BlindHarmony: “Blind” Harmonization for multi-site MR Image processing via Flow model

LABORATORY FOR IMAGING SCIENCE AND TECHNOLOGY

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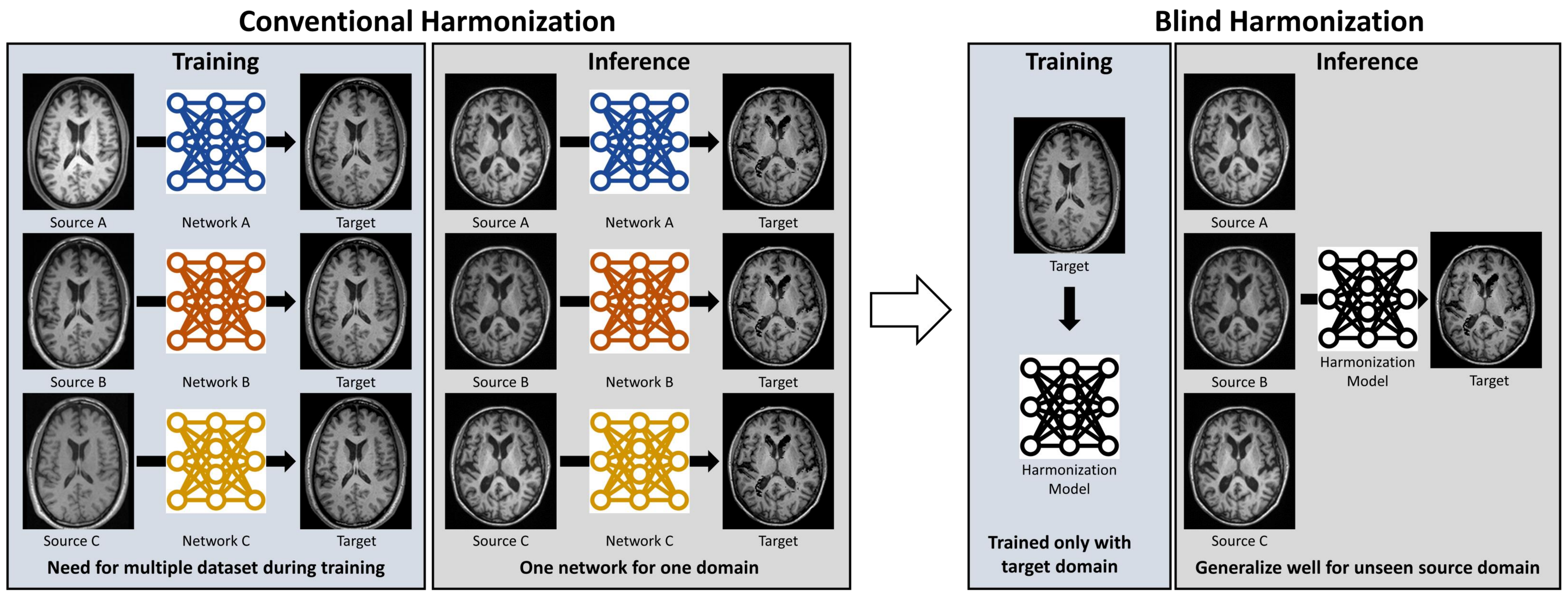
Introduction

- Deep learning has been widely applied to MRI, but generalization is challenging due to domain gaps in MRI data.
- Various harmonization methods have been developed, some requiring diverse datasets.
- Introducing **Blind Harmonization**: Training only with target domain data and generalizable to unseen source domains.
- Introducing BlindHarmony: A flow-based MRI image harmonization framework trained solely on the target domain data.
- Evaluation of BlindHarmony on both simulated and real-world data is presented.



