

Sample Alignment For Image-To-Image Translation Based Medical Domain Adaptation



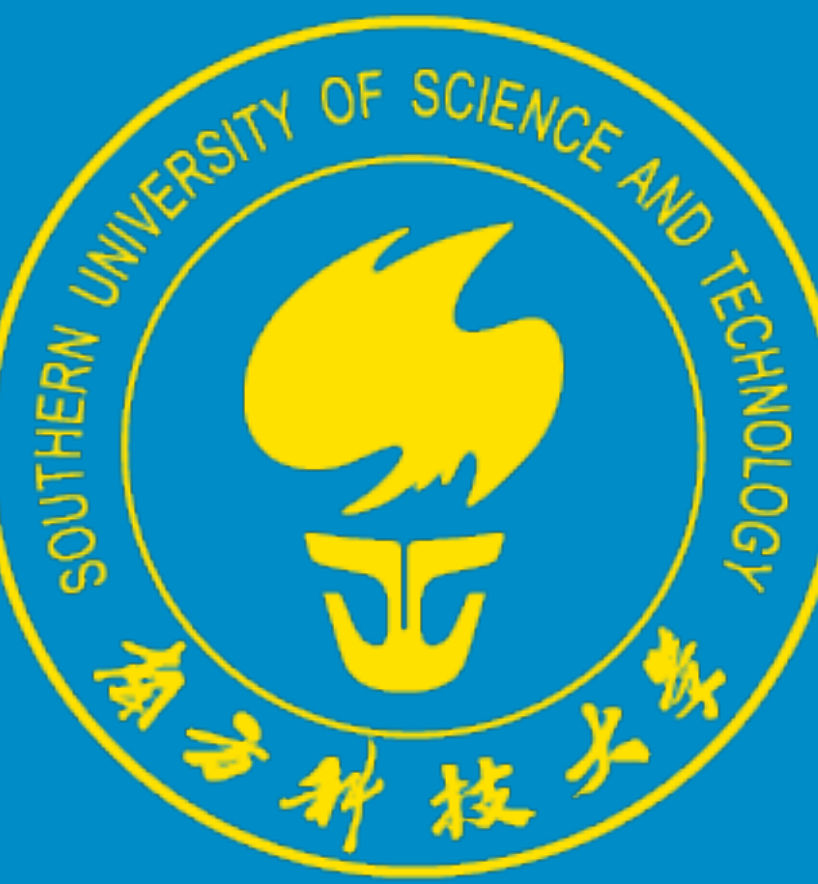
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INTRODUCTION

- 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.

