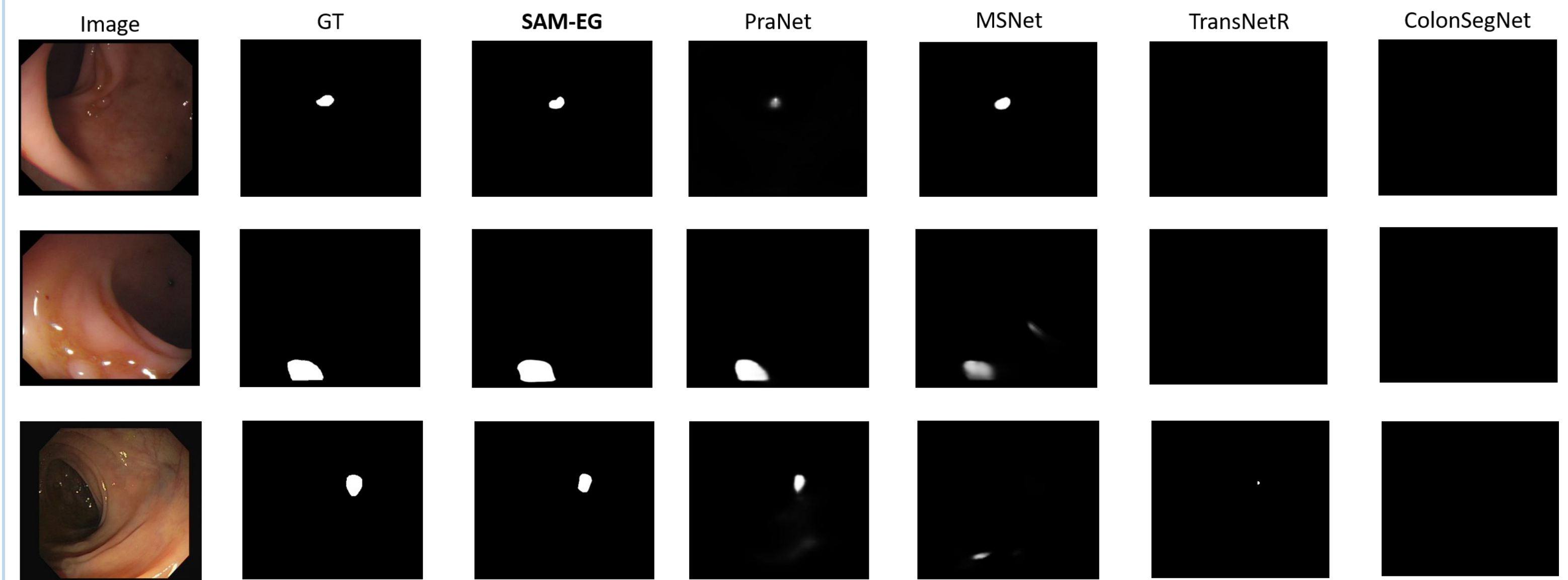


INTRODUCTION

Polyp segmentation is an important task to help early diagnose the colorectal cancer. Previous works achieve high accuracy, however, the extensive **computational cost** is the problem in the production deployment. Recent years, SAM is proposed as the strong foundation model for the Segmentation. Inspired by the **power of SAM**, we leverage this model to guide the segmentation model to learn and improve the based information learning for the better prediction. Moreover, we propose the **Edge Guiding module**, to support the segmentation model deal with the challenge in the boundary, thus can alleviate the boundary challenge of the segmentation from the small model. From extensive experiments, our method achieves competitive performance with state-of-the-art method with the small size of the model

VISUALIZATION

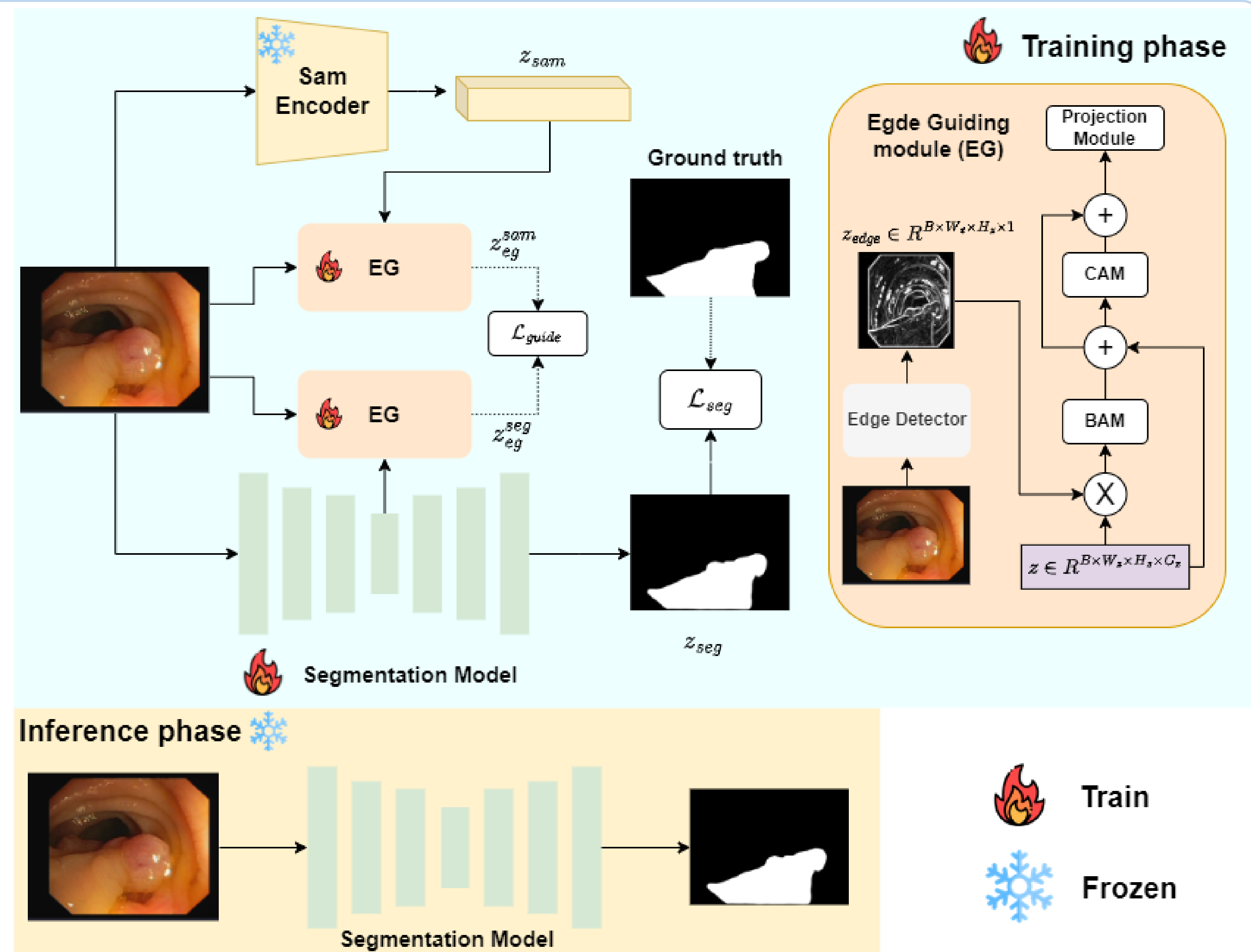
Below is our visualization comparison with previous works on both normal setting, and light-weight setting



