



HAL
open science

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

Alexandre Stenger, Étienne Baudrier, Nicolas Passat, Benoît Naegel, Patrick Schultz

► To cite this version:

Alexandre Stenger, Étienne Baudrier, Nicolas Passat, Benoît Naegel, Patrick Schultz. L'hypothèse du décalage de covariable à la rencontre des modèles de diffusion pour l'adaptation de domaine non supervisée. Colloque Français d'Intelligence Artificielle en Imagerie Biomédicale (IABM), Mar 2024, Grenoble, France. hal-04440876

HAL Id: hal-04440876

<https://hal.science/hal-04440876v1>

Submitted on 28 Mar 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Covariate shift assumption meets Diffusion models for Unsupervised Domain Adaptation

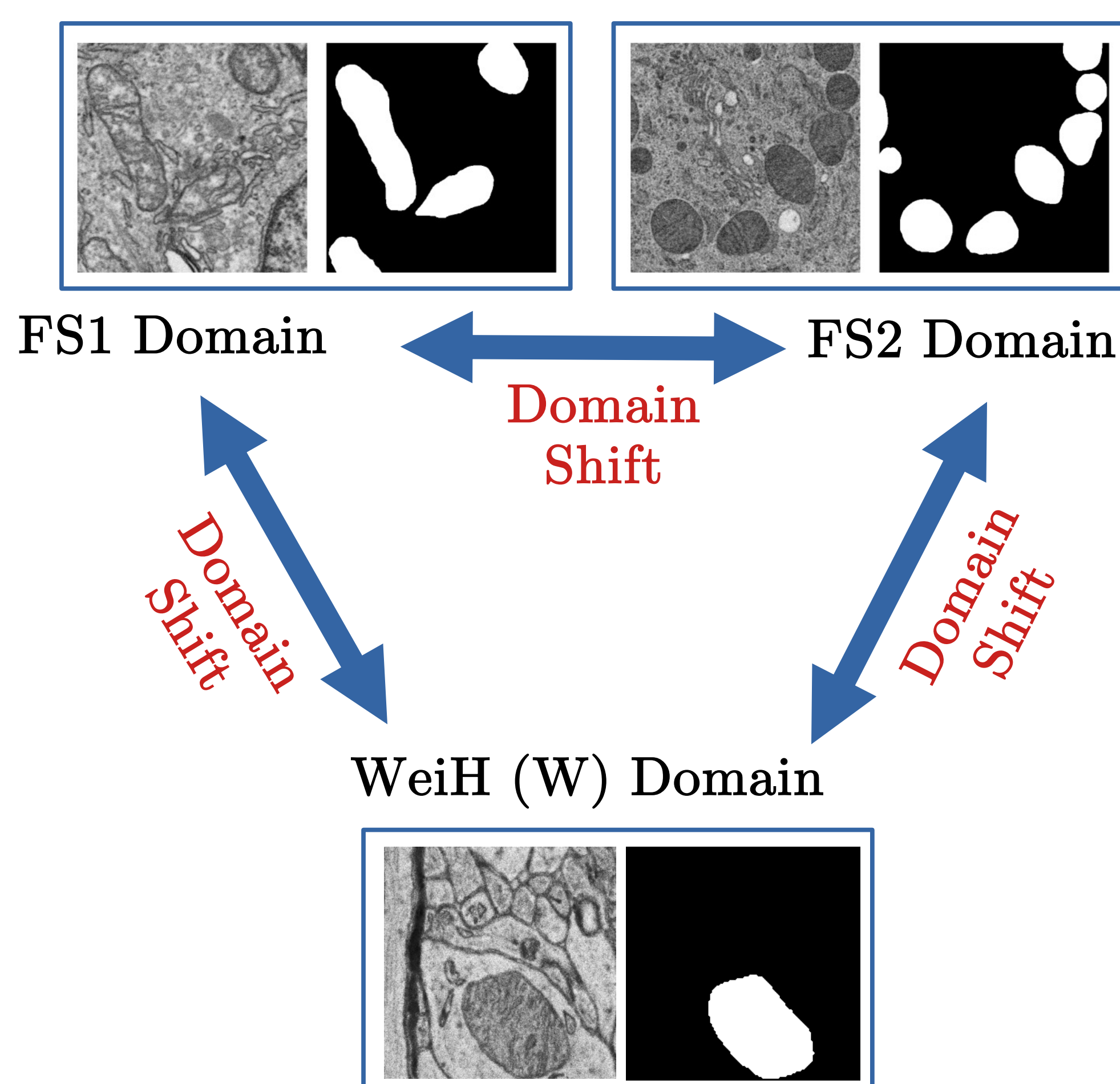
Alexandre STENGER, Étienne BAUDRIER, Nicolas PASSAT, Benoît NAEGEL, Patrick SCHULTZ

