Information

Domain Adaptive Medical Image Segmentation via Adversarial Learning of Disease-Specific Spatial Patterns

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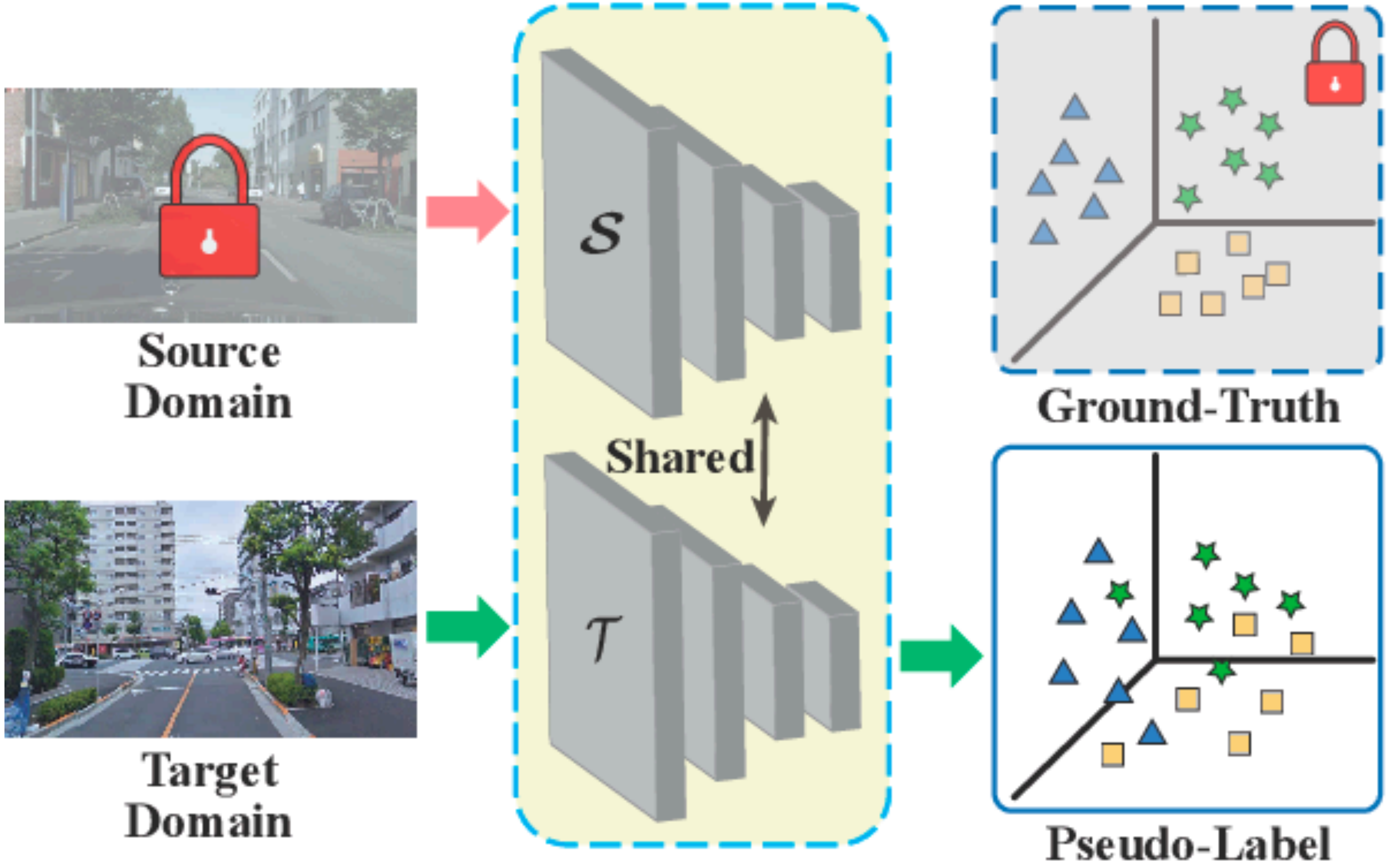
Introduction

