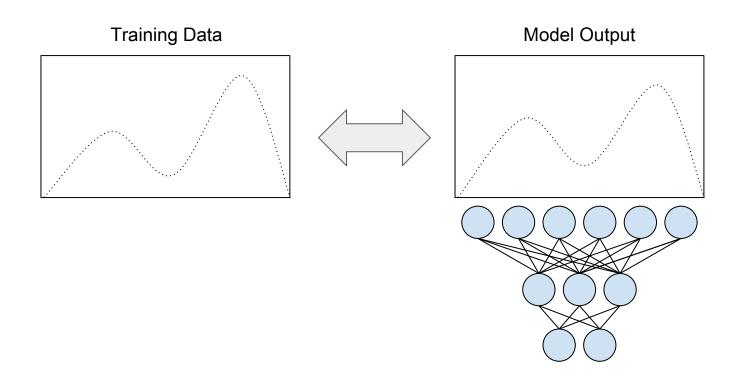
#### Our statement:

Image translation (via distribution matching) should not be used for direct interpretation.



Losses like in CycleGAN just match distributions

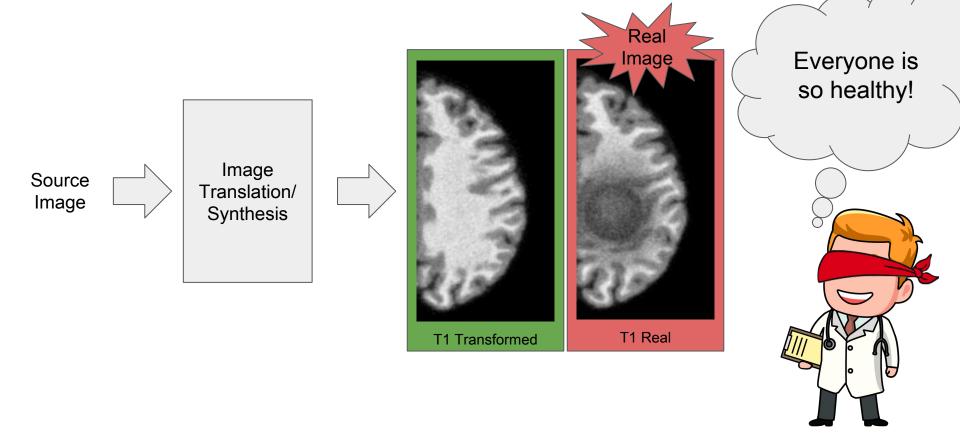


[Karras, 2018]



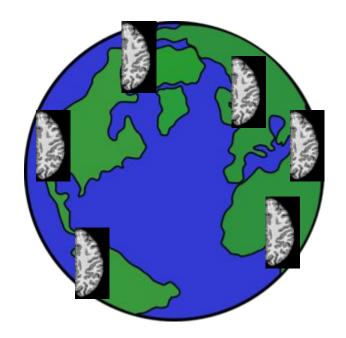
[CycleGAN, Zhu 2017]

They are very good at distribution matching



But a bias in training data can lead to incorrect translation

Time t



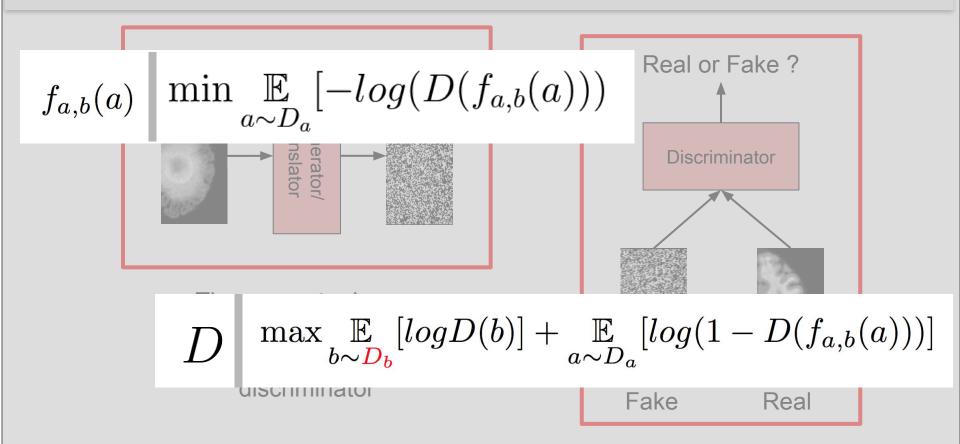
Even with all the training data in the world today.

