HEAL: Learning-Free Source Free Unsupervised Domain Adaptation for Cross-Modality Medical Image Segmentation

Northeastern University, Shenyang, China

Yulong Shi, Jiapeng Li, Lin Qi*

BMVC 2025

Abstract

Growing demands for clinical data privacy and storage constraints have spurred advances in Source Free Unsupervised Domain Adaptation (SFUDA). SFUDA addresses the domain shift by adapting models from the source domain to the unseen target domain without accessing source data, even when target-domain labels are unavailable. However, SFUDA faces significant challenges: the absence of source data and label supervision in the target domain due to source-free and unsupervised settings. To address these issues, we propose **HEAL**, a novel SFUDA framework that integrates **H**ierarchical denoising, **E**dge-guided selection, size-**A**ware fusion, and **L**earning-free characteristic. Large-scale cross-modality experiments demonstrate that our method outperforms existing SFUDA approaches, achieving SOTA performance. The source code is publicly available at: ***https://github.com/derekshiii/HEAL***.

Methods

2.1 Hierarchical Denoising

To further mitigate fine-grained pseudo-label errors, we introduce NIG denoising. Specifically, we model the class probability p of each voxel in Y_T as a Gaussian distribution $\mathcal{N}(\mu, \sigma^2)$, where the mean μ and variance σ^2 are governed by a NIG prior.

$$p(\mu, \sigma^2 \mid \alpha, \beta, \gamma, \omega) = \frac{\beta^\alpha \sqrt{\omega}}{\Gamma(\alpha)\sqrt{2\pi\sigma^2}} \left(\frac{1}{\sigma^2}\right)^{\alpha+1} \exp\left\{-\frac{2\beta + \omega(\gamma-\mu)^2}{2\sigma^2}\right\} \tag{3}$$

Where $\Gamma(\cdot)$ is the gamma function and the NIG parameters $\gamma, \omega, \alpha, \beta$ are calculated from $Y_T^{entropy}$. Specifically, γ is directly governed by $Y_T^{entropy}$, which anchors the distribution center to high-confidence regions. In contrast, α is modulated by the discrepancy between Y_T and $Y_T^{entropy}$. Meanwhile, ω and β are dynamically tuned based on the regional entropy $E(v)$, ensuring finer adjustments in regions of higher uncertainty.

2.2 Edge-Guided Selection

First, we use the diffusion model to generate n samples. Then, we apply n sets of Canny edge detectors, where each set consists of two independent detectors:

$$\{\{E_{I_1}, E_{Y_T^*}\}, \{E_{I_2}, E_{Y_T^*}\}, ..., \{E_{I_n}, E_{Y_T^*}\}\} = \text{Canny}(\{I_1, I_2, ..., I_n\}, Y_T^*) \tag{6}$$

Where E_{I_i} represents the edge map of the i_{th} generated image I_i. $E_{Y_T^*}$ represents the edge map of the corresponding diffusion model conditions Y_T^*. $\text{Canny}(\cdot,\cdot)$ denotes the application of the Canny edge detector. To quantify the consistency between the generated image and the conditions, we calculate the structural consistency metric S_i for each generated image I_i:

$$S_i = \frac{|E_{I_i} \cap E_{Y_T^*}|}{|E_{Y_T^*}|} \tag{7}$$

2.3 Size-Aware Fusion

$$\widehat{Y}_T = \sum_{k=1}^{C} \lambda_k \cdot [\mathbb{I}(v_k = v_{min}) \cdot Y_T^* + \mathbb{I}(v_k \neq v_{min}) \cdot M_S(I_B)] \tag{8}$$

Where $v_{min} = min\{v_1, v_2, ..., v_C\}$ denotes the fewest voxels of the target category, $M_S(I_B)$ is the segmentation of the EGS-selected sample I_B , and $\lambda_k = \frac{v_k^{-1}}{\Sigma v_i^{-1}}$ is the dynamic weight of the smallest target.

