89.45 $\pm$ 0.31	91.09 $\pm$ 0.36	4.7M
PH2	88.34 $\pm$ 0.52	89.83 $\pm$ 0.46	91.52 $\pm$ 0.38	92.66 $\pm$ 0.35	93.56 $\pm$ 0.39	90.12 $\pm$ 0.44	90.34 $\pm$ 0.43	92.15 $\pm$ 0.49	96.67 $\pm$ 0.32 †	4.7M
Histopathology & Ultrasound										
GlaS	91.57 $\pm$ 0.39	91.40 $\pm$ 0.41	90.40 $\pm$ 0.46	89.01 $\pm$ 0.53	89.92 $\pm$ 0.48	91.18 $\pm$ 0.42	88.73 $\pm$ 0.55	91.67 $\pm$ 0.07	93.83 $\pm$ 0.38	4.7M
BUSI	76.77 $\pm$ 0.61	78.35 $\pm$ 0.56	79.48 $\pm$ 0.52	82.52 $\pm$ 0.49	82.11 $\pm$ 0.51	79.04 $\pm$ 0.58	78.13 $\pm$ 0.63	81.34 $\pm$ 0.73	85.07 $\pm$ 0.45 †	4.7M
Surgical Robotics (EndoVis-2017)										
Binary	95.93 $\pm$ 0.26	95.32 $\pm$ 0.29	95.24 $\pm$ 0.30	95.24 $\pm$ 0.30	95.45 $\pm$ 0.28	95.53 $\pm$ 0.27	95.11 $\pm$ 0.31	95.78 $\pm$ 0.36	95.95 $\pm$ 0.28	4.7M
Multiclass	61.07 $\pm$ 1.12	70.93 $\pm$ 0.89	73.86 $\pm$ 0.76	73.22 $\pm$ 0.78	74.74 $\pm$ 0.72	74.29 $\pm$ 0.75	73.88 $\pm$ 0.87	74.81 $\pm$ 0.19	83.43 $\pm$ 0.63 †	4.7M
Brain Tumor MRI										
BraTS2020	65.67 $\pm$ 0.84	66.05 $\pm$ 0.82	66.44 $\pm$ 0.81	69.86 $\pm$ 0.73	68.36 $\pm$ 0.77	62.88 $\pm$ 0.91	66.93 $\pm$ 0.79	67.82 $\pm$ 0.12	79.96 $\pm$ 0.58 †	4.7M
Cardiac MRI										
ACDC	89.52 $\pm$ 0.42	90.15 $\pm$ 0.45	91.11 $\pm$ 0.38	92.32 $\pm$ 0.37	92.44 $\pm$ 0.36	91.57 $\pm$ 0.48	92.13 $\pm$ 0.38	91.45 $\pm$ 0.20	93.09 $\pm$ 0.43	4.7M
Retinal Vessel Segmentation										
STARE	81.18 $\pm$ 0.54	81.73 $\pm$ 0.51	82.94 $\pm$ 0.47	83.86 $\pm$ 0.44	83.10 $\pm$ 0.46	82.05 $\pm$ 0.58	81.41 $\pm$ 0.62	82.34 $\pm$ 0.38	84.45 $\pm$ 0.48	4.7M
DRIVE	79.02 $\pm$ 0.56	80.18 $\pm$ 0.59	81.94 $\pm$ 0.49	83.07 $\pm$ 0.48	81.45 $\pm$ 0.50	82.18 $\pm$ 0.58	81.39 $\pm$ 0.57	82.94 $\pm$ 0.12	84.06 $\pm$ 0.49	4.7M
CHASE-DB	81.51 $\pm$ 0.52	81.65 $\pm$ 0.51	81.47 $\pm$ 0.52	83.12 $\pm$ 0.49	82.93 $\pm$ 0.47	82.90 $\pm$ 0.59	83.16 $\pm$ 0.58	83.21 $\pm$ 0.29	84.95 $\pm$ 0.48	4.7M
Average	83.98	85.09	86.29	87.04	86.46	85.42	86.47	86.72	90.07	4.7M

† RAPUNet follows PraNet data split for polyp datasets; S2M-Net uses DuckNet split. Direct numerical comparison on CVC-ColonDB is not fully appropriate without matching distributions. FNet/GFNet excluded: classification-only, no decoder. (Lee & Yoo, 2024; Lee-Thorp et al., 2022; Rao et al., 2021)

Results and Ablation Studies

Table 2. Architecture vs. MASL disentanglement. S2M-Net evaluated under standard Dice+CE loss to isolate architectural gains from loss design. Dice (%).