Time t+1



There will be new diseases tomorrow that are out of distribution.

## What is image translation via distribution matching?



## Model Breakdown

Optimizing

$$D = \max_{b \sim D_b} \mathbb{E}[logD(b)] + \mathbb{E}_{a \sim D_a}[log(1 - D(f_{a,b}(a)))]$$

Optimizing

$$f_{a,b}(a) \min_{a \sim D_a} \mathbb{E}\left[-log(D(f_{a,b}(a)))\right]$$

- $f_{a,b}(a)$  should produce examples in  $D_b$
- $D_a$  can be anything non-finite, like a Gaussian
- No guarantee mapping maintains phenotypes

**L1** 

**Optimizing** 

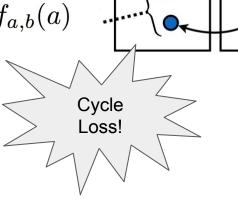
$$\max_{b \sim D_b} \mathbb{E}[log D(b)] + \mathbb{E}_{a \sim D_a}[log(1 - D(f_{a,b}(a)))]$$

Optimizing 
$$a\sim D_b$$
  $a\sim D_a$   $f_{a,b}(a)$   $\min \mathop{\mathbb{E}}_{a\sim D_a}[-log(D(f_{a,b}(a)))+||f_{b,a}(f_{a,b}(a))-a||_1]$ 

Add a reconstruction loss regularizer for the func  $f_{a,b}(a)$ 

Loss term still matches distribution  $D_h$ 

No guarantee mapping maintains phenotypes



**Optimizing** 

$$X_{(a}$$

 $\max \underset{(\boldsymbol{a},b)\sim(D_a,\boldsymbol{D_b})}{\mathbb{E}}[logD(b,\boldsymbol{a})] + \underset{a\sim D_a}{\mathbb{E}}[log(1-D(f_{a,b}(a),\boldsymbol{a}))]$ 

**Optimizing** 

$$f_{a,b}(a) \min_{a \sim D_a} \mathbb{E}\left[-log(D(f_{a,b}(a)))\right]$$

- *D* is given paired examples allowing detection of what to preserve
- $D_h$  still plays a role in what D learns
- No guarantee mapping maintains phenotypes