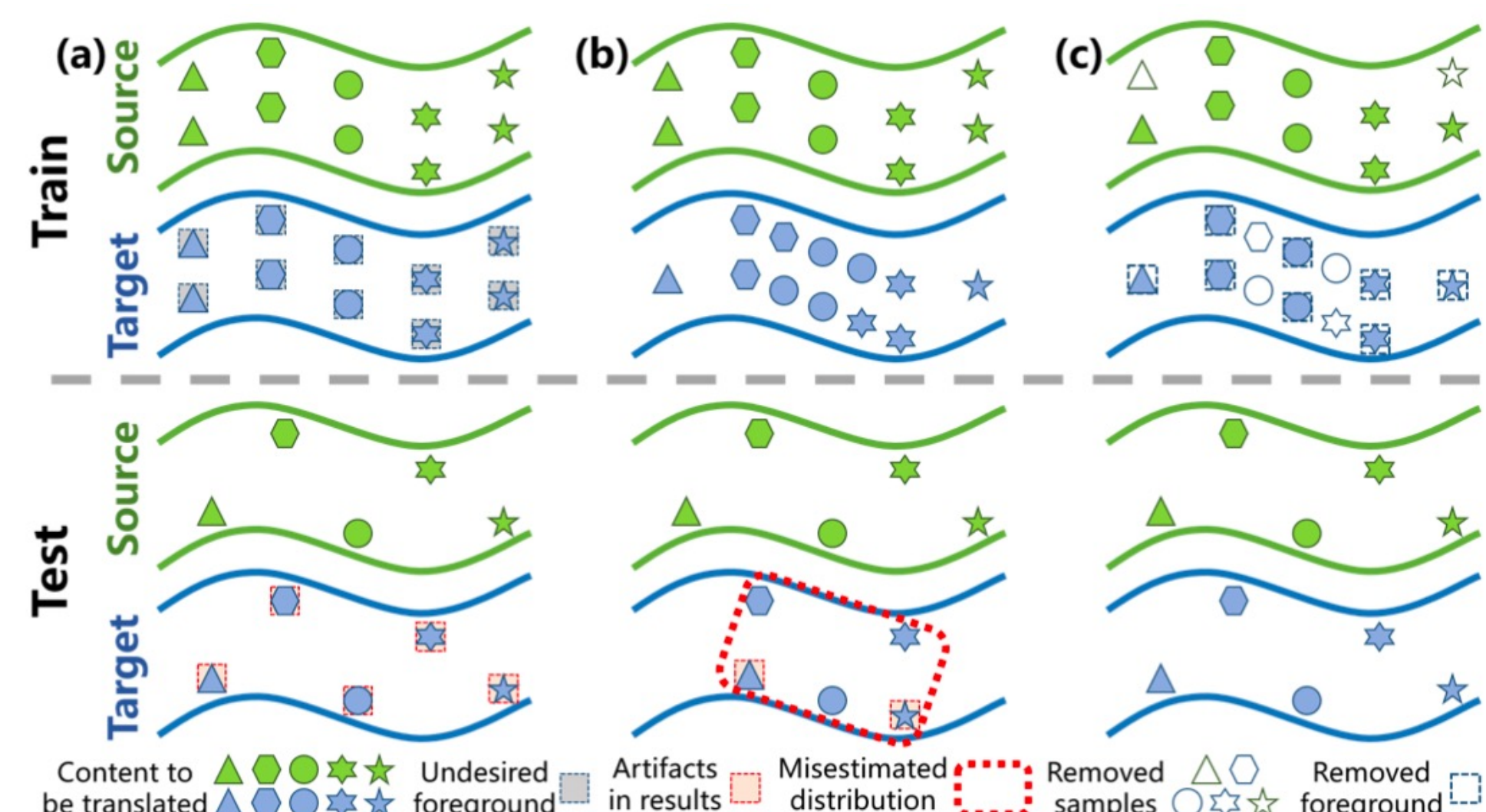


Figure 1: Sample bias in the training of I2I translation models leads to undesired artifacts in DA. (a) the different foreground distributions in paired samples (b) the non-uniform sampling (c) the proposed algorithm

AIM

In this paper, we aim to boost the Image-To-Image translation based on Domain Adaptation by proposing a sample alignment (SA) algorithm to fundamentally correct the sampling bias

CONCLUSIONS

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.

