ICVRV 2025

2025 International Conference on Virtual Reality and Visualization

Author(s): Junkai Lin, Weitong Li, Di Li

Affiliation: Beijing Normal-Hong Kong Baptist University

Domain-Adaptive Fine-Tuning of HI-Diff for Enhanced Microscopy Deblurring & Bacterial Flagellar Motor Localization

1. Introduction

Motivation: Fluorescence microscopy suffers from defocus blur, obscuring nanoscale structures like bacterial flagellar motors.

Challenges:

- Traditional methods (e.g., Blind Deconvolution) struggle with noise amplification.
- Pre-trained Deep Learning models fail due to severe **Domain Shift**.

Contributions:

- Proposed domain-adaptive fine-tuning for HI-Diff.
- Achieved **40.31 dB PSNR** on Leishmania dataset (SOTA).
- Developed MHAF-YOLO for 3D localization (Top 5% in Kaggle).

2. HI-Diff Methodology

Architecture: Combines Latent Diffusion Model (LDM) with a Regression Transformer.

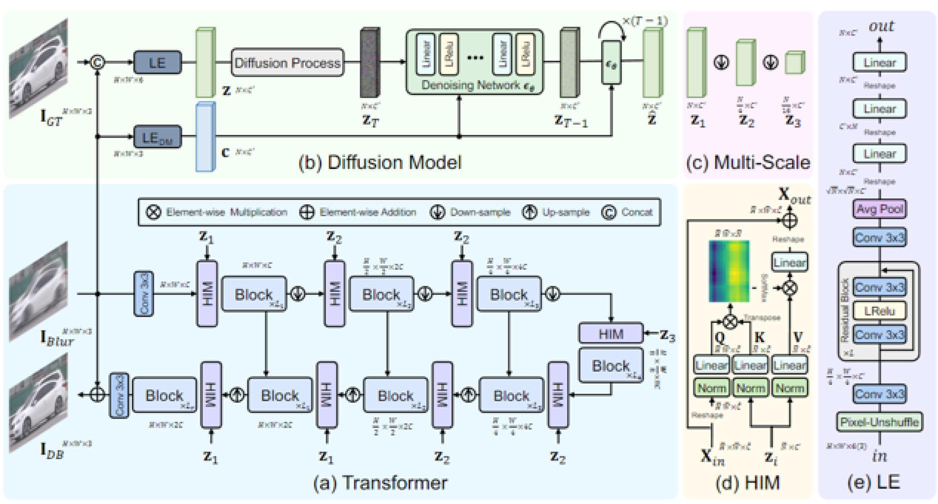

Fig 1. HI-Diff Architecture

Fine-Tuning Strategies:

- **1. Joint Training:** Merge Leishmania & BPAEC datasets.
- **2. Sequential (Source → Target):** Pre-train on structure (BPAEC), fine-tune on target (Leishmania). **(Optimal Strategy)**

Fig. 1. Joint-Small Model Deblurring (Leishmania) **[Blur, Deblur, Oringin]**

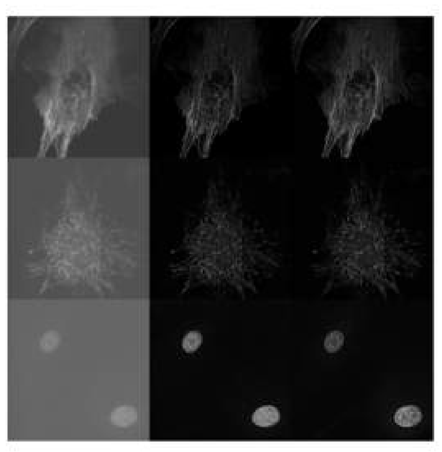

Fig 2.1. Visual Comparison (Blur vs Ours vs GT)

3. Deblurring Results (Visual)

Comparison on Leishmania Dataset. Note the recovery of fine parasite structures.