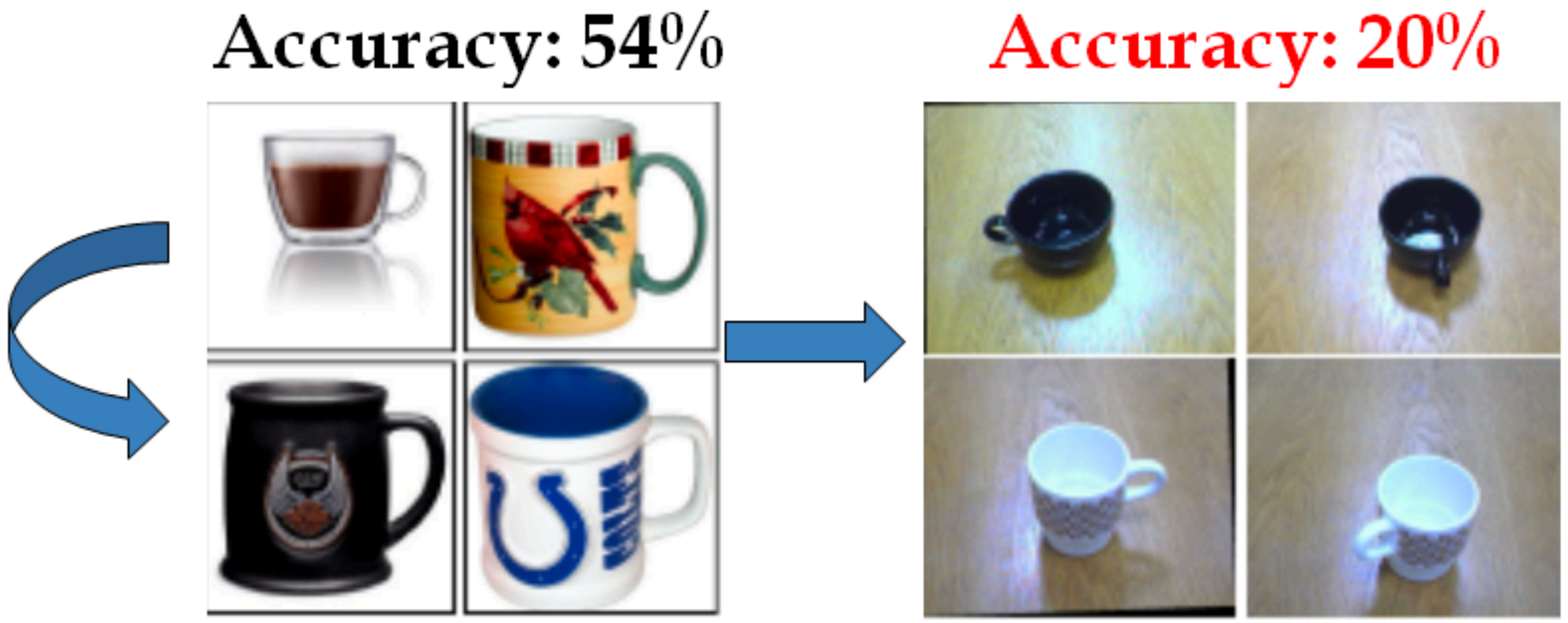
What is Domain Adaption



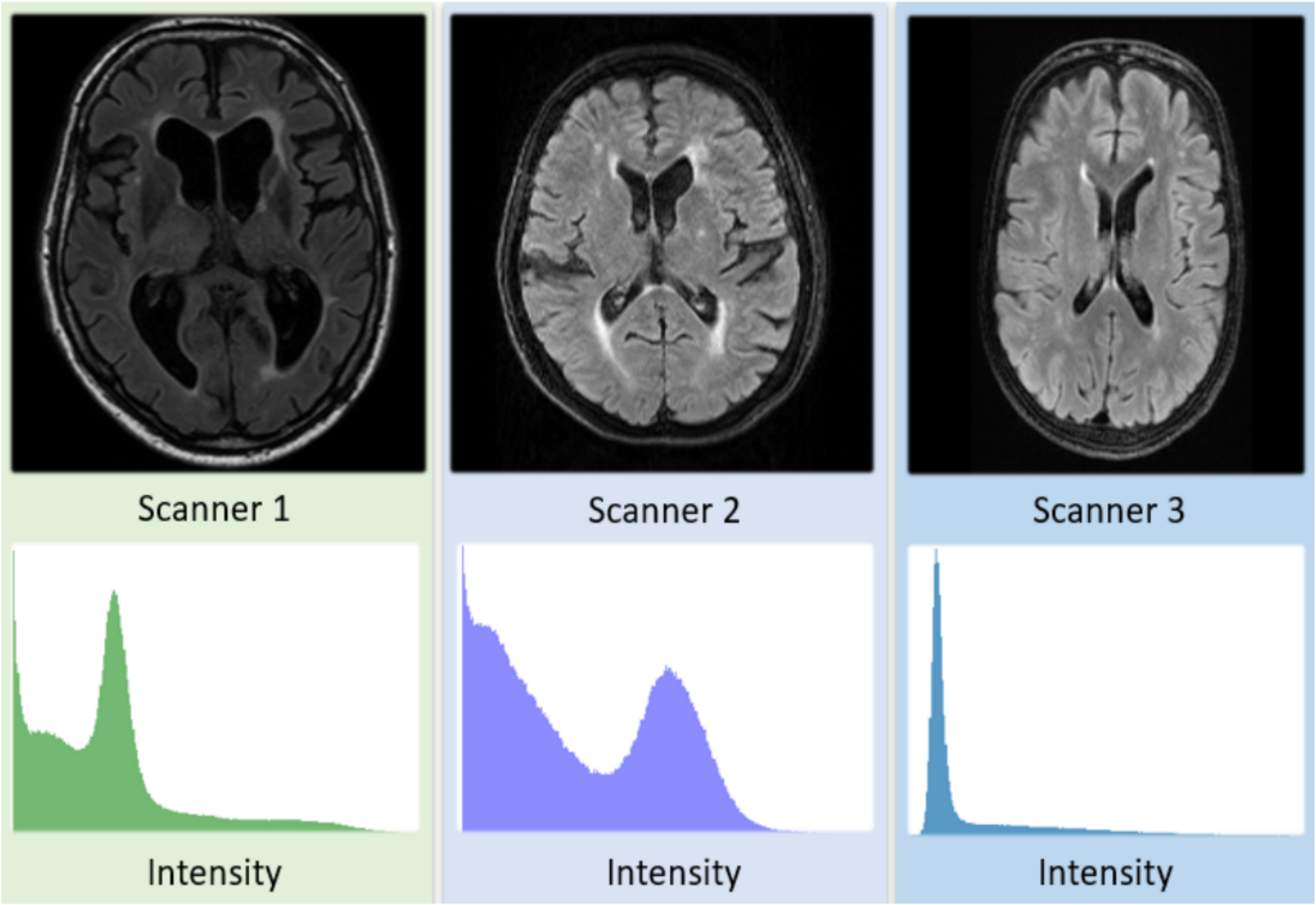
Introduction

Why we need domain adaption in medical image

- **Most DL tasks is data-driven**: CNN based tasks like segmentation which require a large amount of annotated