SAM-EG

Include three modules:

- **SAM Encoder:** SAM teacher model to encode the base feature of the Polyp images.
- **Segmentation model:** Student segmentation model is trained for the segmentation
- **Edge Guiding Module (EG):** to guide edge for student model



RESULTS

To evaluate SAM-EG, we do the benchmark on two settings: compare with state-of-the-art and compare with the light-weight model

| Method | Params(M) | ClinicDB | | ColonDB | | Kvasir | | ETIS | |
|---------------------------------|-----------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | | mDice | mIoU | mDice | mIoU | mDice | mIoU | mDice | mIoU |
| UNet (2015) [18] | 7.6 | 0.824 | 0.767 | 0.519 | 0.449 | 0.821 | 0.756 | 0.406 | 0.343 |
| UNet++ (2018) [32] | 9.0 | 0.794 | 0.729 | 0.483 | 0.410 | 0.820 | 0.743 | 0.401 | 0.344 |
| PraNet (2019) [7] | 32.6 | 0.899 | 0.849 | 0.712 | 0.640 | 0.898 | 0.840 | 0.628 | 0.567 |
| MSNet (2021) [31] | 29.7 | 0.921 | <u>0.879</u> | <u>0.755</u> | 0.678 | 0.907 | 0.862 | <u>0.719</u> | <u>0.664</u> |
| Polyp-PVT (2022) [3] | 3.7 | <u>0.924</u> | 0.867 | 0.756 | 0.668 | 0.894 | 0.835 | 0.747 | 0.675 |
| PEFNet (2023) [17] | 28.0 | 0.866 | 0.814 | 0.710 | 0.638 | 0.892 | 0.833 | 0.636 | 0.572 |
| M ² UNet (2023) [26] | 28.7 | 0.901 | 0.853 | 0.767 | <u>0.684</u> | 0.907 | 0.855 | 0.670 | 0.595 |
| HarDNet-CPS (2023) [29] | --- | 0.917 | 0.887 | 0.729 | 0.658 | <u>0.911</u> | <u>0.856</u> | 0.69 | 0.619 |
| SAM-EG | 3.7 | 0.931 | <u>0.879</u> | <u>0.774</u> | <u>0.689</u> | 0.915 | 0.862 | 0.757 | 0.681 |

Table 1: Qualitative results of SAM-EG on various datasets

| Method | Params(M) | FLOPs (G) | ClinicDB | | ColonDB | | Kvasir | | ETIS | |
|-------------------------|-----------|-----------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | | | mDice | mIoU | mDice | mIoU | mDice | mIoU | mDice | mIoU |
| ColonSegNet (2021) [11] | 5.0 | 6.22 | 0.28 | 0.21 | 0.12 | 0.10 | 0.52 | 0.39 | 0.16 | 0.12 |
| TransNetR (2023) [12] | 27.3 | 10.09 | 0.87 | 0.82 | 0.68 | 0.61 | 0.87 | 0.80 | 0.60 | 0.53 |
| MMFIL-Net (2023) [16] | 6.7 | 4.32 | 0.890 | 0.838 | 0.744 | 0.659 | 0.909 | <u>0.858</u> | 0.743 | 0.670 |
| KDAS (2024) [24] | 3.7 | 2.01 | <u>0.925</u> | <u>0.872</u> | <u>0.759</u> | <u>0.679</u> | <u>0.913</u> | 0.848 | <u>0.755</u> | <u>0.677</u> |
| SAM-EG | 3.7 | 2.12 | 0.931 | 0.879 | 0.774 | 0.689 | 0.915 | 0.862 | 0.757 | 0.681 |

Table 2: Comparison of model from SAM-EG with real-time model