

Hard Negative Sample Mining for Whole Slide Image Classification

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Table 4: Comparison result on Camelyon16 and TCGA-LUAD mutation datasets, including standard deviations.

Method	Camelyon16		TCGA-LUAD mutation			
	AUC		EGFR AUC	KRAS AUC	STK11 AUC	TP53 AUC
Max-pooling	0.8641 ± 0.0132	0.6643 ± 0.0033	0.5746 ± 0.0027	0.6702 ± 0.0036	0.6109 ± 0.0022	
ABMIL[1]	0.8652 ± 0.0086	0.6848 ± 0.0026	0.5994 ± 0.0033	0.6784 ± 0.0031	0.6520 ± 0.0034	
DSMIL[2]	0.9095 ± 0.0075	0.6956 ± 0.0035	0.6026 ± 0.0029	0.6885 ± 0.0037	0.6344 ± 0.0031	
Its2CLR[3]	0.9465 ± 0.0023	0.7103 ± 0.0030	0.6135 ± 0.0025	0.7111 ± 0.0032	0.6703 ± 0.0024	
Ours	0.9604 ± 0.0022	0.7235 ± 0.0025	0.6473 ± 0.0034	0.7396 ± 0.0037	0.7071 ± 0.0028	

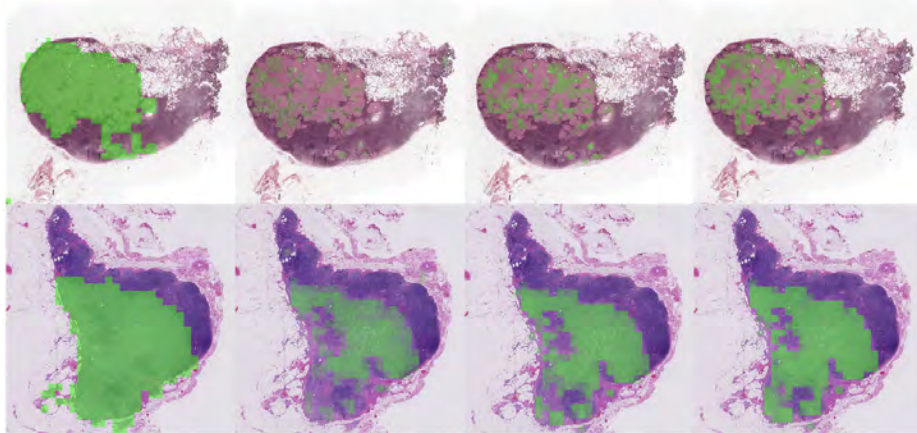


Fig. 4: Magnified version of Figure 3. The first column displays the instance ground truth label. The second, third, and fourth columns visualize the instance prediction probabilities generated by DSMIL, Its2CLR, and our method, respectively. Patches with threshold probabilities below 0.3 are rendered transparent.

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Table 5: Threshold for pseudo labeling, patches with prediction scores exceeding the threshold are marked as positive.

	CAMELYON16	TCGA-LUAD mutation			
		EGFR	KRAS	STK11	TP53
Threshold	0.3	0.1	0.25	0.1	0.5

References

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