- **Existence of domain shift**: Domain shift is a change in the data distribution. The problem of domain shift is **ubiquitous** in biomedical image analysis as images acquired by **various institutions** due to difference in image acquisition parameters used for capturing data



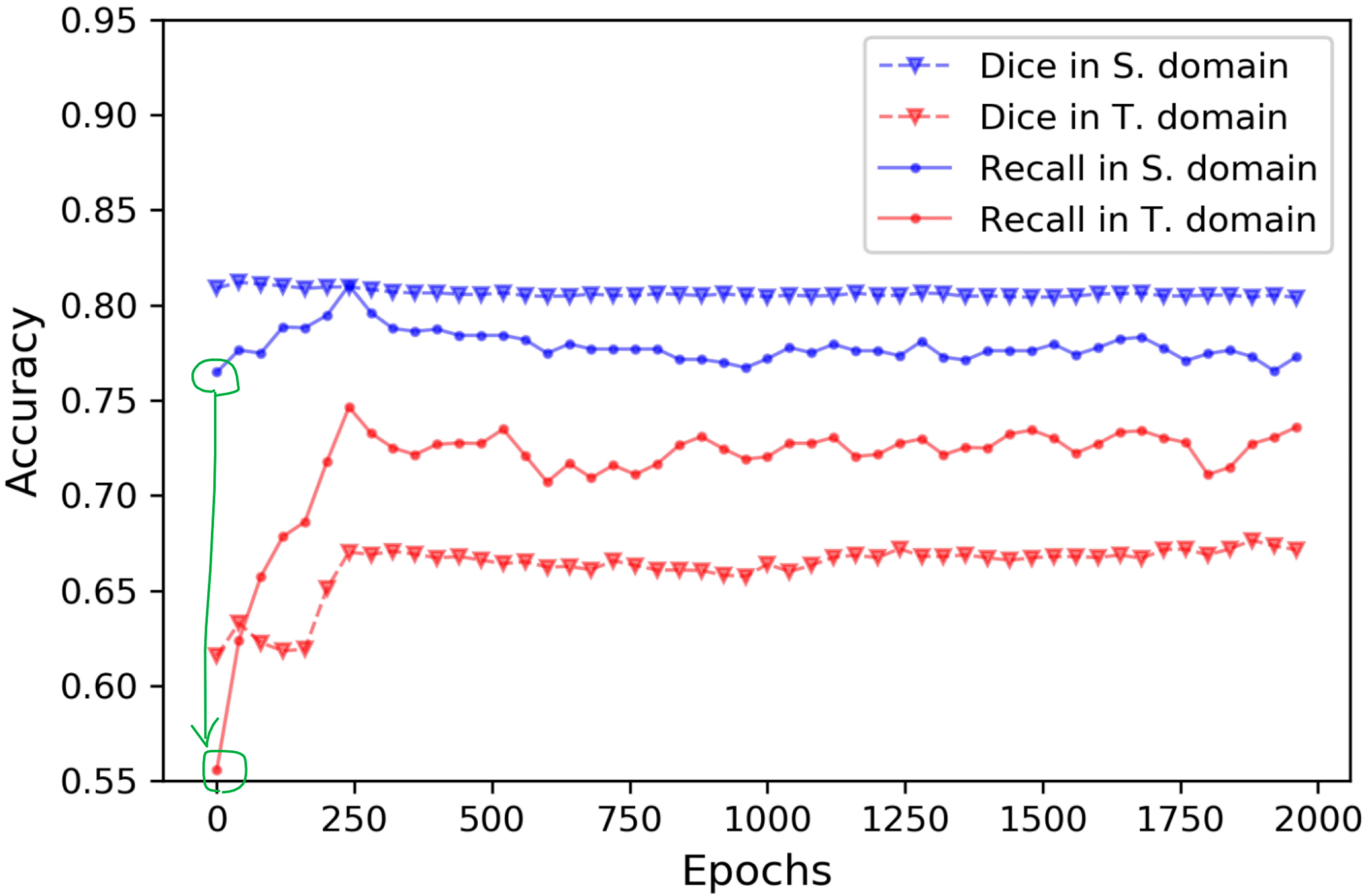
Dataset: MS lesion & White Matter Hyperintensities