BlindHarmony

[Harmonization model] When considering x_s as the source domain image and x_h as its corresponding harmonized version in the target domain, the following equations are applicable:

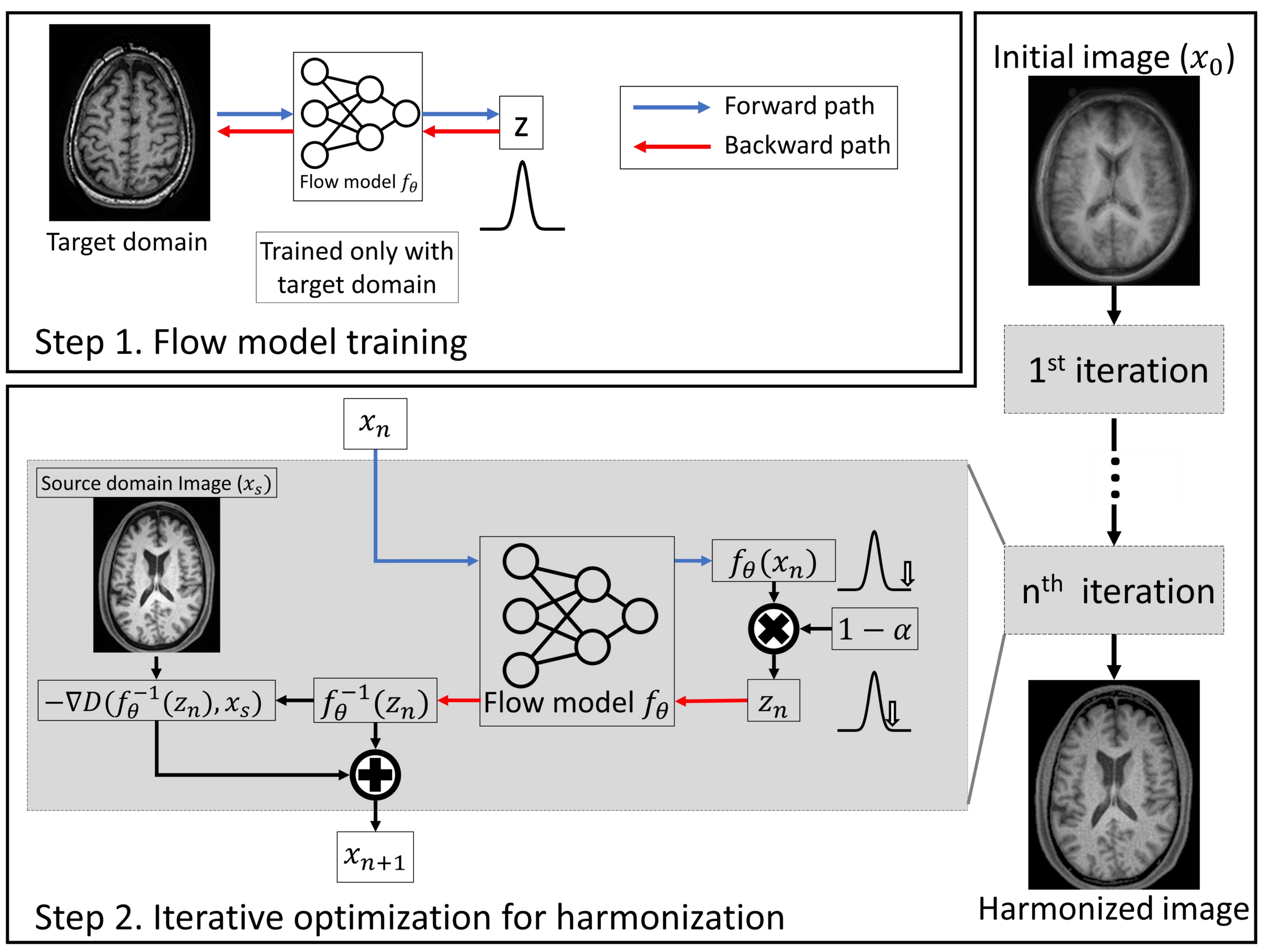
$$NCC(x_h, x_s) \approx 1 \text{ (High correlation)},$$
$$\|MGx_h\|_1 \approx 0 \text{ (Edge coincidence)}.$$

Here NCC: normalized cross correlation, $\| \quad \|_1$: L1 norm, M: non-edge mask of x_s, G: gradient operator. The harmonization distance can be defined as:

