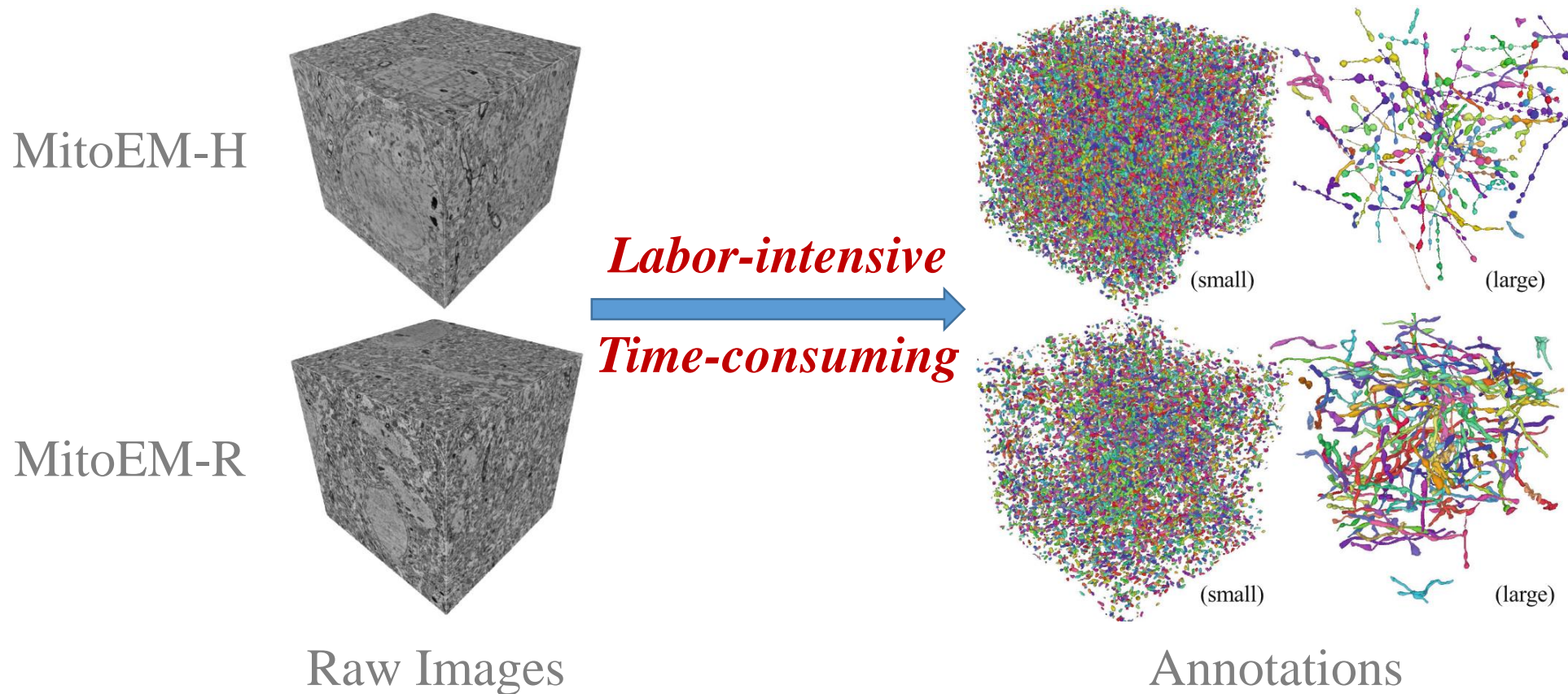# Domain Adaptive Mitochondria Segmentation via Enforcing Inter-Section Consistency

Wei Huang[1], Xiaoyu Liu[1], Zhen Cheng[1], Yueyi Zhang[1,2], and Zhiwei Xiong[1,2(✉)]

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➤ **Sufficient annotations are expensive**

MitoEM-H

MitoEM-R

Labor-intensive

Time-consuming

(small)   (large)

(small)   (large)

Raw Images

Annotations

Wei, D., Lin, Z., Franco-Barranco, D., Wendt, N., Liu, X., Yin, W., Huang, X., Gupta, A., Jang, W.D., Wang, X., et al.: Mitoem dataset: large-scale 3d mitochondria instance segmentation from em images. In: MICCAI (2020)

➤ **Sufficient annotations are expensive**

How to mitigate the burden of manual annotation?

Is it possible to avoid labeling a new dataset (target) by exploiting the labeled dataset (source)?

