InstaSAM: Instance-aware Segment Any Nuclei Model with Point Annotations

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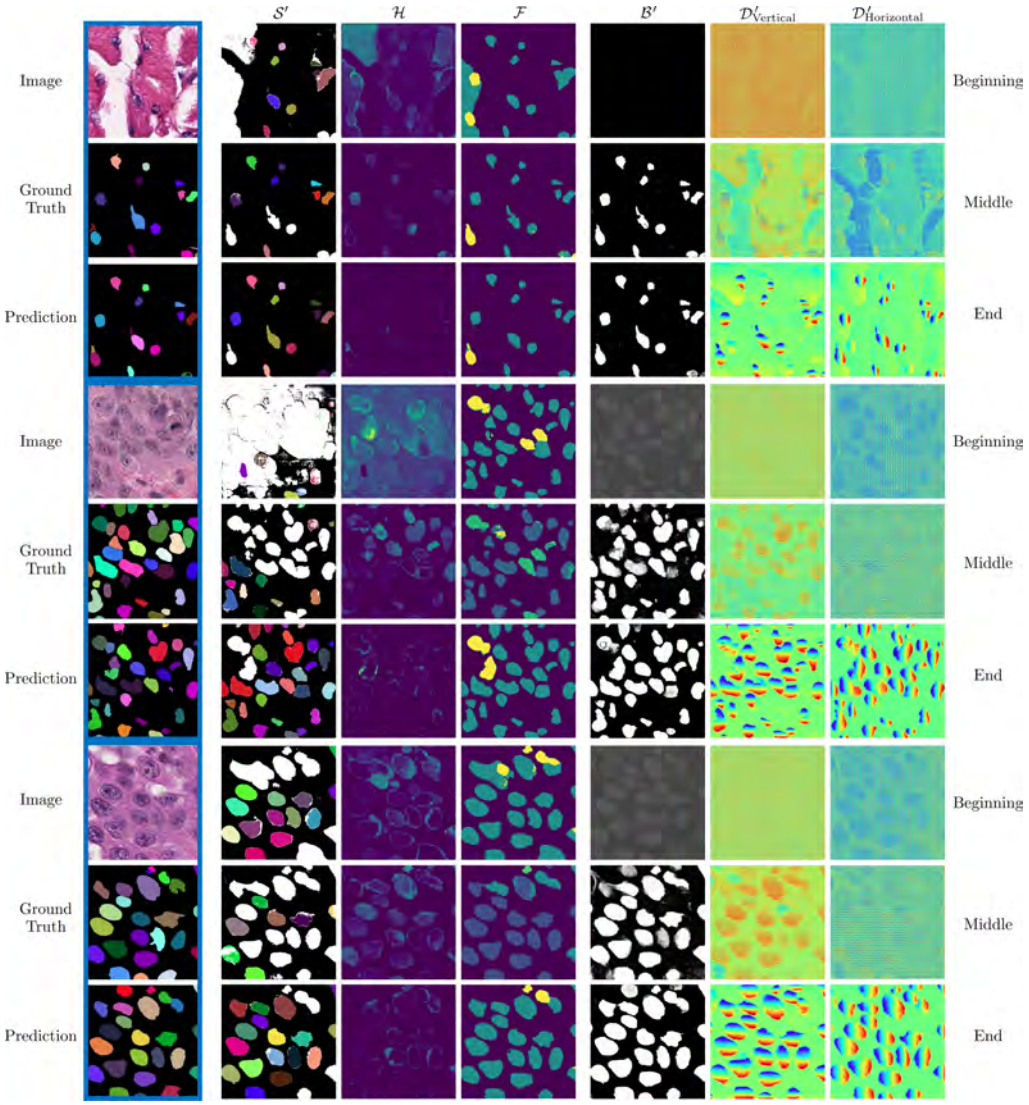

Fig. 1. The evolution of the pseudo instance map and the prediction maps. In the very beginning of train, the entropy map $\mathcal{H}$ and foreground map $\mathcal{F}$ have high value at tissue area. Since $\mathcal{H}$ and $\mathcal{F}$ predict tissue area as nuclei, the pseudo instance map $\mathcal{S}'$ refined with $\mathcal{H}$ and $\mathcal{F}$ is inaccurate. Similarly, the predictions of Nuclei Decoder, binary map $\mathcal{B}'$ and distance map $\mathcal{D}'$, miserable in both nuclei separation and nuclei/tissue separation. As InstaSAM gradually learns the difference between nuclei and tissue area, the high entropy of tissue area removed, and the separation of foreground and background also much clear compared to very beginning. At the end of the training, the high entropy area only limited to nuclei border and foreground map cleared background map completely.