- Input: MRI
- Dim: 3D
- Output: Segmentation

Centres	Scanner	Voxel Size (mm^3)	Volume Size
Utrecht	3T Philips Achieva	$0.96 \times 0.95 \times 3.00$	$240 \times 240 \times 48$
Singapore	3T Siemens TrioTim	$1.00 \times 1.00 \times 3.00$	$252 \times 232 \times 48$
Amsterdam	3T GE Signa HDxt	$0.98 \times 0.98 \times 1.20$	$132 \times 256 \times 83$

- **domain shift**



Introduction

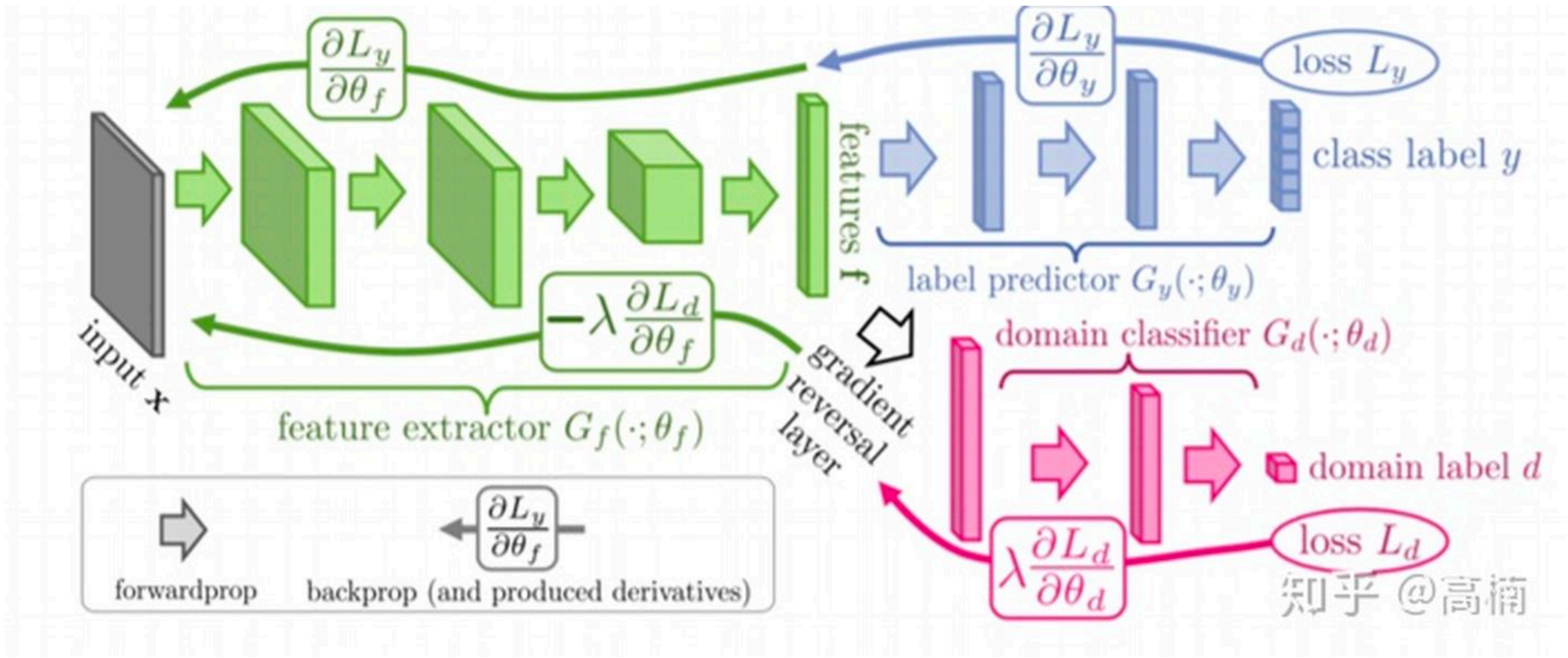
Why we can apply domain adaption in medical image