Wei, D., Lin, Z., Franco-Barranco, D., Wendt, N., Liu, X., Yin, W., Huang, X., Gupta, A., Jang, W.D., Wang, X., et al.: Mitoem dataset: large-scale 3d mitochondria instance segmentation from em images. In: MICCAI (2020)

➢ **An intuitive solution**

- Training on the source dataset and directly testing on the target dataset

Source dataset with labels

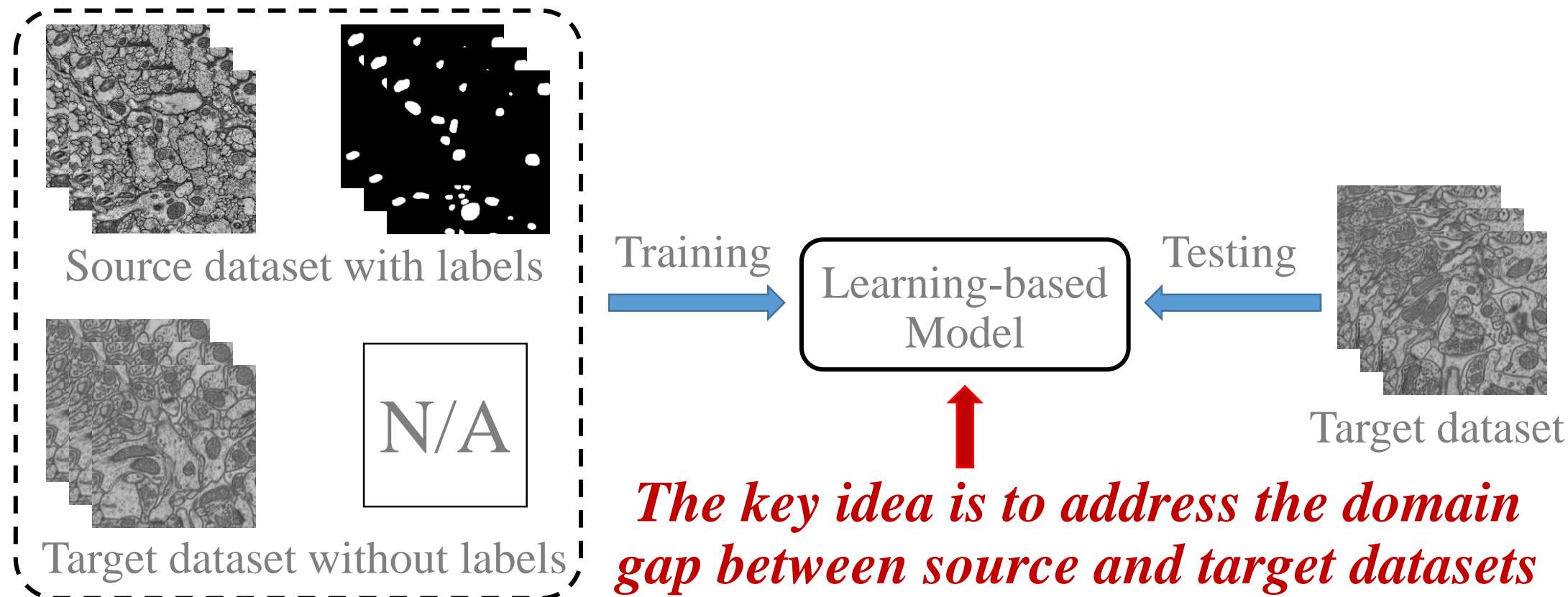Training

Learning-based Model

Testing
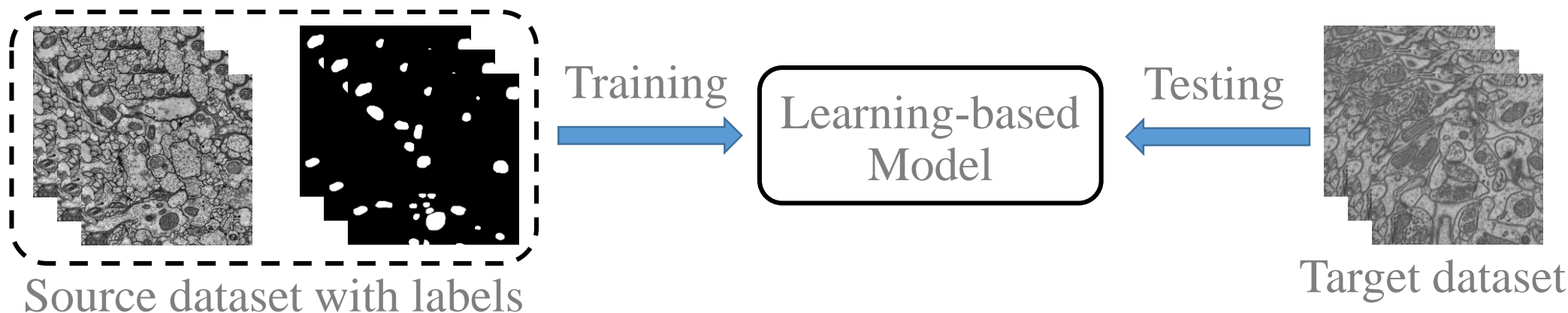
Target dataset

➢ **Domain gap between source and target datasets**

- **Intra-section gap**: different shapes and distributions of mitochondria within an individual section