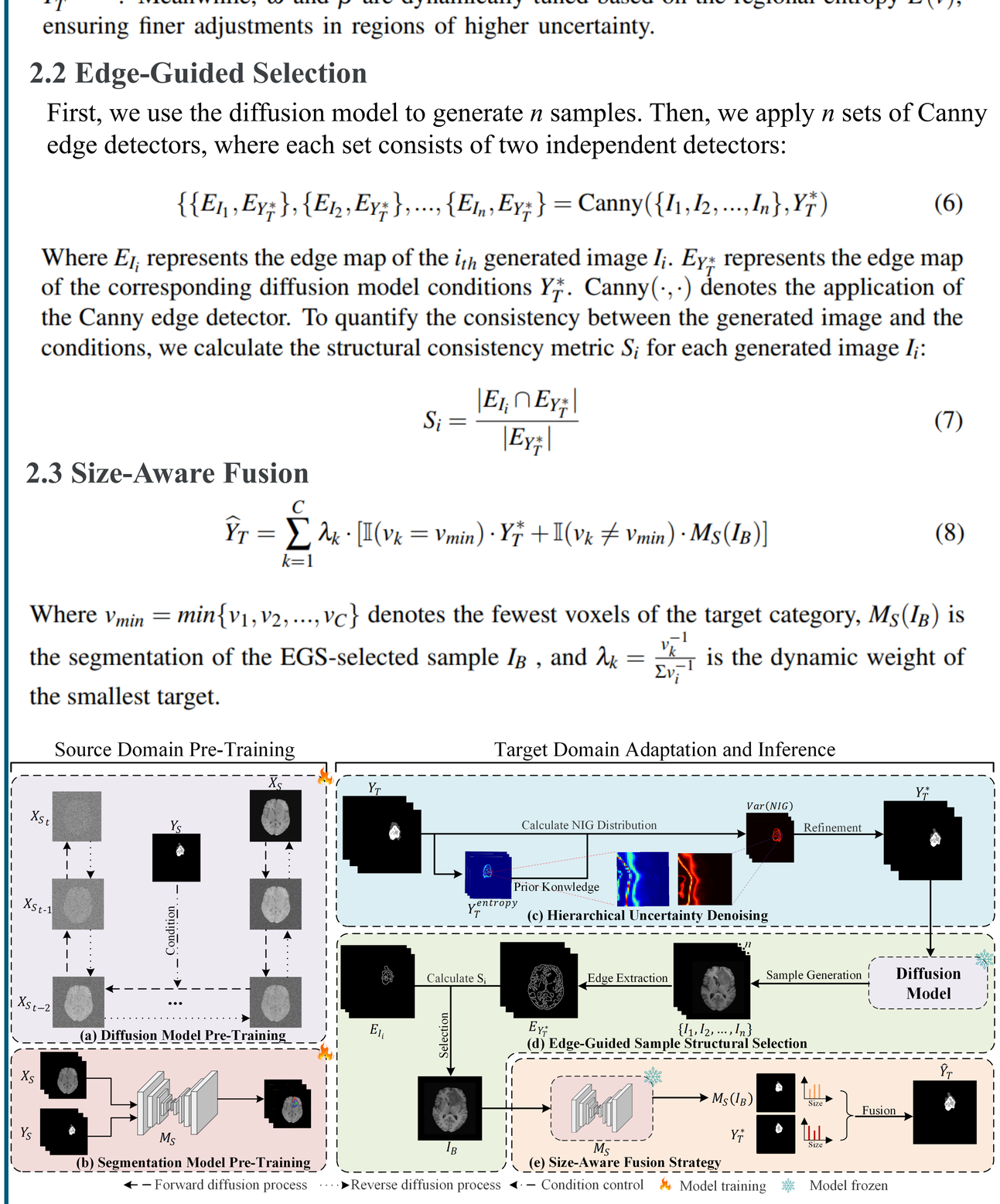

Figure 1. An overview of HEAL, illustrating its key components: hierarchical denoising, edge-guided selection, and size-aware fusion.

Results

3.2 Comparison with SOTA Methods

Method	T1→T1ce								T2→FLAIR							
	Dice (%) ↑				ASD (mm) ↓				Dice (%) ↑				ASD (mm) ↓			
	WT	TC	ET	Mean	WT	TC	ET	Mean	WT	TC	ET	Mean	WT	TC	ET	Mean
No Adaptation	64.3	57.2	55.1	58.9	3.3	2.0	3.2	2.8	67.2	63.0	50.9	60.4	3.2	5.1	2.4	3.6
Supervised	86.2	93.1	73.2	84.2	1.3	0.6	1.4	1.1	93.0	84.3	81.1	86.1	0.8	1.4	1.0	1.1
ProtoContra[25]	46.1	47.9	33.4	42.5	6.0	5.5	4.0	5.2	63.3	56.7	37.6	52.5	4.3	5.8	4.4	4.8
DPL[4]	54.3	49.9	44.8	49.7	5.3	3.7	3.6	4.2	58.8	36.4	18.5	37.9	4.0	7.0	7.8	6.3
IAPC[3]	59.4	58.8	34.8	51.0	7.3	6.1	6.1	6.5	65.1	53.4	30.9	49.8	4.5	5.4	5.8	5.2
UPL[22]	66.1	67.7	60.0	64.6	4.9	3.6	2.8	3.7	54.0	48.4	27.7	43.4	9.9	7.4	6.5	7.9
HEAL	**80.7**	**82.9**	**68.1**	**77.3**	**2.5**	**1.5**	**2.0**	**2.0**	**82.9**	**74.5**	**63.0**	**73.5**	**2.8**	**2.6**	**2.4**	**2.6**

