

DoNet: Deep De-overlapping Network for Cytology Instance Segmentation

Hao Jiang^{1*}, Rushan Zhang^{1*}, Yanning Zhou², Yumeng Wang¹, Hao Chen¹



¹ The Hong Kong University of Science and Technology

² Tencent AI Lab



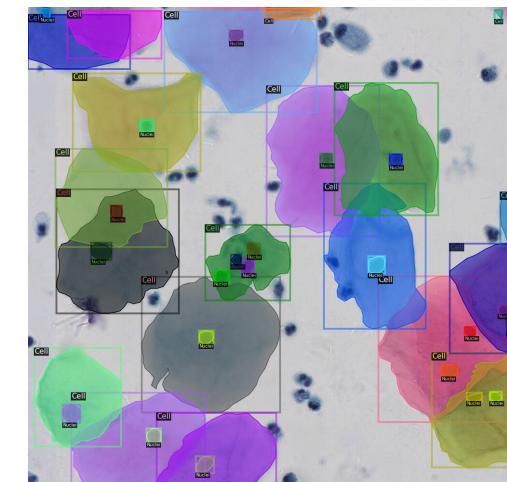
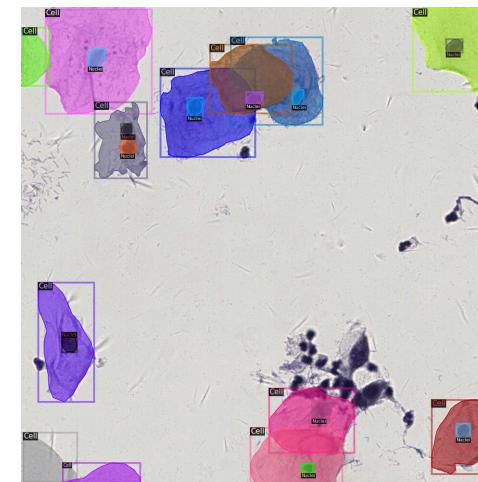
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Motivation

Cytology instance segmentation has been essential for cancer screening and earlier diagnosis, such as quantitative identification of cellular morphology, nuclei size, and nuclear-cytoplasmic ratio.

Challenges

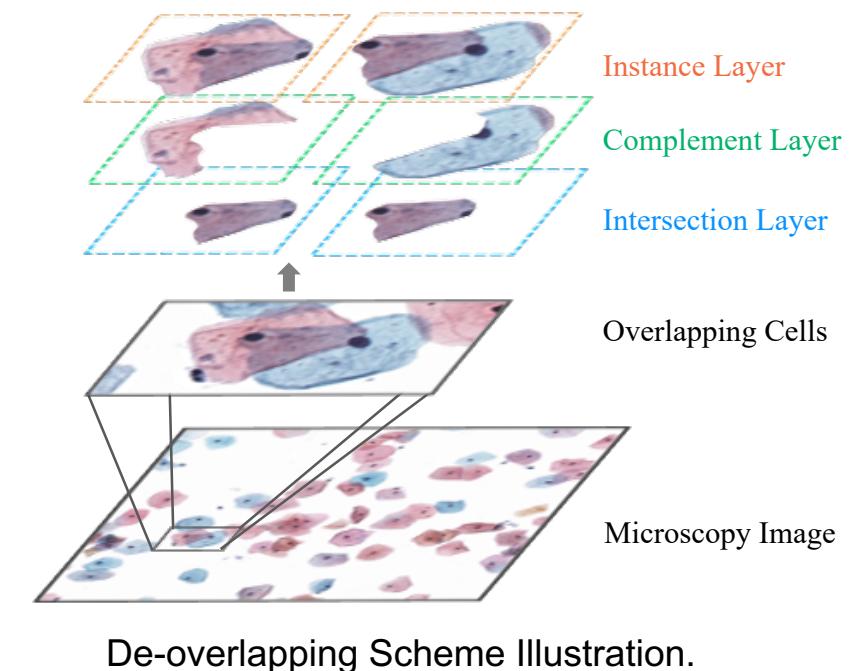
- The extensive **overlapping** translucent cell clusters that cause the ambiguous boundaries;
- The confusion of **mimics** and debris as nuclei.



Cytology Instance Segmentation.

Motivation

- Motivated by the amodal perception, we propose a **De-overlapping Network (DoNet)** in a **decompose-and-recombined** strategy.
- **Implicitly** learning the hidden interaction of sub-regions by predicting instance masks from clusters.
- **Explicitly** models the components and their relationships via the intersection layer, complement layer, and instance layer.

