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# L'hypothèse du décalage de covariable à la rencontre des modèles de diffusion pour l'adaptation de domaine non supervisée

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# Covariate shift assumption meets Diffusion models for Unsupervised Domain Adaptation

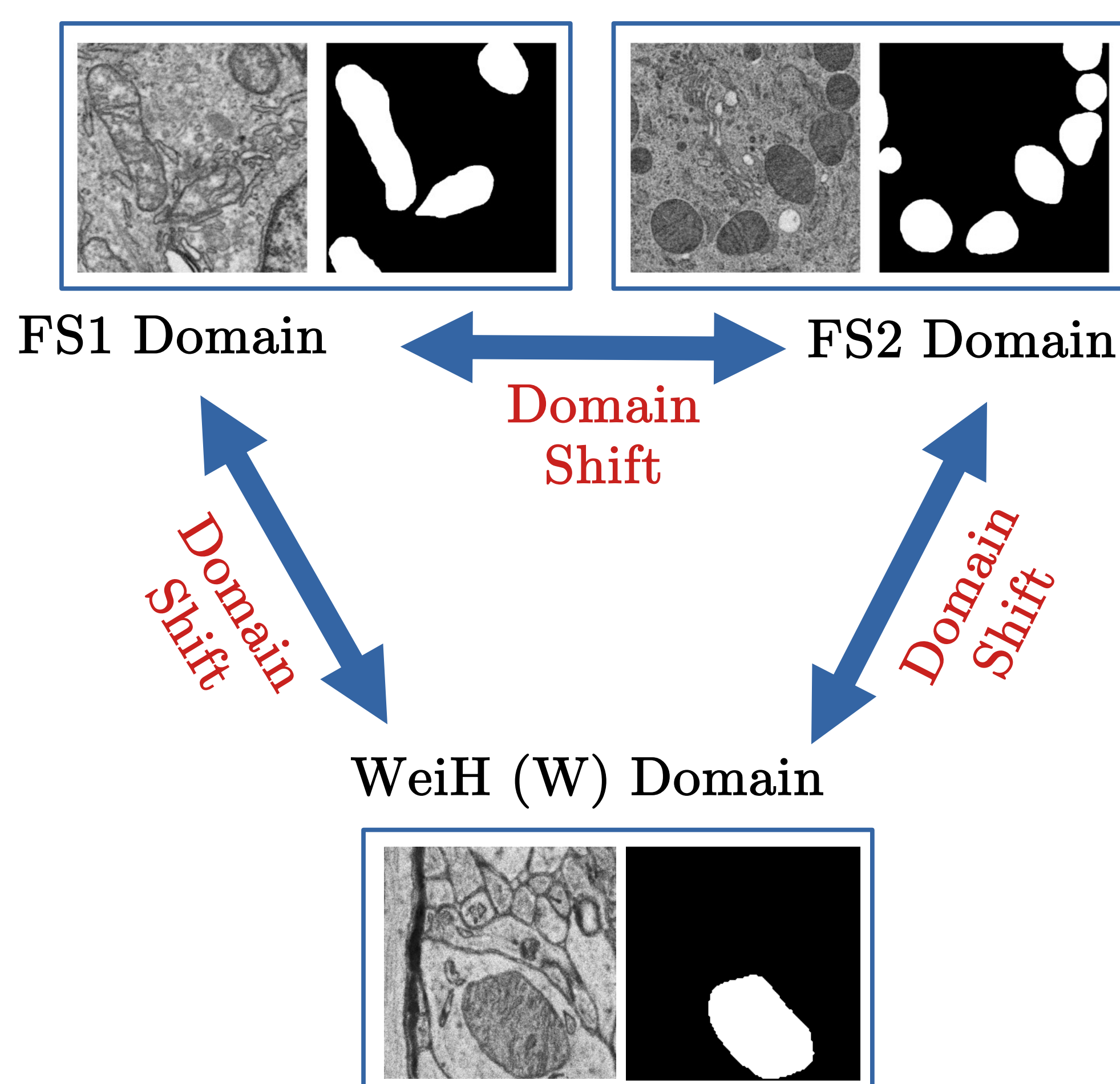
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## Abstract

Cell image segmentation is a critical task in biomedical image analysis. However, the performance of segmentation models often suffers when applied to new cell images. To avoid training new models, we use Unsupervised Domain Adaptation (UDA) in order to get a more robust segmentation framework.

