

Self-Attentive Adversarial Stain Normalization

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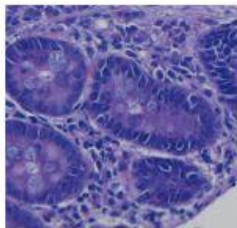
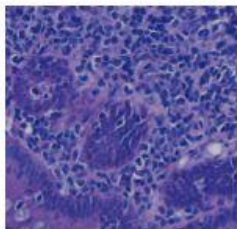
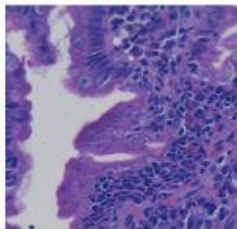
Introduction

- With the success of deep learning, Hematoxylin and Eosin (H&E) stained Whole Slide Images (WSIs) are being used for model-based diagnostic assessment of diseases.
- Variation in the H&E stains across different lab sites can lead to undesirable bias in both human and model-based assessment.
- Traditionally used stain normalization strategies can handle the human level bias. But deep learning models can easily disentangle the linear transformation used in these approaches.
- To handle these limitations, we propose a Self-Attentive Adversarial Stain Normalization (SAASN) approach for the normalization of multiple stain appearances to a common domain.

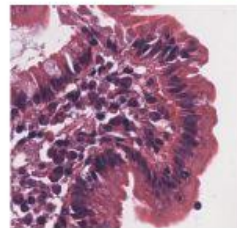
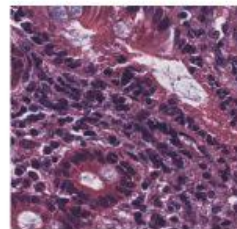
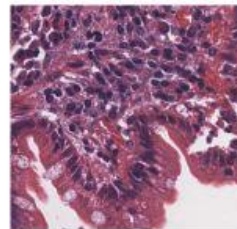
Task

Biopsy data sourced from different lab sites generally contain a unique stain color distribution

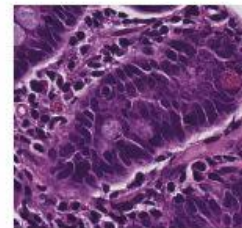
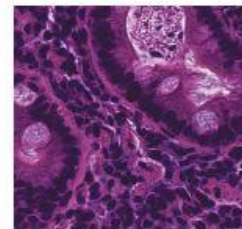
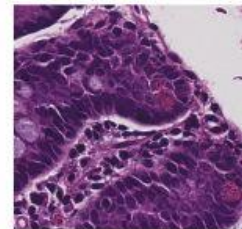
Our approach aims to tackle multiple stain distributions together for many-to-one stain transfer.



Site 1 ($X^{(1)}$)



Site 2 ($X^{(2)}$)



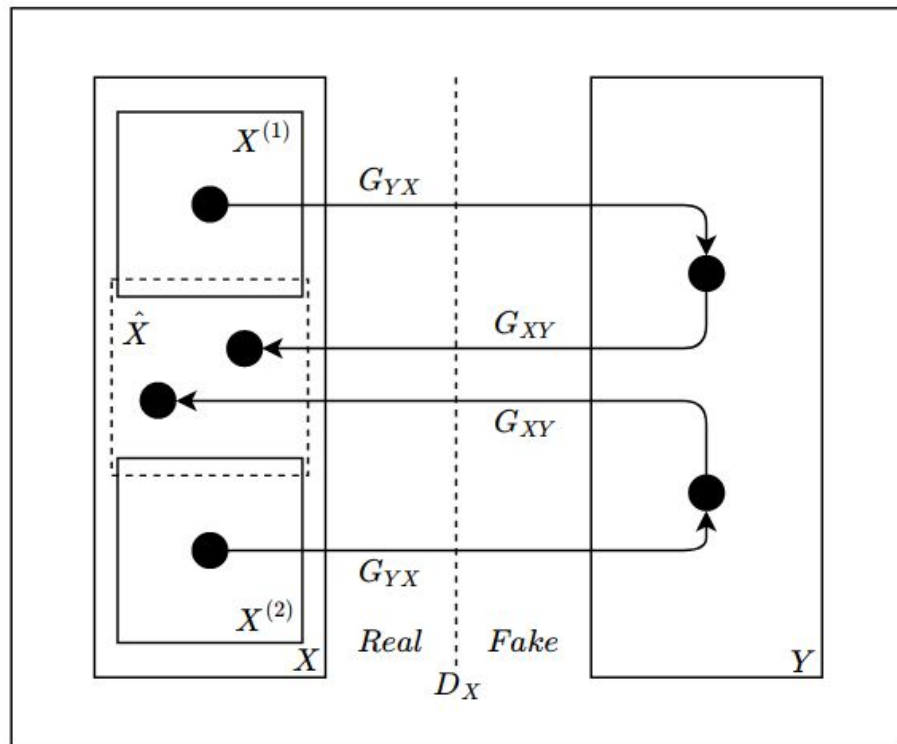
Site 3 (Y)

