

Adversarial Domain Adaptation for Cell Segmentation

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Introduction

- In Cell Segmentation problem, we want to segment the **cells** (nuclei) from the **background**

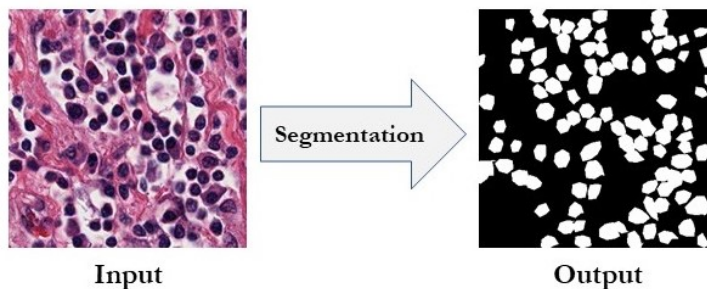


Figure: Cell Segmentation

- To successfully train a cell segmentation network in **fully-supervised** manner, we need **ground-truth annotations** of a dataset
- However, such annotated dataset is highly unavailable because
 - labeling process is **tedious**
 - it requires **domain experts** (pathologists)
 - it is **expensive**

Proposed solution

- We observed that, **images from different cell datasets/organs exhibit dissimilarity while their corresponding segmentation ground-truth labels are quite similar**

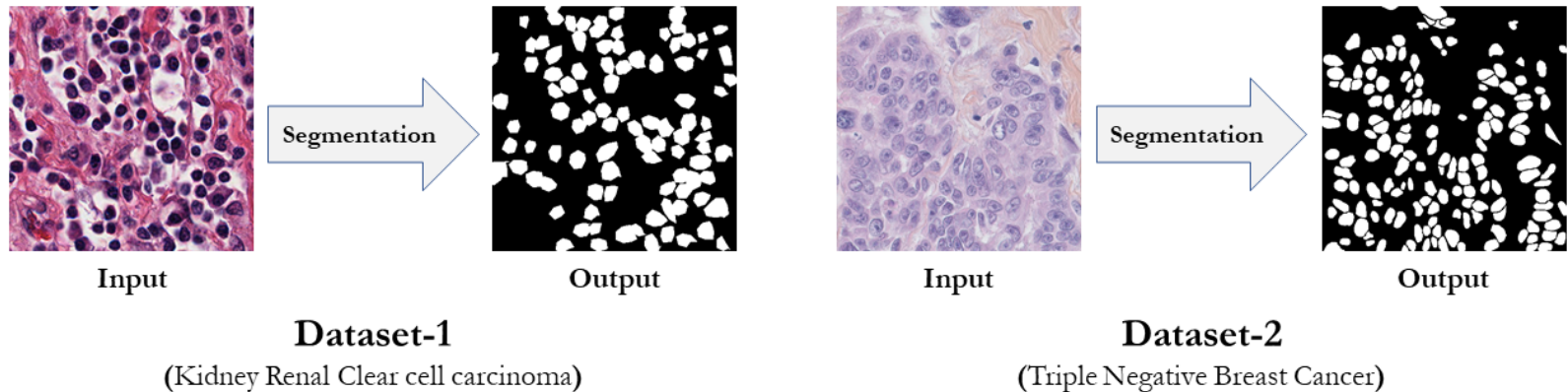


Figure: Motivation behind the proposed solution

- Let's assume, we have **two datasets** from **two different organs**
 - one with annotations (source domain), another without annotation (target domain)
- We apply a technique called **Domain Adaptation** with help of the annotated dataset