Optimizing

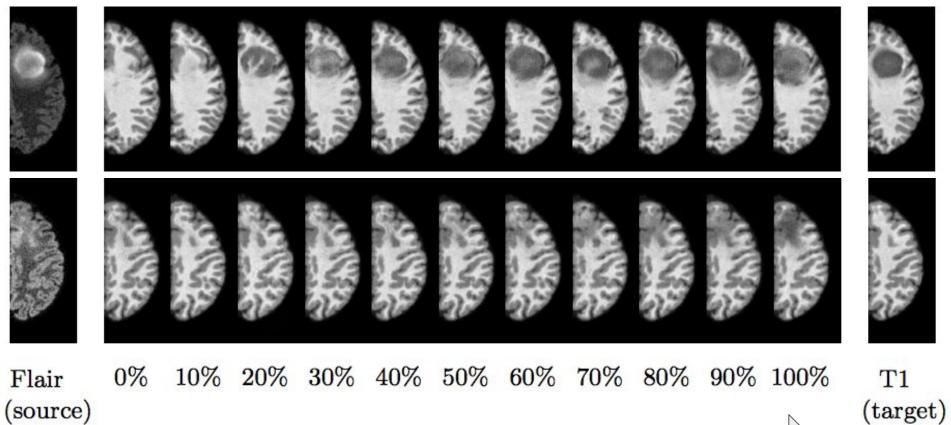
 $\Gamma$ 

$$f_{a,b}(a) \min_{(a,b)\sim(D_a, \mathbf{D_b})} ||f_{a,b}(a) - b||_1$$

- ullet  $f_{a,b}(a)$  should produce examples in  $D_b$
- Pixel-wise loss
- No guarantee mapping maintains phenotypes