- **Inter-section gap**: the shape and distribution variation of mitochondria across sections

Limited generalizability for supervised methods on the target dataset

➢ **Domain Adaptive learning**

Source dataset with labels

Target dataset without labels

N/A

Training

Learning-based
Model

Testing

Target dataset

*The key idea is to address the domain
gap between source and target datasets*
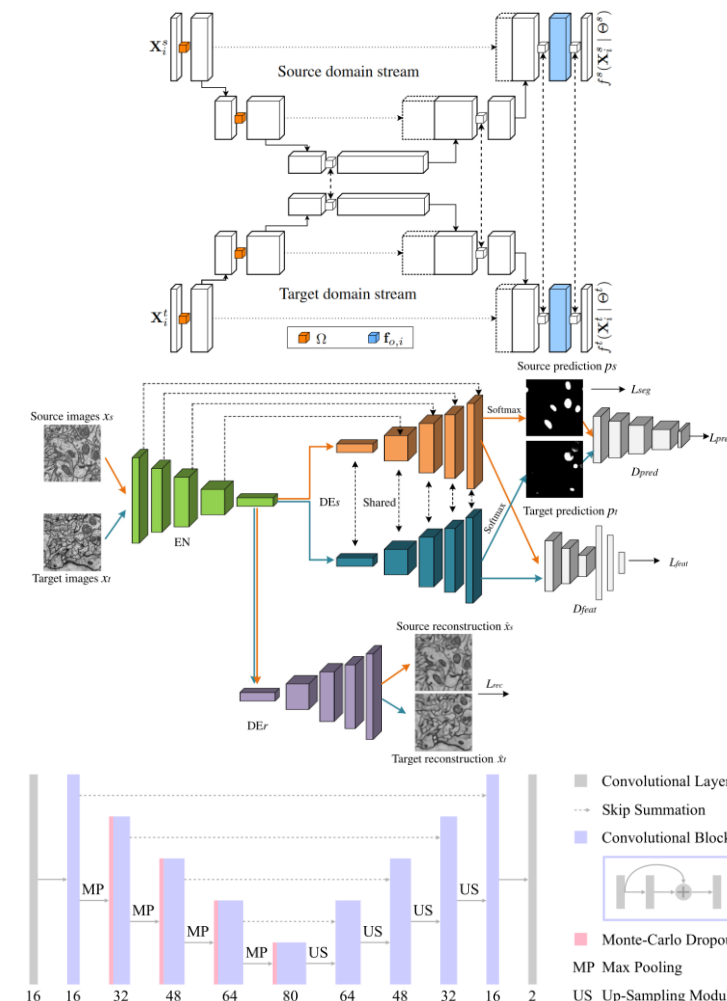
➢ **Statistical distance metrics [1]**

- Minimize the maximum mean discrepancy (MMD)

➢ **Domain-adversarial learning [2]**

- Align the distribution of features and outputs
- Reconstruct the target images

➢ **Pseudo-labeling [3]**

- Rectify pseudo labels via an uncertainty-aware model

[1] Bermúdez-Chacón, R., Márquez-Neila, P., Salzmann, M., Fua, P.: A domain-adaptive two-stream u-net for electron microscopy image segmentation. In: ISBI (2018)
[2] Peng, J., Yi, J., Yuan, Z.: Unsupervised mitochondria segmentation in em images via domain adaptive multi-task learning. IEEE Journal of Selected Topics in Signal Processing 14(6), 1199–1209 (2020)
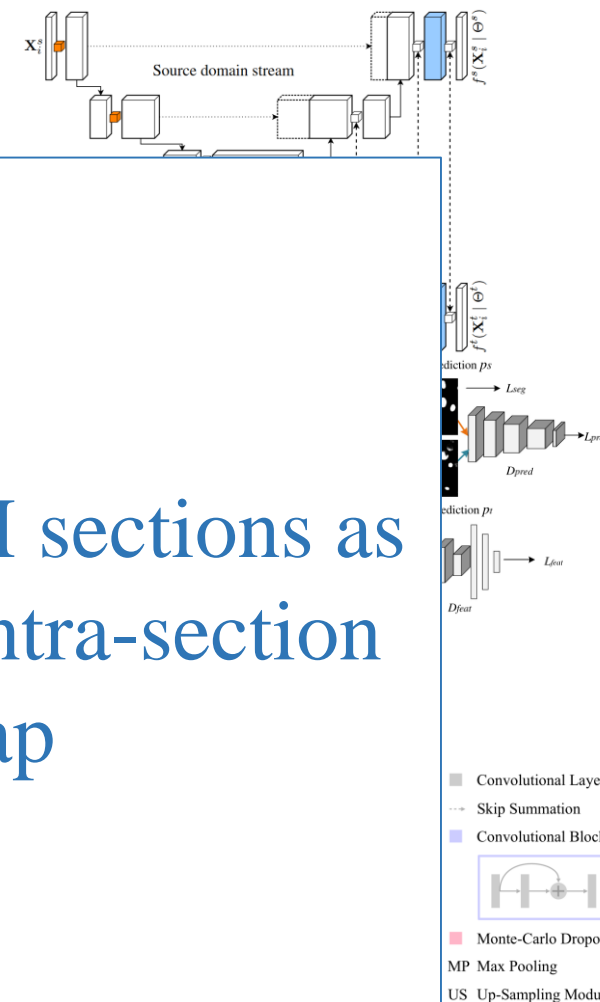[3] Wu, S., Chen, C., Xiong, Z., Chen, X., Sun, X.: Uncertainty-aware label rectification for domain adaptive mitochondria segmentation. In: MICCAI (2021)

