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SAMPLE ALIGNMENT FOR IMAGE-TO-IMAGE TRANSLATION BASED MEDICAL DOMAIN ADAPTATION

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Introduction

- Whenever target data is either not available, or expensive to collect and label it, the typical approach is to use available datasets, which leads to suboptimal performance. Domain adaptation has been developed to address the issue.
- I2I translation, which learns the mapping from a given image to a specific target image, can be employed to align the source and target domain.
- For boosting the I2I translation based DA in medical scenarios, a sample alignment algorithm is proposed to correct the sample bias in medical data.

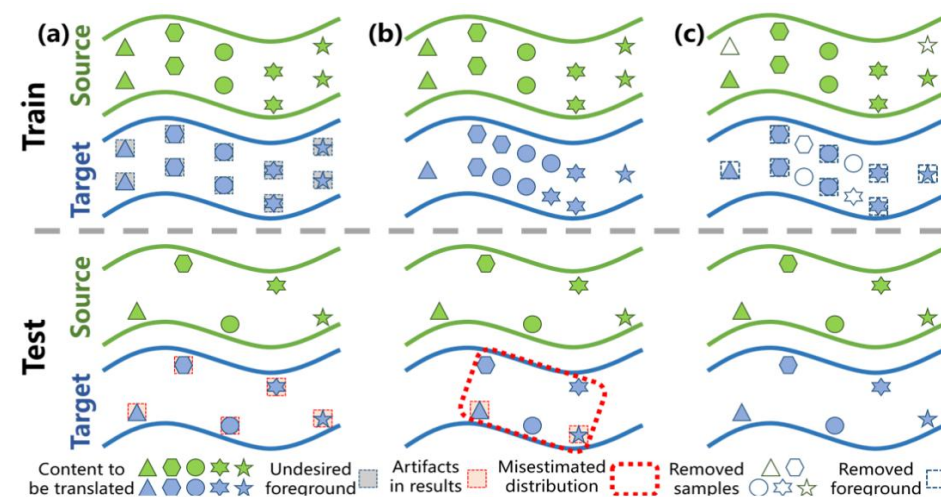


Figure 1: Sample bias in the training of I2I translation models leads to undesired artifacts in DA. (a) the different foreground distributions in paired samples (b) the non-uniform sampling (c) the proposed algorithm

Method

- ❑ Sample alignment
- ❑ Structure alignment by diffeomorphic transformation
- ❑ Symmetric resampling
- ❑ Weakly paired 2D data
- ❑ Unpaired 3D data