Hypothesis: Disease-specific patterns in segmentation tasks are domain-invariant, for example:

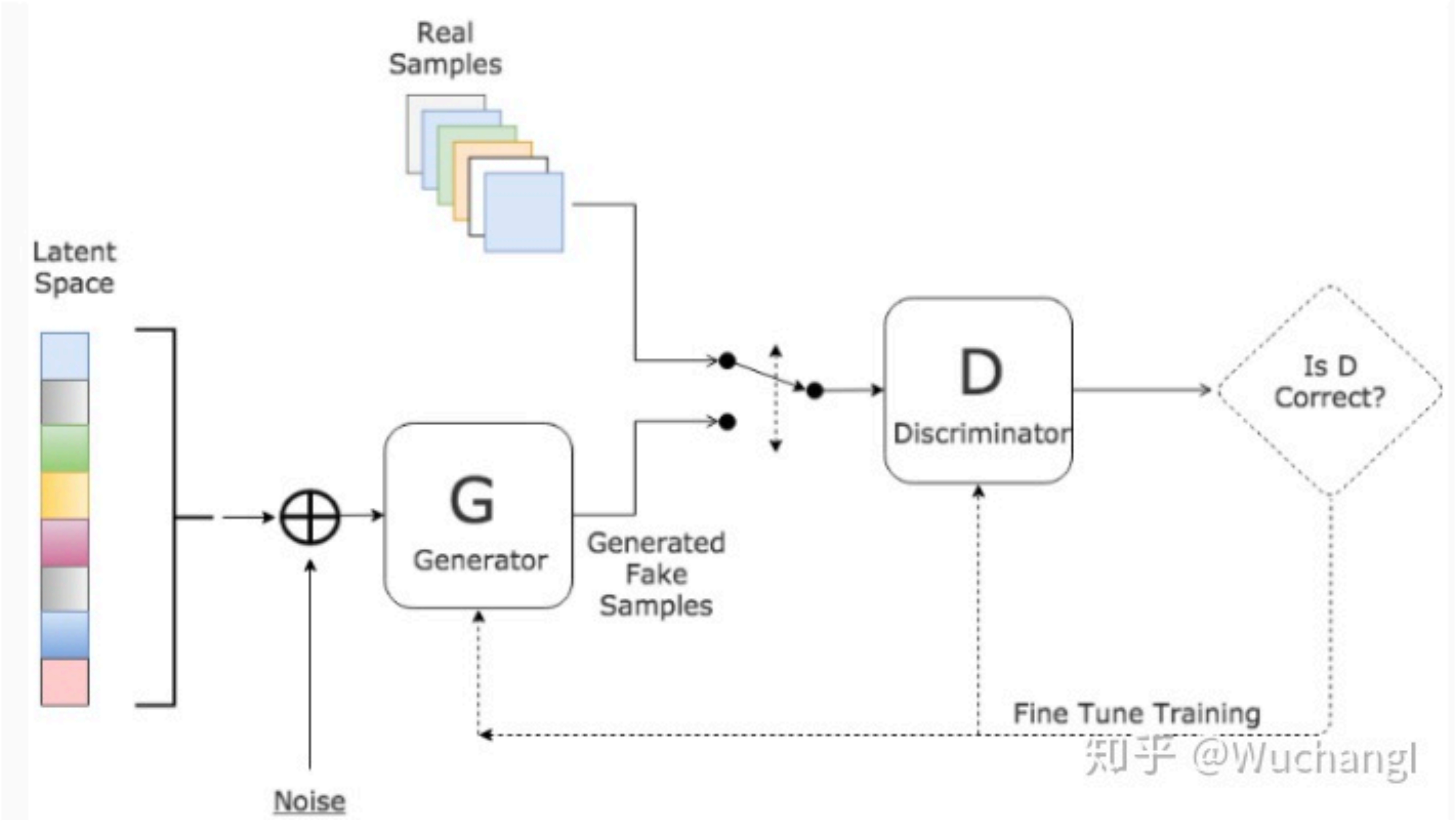
- the structure or morphology of lesions is invariant to domain shifts
- the spatial manifestation of the disease-specific pattern

Core Concept

- Adversarial-based methods: 将target domain提取的特征看作generator的输出, source domain的特征看作real image，使用discriminator来判断backbone的输出属于哪个域, 以此引导backbone提取出domain invariant的特征.



