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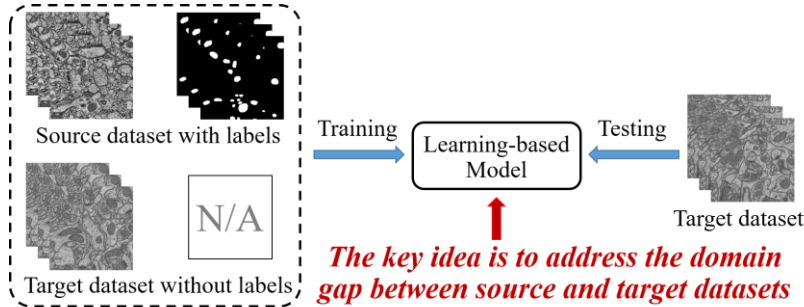[1] University of Science and Technology of China,   [2] Institute of Artificial Intelligence, Hefei Comprehensive National Science Center

Introduction

Domain adaptive learning

➢ Avoid labeling a new dataset (target) by exploiting the labeled dataset (source)

*The key idea is to address the domain gap between source and target datasets*

Domain gap

➢ **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

However, existing domain adaptation methods only consider the intra-section gap but ignore the inter-section gap
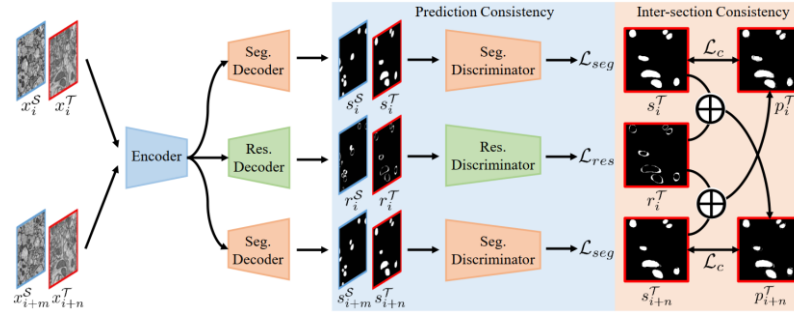
Contributions

➢ Propose the *inter-section residual* to describe the inter-section distribution
➢ Align the intra-section and inter-section distribution between source and target datasets simultaneously
➢ Enforce the inter-section consistency on the target dataset

Adjacent labels   Inter-section residual
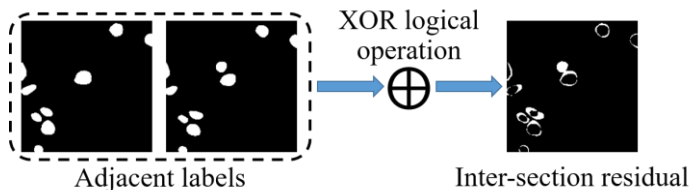
Method

Overall Pipeline

➢ Predict the segmentation results and the inter-section residual maps simultaneously using a CNN
➢ Align the intra-section and inter-section distribution between source and target domains via adversarial learning
➢ Enforce inter-section consistency on the target domain by the aligned inter-section residual map

Loss Function

Supervised loss: $\mathcal{L}_s = CE(s_i^{\mathcal{S}}, y_i^{\mathcal{S}}) + CE(s_{i+m}^{\mathcal{S}}, y_{i+m}^{\mathcal{S}}) + CE(r_i^{\mathcal{S}}, g_i^{\mathcal{S}})$.

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

Consistency loss: $\mathcal{L}_c = CE(s_i^{\mathcal{T}}, p_i^{\mathcal{T}}) + CE(s_{i+n}^{\mathcal{T}}, p_{i+n}^{\mathcal{T}})$.
$$\mathcal{L}_{total} = \alpha\mathcal{L}_s + \beta(\mathcal{L}_{seg} + \mathcal{L}_{res}) + \gamma\mathcal{L}_c,$$

Four representative and diverse EM datasets

Name	VNC III [4]	Lucchi [13]	MitoEM-R [23]	MitoEM-H [23]
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	-	$165 \times 768 \times 1024$	$100 \times 4096 \times 4096$	$100 \times 4096 \times 4096$

Evaluation

Quantitative and qualitative comparisons

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**

Groundtruth   UALR   DAMT-Net   DA-VSN   Ours