➢ **Statistical distance metrics [1]**

-

➢ **D**

-
-

➢ **Ps**

-

However, these methods view sequential EM sections as independent images and only consider the intra-section gap, but ignore the inter-section gap

Convolutional Layer
Skip Summation
Convolutional Block

Monte-Carlo Dropout
MP Max Pooling
US Up-Sampling Module

[1] Bern
image se
[2] Peng, J., Yi, J., Yuan, Z.: Unsupervised mitochondria segmentation in em images via domain adaptive multi-task learning. IEEE Journal of Selected Topics in Signal Processing 14(6), 1199–1209 (2020)
[3] Wu, S., Chen, C., Xiong, Z., Chen, X., Sun, X.: Uncertainty-aware label rectification for domain adaptive mitochondria segmentation. In: MICCAI (2021)

How to describe the inter-section distribution?

Our answer is the inter-section residual

Adjacent labels   XOR logical operation   Inter-section residual
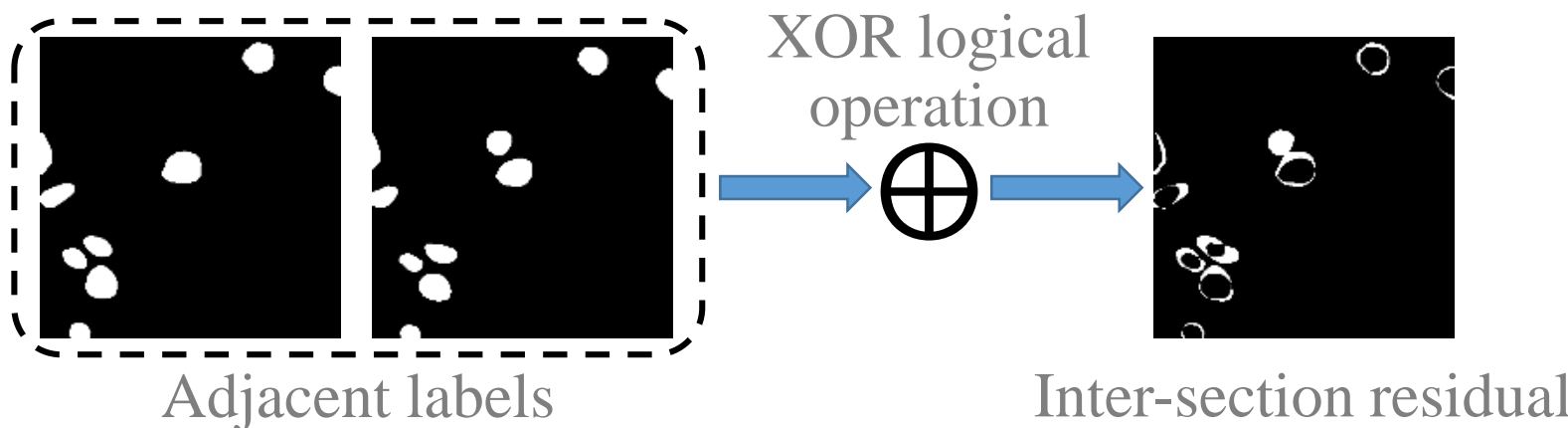
How to address the inter-section gap and maintain the inter-section consistency?

