

Supplementary Material for "Mining Gold from the Sand: Weakly Supervised Histological Tissue Segmentation with Activation Relocalization and Mutual Learning"

Table 1. Comparison with fully supervised methods on BCSS dataset. The results are reported in mean \pm std.

Supervision	Backbone	TUM	STR	LYM	NEC	mIoU	Dice	ACC
Fully	MixTransformer	81.35 \pm 0.27	74.75 \pm 0.13	63.50 \pm 1.08	63.69 \pm 1.53	70.87 \pm 0.14	82.72 \pm 0.10	86.28 \pm 0.39
	ResNet38	79.56 \pm 0.33	73.33 \pm 0.14	61.14 \pm 1.37	60.07 \pm 1.03	68.52 \pm 0.27	80.99 \pm 0.17	85.02 \pm 0.46
	ResNeSt101	79.79 \pm 0.18	73.66 \pm 0.09	62.26 \pm 1.44	64.64 \pm 0.98	70.09 \pm 0.20	82.21 \pm 0.13	85.46 \pm 0.28
Weakly (Ours)	MixTransformer	79.97 \pm 0.41	73.09 \pm 0.38	57.72 \pm 0.95	65.02 \pm 0.33	68.95 \pm 0.39	81.33 \pm 0.22	85.08 \pm 0.44
	ResNet38	78.87 \pm 0.55	73.18 \pm 0.73	58.85 \pm 1.04	66.55 \pm 0.36	69.36 \pm 0.41	81.68 \pm 0.25	84.88 \pm 0.67
	ResNeSt101	79.20 \pm 0.30	73.83 \pm 0.17	60.25 \pm 0.14	68.96 \pm 0.44	70.56 \pm 0.19	82.48 \pm 0.10	85.63 \pm 0.17

Table 2. Ablation study of different relation loss in \mathcal{L}_{st} (Eq. 8) on BCSS dataset. CE means the baseline with standard cross entropy loss. The results are reported in mean \pm std.

Method	mIoU	Dice
CE	67.97 \pm 0.28	80.67 \pm 0.22
\mathcal{L}_{st} w/o \mathcal{L}_{ang}	69.07 \pm 0.37	81.47 \pm 0.28
\mathcal{L}_{st} w/o \mathcal{L}_{dist}	69.34 \pm 0.30	81.65 \pm 0.19
\mathcal{L}_{st}	70.56 \pm 0.19	82.48 \pm 0.10

Table 3. Different mIoU results on BCSS validation set when λ in different values. Thus we set $\lambda = 0.2$ in final segmentation loss \mathcal{L} .

λ	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9
mIoU	67.01	67.87	66.55	66.89	67.13	66.82	66.35	65.96	65.18

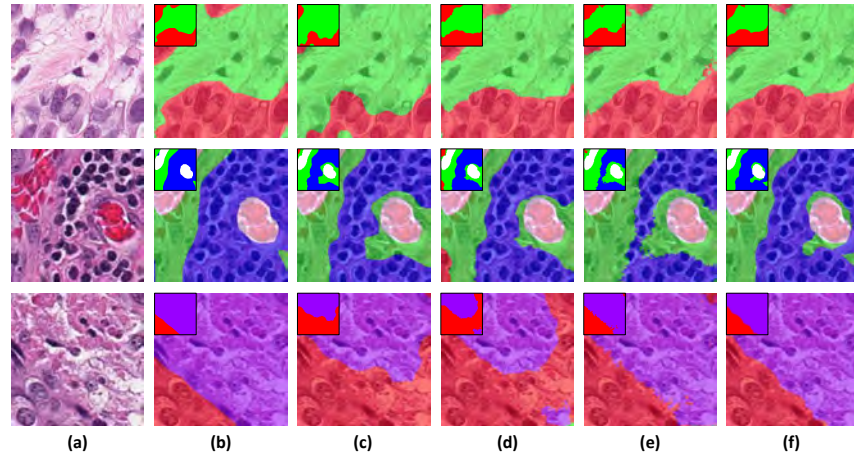


Fig. 1. Visualization of tissue segmentation on BCSS dataset. (a) Test image. (b) Ground truth. (c) OEEM. (d) MLPS. (e) TPRO. (f) Our ARML with ResNeSt101 backbone. TUM is shown in red, STR is shown in green, LYM is shown in blue and NEC is shown in violet. The results are overlaid on test images, and the segmentation masks are put in the top-left corner. Best view in color.

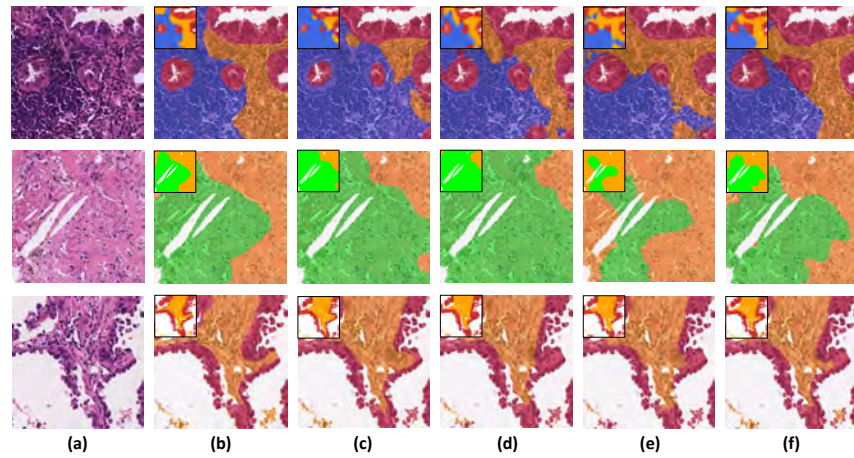


Fig. 2. Visualization of tissue segmentation on LUAD-HistoSeg dataset. (a) Test image. (b) Ground truth. (c) OEEM. (d) MLPS. (e) TPRO. (f) Our ARML with ResNeSt101 backbone. TE is shown in red, NEC is shown in green, LYM is shown in blue and TAS is shown in orange. The results are overlaid on test images, and the segmentation masks are put in the top-left corner. Best view in color.