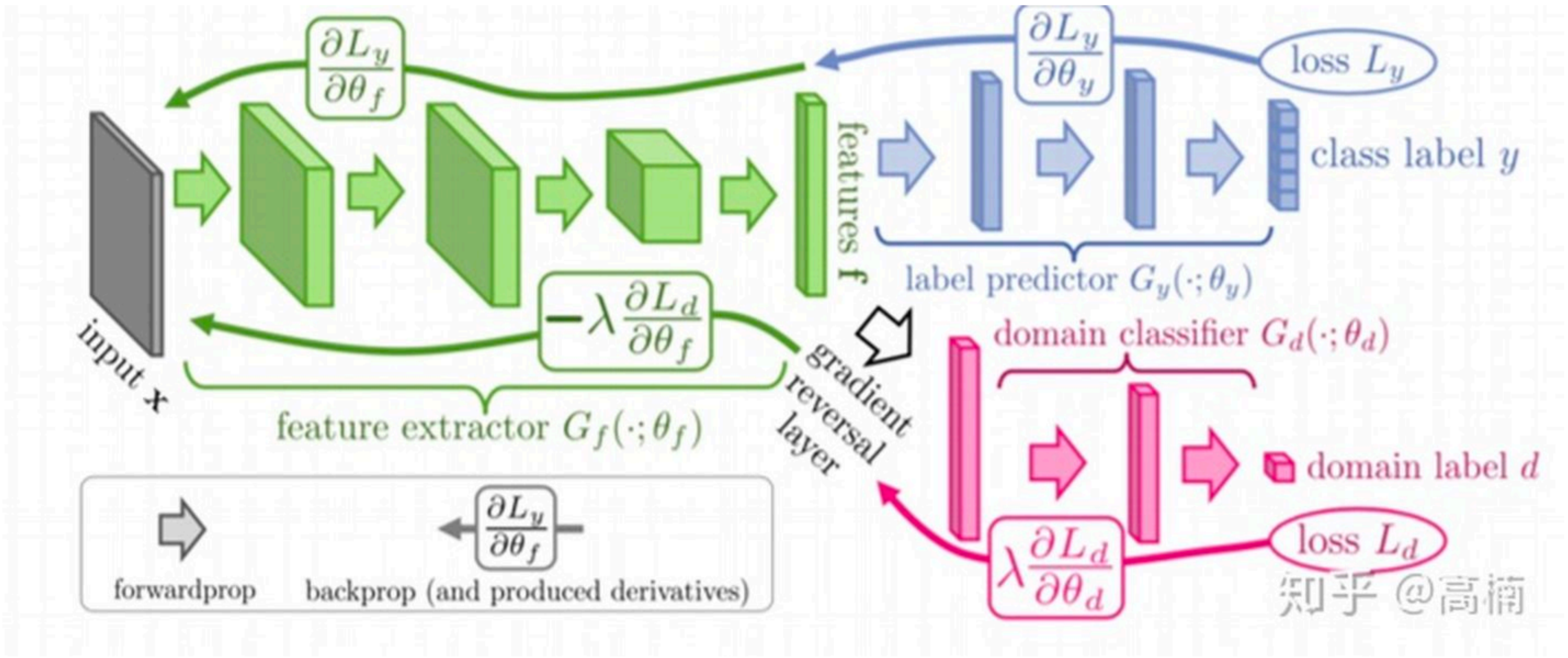
Relevant Work: GAN（生成对抗网络）



生成对抗网络包含一个**生成器（Generator）**和一个**判别器（Discriminator）**。两者互相博弈，直到网络收敛 (即生成器生成的图片可以骗过判别器)

