Medical Image Seminar

Yicheng Jiang CUHK, Shenzhen July 2, 2020

Paper List

MICCAI 2019	Unsupervised Domain Adaptation via Disentangled Representations: Application to Cross-Modality Liver Segmentation				
MICCAI 2019	Integrating cross-modality hallucinated MRI with CT to aid mediastinal lung tumor segmentation				
MICCAI 2018	Tumor-Aware, Adversarial Domain Adaptation from CT to MRI for Lung Cancer Segmentation				
CVPR 2018	Task Driven Generative Modeling for Unsupervised Domain Adaptation: Application to X-ray Image Segmentation				



Background

Domain Adaptation (领域自适应)

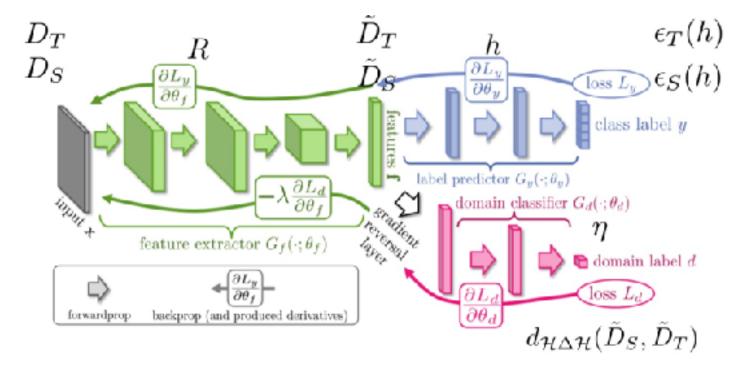
领域自适应即**Domain Adaptation**,是 利用信息丰富的 **源域样本source domain** 来提升 **目标域target domain** 模型的性能。通常指,特征层面自适应,目的是把分布不同的源域和目标域的数据,映射到一个特征空间中,使其在该空间中的距离尽可能近。于是在特征空间中对source domain训练的目标函数,就可以迁移到target domain上,提高target domain上的准确率。

Example:

Gf: 将数据映射到feature space

Gy: 对feature space的source domain进行分类, 尽可能分出正确的label。

Gd: 对feature space的数据进行 领域分类, 尽量分辨出数据来自于哪一个domain。



Paper Information

TITLE

Unsupervised Domain Adaptation via Disentangled Representations: Application to Cross-Modality Liver Segmentation

Authors

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Problem

Target

Learn a liver segmentation model from the more accessible CT data that also performs well on MRI images.

Source Domain: CT

Target Domain: MRI

Challenge

Achieve domain adaptation between CT and MRI while maintaining the complex relationship between the two domains. exhibit quite different visual appearance with the same anatomical structure shared behind them.

Assumption

Many-to-Many Mapping

MRI and CT images exhibit quite different visual appearance with the same anatomical structure shared behind them.

A shared domain-invariant space that preserves the anatomical information

A domain-specific style code for each modality

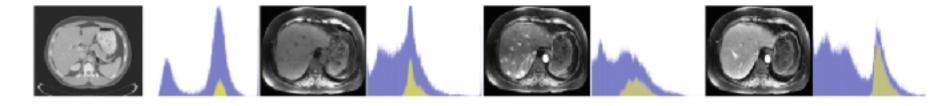


Fig. 1. Images and histograms of liver (yellow) and whole image (blue). From left to right: CT, multiphasic MRI sequence at three time points (pre-contrast, 20s post-contrast i.e. arterial phase, 70s post-contrast i.e. portal venous phase) (Color figure online)

Domain Adaptation via Disentangled Representations (DADR)

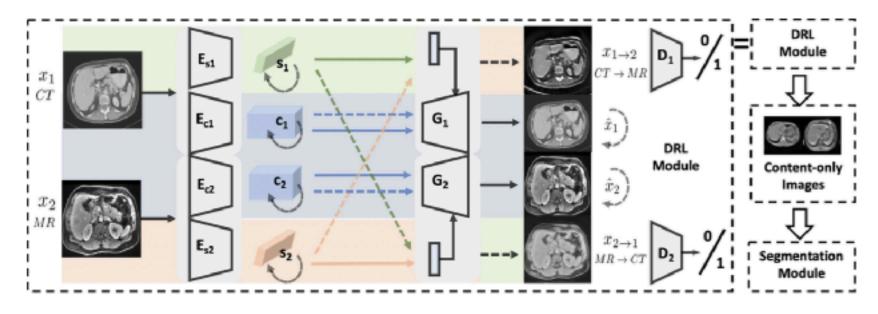


Fig. 2. Left: Framework for Disentangled Representation Learning Module. Solid line: in-domain reconstruction, Dotted line: cross-domain translation. Right: Pipeline of Domain Adaptation via Disentangled Representations (DADR)