$$D(x_h, x_s) = \beta_1\{1 - NCC(x_h, x_s)\} + \beta_2\|MGx_h\|_1$$

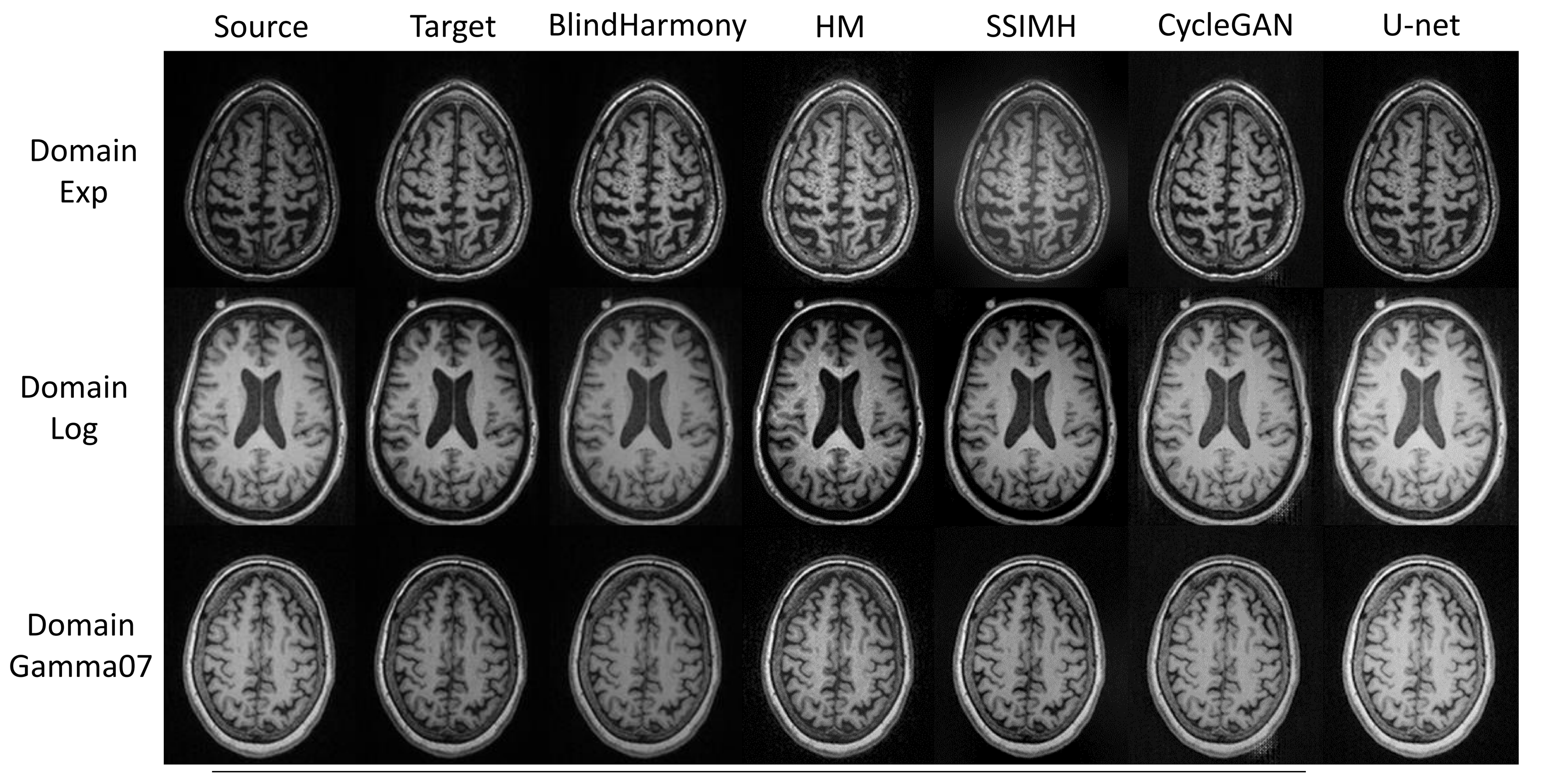
[BlindHarmony] The distribution of target domain image is trained by using an unconditional flow model f_θ (ONLY target domain is used for training). Iterative optimization is performed in both the image and latent vector domains to satisfy the following equation:

$$\widehat{z_h} = \underset{z}{argmin}\, D\left(f_\theta^{-1}(z), x_s\right) + \alpha|z|^2$$