de Strasbourg

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

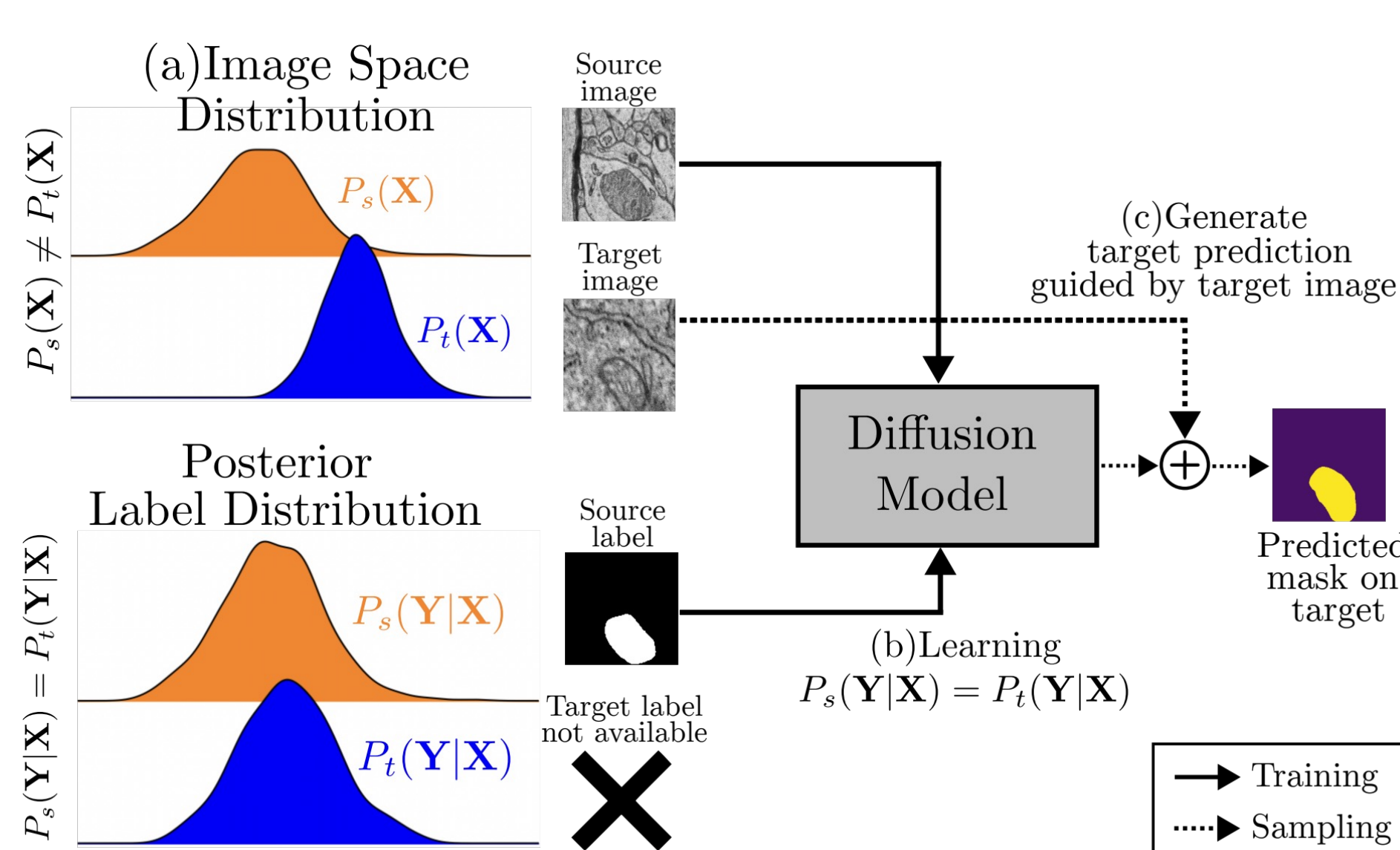


Covariate Shift Hypothesis