Loss

$$L_{total} = \alpha L_{recon} + \beta L_{adv} + \gamma L_{latent} \tag{1}$$

(a) In-domain reconstruction, $L_{recon} = L_{recon}^1 + L_{recon}^2$

$$L_{recon}^{i} = \mathbb{E}_{x_{i} \sim X_{i}} ||G_{i}(E_{ci}(x_{i}), E_{si}(x_{i})) - x_{i}||_{1}$$
(2)

(b) Cross-domain translation, $L_{adv} = L_{adv}^{1 \to 2} + L_{adv}^{2 \to 1}$

$$L_{adv}^{1\to 2} = \mathbb{E}_{c_1 \sim p(c_1), s_2 \sim p(s_2)}[log(1 - D_2(x_{1\to 2}))] + \mathbb{E}_{x_2 \sim X_2}[log(D_2(x_2))]$$
(3)

(c) Latent space reconstruction, $L_{latent} = L_{recon}^{c_1} + L_{recon}^{s_1} + L_{recon}^{c_2} + L_{recon}^{s_2}$

$$L_{recon}^{c_1} = ||E_{c_2}(x_{1\to 2}) - c_1||_1, L_{recon}^{s_2} = ||E_{s_2}(x_{1\to 2}) - s_2||_1$$
(4)



Data

- Unpaired CT slices of 130 patients from LiTS challenge 2017
- Multi-phasic MRI slices of 20 local patients with HCC

Exp1: Segmentation with Domain Adaptation

Note: Domain Adaptation with CycleGAN (DACGAN) (MICCAI 2018)

Table 1. Comparison of Segmentation Results

Method	DICE	std
UNet w/o DA	0.26	0.07
DACGAN	0.72	0.05
DADR	0.81	0.03



Fig. 5. Two examples of segmentation results. Left to right: pre-contrast MR, liver mask, predictions from UNet w/o DA, DACGAN, DADR

Exp2: Joint-Domain Learning

Table 2. Joint-domain Learning with DADR

Method	CT tested DSC	MR tested DSC
CT trained	0.901(0.020)	0.260(0.072)
MR trained	0.134(0.091)	0.869(0.044)
Joint CT & MR	0.912(0.012)	0.891(0.040)

- Exp3: Multi-modal Target Domain
- Multi-phasic MR with three phases as multi-modal target domain

- Exp3: Multi-modal Target Domain
- A. Robust Domain Adaptation

Table 3. DA on Multimodal Target Domain

Method	DICE	std
DACGAN	0.52	0.06
DADR	0.74	0.04

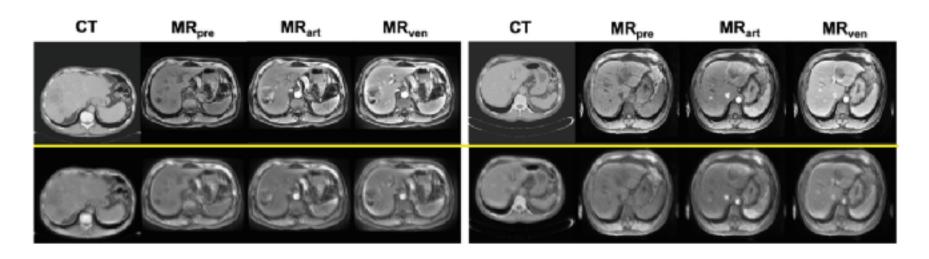
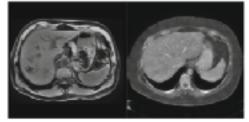
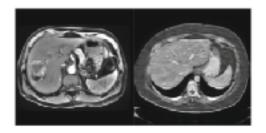


Fig. 6. Two examples of content-only images via disentangled representations for multi-phasic MR. first row: original images, second row: content-only images.

- Exp3: Multi-modal Target Domain
- B. Diverse Style Transfer.