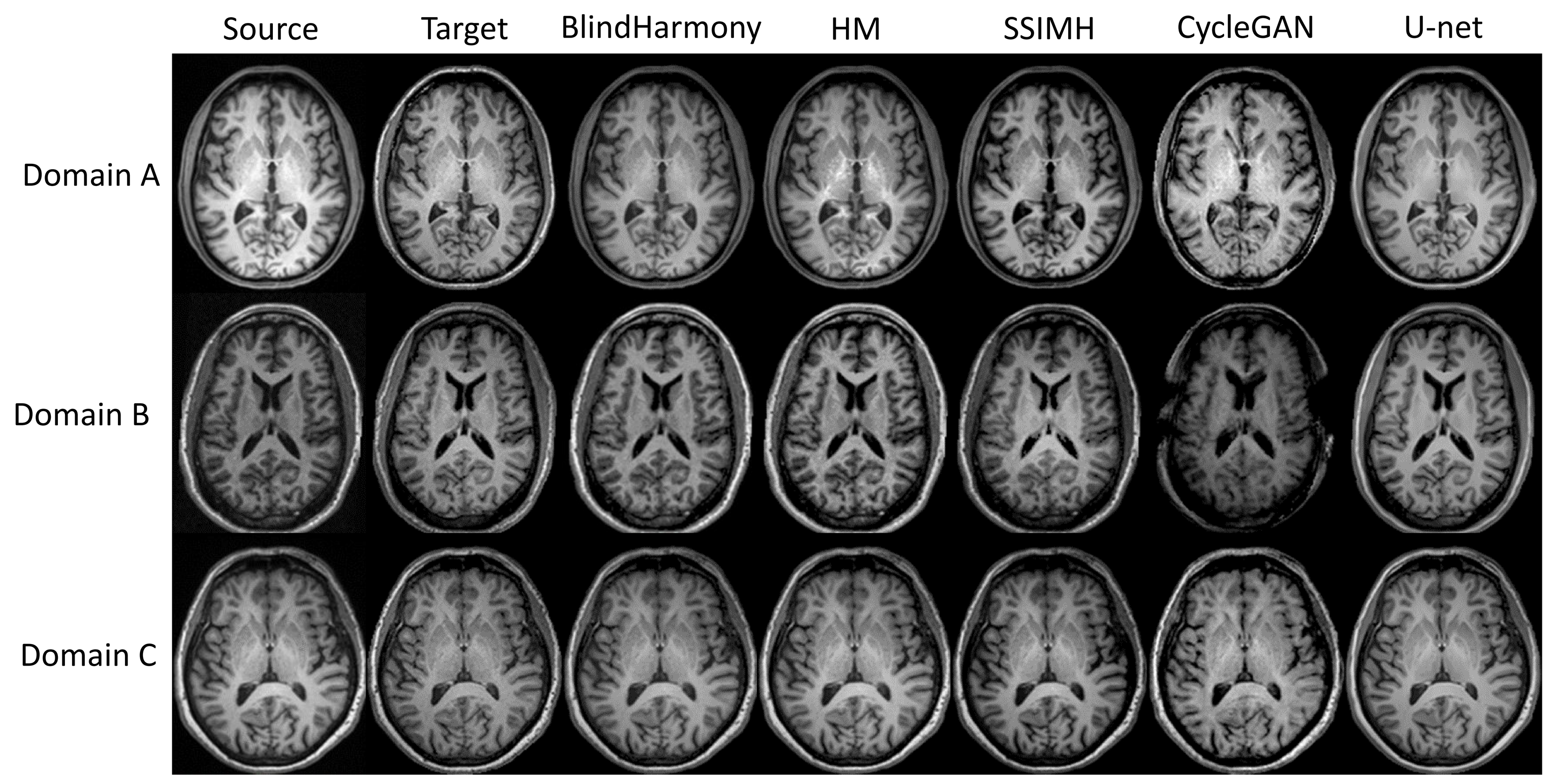
Results

[Simulated dataset] When BlindHarmony was applied to the simulated source domain dataset, it successfully harmonized the images, bringing them closer to the target domain images.