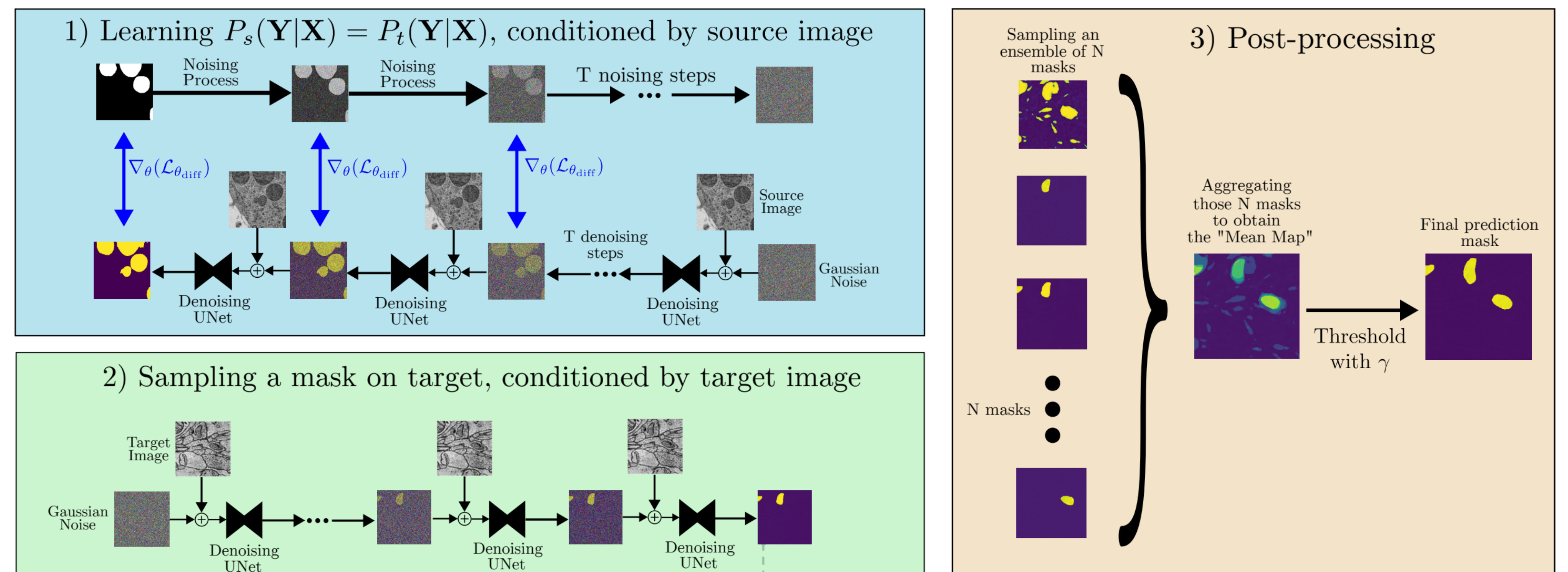
$$\begin{cases} P_s(\mathbf{X}) \neq P_t(\mathbf{X}) \\ P_s(\mathbf{Y}|\mathbf{X}) = P_t(\mathbf{Y}|\mathbf{X}) \end{cases}$$