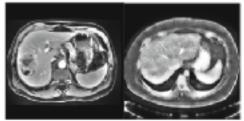


Fig. 7. Three examples of multi-modal style generation with reference, from left to right: CT, three pairs of reference MR and generated MR (pre-contrast, arterial, portal venous phase)

Contribution

- First to achieve unsupervised domain adaptation for segmentation via disentangled representations in the field of medical imaging.
- Superior performance on a liver segmentation task with crossmodality domain adaptation to the state-of-art CycleGAN.
- Demonstrate the generalizability of our model to joint-domain learning and robust adaptation to a multi-modal target domain with large variety

Paper Information

TITLE

Integrating cross-modality hallucinated MRI with CT to aid mediastinal lung tumor segmentation

Authors

Jiang Jue¹, Hu Jason¹, Tyagi Neelam¹, Rimner Andreas², Berry L. Sean¹, Deasy O. Joseph¹, and Veeraraghavan Harini¹ *

- Medical Physics, Memorial Sloan Kettering Cancer Center
- ² Radiation Oncology, Memorial Sloan Kettering Cancer Center

Problem

- Target
- CT肺部肿瘤分割
- Challenge
- 通过领域自适应的学习方式,将MRI图像中的特征信息,结合到CT图像中,以提高CT的肺部肿瘤分割结果

Cross-Modality Educed Deep Learning (CMEDL)

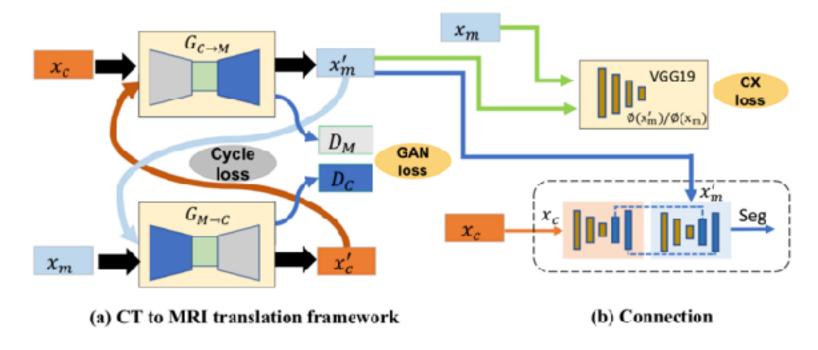


Fig. 1: Overview of the comparison of different combinations. x_c is the CT image; x_m is the MRI image; $G_{C\to M}$ and $G_{M\to C}$ are the CT and MRI transfer networks; x_m is the translated MRI image from x_c ; x_c is the translated MRI image from x_m .

CX Loss

$$CX(g,m) = \frac{1}{N} \sum_{i} \max_{i} CX(g_j, m_i), \tag{1}$$

$$L_{cx} = -log(CX(f(G(X_{CT})), f(X_{MR})).$$
(2)

Segment Loss

$$L_{seg} = \mathbb{E}_{x_c \sim X_{CT}} \left[-logP(S_{MR}(G_{CT \to MR}(x_c))) - logP(S_{CT}(x_c)) \right] +$$

$$\|\phi_{CT}(x_c) - \phi_{MR}(G_{CT \to MR}(x_c))\|_F^2,$$
(3)

Total Loss

$$Loss = L_{adv} + \lambda_{cyc}L_{cyc} + \lambda_{cx}L_{CX} + \lambda_{seg}L_{seg}, \tag{4}$$

Data

- 1. the Cancer Imaging Archive (TCIA) with non-small cell lung cancers (NSCLC) consisting of 377 patients (training)
- 2. 81 longitudinal T2-weighted MR scans (scanned on Philips 3T Ingenia) from 21 patients treated with radiation therapy, and (training)
- 3. 637 contrast-enhanced tumors treated with immunotherapy at our institution for validation (N=304) and testing (N=333)

Tumor Detection Rate and Segmentation Accuracy

Table 1: Detection and segmentation accuracy using the two networks.

	Validation			Test		
Method	Detection rate	DSC	HD95 mm	Detection rate	DSC	HD95 mm
U-net CT	80%	$0.67 {\pm} 0.18$	7.44 ± 7.18	79%	0.68 ± 0.17	9.35±7.08
DenseFCN CT	77%	0.70 ± 0.15	7.25 ± 6.71	75%	0.68 ± 0.16	9.34 ± 9.68
U-net CMEDL	85%	0.71 ± 0.15	6.57 ± 7.15	85%	0.72 ± 0.14	8.22±6.89
DenseFCN CMEDL	84%	0.74 ± 0.12	5.89 ± 5.87	84%	0.73 ± 0.12	7.19 ± 8.55

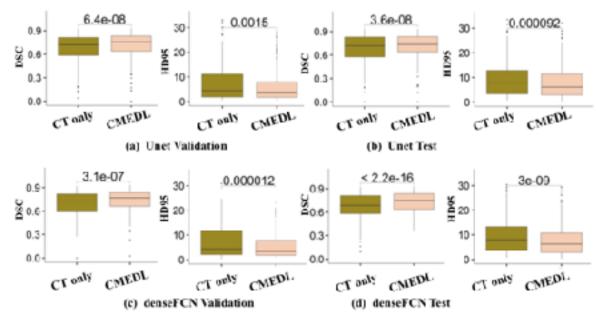


Fig. 2: Box plots comparing CT-only and CMEDL-based networks.