Methodology

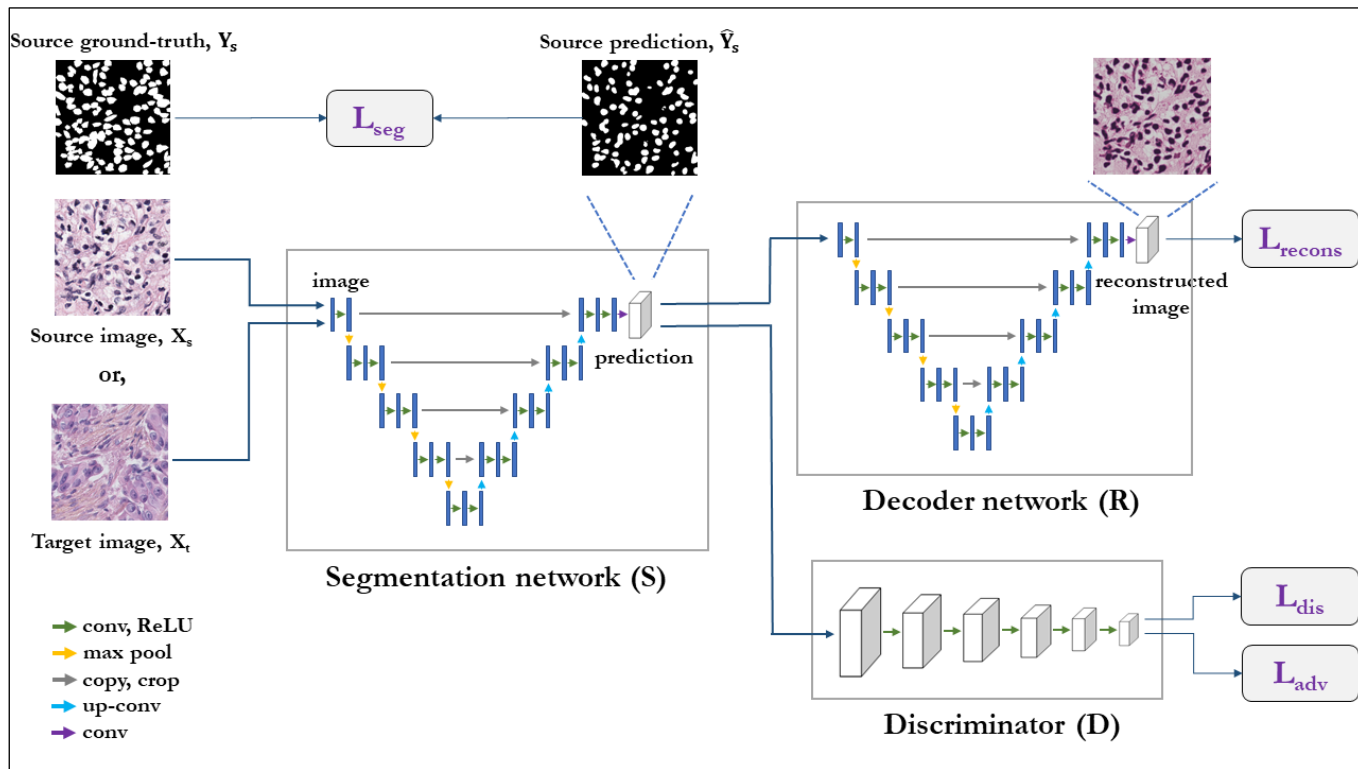


Figure: Complete architecture of CellSegUDA

- **Segmentation network** takes input images, and produces segmentation predictions
- **Discriminator** distinguishes between source-domain and target-domain prediction
- **Decoder** ensures that target domain predictions spatially correspond to target domain images

Experiments

- **Datasets**

- **Dataset-1: KIRC** (Kidney Renal Clear cell carcinoma)
 - 486 patches of size 400x400
- **Dataset-2: TNBC** (Triple Negative Breast Cancer)
 - 50 patches of size 512x512

- **Experimental setups of CellSegUDA** (unsupervised domain adaptation)

	Experiment 1 (KIRC → TNBC)	Experiment 2 (TNBC → KIRC)
Training	100% of KIRC (with labels) + 80% of TNBC (w/o labels)	100% of TNBC (with labels) + 80% of KIRC (w/o labels)
Validation	10% of TNBC (with labels)	10% of KIRC (with labels)
Testing	10% of TNBC	10% of KIRC

- For **CellSegSSDA** (semi-supervised domain adaptation), we utilize incremental percentage (10%, 25%, 50% and 75%) of target dataset labels while training

Experimental results

Method	Experiment 1 (KIRC → TNBC)		Experiment 2 (TNBC → KIRC)	
	IoU%	Dice score	IoU%	Dice score
U-Net (source-trained) ^[1]	52.66	0.6875	54.82	0.7056
DA-ADV ^[2]	54.93	0.7079	55.43	0.7107
CellSegUDA w/o recons	56.56	0.72	56.91	0.7224
CellSegUDA	59.02	0.7394	57.09	0.7242
U-Net (source 100% + target 10%)	60.74	0.7534	56.89	0.7194
CellSegSSDA (source 100% + target 10%)	60.96	0.7557	58.81	0.7377
U-Net (source 100% + target 25%)	61.67	0.7607	59.32	0.7405
CellSegSSDA (source 100% + target 25%)	62.94	0.771	59.73	0.7443
U-Net (source 100% + target 50%)	56.73	0.7208	59.95	0.7464
CellSegSSDA (source 100% + target 50%)	63.59	0.7748	60.32	0.7494
U-Net (source 100% + target 75%)	59.06	0.7394	61.63	0.7592
CellSegSSDA (source 100% + target 75%)	64.96	0.7862	61.01	0.7541
U-Net (target-trained)	66.57	0.7985	62.04	0.7621