Method	Loss	Kvasir	DRIVE	EV17-MC	BraTS20	Avg
TransUNet	Dice+CE	92.17	80.92	71.83	66.42	77.84
Swin-Unet	Dice+CE	91.84	82.14	70.54	67.91	78.11
S2M-Net	Dice+CE	93.89	82.74	78.91	74.83	82.59
S2M-Net	MASL	96.05	84.06	83.43	79.96	85.88
Arch. gain (S2M vs. best@Dice+CE)		+1.72	+0.60	+7.08	+6.92	+4.48
MASL gain (MASL vs. Dice+CE)		+2.16	+1.32	+4.52	+5.13	+3.29

Table 4. Spectral energy retention across medical imaging modalities. $K = 32$ retains 94.8% average energy while representing only 0.83% of frequency coefficients at 352×352 resolution. Medical images show stronger concentration than natural images, validating domain-specific truncation.

Modality	K=16	K=24	K=32	K=48
Colonoscopy	89.3±2.1%	93.7±1.4%	95.2±1.2%	97.1±0.9%
Fundus	91.2±1.8%	94.8±1.2%	96.4±0.9%	97.8±0.7%
Brain/Cardiac MRI	87.6±2.4%	92.1±1.6%	94.1±1.3%	96.2±1.0%
Ultrasound	85.9±3.2%	90.8±2.1%	93.3±1.7%	95.4±1.3%
Average	88.5±2.4%	92.9±1.6%	94.8±1.3%	96.6±1.0%

Table 5. Per-structure segmentation performance comparing $K = 32$ truncation to full-resolution FFT. Mean Dice degradation is 0.24% across tested structures, with differences within confidence intervals. Thin structures ($< 3\text{px}$ vessels, instrument tips) show degradation $< 0.5\%$.

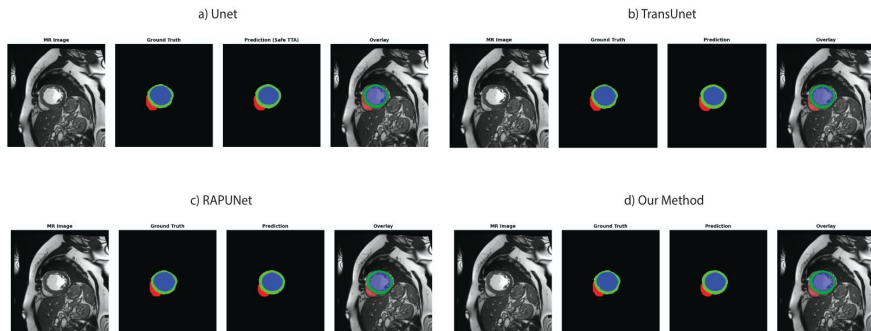
Dataset	Structure	K=32	Full	Δ
DRIVE	Thin vessels ($< 3\text{px}$)	83.6±0.8	83.9±0.9	-0.3%
	Medium vessels	86.7±0.5	86.9±0.6	-0.2%
Kvasir	Small polyps	95.1±0.9	95.3±1.0	-0.2%
	Medium polyps	96.9±0.5	97.0±0.6	-0.1%
EndoVis17	Instrument tips	82.3±1.4	82.7±1.5	-0.4%

Table 3. Ablation study on four medical imaging datasets. Dice coefficient (%) reported for systematic component removal. Full model (bold) includes all components. Differences $\geq 1.0\%$ are statistically significant ($p < 0.001$).