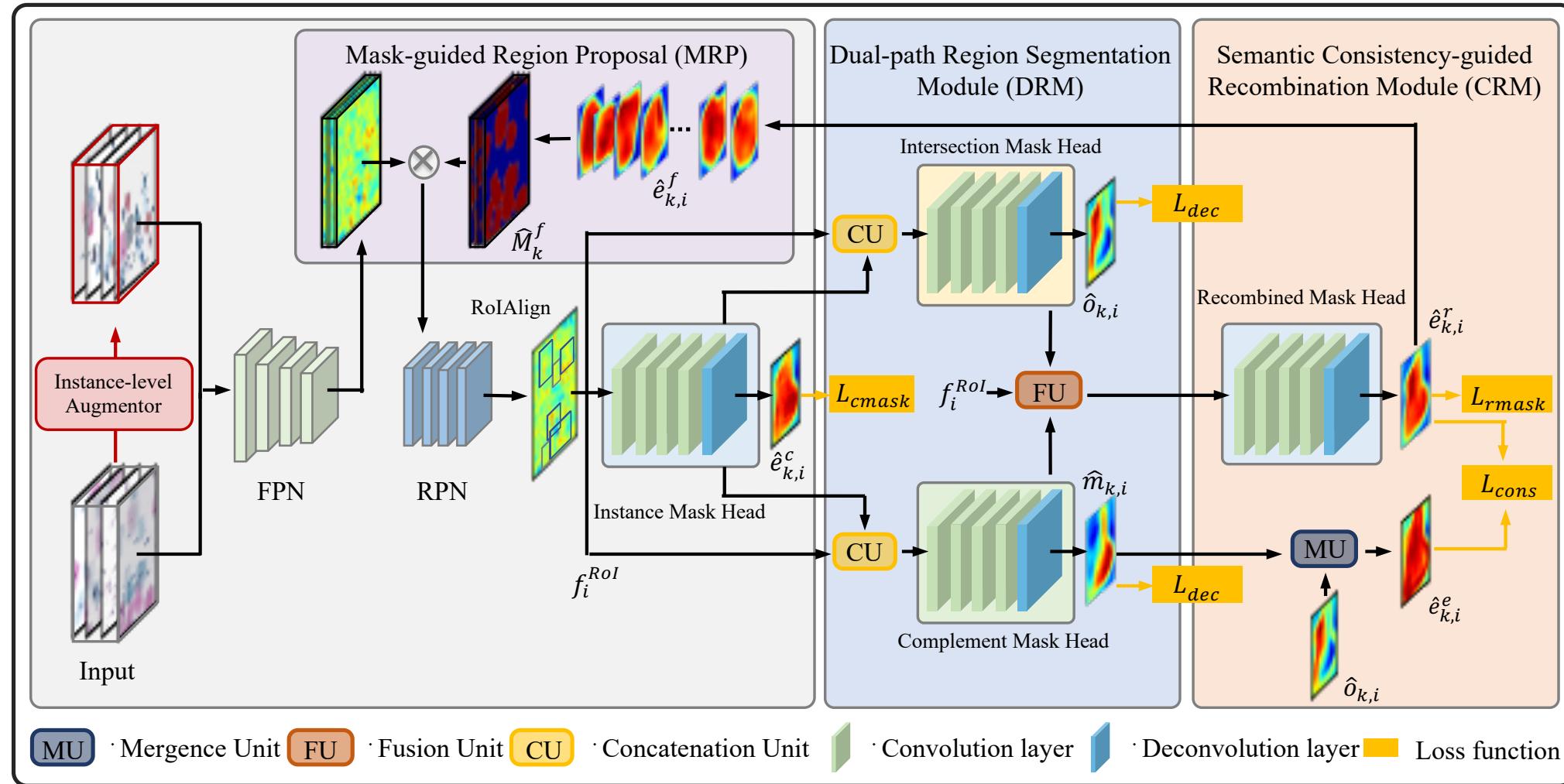


Problem formulation

- Given a cytology dataset $\{(\mathcal{X}_k, \mathcal{Y}_k)\}_{k=1}^K$, contain annotations of bounding boxes $\mathcal{B}_k = \{b_{k,i}\}_{i=1}^{N_k}$, object categories $\mathcal{C}_k = \{c_{k,i}\}_{i=1}^{N_k}$, and instance masks $\mathcal{E}_k = \{e_{k,i}\}_{i=1}^{N_k}$.
- Task: segmenting the nucleus and cytoplasm for cell instance.
- We decompose the instance mask annotations into the intersection region $\mathcal{O}_k = \{o_{k,i}\}_{i=1}^{N_k}$, and the complement region $\mathcal{M}_k = \{m_{k,i}\}_{i=1}^{N_k}$ via the logical operation.
- DoNet **decomposes** instance into intersection $\hat{o}_{k,i}$ and complement $\hat{m}_{k,i}$ via DRM, then **recombines** into instance $\hat{e}_{k,i}^r$ with consistency regularization via CRM, followed by background instance suppression via MRP.