Visual Comparisons

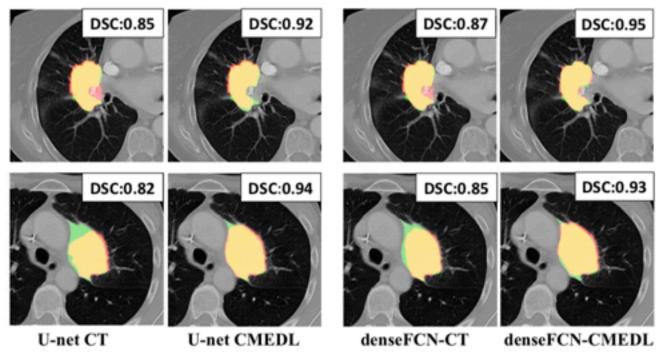


Fig. 3: Representative segmentations produced using CT-only and CMEDL-based segmentations for U-net and DenseFCN networks. The Dice similarity coefficient (DSC) is also shown for each method. Red corresponds to algorithm, green to expert and yellow to overlap between algorithm and expert.

Visual Comparisons

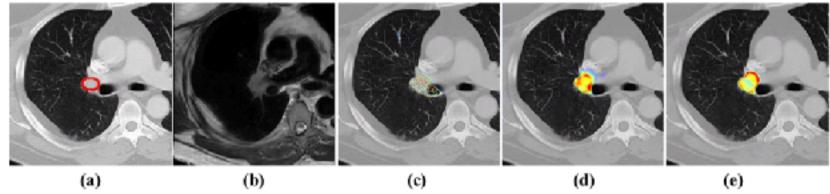


Fig. 4: Feature map activations from the 21 channel of last layer of Unet. (a) the original CT (b) the translated pMRI (c) activation from CT only (d) activation from pMRI (e) activation from CMEDL

Paper Information

TITLE

Tumor-Aware, Adversarial Domain Adaptation from CT to MRI for Lung Cancer

Segmentation

Authors

Jiang Jue
¹, Hu Jason¹, Tyagi Neelam¹, Rimner Andreas², Berry L. Sean¹, Deasy O. Joseph¹, and Veeraraghavan Harini¹ *

- Medical Physics, Memorial Sloan Kettering Cancer Center
- ² Radiation Oncology, Memorial Sloan Kettering Cancer Center

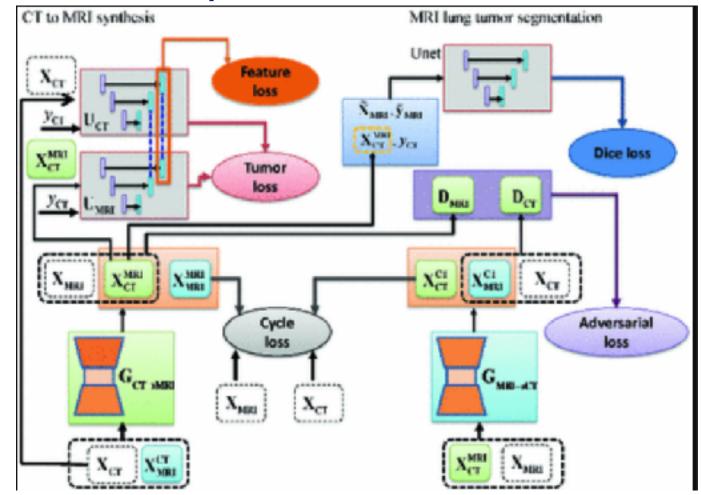
Problem

- Target
- MRI肺部肿瘤分割

Source domain: CT

Target domain: MR

Tumor aware semi-supervised





Data

- 1. the Cancer Imaging Archive (TCIA) with non-small cell lung cancers (NSCLC) consisting of 377 patients (training)
- 2. 81 longitudinal T2-weighted MR scans (scanned on Philips 3T Ingenia) from 21 patients treated with radiation therapy, and (training)

Segmentation Accuracy

Table 1.