METHOD

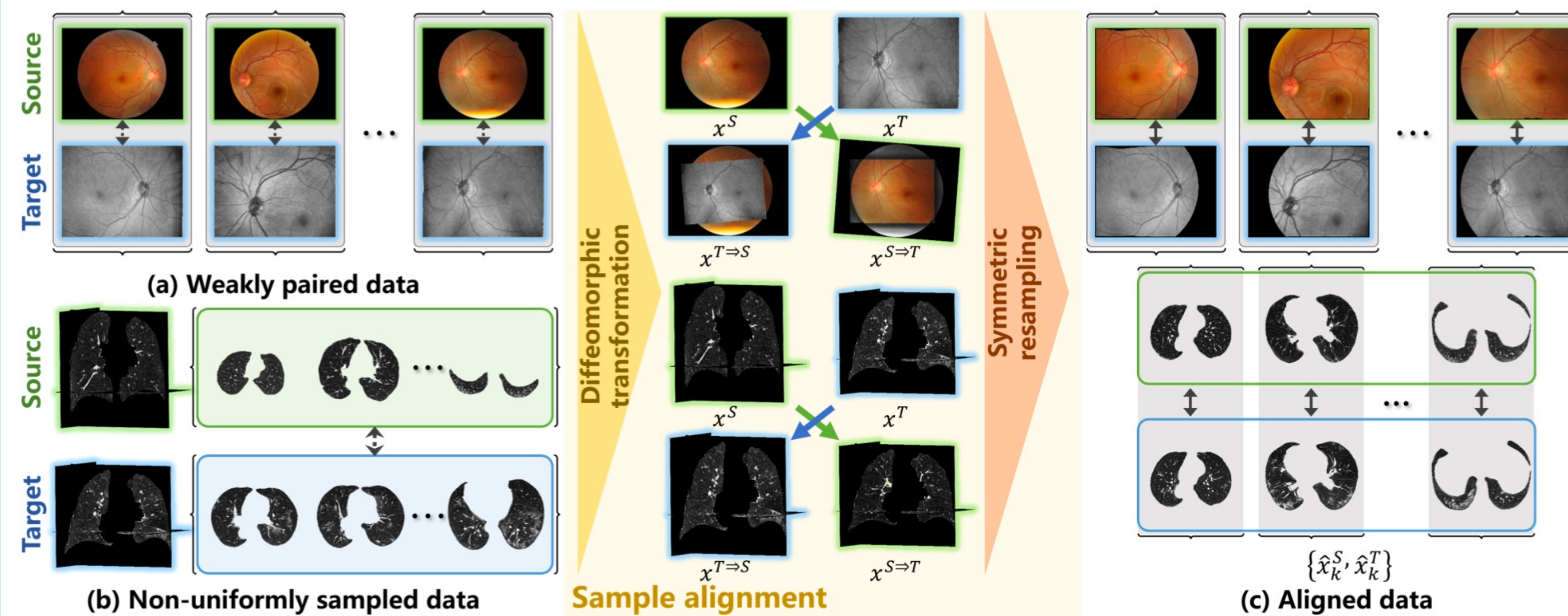


Figure 2: To address the samples bias in (a) and (b), sample alignment is implemented to acquire (c). Using diffeomorphic transformation and symmetric resampling, the aligned data corrects the discrepant foreground distributions in (a) and distribution bias in (b) to boost the training of I2I translation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

• Sample alignment

SA is proposed to correct the sample bias in I2I translation. As shown in Figure. 2, the anatomical structures in original samples are first aligned using diffeomorphic transformation, and then symmetric resampling is performed to eliminate the bias.

• Structure alignment by diffeomorphic transformation

Structure alignment is conducted between the source and target samples by registering the anatomical topologies. Diffeomorphic transformation is employed to implement the registration. Meanwhile, diffeomorphic transformation defines a time-dependent, smooth velocity field.

• Symmetric resample

Images without bias are symmetrically resampled from the structure aligned samples to learn the mapping $M^{S \rightarrow T}$.

• Weakly paired 2D data

$$\text{if } \theta \in \mathbb{R}^2, \{\hat{x}_k^S, \hat{x}_k^T\} = \{x_k^S(\theta), x_k^T \circ M(x_k^S(\theta))\} \odot [M(x_k^S(\theta)) \cap M(x_k^T \circ M(x_k^S(\theta)))]$$

Where we denote the foreground mask as $M(\cdot)$. K is the index of samples and \odot represents the element-wise multiplication

• Unpaired 3D data

$$\text{if } \theta \in \mathbb{R}^3, \{\hat{x}_{i,j}^S, \hat{x}_{i,j}^T\} = \{x_{i,j}^S(\theta), x_{i,j}^T \circ M(x_{i,j}^S(\theta))\} \odot [M(x_{i,j}^S(\theta)) \cap M(x_{i,j}^T \circ M(x_{i,j}^S(\theta)))]$$

where i and j are the indexes of source and target samples.

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RESULTS

To validate the effectiveness of the proposed sample alignment, we implement it in two DA scenarios of medical image translation :

- 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

Qualitative evaluation is exhibited in Figure. 3. Due to the discrepancy in foreground distribution, the OCT images synthesized without SA attempt to fill the background of fundus images. And as a result of the non-uniform sampling, the translation models make efforts on extending the foreground of the lung area.