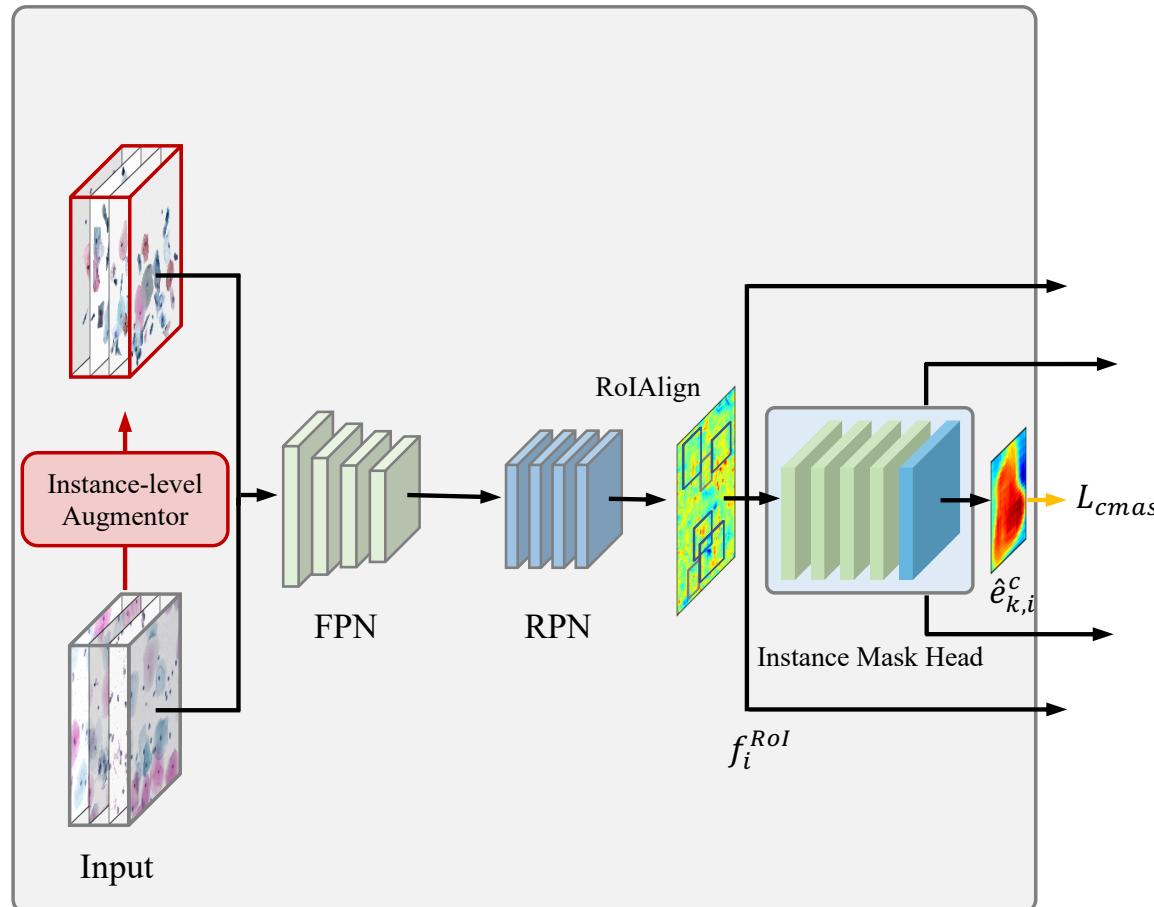
Method

DoNet consists of four parts: (1) Baseline; (2) DRM; (3) CRM; (4) MRP



Method

(1) Baseline: Mask R-CNN

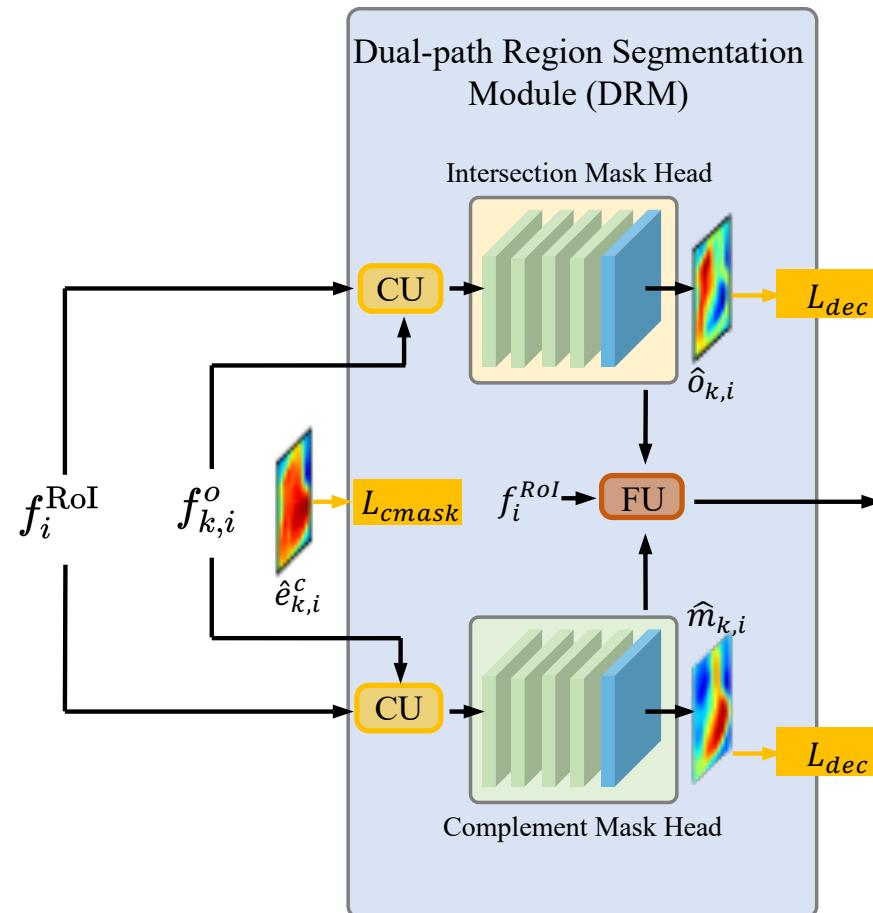


- Instance-level Augmentor
- **Instance Mask Head**
Coarse Mask Segmentation

$$\mathcal{L}_{\text{coarse}} = \mathcal{L}_{\text{reg}} + \mathcal{L}_{\text{cls}} + \mathcal{L}_{\text{cmask}}$$