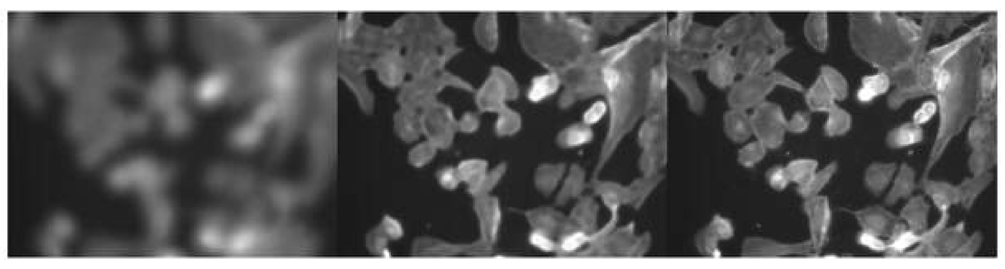

Fig. 3. Joint-Small Model Deblurring (BBBC06) **[Blur, Deblur, Oringin]**

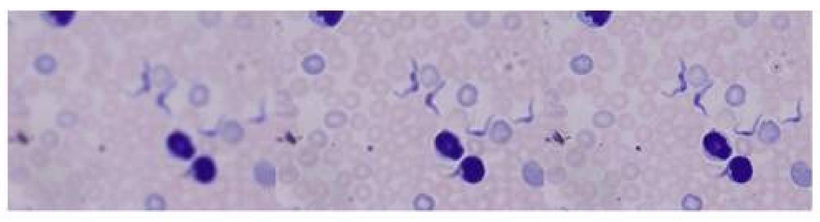

Fig. 4. Joint-Small Model Deblurring (Tryp.) **[Blur, Deblur, Oringin]**

Fig 2.2. Visual Comparison (Blur vs Ours vs GT)

4. Quantitative Analysis

1. Target Domain Evaluation (Leishmania): Sequential Fine-Tuning (Source → Target) yields the best performance (+3.24 dB). Note that "Reverse" order causes severe collapse, confirming domain directionality matters.

Model Variant	Training Strategy	PSNR (dB)	SSIM
Baseline	Pre-trained (GoPro)	37.07	0.9335
Joint (5k)	Mixed Dataset	39.74	0.9578
Seq. (Reverse)	Lei → BPAEC	17.05	0.8806
Seq. (Ours)	**BPAEC → Lei**	**40.31**	**0.9599**

2. Robustness & Generalization Analysis:

- **Catastrophic Forgetting (BPAEC):** Fine-tuning on Leishmania degrades performance on the source domain (BPAEC), indicating a trade-off between specialization and generalist capability.
- **Complex Structures (BBBC06):** Joint training on large datasets enables the model to handle complex grayscale structures where the baseline fails.

Test Dataset	Metric	Strategy	Score	Δ vs Base
BPAEC (Source Domain)	Avg PSNR	Baseline	11.87	-
		BPAEC-Only	**31.98**	+20.11
		Seq. (Ours)	24.33	*-7.65 (Forget)*
BBBC06 (Unseen Complex)	Avg PSNR	Baseline	11.87	-
		Joint-Large	**36.17**	**+24.30**

Conclusion: Use **Sequential** strategies for peak performance on specific targets, and **Joint Training** for broad generalization across diverse biological samples.

5. Flagellar Motor Localization (Kaggle)

Task: 3D localization of bacterial flagellar motors in Cryo-ET tomograms. textbfMetric: Modified F_2-Score (Recall-focused) with distance tolerance $< 150\mathring{A}$.

Fig 3. BYU-LBFM 2025: 3D Tomogram Visualization

Methodology: MHAF-YOLO Pipeline We employed a slice-wise detection approach with 3D aggregation:

- **Model:** Multi-Head Attention Fusion YOLOv10 for small objects.
- **TTA:** Test-Time Augmentation (Horizontal Flip) to boost robustness.
- **Post-Processing:** Weighted Box Fusion (WBF) and 3D NMS for precise volumetric aggregation.

Competition Results (Top 5%): Our method achieved significant improvements over the baseline on the hidden test set.

Model	Public Score	Private Score	Rank
Baseline	0.81047	0.79927	-
Ours	**0.82716**	**0.80849**	**59 / 1180**

6. Conclusion

- **Strategy:** Sequential Fine-Tuning yields best deblurring results (40.31 dB).
- **Generalization:** Model works well on unseen domains.
- **Future Work:** Integrate deblurring as pre-processing to boost detection.