Segmentation accuracy

Method	Validation		Test		
	DSC	HD95 mm	DSC	HD95 mm	
Week one only	0.63 ± 0.27	7.22 ± 7.19	0.55 ± 0.25	13.23 ± 0.75	
Cycle-GAN [5]	0.57 ± 0.24	11.41 ± 5.57	0.66 ± 0.16	11.91 ± 4.44	
Masked cycle-GAN [8]	0.67 ± 0.21	7.78 ± 4.40	0.63 ± 0.24	11.65 ± 6.53	
Tumor aware unsupervised	0.62 ± 0.26	7.47 ± 4.66	0.74 ± 0.15	8.88 ± 4.83	
Tumor aware semi-supervised	$\textbf{0.70} \pm \textbf{0.19}$	$\textbf{5.88} \pm \textbf{2.88}$	$\textbf{0.80} \pm \textbf{0.08}$	7.16 ± 4.52	

Segmentation Accuracy

Val

Fig. 4.

红色: GT; 黄色: 分割结果

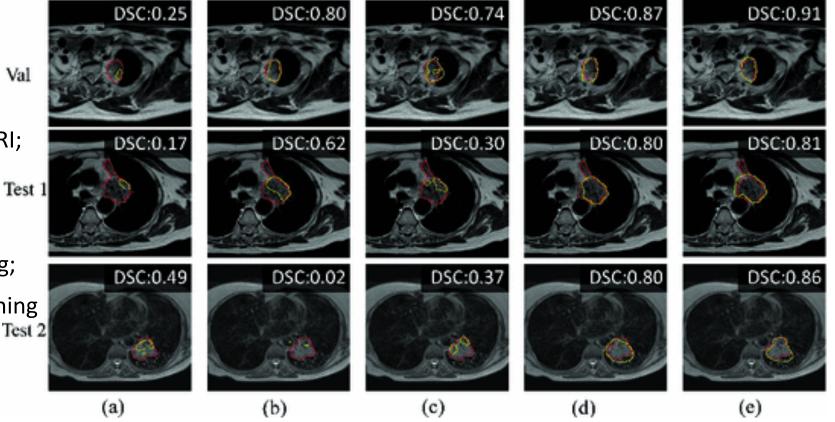
(a) segmentation with only week 1 MRI;

(b) cycle-GAN;

(c) masked cycle-GAN;

(d) tumor-aware unsupervised learning;

(e) tumor-aware semi-supervised learning Test 2



Paper Information

TITLE

Task Driven Generative Modeling for Unsupervised Domain Adaptation: Application

to X-ray Image Segmentation

Authors

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Problem

- Target
- Learn a multi-organ segmentation model on unlabeled X-ray images using pixel-wise annotated DRRs data.

Task Driven GAN (TD-GAN)

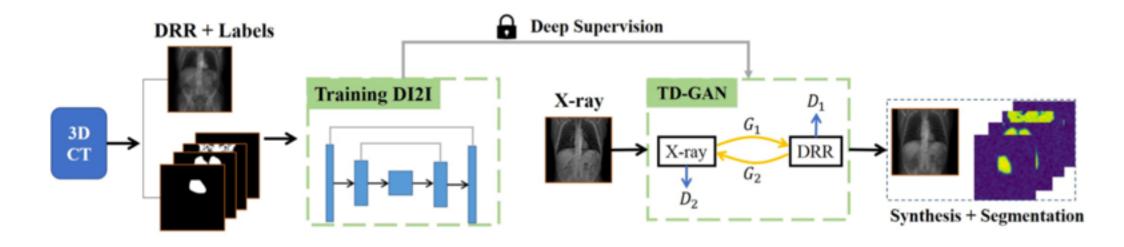


Fig. 1. Overview of the proposed task driven generative model framework.