Table 1: Performance comparison of SFUDA methods for brain tumor segmentation. Best results are in **bold**, second best are underlined.

Method	Kvasir-SEG→CVC-ClinicDB		CVC-ClinicDB→Kvasir-SEG	
	Dice (%) ↑	ASD (mm) ↓	Dice (%) ↑	ASD (mm) ↓
No Adaptation	65.1±21.5	5.8±11.1	60.2±27.0	23.7±20.4
Supervised	99.8±0.1	0.36±0.1	97.4±1.3	0.87±1.1
ProtoContra[25]	78.0±12.1	**0.9±0.6**	**68.9±26.4**	9.5±15.0
DPL[4]	67.2±24.0	8.0±12.4	66.1±33.1	**7.8±17.7**
IAPC[3]	73.3±29.6	4.4±7.9	61.2±26.3	13.7±13.2
UPL[22]	67.1±14.6	2.2±0.9	60.2±31.3	11.4±17.2
HEAL	**81.8±22.6**	4.3±8.2	66.5±28.8	9.15±11.6

Table 2: Performance comparison of SFUDA methods for polyp segmentation. Best results are in **bold**, second best are underlined.

3.3 Ablation Study

Method	Kvasir-SEG→CVC-ClinicDB		CVC-ClinicDB→Kvasir-SEG	
	Dice (%) ↑	ASD (mm) ↓	Dice (%) ↑	ASD (mm) ↓
Baseline	65.1±21.5	5.8±11.1	60.2±27.0	23.7±20.4
Entropy-refined	72.6±24.5	5.8±12.2	63.1±33.0	17.9±39.6
HD	76.4±21.3	5.1±10.9	63.8±35.4	16.2±20.8
HEAL (HD+EGS)	**81.8±22.6**	**4.3±8.2**	**66.5±28.8**	**9.15±11.6**

Table 3: Ablation study of HEAL on polyp segmentation. Entropy-refined refers to the pseudo-labels refined by voxel-wise entropy. Best results are in **bold**, second best are underlined.