➢ **Motivations:**

- Describe the inter-section distribution
- Align the inter-section distribution between source and target datasets
- Enforce the inter-section consistency on the target dataset

➢ **Overall architecture**

  ➢ Prediction consistency
  ➢ Inter-section consistency
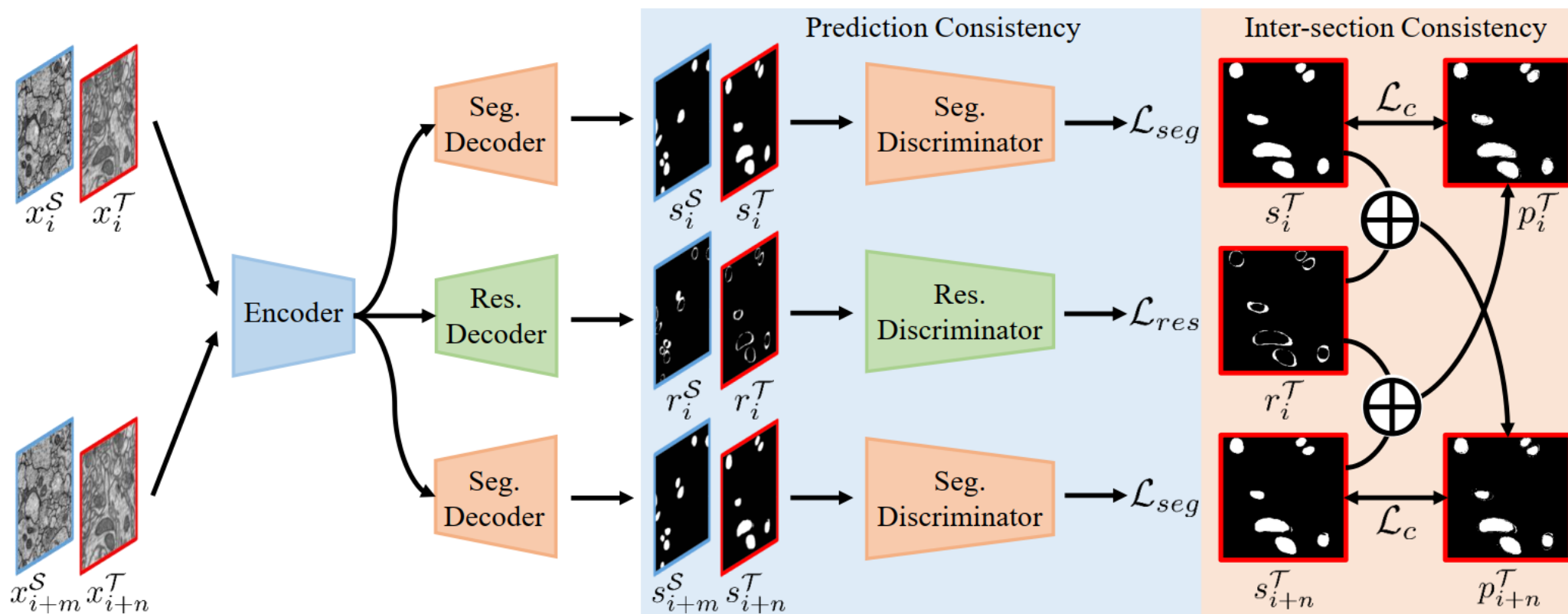
➤ **Overall architecture**
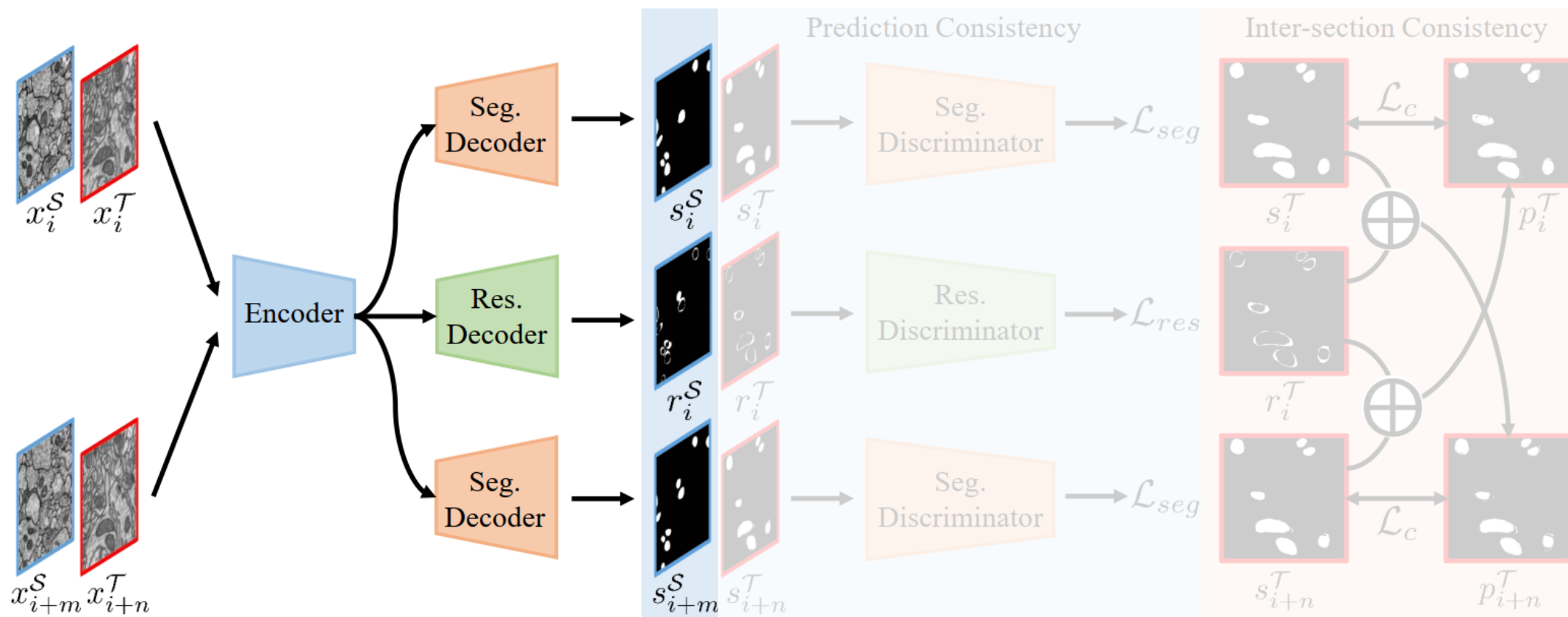
Supervised loss for the source domain: $\mathcal{L}_s = CE(s_i^{\mathcal{S}}, y_i^{\mathcal{S}}) + CE(s_{i+m}^{\mathcal{S}}, y_{i+m}^{\mathcal{S}}) + CE(r_i^{\mathcal{S}}, g_i^{\mathcal{S}})$.