Method

(2) DRM: Dual-path Region Segmentation Module

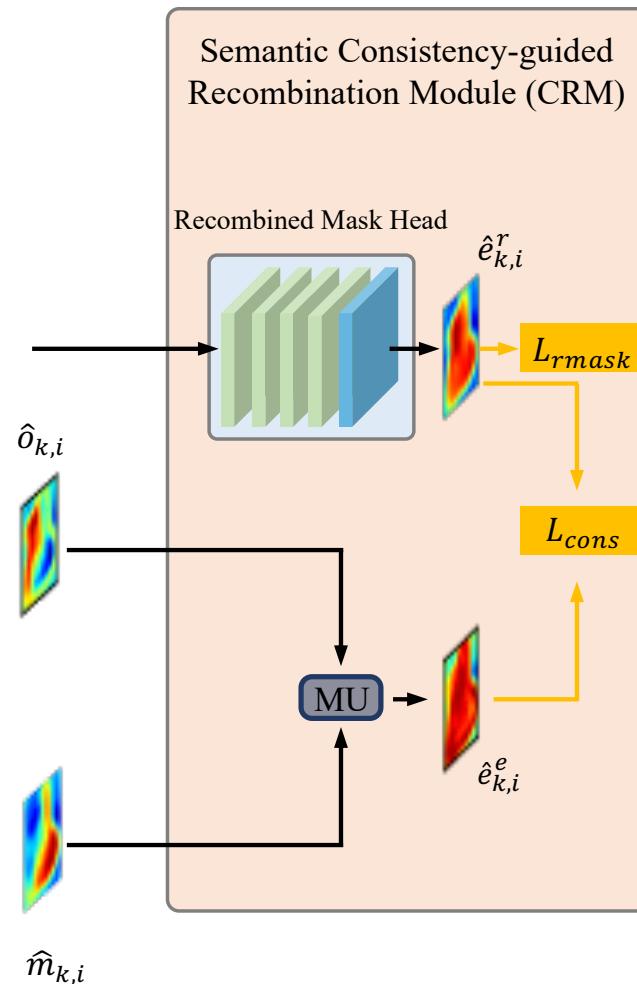


- **Intersection Mask Head**
 - **Complement Mask Head**
- Decomposition Loss

$$\mathcal{L}_{dec} = \frac{1}{K} \sum_{k=1}^K \frac{1}{N_k} \sum_{i=1}^{N_k} (\mathcal{L}_{ce}(\hat{o}_{k,i}, o_{k,i}) + \mathcal{L}_{ce}(\hat{m}_{k,i}, m_{k,i}))$$