- 生成器用来生成能生成尽可能逼真的样本
- 判别器则用来区分, 判别器则希望提高辨别能力防止被骗

Relevant Work: DANN

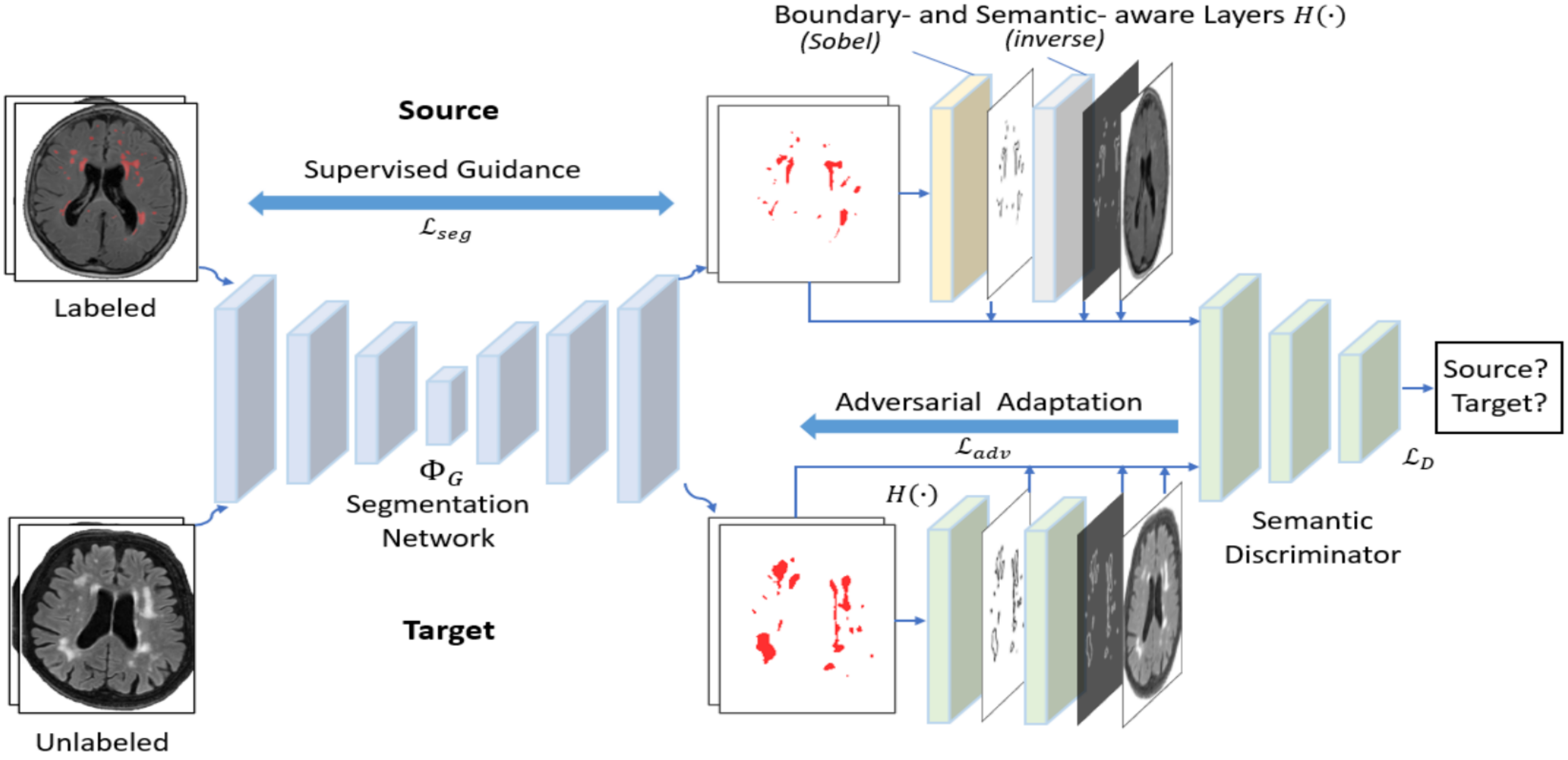


DANN结构主要包含3个部分：

- 特征提取器 （feature extractor） - 图示绿色部分，用来将数据映射到特定的特征空间，使标签预测器能够分辨出来自源域数据的类别的同时，域判别器无法区分数据来自哪个域。
- 标签预测器 （label predictor） - 图示蓝色部分，对来自源域的数据进行分类，尽可能分出正确的标签。
- 域判别器（domain classifier）- 图示红色部分，对特征空间的数据进行分类，尽可能分出数据来自哪个域。

Methodology

Conceptual overview : Training segmentation models for unlabeled data



Results

Conditions	Dice score	H95↓ (mm)	AVD↓	Lesion Recall	Lesion F1	p-value$_{Dice}$ [ours *vs.* others]	p-value$_{H95}$ [ours *vs.* others]
U. + A. → S.							
Baseline	0.682	9.22	45.95	0.641	0.592	<0.001	<0.001
U-Net Ensembles [32]	0.703	8.83	37.21	0.672	0.642	<0.001	0.008
CyCADA [40]	0.452	15.23	67.13	0.462	0.344	<0.001	<0.001
BigAug [26]	0.711	8.25	35.41	0.691	0.651	<0.001	0.012
Ours (with a few shots)	0.780	7.54	24.75	0.666	**0.657**	0.325	0.599
Ours (with full set)	**0.782**	**7.51**	**22.14**	**0.754**	0.649	-	-
U. + S. → A.							
Baseline	0.674	11.51	37.60	0.692	0.673	0.002	<0.001
U-Net Ensembles [32]	0.694	9.90	31.01	0.720	0.691	0.008	0.002
CyCADA [40]	0.412	18.21	89.23	0.402	0.292	<0.001	<0.001
BigAug [26]	0.691	9.77	30.64	0.709	0.704	0.012	0.008
Ours (with a few shots)	0.733	7.90	**16.01**	0.785	0.725	0.530	0.357
Ours (with full set)	**0.737**	**7.53**	30.97	**0.841**	**0.739**	-	-
A. + S. → U.							
Baseline	0.430	11.46	54.84	0.634	0.561	<0.001	<0.001
U-Net Ensembles [32]	0.452	10.38	50.33	0.652	0.565	<0.001	<0.001
CyCADA [40]	0.422	13.91	77.45	0.544	0.385	<0.001	<0.001
BigAug [26]	**0.534**	**9.49**	**47.46**	0.643	**0.577**	0.262	0.470
Ours (with a few shots)	0.489	11.02	57.01	0.639	0.533	0.008	0.002
Ours (with full set)	0.529	10.01	54.95	**0.652**	0.546	-	-