➤ **Overall architecture**
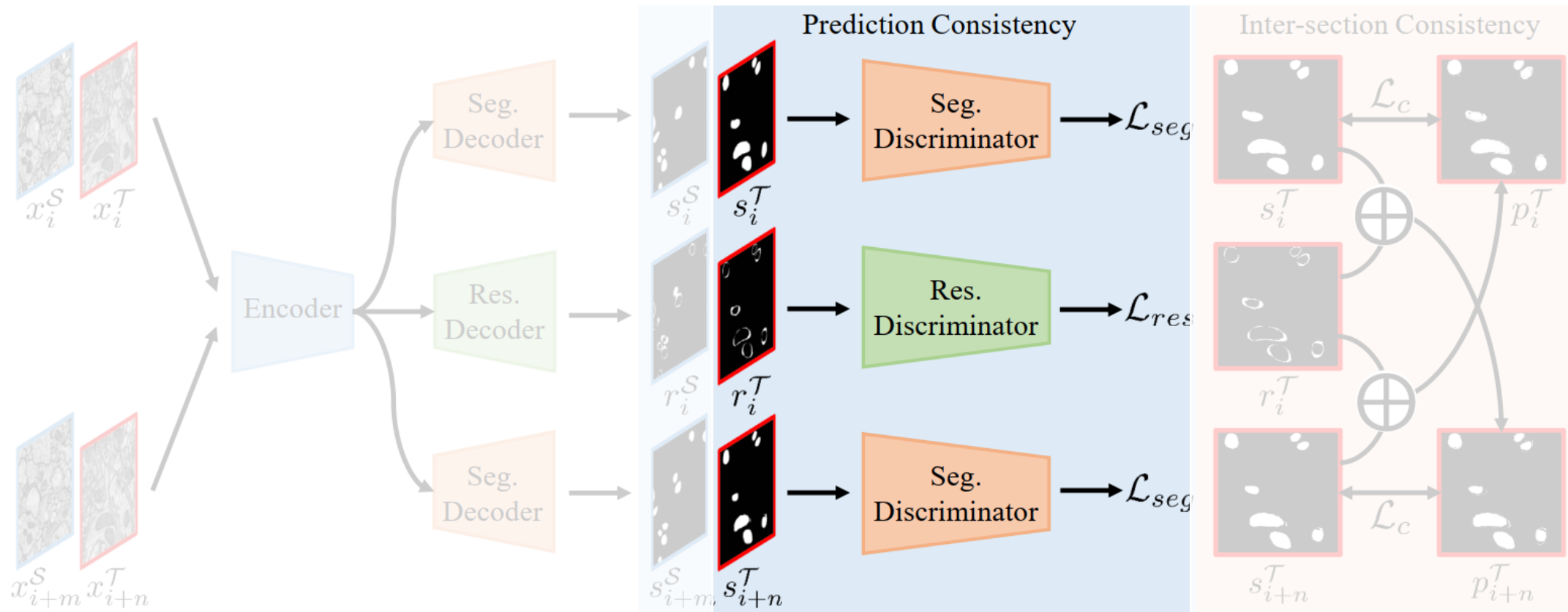
Align the intra-section and inter-section distribution via adversarial loss:

$$\mathcal{L}_{seg} = log(\mathbb{D}_{seg}(s_i^{\mathcal{S}})) + log(1 - \mathbb{D}_{seg}(s_i^{\mathcal{T}}))$$
$$+ log(\mathbb{D}_{seg}(s_{i+m}^{\mathcal{S}})) + log(1 - \mathbb{D}_{seg}(s_{i+n}^{\mathcal{T}})).$$
$$\mathcal{L}_{res} = log(\mathbb{D}_{res}(r_i^{\mathcal{S}})) + log(1 - \mathbb{D}_{res}(r_i^{\mathcal{T}})).$$