Method

(3) CRM: Semantic Consistency-guided Recombination Module



- **Recombined Mask Head**
Recombination loss

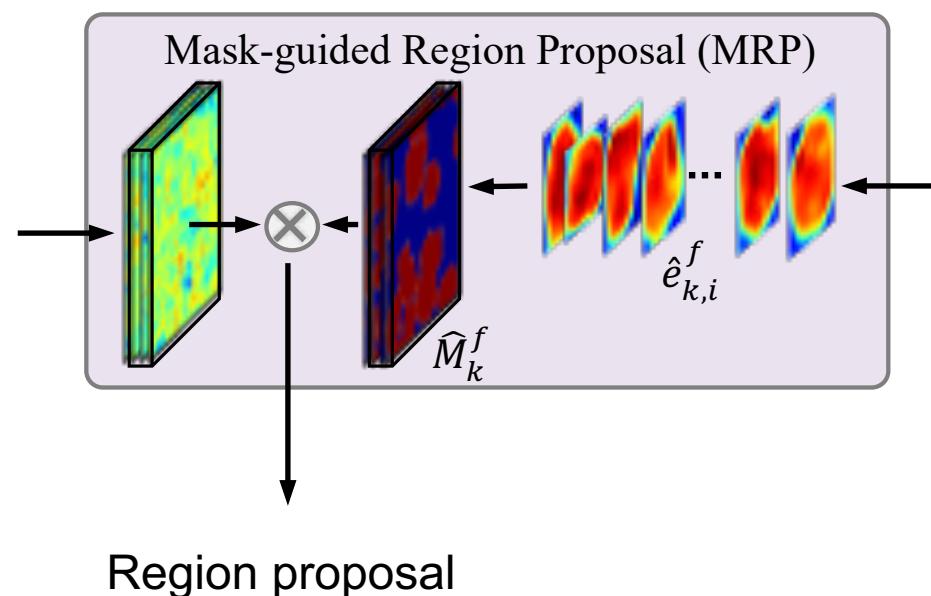
$$\mathcal{L}_{rmask} = \frac{1}{K} \sum_{k=1}^K \frac{1}{N_k} \sum_{i=1}^{N_k} \mathcal{L}_{ce}(\hat{e}_{k,i}^r, e_{k,i})$$

Semantic consistency regularization

$$\mathcal{L}_{cons} = \frac{1}{K} \sum_{k=1}^K \frac{1}{N_k} \sum_{i=1}^{N_k} \mathcal{L}_{ce}(\hat{e}_{k,i}^r, \mathcal{F}_{\text{merge}}(\hat{o}_{k,i}, \hat{m}_{k,i}))$$

