Supplementary Material for
MetaStain: Stain-generalizable Meta-learning for cell segmentation and classification with limited exemplars

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Table 1. SOTA Comparison with baselines for 5-class segmentation and classification in PR target stain

Methods	PR samples in the inference (DSC, Acc)		
	5% samples	10% samples	20% samples
PANet	0.66, 0.70	0.69, 0.72	0.74, 0.72
HSNet	0.75, 0.72	0.78, 0.72	0.80, 0.74
DCAMA	0.74, 0.71	0.76, 0.73	0.77, 0.73
AAformer	0.76, 0.70	0.78, 0.72	0.80, 0.74
PATNet	0.81, 0.72	0.83, 0.74	0.86, 0.75
PMNet	0.79, 0.77	0.80, 0.79	0.83, 0.79
MLDG-Seg	0.75, 0.70	0.78, 0.73	0.81, 0.74
MetaMedSeg	0.79, 0.67	0.77, 0.69	0.80, 0.70
iMAML	0.80, 0.76	0.82, 0.75	0.83, 0.78
Ours	**0.85, 0.81**	**0.86, 0.81**	**0.87, 0.82**

Table 2. SOTA Comparison with non-meta learning DG methods for 5-class segmentation and classification in Ki67 and ER target stains with no support samples

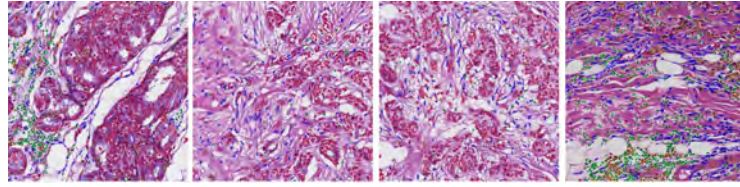| Methods	0% support samples (DSC, Acc)	
	Ki67	ER
DCA-Net	0.79, 0.67	0.74, 0.68
DCAC	0.73, 0.64	0.69, 0.61
Ours	**0.84, 0.79**	**0.80, 0.79**

Fig. 1. Segmentation results of 5 types of cells (Neoplastic - red, Inflammatory - green, Connective - blue, Necrosis - Yellow, Non-neoplastic epithelial - Orange) on H&E target stain.

Table 3. Avg and std scores for DSC based on 10 random runs.

Methods	Ki67 samples in inference (DSC, Acc)			ER samples in inference (DSC, Acc)		
	5%	10%	20%	5%	10%	20%
PANet	0.64, 0.06	0.67, 0.05	0.70, 0.07	0.60, 0.06	0.63, 0.06	0.69, 0.05
HSNet	0.73, 0.07	0.78, 0.06	0.80, 0.05	0.70, 0.06	0.74, 0.04	0.76, 0.05
DCAMA	0.78, 0.05	0.80, 0.04	0.84, 0.05	0.72, 0.06	0.75, 0.05	0.78, 0.04
AAformer	0.77, 0.06	0.82, 0.05	0.82, 0.06	0.77, 0.04	0.75, 0.05	0.79, 0.04
PATNet	0.82, 0.04	0.85, 0.04	0.85, 0.04	0.82, 0.04	0.82, 0.04	0.83, 0.03
PMNet	0.80, 0.05	0.82, 0.04	0.87, 0.03	0.77, 0.05	0.81, 0.04	0.82, 0.04
MLDG-Seg	0.82, 0.05	0.79, 0.04	0.86, 0.03	0.79, 0.04	0.80, 0.03	0.81, 0.05
MetaMedSeg	0.80, 0.03	0.78, 0.06	0.85, 0.04	0.77, 0.06	0.81, 0.05	0.82, 0.04
iMAML	0.82, 0.06	0.82, 0.07	0.86, 0.03	0.80, 0.06	0.82, 0.04	0.84, 0.03
DCA-Net	0.80, 0.04	0.81, 0.05	0.85, 0.04	0.76, 0.06	0.80, 0.04	0.82, 0.05
DCAC	0.75, 0.06	0.77, 0.03	0.78, 0.04	0.74, 0.06	0.74, 0.07	0.76, 0.05
Ours	**0.87, 0.03**	**0.89, 0.04**	**0.92, 0.02**	**0.84, 0.04**	**0.88, 0.05**	**0.89, 0.05**

Table 4. Avg and std scores for Acc based on 10 random runs.

| Methods	Ki67 samples in inference (DSC, Acc)			ER samples in inference (DSC, Acc)		
	5%	10%	20%	5%	10%	20%
PANet	0.69, 0.07	0.70, 0.06	0.72, 0.06	0.63, 0.08	0.66, 0.08	0.68, 0.07
HSNet	0.69, 0.08	0.70, 0.09	0.74, 0.06	0.67, 0.06	0.71, 0.07	0.73, 0.06
DCAMA	0.72, 0.05	0.75, 0.06	0.78, 0.04	0.71, 0.07	0.74, 0.04	0.75, 0.06
AAformer	0.71, 0.07	0.74, 0.08	0.77, 0.04	0.70, 0.05	0.73, 0.05	0.75, 0.07
PATNet	0.74, 0.06	0.75, 0.05	0.78, 0.06	0.72, 0.06	0.75, 0.07	0.78, 0.05
PMNet	0.75, 0.06	0.76, 0.08	0.78, 0.06	0.71, 0.06	0.74, 0.06	0.76, 0.07
MLDG-Seg	0.71, 0.08	0.73, 0.06	0.75, 0.05	0.71, 0.09	0.73, 0.07	0.74, 0.07
MetaMedSeg	0.72, 0.06	0.72, 0.07	0.73, 0.05	0.69, 0.05	0.70, 0.07	0.72, 0.08
iMAML	0.75, 0.07	0.77, 0.05	0.81, 0.04	0.76, 0.05	0.78, 0.04	0.79, 0.05
DCA-Net	0.74, 0.04	0.76, 0.06	0.78, 0.05	0.70, 0.07	0.72, 0.08	0.75, 0.07
DCAC	0.71, 0.05	0.73, 0.05	0.74, 0.07	0.69, 0.07	0.70, 0.05	0.72, 0.06
Ours	**0.83, 0.04**	**0.84, 0.03**	**0.85, 0.03**	**0.83, 0.04**	**0.84, 0.06**	**0.86, 0.04**
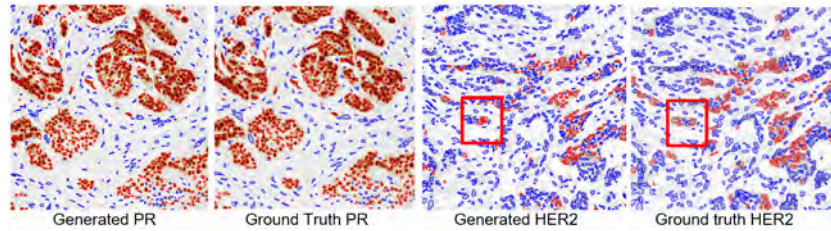
Fig. 2. Segmentation results of IHC+ (red) and IHC- (blue) cells on two different target stains (PR, HER2). Regions with inconsistent outputs are highlighted with red bounding boxes.