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

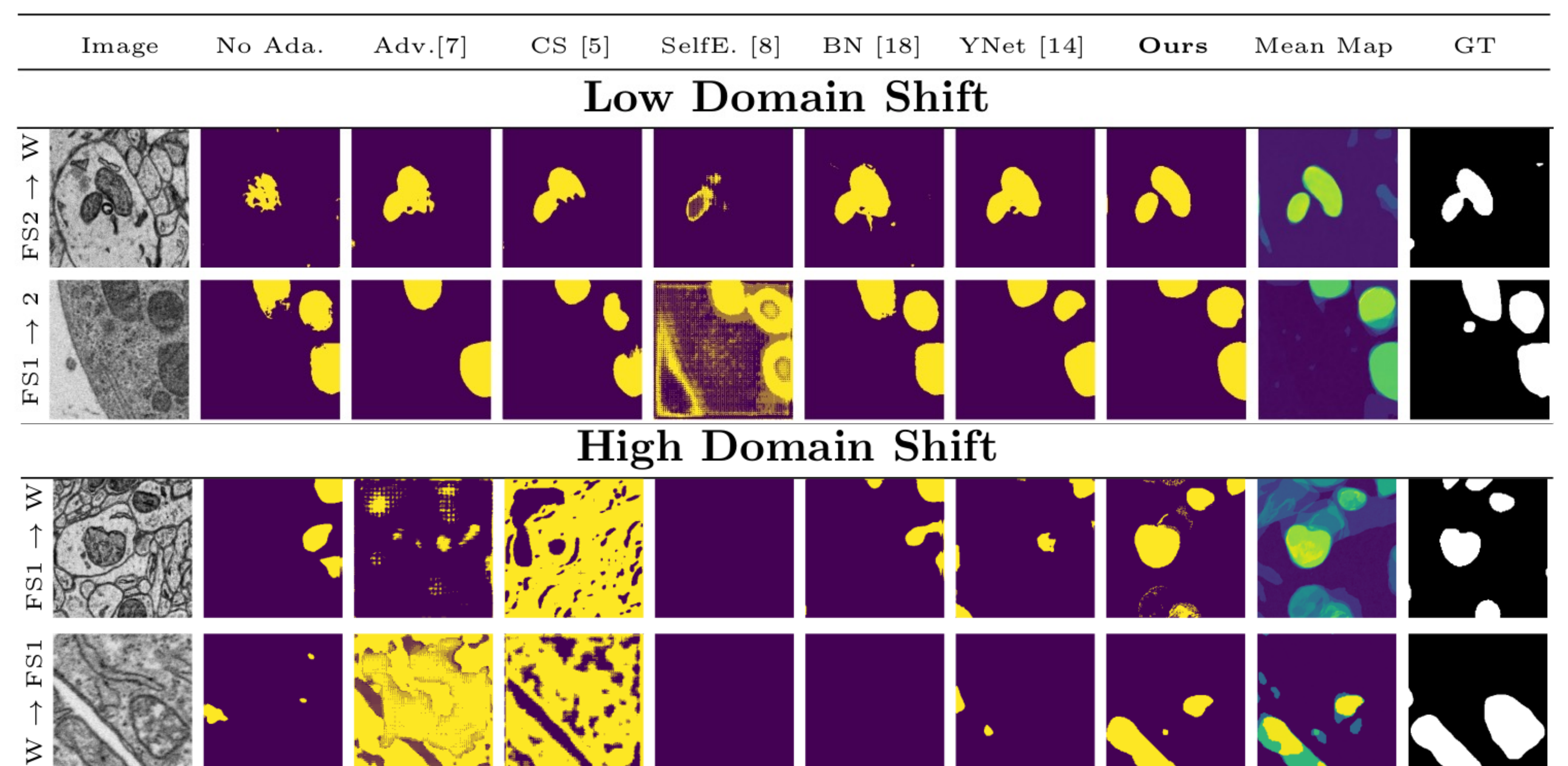


Methods



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	0.62	0.72	0.81
Adv. [7]	0.17	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	0.50	0.62	0.64	0.75
SelfEns. [8]	0.17	0.27	0.01	0.01	0.18	0.27	0.33	0.48
Ours	0.17	0.35	0.22	0.36	0.45	0.62	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

- Haq et al. "Adversarial domain adaptation for cell segmentation", PMLR, 2020.
- Javanmardi, et al. Domain adaptation for biomedical image segmentation using adversarial training. In *2018 IEEE ISBI*.
- Li, C. et al. Unsupervised domain adaptation for the histopathological cell segmentation through self-ensembling. In *MICCAI 2021*, PMLR.
- Roels, J. et al. Domain adaptive segmentation in volume electron microscopy imaging. In *2019 IEEE ISBI*.
- Stenger, A., Vedrenne et al. Fast and Interpretable Unsupervised Domain Adaptation for FIB-SEM Cell Segmentation. In *2023 IEEE ISBI*