Method

(3) MRP: Mask-guided Region Proposal



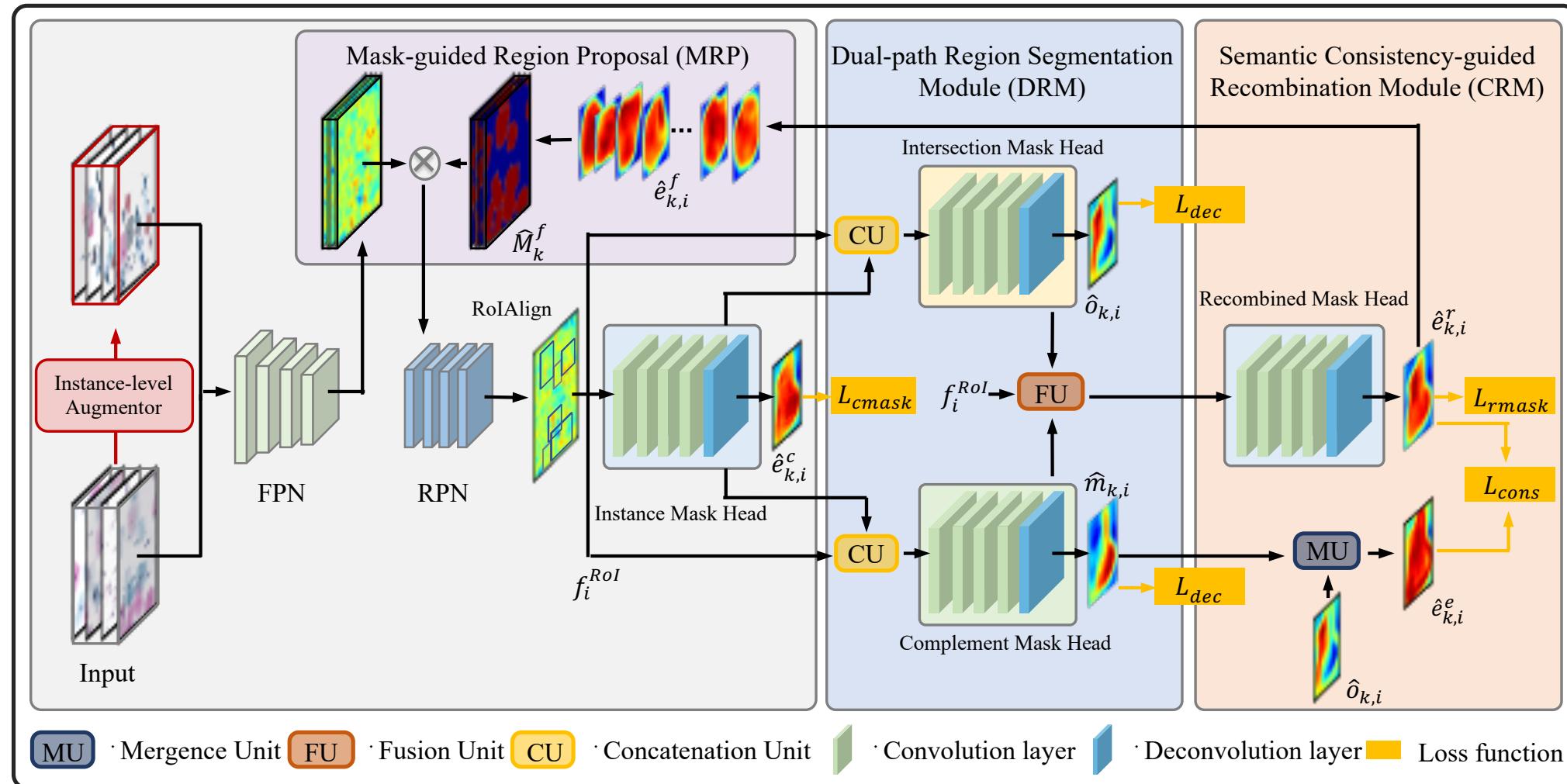
Encourage the model to generate nuclei proposals in intra-cellular regions

Re-weight for nuclei region proposal

$$f_k^w = \hat{M}_k \circ f_k$$

Method

DoNet consists of four parts: (1) Baseline; (2) DRM; (3) CRM; (4) MRP



Experiments

Dataset

- **ISBI2014** (*Overlapping Cervical Cytology Image Segmentation Challenge*), real and corresponding synthetic cervical cytology images (945 totally, split and train following the challenge settings).
- **CPS**, liquid-based cytology dataset contains 137 labeled images (4439 cytoplasm and 4789 nuclei annotations, 3 fold cross validation).

Evaluation metrics

- Aggregated Jaccard index (AJI)
- Average Dice coefficient (Dice)
- F1-score (F1)
- Mean of Average Precision (mAP)