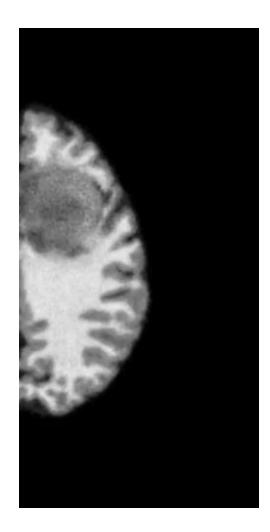
## Visual Evaluation

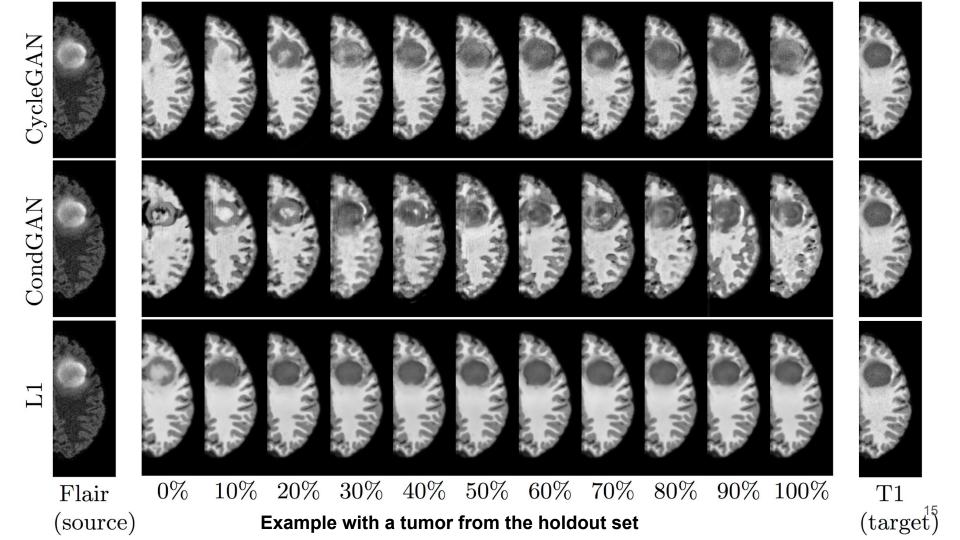
#### CycleGAN results

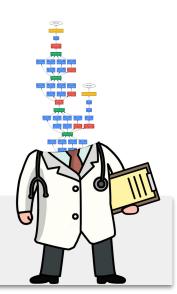


% training data with tumor

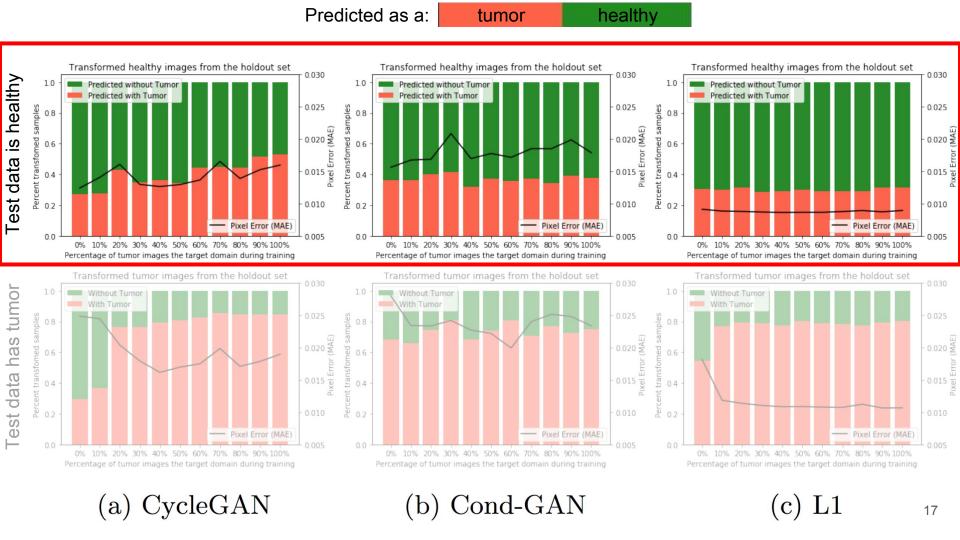
13

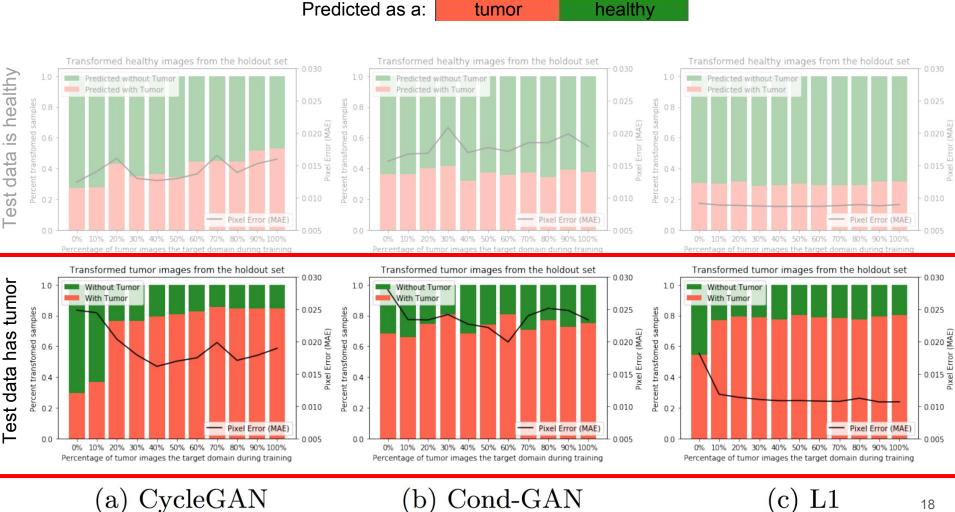






## **Quantitative Evaluation**





#### Our statement:

Image translation (via distribution matching) should not be used for direct interpretation.

### Where do go from here?

1. How to guarantee image translation? (I doubt it)

- 2. Where should distribution matching be used in medical imaging?
  - a. Data augmentation (for classification, segmentation, registration)
  - b. Better features (for unsupervised learning)
  - c. To correct model predictions [Zhang MICCAI 2017]

#### Limitations

- We test only a subset of loss terms which compose most methods
- The synthetic BRATS 2013 data had tumors added to healthy brains (in real data the entire brain is sick)



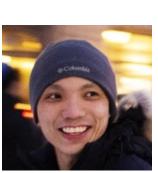
Joseph Paul Cohen, PhD







**Martin Weiss** 





Tristan Sylvain



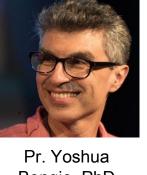
Margaux Luck, PhD



Sina Honari



Assya Trofimov



Bengio, PhD



Vincent Frappier, PhD

#### Thanks!

























# Distribution Matching Losses Can Hallucinate Features in Medical Image Translation



Joseph Paul Cohen



Margaux Luck



Sina Honari

See us at poster M-60 https://arxiv.org/abs/1805.08841