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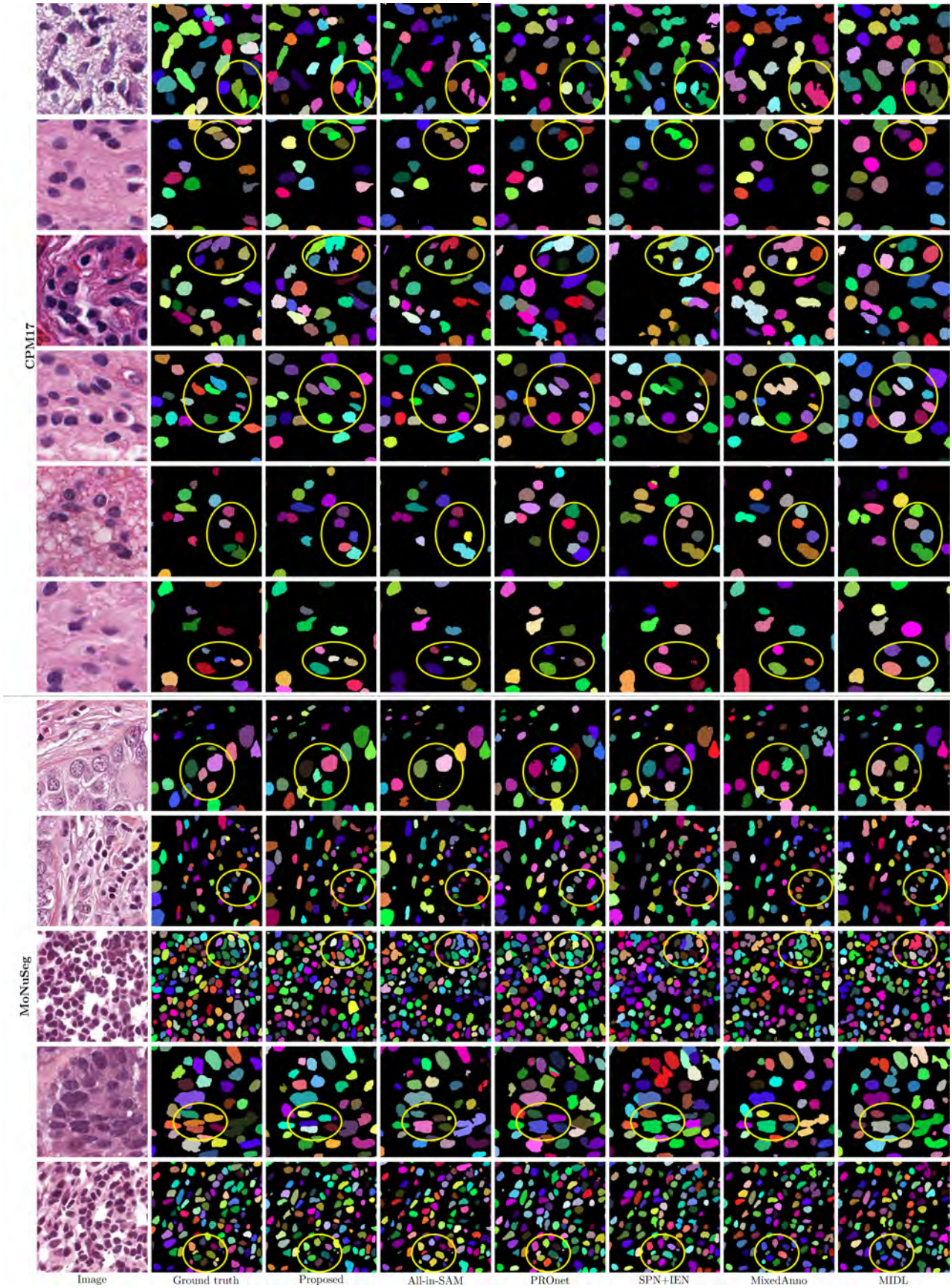

Fig. 2. Results for nuclei instance segmentation on the CPM17 and MoNuSeg datasets. All-in-SAM, MixedAnno, and MIDL methods have a common limitation for separating adjacent nuclei. SPN-IEN appears to perform well on the MoNuSeg dataset but exhibits numerous noisy predictions on the CPM17 data. PROnet, on the other hand, tends to segment all cells into round shapes, which is a significant limitation. InstaSAM successfully segments nuclei according to their actual shapes and achieves state-of-the-art performance.