Experiments

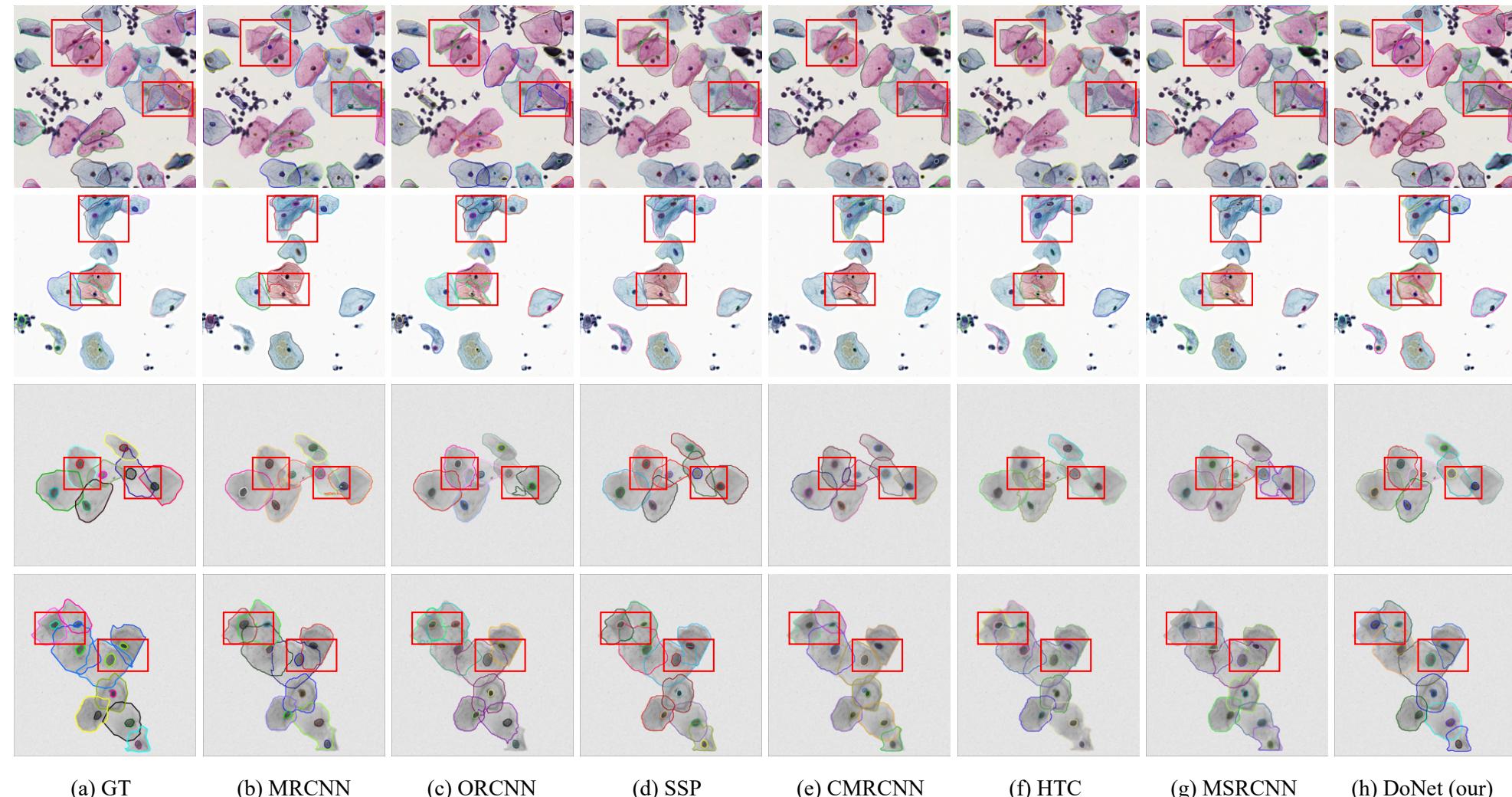
Quantitative results

Table 1. Quantitative segmentation results of DoNet and other state-of-the-art methods on CPS and ISBI2014.

Methods	ISBI2014				CPS			
	mAP↑	Dice↑	F1↑	AJI↑	mAP↑	Dice↑	F1↑	AJI↑
Mask R-CNN [11]	59.09	91.15	92.54	77.07	48.28 ± 3.10	89.32 ± 0.50	85.07 ± 2.01	69.20 ± 2.27
Cascade R-CNN [2]	62.45	91.29	92.51	77.91	47.87 ± 3.27	89.24 ± 0.44	83.33 ± 1.65	68.86 ± 3.55
Mask Scoring R-CNN [13]	63.56	91.28	91.87	75.14	48.38 ± 3.13	89.39 ± 0.24	82.98 ± 1.86	67.45 ± 2.45
HTC [8]	59.62	91.39	88.08	75.00	47.60 ± 3.56	89.08 ± 0.51	81.30 ± 2.56	66.35 ± 2.84
Occlusion R-CNN [9]	62.35	91.75	93.18	78.64	48.14 ± 2.84	89.08 ± 0.28	85.69 ± 2.28	69.51 ± 2.45
Xiao et al. [37]	57.34	91.70	92.75	78.29	48.53 ± 2.85	89.29 ± 0.24	85.46 ± 2.60	69.37 ± 2.88
DoNet	64.02	92.13	93.23	79.05	49.43 ± 3.83	89.54 ± 0.25	85.51 ± 2.33	70.08 ± 2.84
DoNet w/ Aug.	-	-	-	-	49.65 ± 3.52	89.50 ± 0.38	86.30 ± 2.01	70.56 ± 2.34

Experiments

Visualization



Experiments

Ablation: effect of proposed modules

Table 3. Effect of each proposed module on CPS and ISBI2014 datasets. ✓ denotes adding the corresponding module.

Base	DRM	CRM	MRP	ISBI2014				CPS			
				mAP↑	Dice↑	F1↑	AJI↑	mAP↑	Dice↑	F1↑	AJI↑
✓				59.09	91.15	92.54	77.07	48.28 ± 3.10	89.32 ± 0.50	85.07 ± 2.01	69.20 ± 2.27
✓	✓			61.01	91.61	92.86	78.06	48.03 ± 3.48	89.13 ± 0.30	84.63 ± 2.57	68.56 ± 2.57
✓	✓	✓		63.43	91.87	94.16	79.88	49.12 ± 3.26	89.47 ± 0.31	84.82 ± 2.73	69.26 ± 2.63
✓	✓	✓	✓	64.02	92.13	93.23	79.05	49.43 ± 3.83	89.54 ± 0.25	85.51 ± 2.33	70.08 ± 2.84