## Data

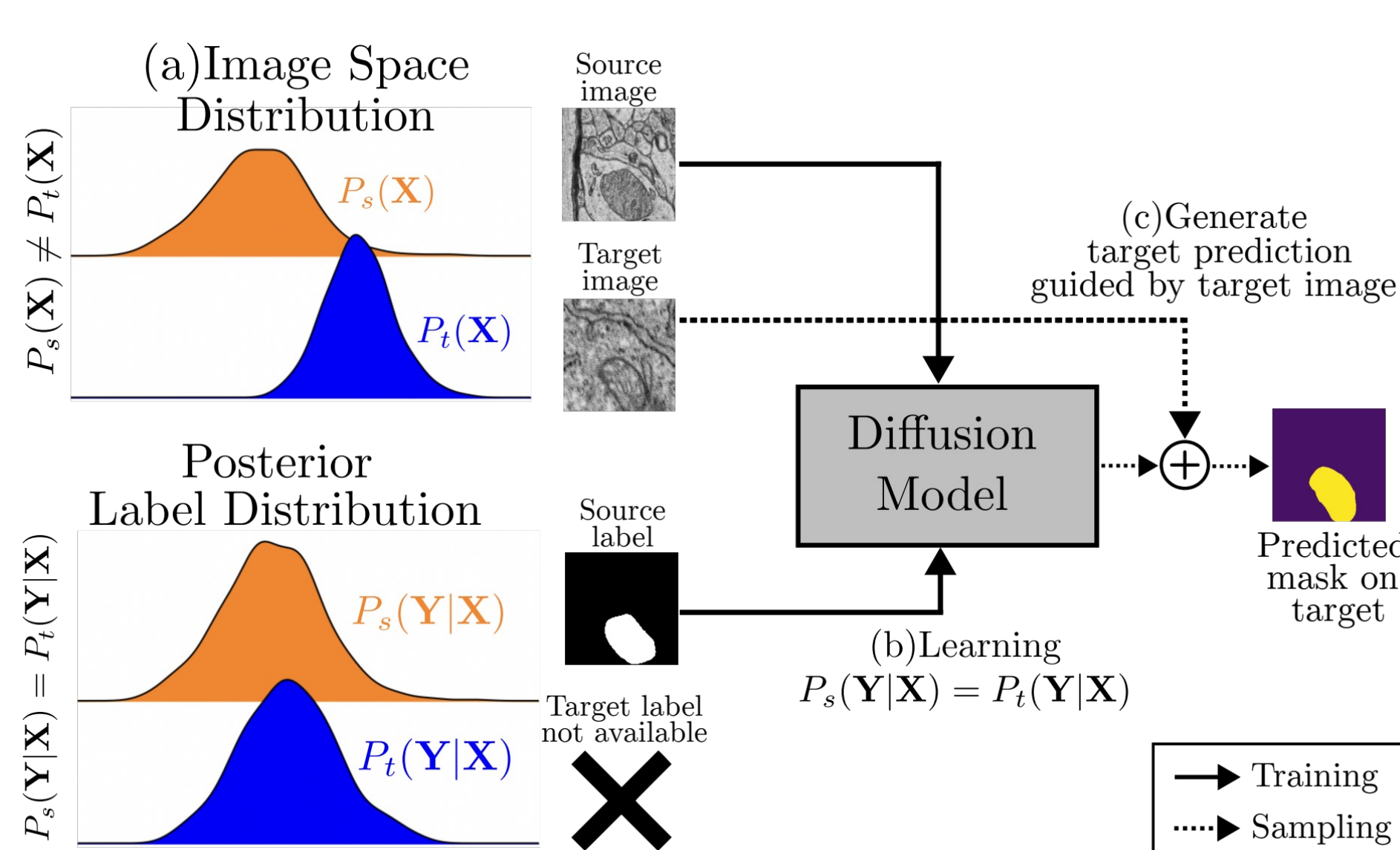


## Covariate Shift Hypothesis

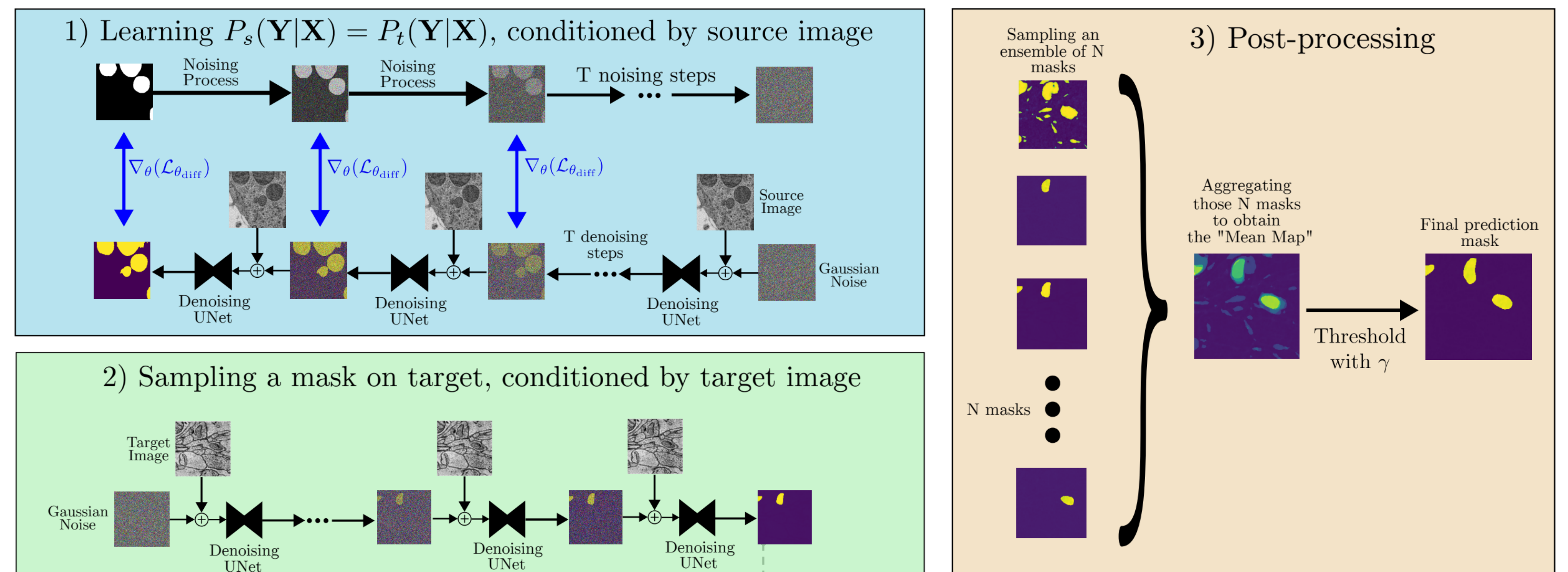
$$\begin{cases} P_s(\mathbf{X}) \neq P_t(\mathbf{X}) \\ P_s(\mathbf{Y}|\mathbf{X}) = P_t(\mathbf{Y}|\mathbf{X}) \end{cases}$$

## Idea

We propose to obliterate the covariate shift (a) by learning source posterior label distributions (b) with Diffusion Models to enforce (c) target segmentation to be consistent