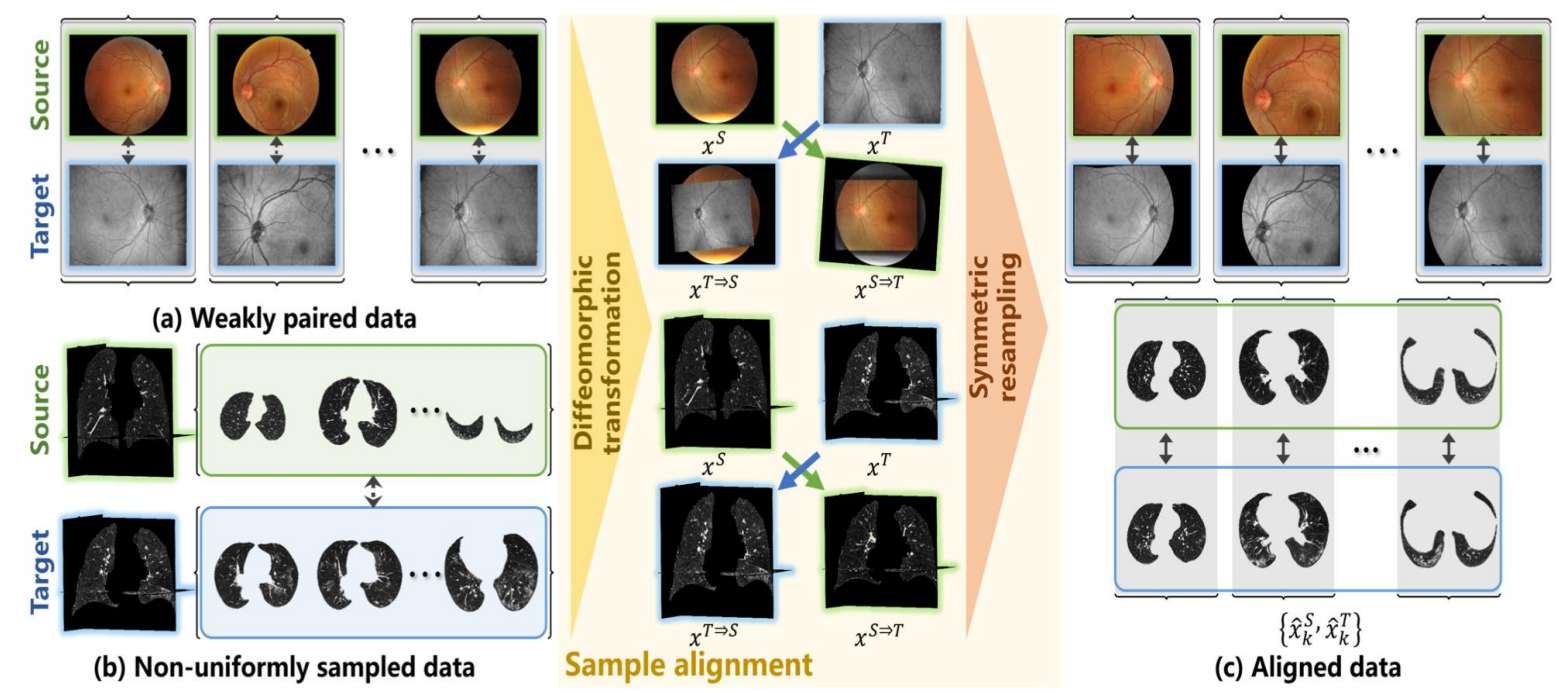


Figure 2: To address the samples bias in (a) and (b), sample alignment is implemented to acquire (c). Using diffeomorphic transformation and symmetric resampling, the aligned data corrects the discrepant foreground distributions in (a) and distribution bias in (b) to boost the training of I2I translation models.

Implementation scenarios

- The cross-modality translation between the weakly paired color fundus photography and En face OCT
- The pathological image synthesis of CT scans with COVID-19

Synthesis quality evaluation

Table 1. Quantitative evaluation of the synthesis quality.

Methods	2D fundus		3D lung	
	PA	mIoU	PA	mIoU
pix2pix	—	—	—	—
CycleGAN	0.896	0.644	0.964	0.910
CUT	0.847	0.478	0.918	0.835
SA+pix2pix	0.983	0.927	0.993	0.977
SA+CycleGAN	0.988	0.957	0.995	0.985
SA+CUT	0.905	0.704	0.986	0.962

Boosting of clinical diagnosis

Table 2. Diagnosis accuracy with I2I translation based DA.

Methods	VGG16	ResNet18
Original Data	0.853	0.862
pix2pix / SA+pix2pix	— / 0.871	— / 0.885
CycleGAN / SA+CycleGAN	0.811 / 0.903	0.830 / 0.906
CUT / SA+CUT	0.844 / 0.872	0.819 / 0.874

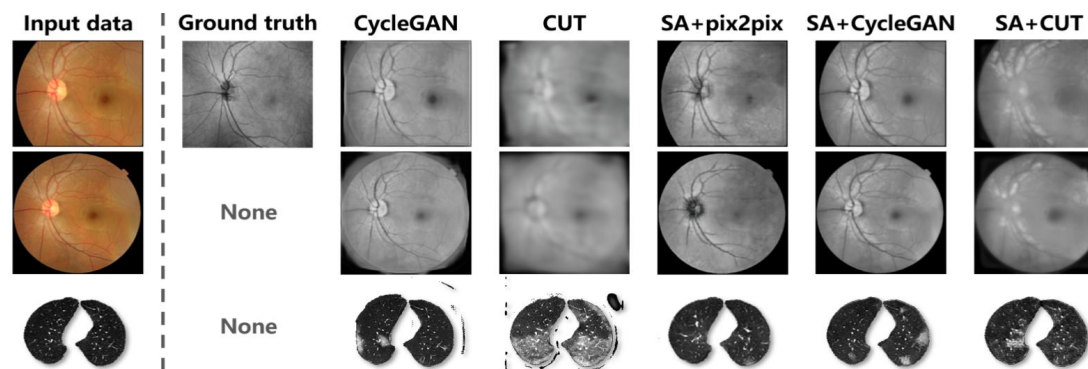


Figure 3: Visual comparison of the synthesis results. The first two row present the cross-modality translation of fundus images using the aligned and original data, and the third row is the synthesis of COVID-19 infected CT scan.

Conclusion

- To boost the I2I translation based DA in the attendance of sample bias, a sample alignment algorithm is proposed in this paper.
- The structures in samples are first aligned by diffeomorphic transformation, and paired data are symmetrically resampled from the aligned ones.
- The experiments demonstrate the effectiveness of the proposed algorithm, it suppresses the artifacts in synthesized images and improved the performances of DA on diagnosis models



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Thank You !