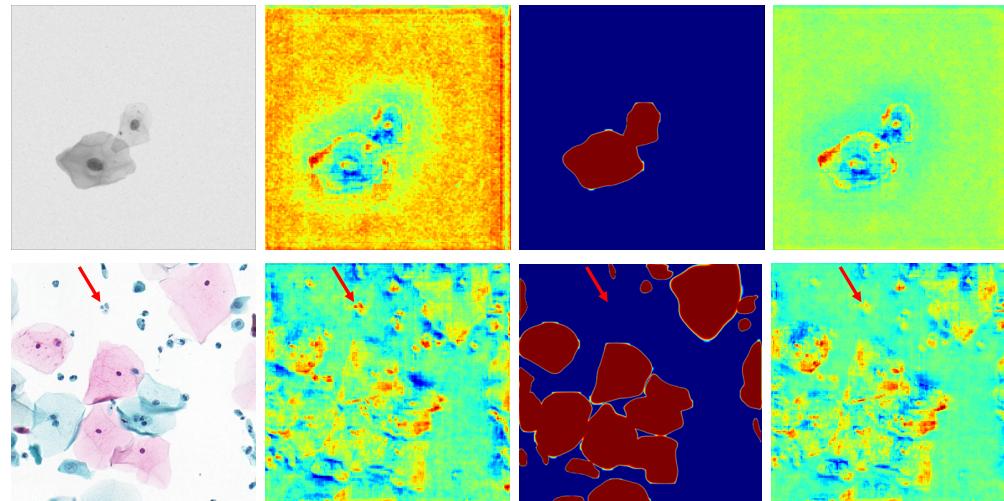
Ablation: effect of proposed components

Table 4. Ablation study of DRM and CRM on the ISBI2014 dataset. ✓ denotes adding the corresponding component or strategy.

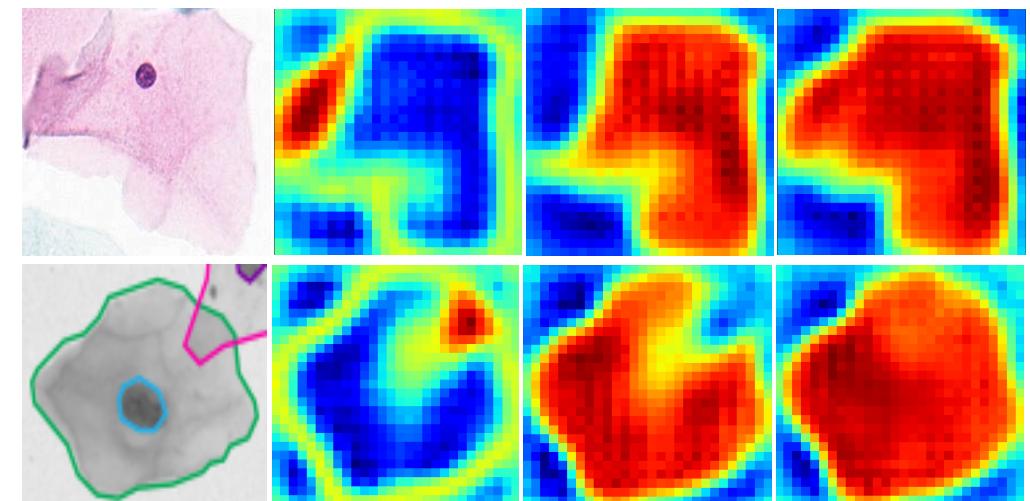
H_i	H_o	H_m	FU	\mathcal{L}_{cons}	mAP↑			Dice↑			F1↑			AJI↑		
					Cyt.	Nuc.	Avg.									
✓					50.71	67.46	59.09	90.72	91.59	91.15	86.96	98.13	92.54	70.55	83.60	77.07
✓	✓				54.84	65.94	60.39	91.56	91.54	91.55	87.00	97.68	92.34	72.07	82.67	77.37
✓	✓	✓			57.41	66.49	61.95	91.79	91.53	91.66	88.67	97.98	93.32	74.00	83.27	78.63
✓	✓	✓	✓		58.40	67.82	63.11	92.22	91.74	91.98	89.21	98.07	93.64	74.94	83.70	79.32
✓	✓	✓	✓	✓	59.31	67.56	63.43	92.03	91.71	91.87	90.13	98.18	94.16	75.86	83.91	79.88

Experiments

Noise suppression in MRP



Heatmaps of cellular regions



Comparisons of instance segmentation methods



baseline

Multi-task

Amodal

DoNet