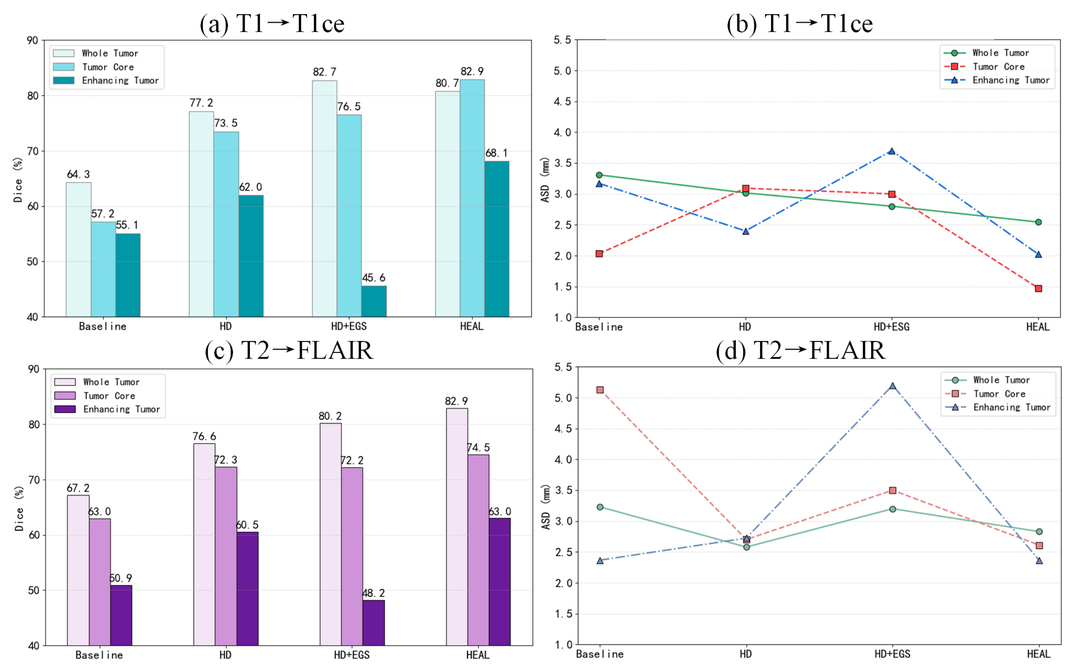

Figure 2. Ablation study of each component in HEAL on brain tumor segmentation

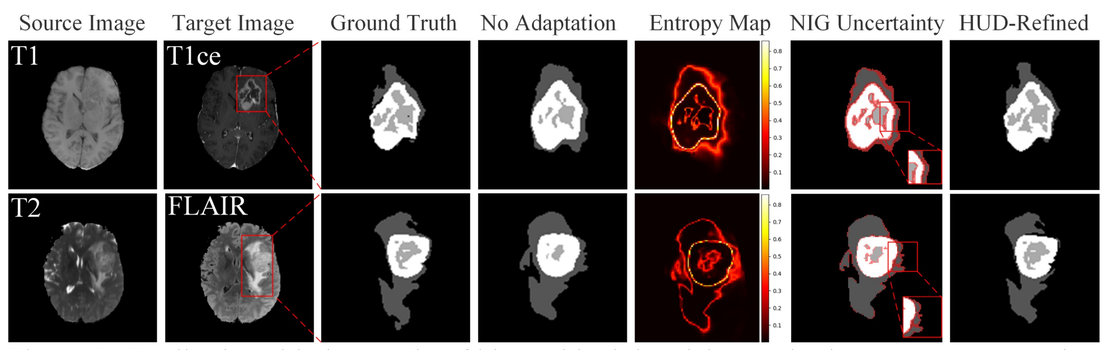

Figure 3. Qualitative ablation study of hierarchical denoising on brain tumor segmentation. The first row corresponds to patient #0000, and the second row to patient #0051.

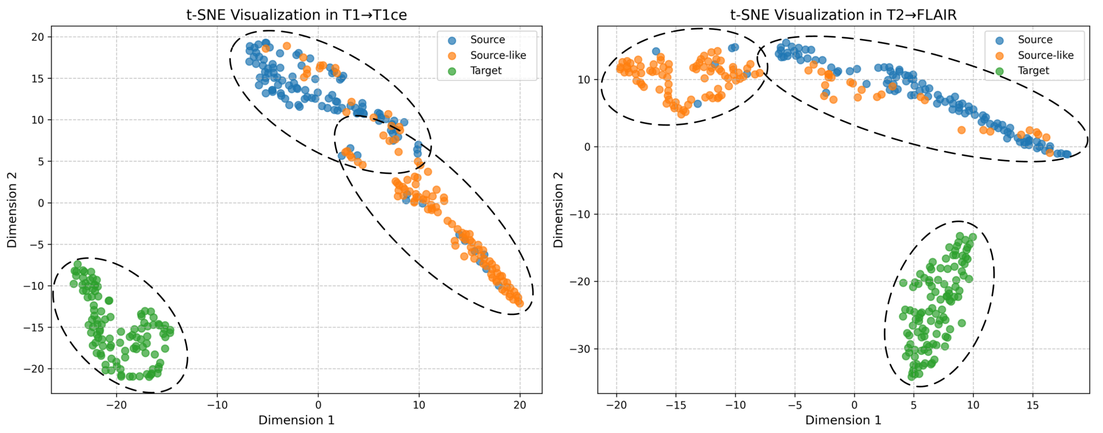

Figure 4. t-SNE visualizations of feature distribution in T1→T1ce and T2→FLAIR.

References

Isensee *et al*. nnu-net: a self-configuring method for deep learning-based biomedical image segmentation. *Nature methods*, 18(2):203–211, 2021.

Dorjsembe *et al.* Conditional diffusion models for semantic 3d brain mri synthesis. IEEE Journal of Biomedical and Health Informatics, 28(7):4084–4093, 2024.

Zeng *et al.* Reliable source approximation: Source-free unsupervised domain adaptation for vestibular schwannoma mri segmentation. In MICCAI 2024, pages 622–632. Springer, 2024.