➢ **Overall architecture**

Enforce the inter-section consistency on the target domain via consistency loss:

$$p_i^{\mathcal{T}} = s_{i+n}^{\mathcal{T}} \oplus r_i^{\mathcal{T}} \quad p_{i+n}^{\mathcal{T}} = s_i^{\mathcal{T}} \oplus r_i^{\mathcal{T}}$$
$$\mathcal{L}_c = CE(s_i^{\mathcal{T}}, p_i^{\mathcal{T}}) + CE(s_{i+n}^{\mathcal{T}}, p_{i+n}^{\mathcal{T}}).$$

➢ **Datasets**

- VNC III [1]
- Lucchi [2]
- MitoEM-R [3]
- MitoEM-H [3]

➢ **Metrics**

- mean Average Precision (mAP)
- F1 score
- Mattews Correlation Coefficient (MCC)
- Intersection over Union (IoU)

Name	VNC III	Lucchi	MitoEM-R	MitoEM-H
Organism	Drosophila	Mouse	Rat	Human
Tissue	Ventral nerve cord	Hippocampus	Cortex	Cortex
Device	ssTEM	FIB-SEM	mbSEM	mbSEM
Resolution	$50 \times 5 \times 5$ nm	$5 \times 5 \times 5$ nm	$30 \times 8 \times 8$ nm	$30 \times 8 \times 8$ nm
Training set	$20 \times 1024 \times 1024$	$165 \times 768 \times 1024$	$400 \times 4096 \times 4096$	$400 \times 4096 \times 4096$
Test set	-	$165 \times 768 \times 1024$	$100 \times 4096 \times 4096$	$100 \times 4096 \times 4096$

[1] Gerhard, S., Funke, J., Martel, J., Cardona, A., Fetter, R.: Segmented anisotropic sstem dataset of neural tissue. Figshare pp. 0–0 (2013)
[2] Lucchi, A., Li, Y., Fua, P.: Learning for structured prediction using approximate subgradient descent with working sets. In: CVPR (2013)
[3] Wei, D., Lin, Z., Franco-Barranco, D., Wendt, N., Liu, X., Yin, W., Huang, X., Gupta, A., Jang, W.D., Wang, X., et al.: Mitoem dataset: large-scale 3d mitochondria instance segmentation from em images. In: MICCAI (2020)

➤ **Quantitative comparisons on the Lucchi and MitoEM datasets**

Methods	VNC III → Lucchi (Subset1)				VNC III → Lucchi (Subset2)			
	mAP(%)	F1(%)	MCC(%)	IoU(%)	mAP(%)	F1(%)	MCC(%)	IoU(%)
Oracle	-	92.7	-	86.5	-	93.9	-	88.6
NoAdapt	-	57.3	-	40.3	-	61.3	-	44.3
Y-Net [19]	-	68.2	-	52.1	-	71.8	-	56.4
DANN [3]	-	68.2	-	51.9	-	74.9	-	60.1
AdaptSegNet [22]	-	69.9	-	54.0	-	79.0	-	65.5
UALR [24]	80.2	72.5	71.2	57.0	87.2	78.8	77.7	65.2
DAMT-Net [18]	-	74.7	-	60.0	-	81.3	-	68.7
DA-VSN [5]	82.8	75.2	73.9	60.3	91.3	83.1	82.2	71.1
Ours	**89.5**	**81.3**	**80.5**	**68.7**	**92.4**	**85.2**	**84.5**	**74.3**

Methods	MitoEM-R → MitoEM-H				MitoEM-H → MitoEM-R			
	mAP(%)	F1(%)	MCC(%)	IoU(%)	mAP(%)	F1(%)	MCC(%)	IoU(%)
Oracle	97.0	91.6	91.2	84.5	98.2	93.2	92.9	87.3
NoAdapt	74.6	56.8	59.2	39.6	88.5	76.5	76.8	61.9
UALR [24]	90.7	83.8	83.2	72.2	92.6	86.3	85.5	75.9
DAMT-Net [18]	92.1	84.4	83.7	73.0	94.8	86.0	85.7	75.4
DA-VSN [5]	91.6	83.3	82.6	71.4	94.5	86.7	86.3	76.5
Ours	**92.6**	**85.6**	**84.9**	**74.8**	**96.8**	**88.5**	**88.3**	**79.4**