Dense Image-to-Image Network (D2I2)

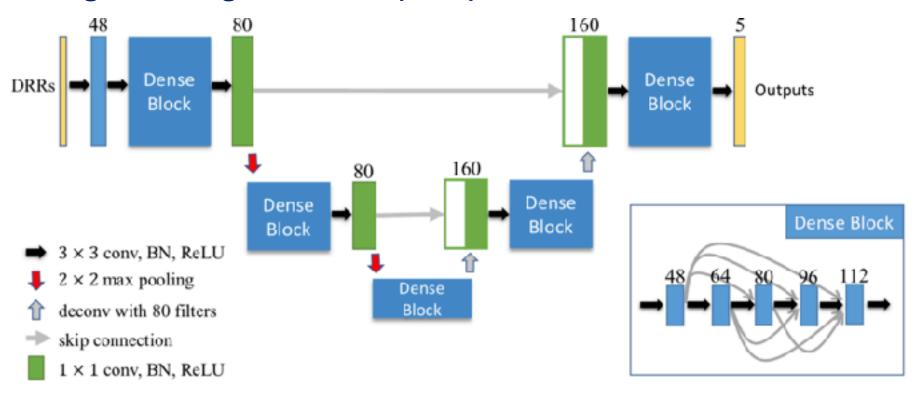


Fig. 2. Illustration of the DI2I for segmentation on DRRs.

Detail for TD-GAN

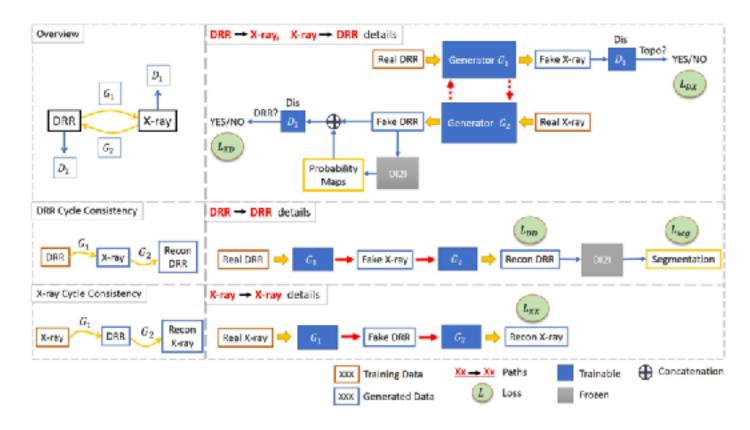


Fig. 3. Proposed TD-GAN architecture. Real X-ray images and DRRs are passed through 4 different paths for simultaneously synthesis and segmentation.



Data

815 labeled DRRs and 153 topograms

X-ray images not mentioned

Dice score(no other compares)

Table 1. Average Dice results of segmentation on topograms.

$\overline{\text{Objects}\big \text{Vanilla}\big \text{CGAN}\big \text{TD-GAN-A}\big \text{TD-GAN-S}\big \text{TD-GAN}\big \text{Supervised}}}$						
Bone	0.401	0.808	0.800	0.831	0.835	0.871
Heart	0.233	0.816	0.846	0.860	0.870	0.880
Liver	0.285	0.781	0.797	0.804	0.817	0.841
Lung	0.312	0.825	0.853	0.879	0.894	0.939
mean	0.308	0.808	0.824	0.844	0.854	0.883

Visual Compares

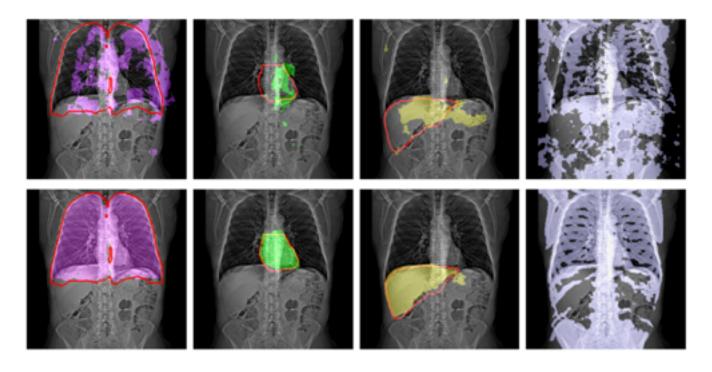


Fig. 4. Visualization of segmentation results on topograms (bottom) against direct application of DI2I (top). The red curves stands for the boundary of the ground truth. The colored fill-in parts are the predictions by TD-GAN and DI2I.

References

- Domain Adaptation Introduction
- https://www.zhihu.com/question/41979241/answer/247421889
- https://zhuanlan.zhihu.com/p/50710267
- Paper Link
- https://doi.org/10.1007/978-3-030-32245-8_29
- https://arxiv.org/abs/1909.04542
- https://link.springer.com/chapter/10.1007%2F978-3-030-00934-2_86
- https://arxiv.org/pdf/1806.07201.pdf
- LiTS Dataset
- http://academictorrents.com/details/
 27772adef6f563a1ecc0ae19a528b956e6c803ce