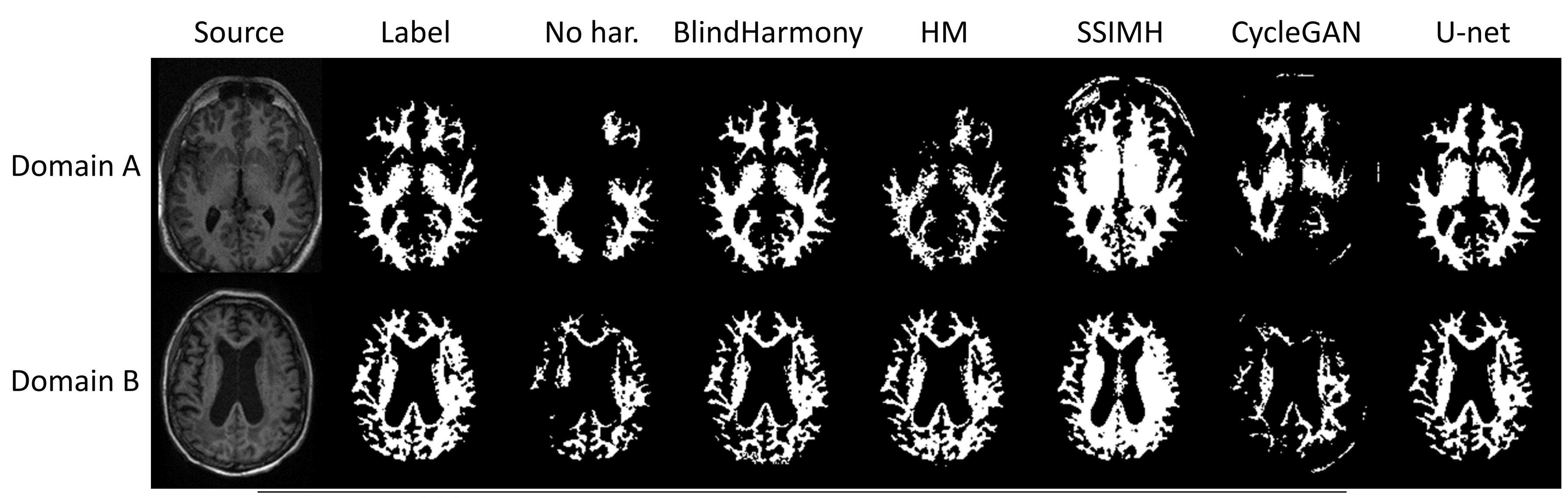
	Domain – Exp		Domain - Log		Domain – Gamma0.7	
	PSNR (↑)	SSIM (↑)	PSNR (↑)	SSIM (↑)	PSNR (↑)	SSIM (↑)
Source	22.6	0.952	21.4	0.958	21.6	0.955
BlindHarmony	29.6	0.985	28.8	0.978	27.4	0.969
HM	26.5	0.961	26.5	0.961	26.5	0.961
SSIMH	26.5	0.972	25.8	0.973	26.3	0.976
CycleGAN (w/ Domain-Exp)	32.6	0.993	23.0	0.951	23.0	0.948
U-net (w/ Domain-Exp)	65.6	0.999	15.9	0.885	15.9	0.879

[Real dataset] Applying BlindHarmony to real source domain images (taken from a different scanner) also demonstrates a strong correspondence with the target domain images.



	Domain A		Domain B		Domain C		Domain D	
	PSNR (↑)	SSIM (↑)	PSNR (↑)	SSIM (↑)	PSNR (↑)	SSIM (↑)	PSNR (↑)	SSIM (↑)
Source	19.6	0.833	19.4	0.836	24.1	0.914	23.0	0.893
BlindHarmony	20.2	0.840	20.8	0.850	24.6	0.912	23.0	0.892
HM	20.4	0.834	20.6	0.840	23.9	0.899	22.5	0.882
SSIMH	20.4	0.831	20.4	0.833	22.6	0.896	22.0	0.882
CycleGAN (each)	7.22	0.451	15.3	0.612	19.8	0.795	6.62	0.442
U-net (each)	25.0	0.919	23.4	0.890	25.1	0.925	25.6	0.920

[Segmentation task] The white matter segmentation network is initially trained on the target domain dataset. When a source domain dataset is inputted, its performance drops. BlindHarmony effectively mitigates this domain gap, resulting in improved performance.



IoU (↑)	Domain A	Domain B	Domain C	Domain D
Source	0.912	0.845	0.938	0.947
BlindHarmony	0.922	0.878	0.938	0.947
HM	0.863	0.854	0.894	0.911
SSIMH	0.777	0.752	0.860	0.862
CycleGAN (each)	0.306	0.408	0.299	0.394
U-net (each)	0.785	0.797	0.870	0.829

Conclusion and Discussion

We propose BlindHarmony, a flow-based blind harmonization method for MR images. Unlike other methods, our approach is trained only on the target domain dataset and can be applied to previously unseen domain images. Both simulated and real-world datasets show acceptable results. This provides a significant advantage in scenarios where access to source domain data is limited or unavailable.

References

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