➢ **Qualitative comparisons on Lucchi and MitoEM datasets**
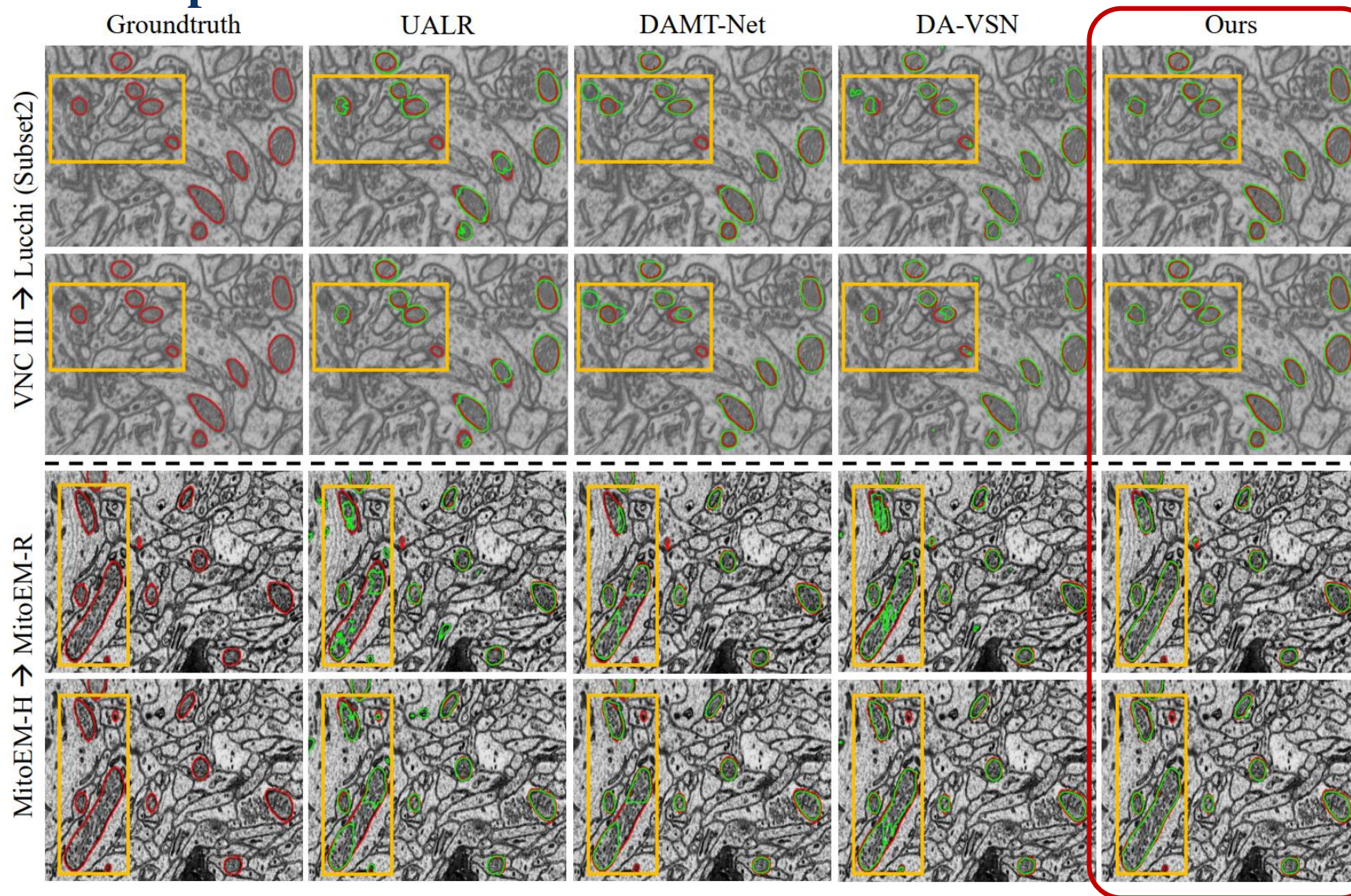
➤ **Ablation results for the effectiveness of each loss term**

VNC III → Lucchi (Subset1)

Settings	$\mathcal{L}_s$	$\mathcal{L}_{seg}$	$\mathcal{L}_{res}$	$\mathcal{L}_c$	mAP(%)	F1(%)	MCC(%)	IoU(%)
i	✓				76.0	68.0	66.7	51.9
ii	✓	✓			80.9	72.5	71.2	57.1
iii	✓		✓		81.1	73.6	72.4	58.8
iv	✓	✓	✓		84.4	74.5	73.3	59.6
v	✓	✓	✓	✓	**89.5**	**81.3**	**80.5**	**68.7**

➤ Propose the inter-section residual to describe the inter-section distribution of EM images

➤ Address both the intra-section and inter-section gap between source and target domains simultaneously

➤ Enforce the inter-section consistency on the target domain using the aligned inter-section residual

Thanks for your listening!