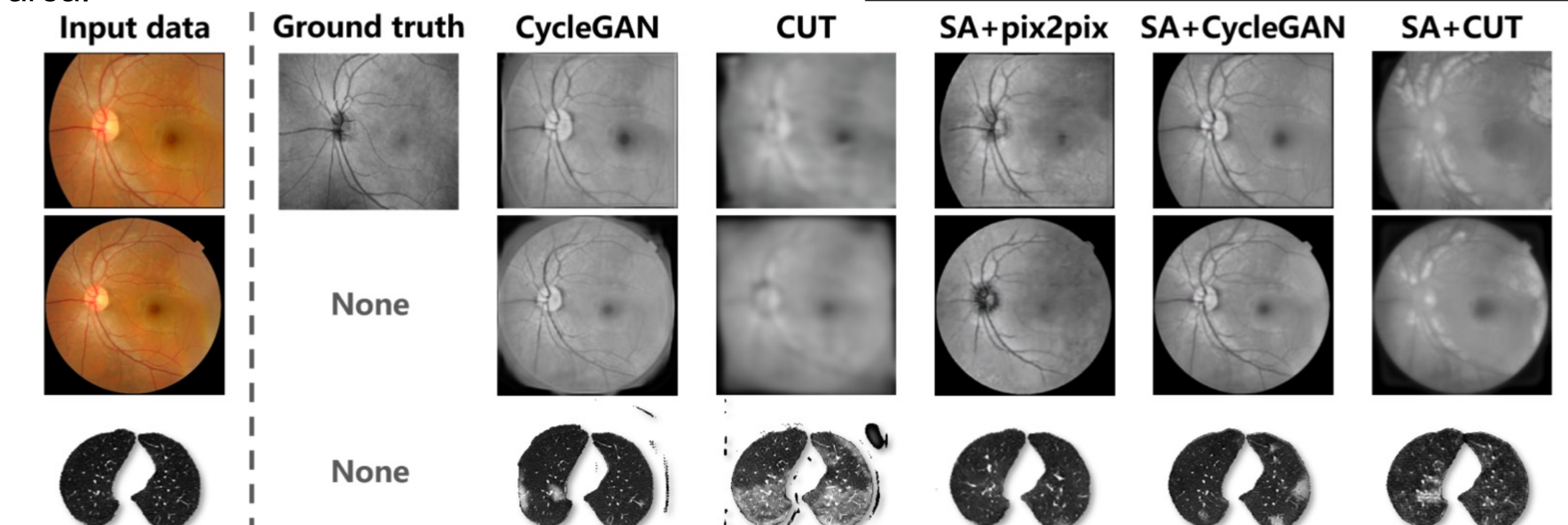


Figure 3: Visual comparison of the synthesis results. The first two rows present the cross-modality translation of fundus images using the aligned and original data, and the third row is the synthesis of COVID-19 infected CT scan.

Boosting of clinical diagnosis

As I2I translation has been extensively used as a paradigm of DA to boost computer-aided diagnosis, DA on the automatic diagnosis of COVID-19 is performed to verify SA. CT scans are augmented by I2I translation with and without SA, then VGG16 and ResNet18 are trained as the classifier to diagnose CT scans infected COVID-19. The diagnosis accuracy is summarized in Table 2

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

Compared to the diagnosis only using original data, the augmentation without SA degrades the diagnosis performance, resulting from the artifacts in synthesized images. Thanks to SA suppressing the artifacts, the training of diagnosis models is boosted by the synthesized images to outperforms the model only learned from the original data.

A quantitative evaluation of the synthesis quality is summarized in Table 1. As the pixel-wise paired ground truth is unavailable in this experiment, the synthesis artifacts are quantified using the segmentation evaluation metrics of pixel accuracy (PA) and mean intersection over union (MIoU) to evaluate the synthesis quality. Table 1 shows that the synthesis artifacts have been effectively suppressed by SA.

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