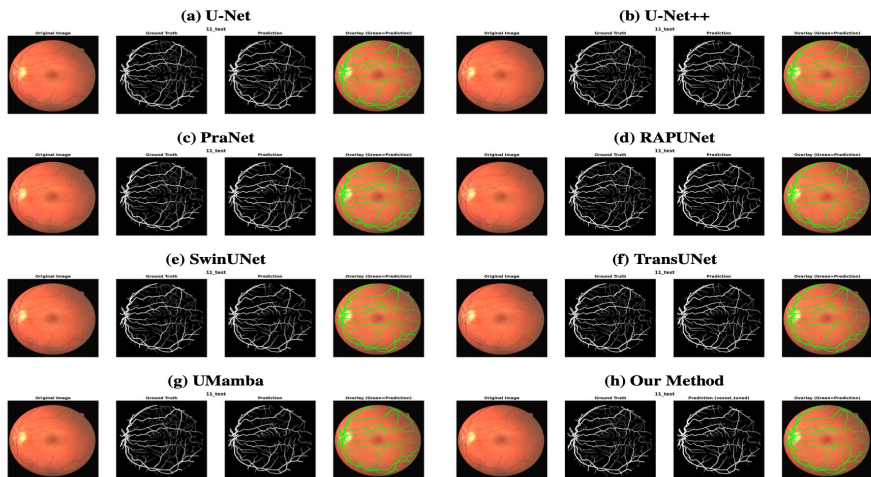
Configuration	Kvasir	DRIVE	GlaS	PH2
Full Model (Ours)	96.05	84.06	93.83	96.67
MASL Loss Components				
w/o Core Loss	92.31	81.12	77.32	93.82
w/o Boundary Loss	87.96	80.45	90.85	89.91
w/o Structure Loss	94.42	82.67	90.17	93.88
w/o Scale-Aware Focal	95.15	83.21	90.43	94.56
w/o Texture Loss	95.68	83.04	88.67	94.01
Adaptive Mechanisms				
Fixed Weights	88.92	78.34	90.38	91.45
No Morphology Modulation	89.37	79.78	90.28	91.92
SSTM Frequency Truncation				
$K=16$	89.87	80.92	88.57	92.34
$K=24$	93.56	82.45	90.43	93.98
$K=32$	96.05	84.06	93.83	96.67
$K=48$	95.98	83.71	89.89	93.38
$K=64$	95.75	83.52	90.42	93.11
Architecture Modules				
w/o SSTM	88.45	77.78	86.92	90.67
w/o BFD Decoder	89.87	79.89	88.34	92.28
w/o MRF-SE	89.23	78.45	87.56	91.78
Vanilla U-Net Baseline	85.67	74.34	86.48	88.45

Qualitative Studies

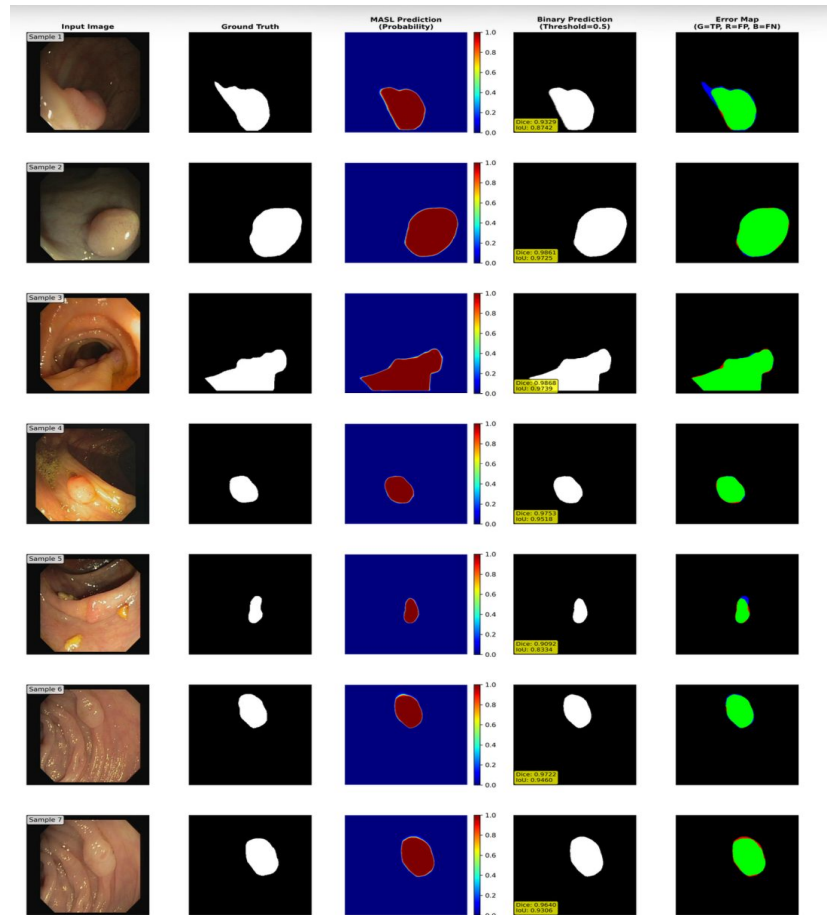
ACDC Multiclass Segmentation



DRIVE Blood Vessel Segmentation



KVASIR-SEG Polyp Segmentation



Thank you