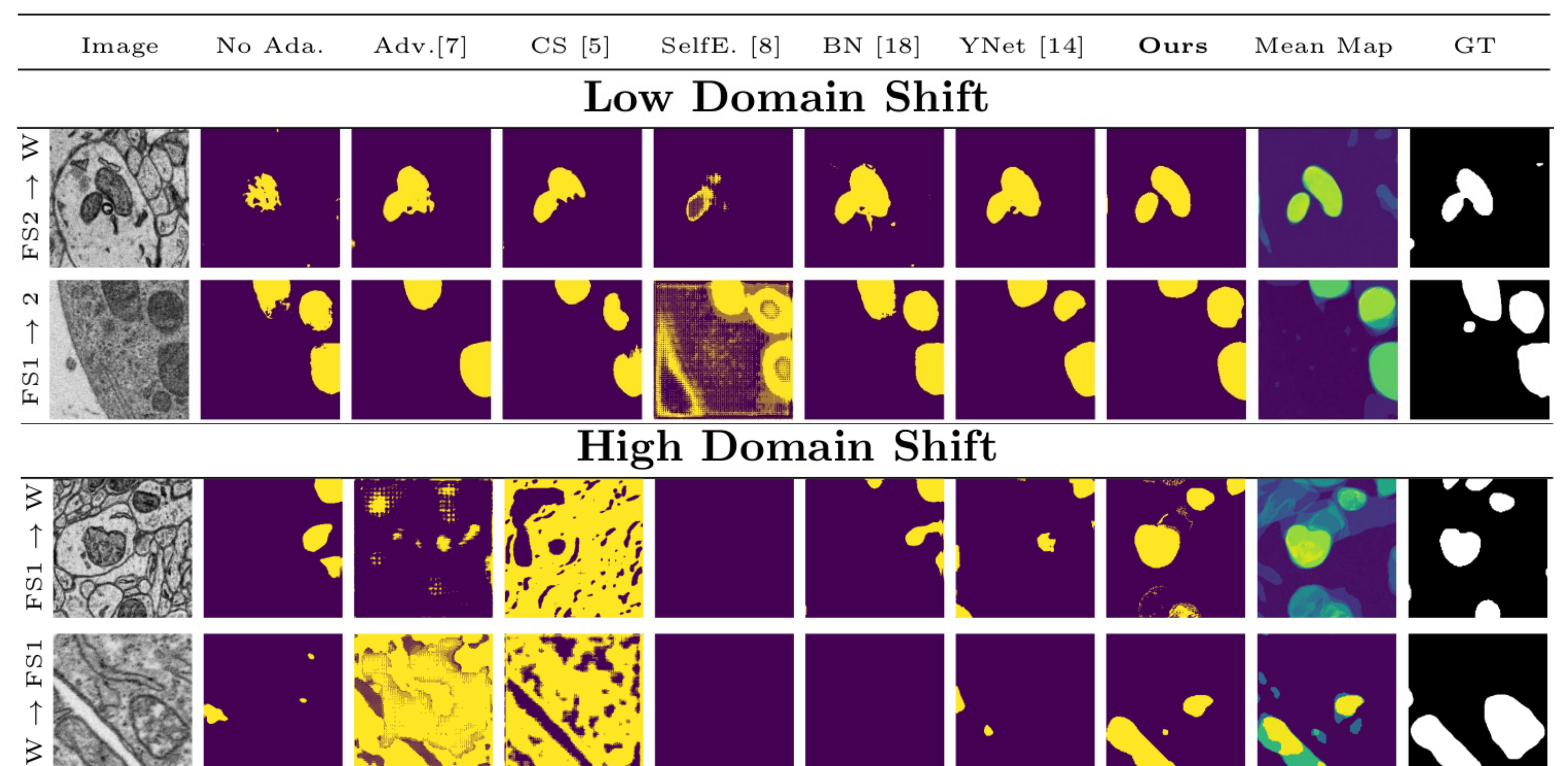


## Methods



1) We gradually add noise to a mask from source domain and then denoise it conditioned by the information in the source image, such that we properly learn  $P_s(\mathbf{Y}|\mathbf{X})$ . 2) We sample a segmentation mask on target domain, conditioned by the target image and the previously learnt posterior label distribution. 3) To enforce the robustness of our method, we generate multiple segmentation masks and threshold over all those predictions to obtain the final predicted mask.

## Results



Settings Methods	W → FS1		FS1 → W		FS2 → W		FS1 → 2	
	IoU (↑)	Dice (↑)	IoU (↑)	Dice (↑)	IoU (↑)	Dice (↑)	IoU (↑)	Dice (↑)
No Adaptation	0.04	0.07	0.07	0.11	0.31	0.42	0.59	0.69
BN [18]	0.03	0.04	0.10	0.16	0.48	<b>0.62</b>	<b>0.72</b>	<b>0.81</b>
Adv. [7]	<b>0.17</b>	0.28	0.08	0.15	0.46	0.59	0.43	0.57
CellSeg. [5]	0.16	0.29	0.10	0.18	0.29	0.41	0.44	0.59
YNet [14]	0.07	0.10	0.17	0.25	<b>0.50</b>	<b>0.62</b>	0.64	0.75
SelfEns. [8]	<b>0.17</b>	0.27	0.01	0.01	0.18	0.27	0.33	0.48
<b>Ours</b>	<b>0.17</b>	<b>0.35</b>	<b>0.22</b>	<b>0.36</b>	0.45	<b>0.62</b>	0.60	0.75
Supervised on target	0.80	0.85	0.73	0.80	0.73	0.80	0.82	0.87

## Conclusion

- Generative processes successfully overcome large domain shift
- Rely on the similarity of the label distribution to constraint adaptation to be consistent
- Future works include improvement of the latent representation

## References

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