[1] U-net: Convolutional networks for biomedical image segmentation, MICCAI 2015

[2] Unsupervised domain adaptation for automatic estimation of cardiothoracic ratio, MICCAI 2018

Visualizations

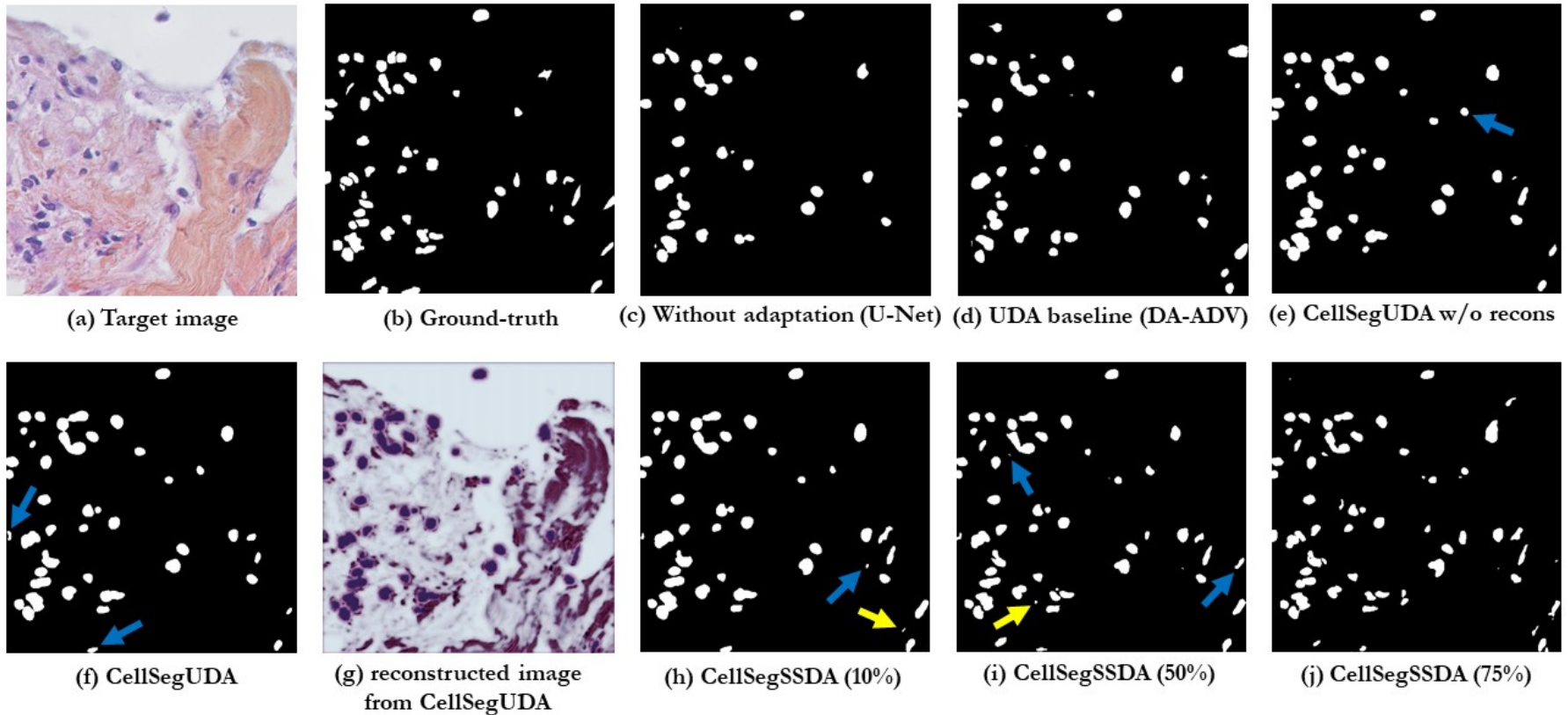


Figure: Visualization of segmentation for KIRC \rightarrow TNBC.

Blue arrows indicate missing cells of previous methods, and Yellow arrows indicate false positives which are removed by following method.

Conclusion

- A novel **unsupervised domain adaptation** framework is proposed for **segmenting cells** in **unannotated datasets** utilizing
 - adversarial learning
 - domain adaptation in output space
 - decoder network
- Then, it is extended to **semi-supervised domain adaptation** considering
 - a few annotations available from the target domain
- In both cases, **significant improvement** is achieved as compared with the baseline methods
- Have questions?
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