Results

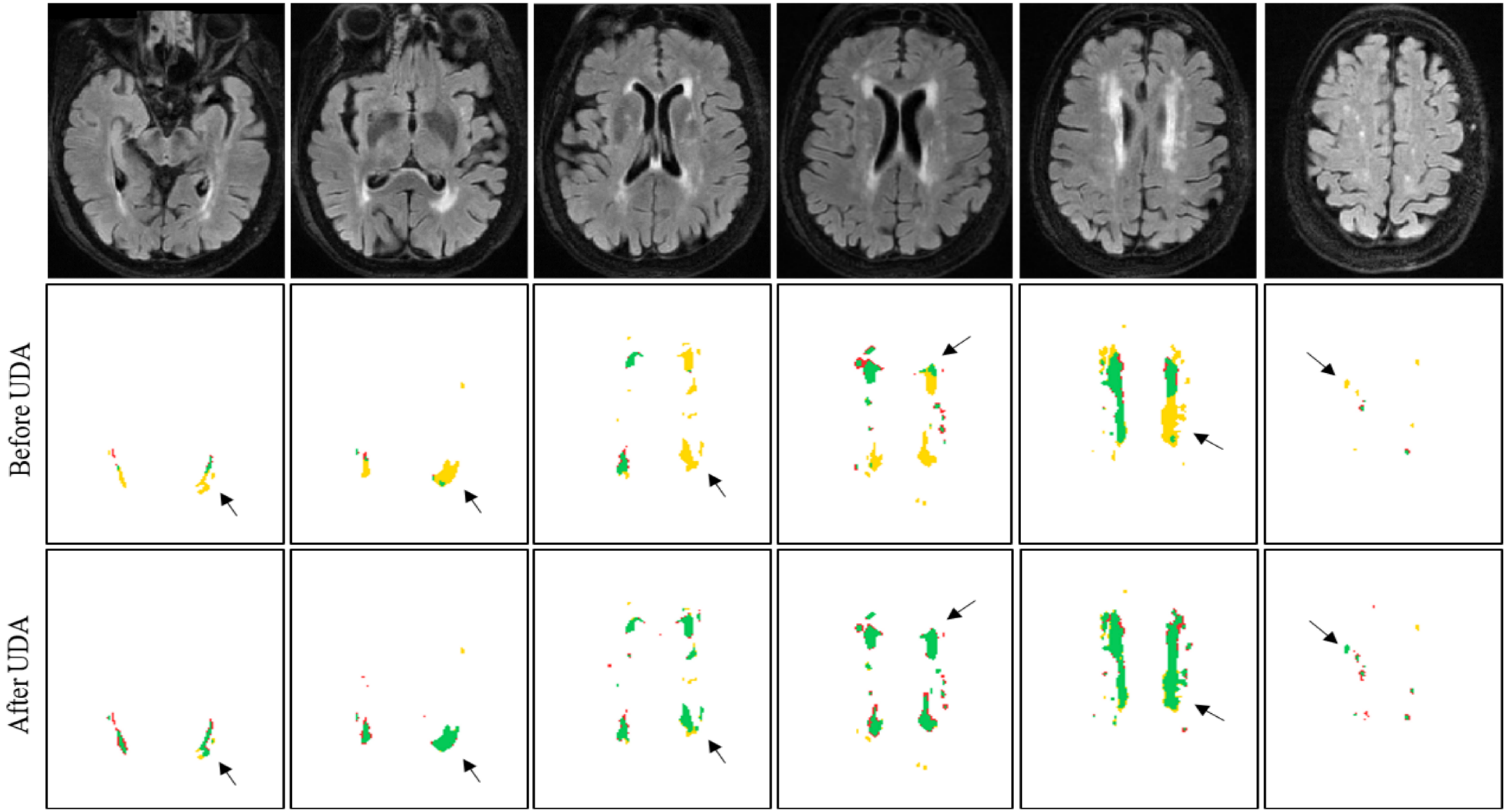


Fig. 3: From left to right: results on six axial slices of the same subject. From top to bottom: FLAIR axial-view images, the segmentation results before UDA, the segmentation results using the proposed method. Green color indicates overlap between the segmentation result and the ground truth masks; red color false positives; gold color false negatives. (Best viewed in color)