H&E stained duodenal biopsy patches created from whole slide images sourced from different locations.

Architecture

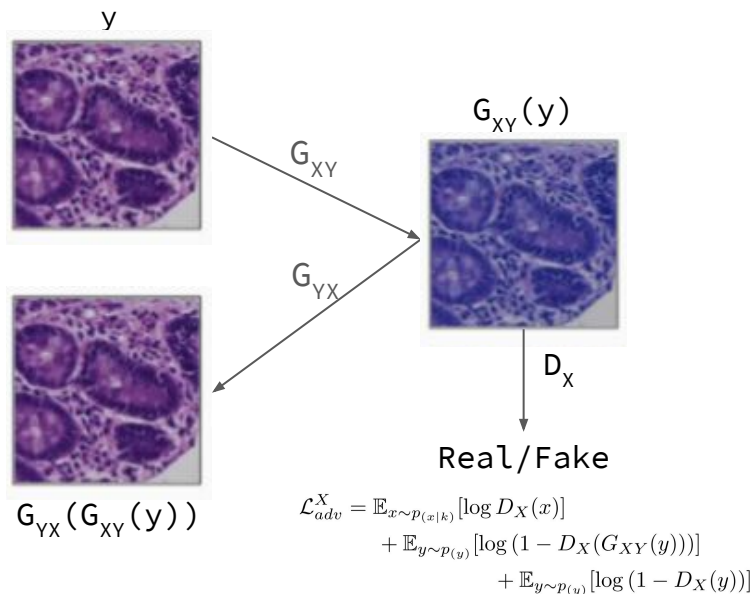
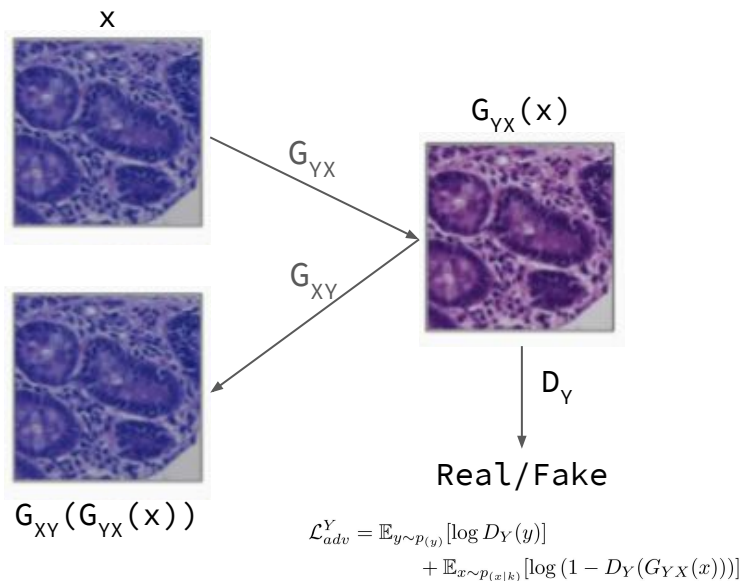
We use two Generators G_{XY} and G_{YX} to perform translations from Y to X and X to Y respectively

Two different stains are present as inputs within X : X^1 and X^2 . Both of these domains are translated to Y with G_{XY} . To complete the cycle, G_{YX} returns the image back to the X domain.



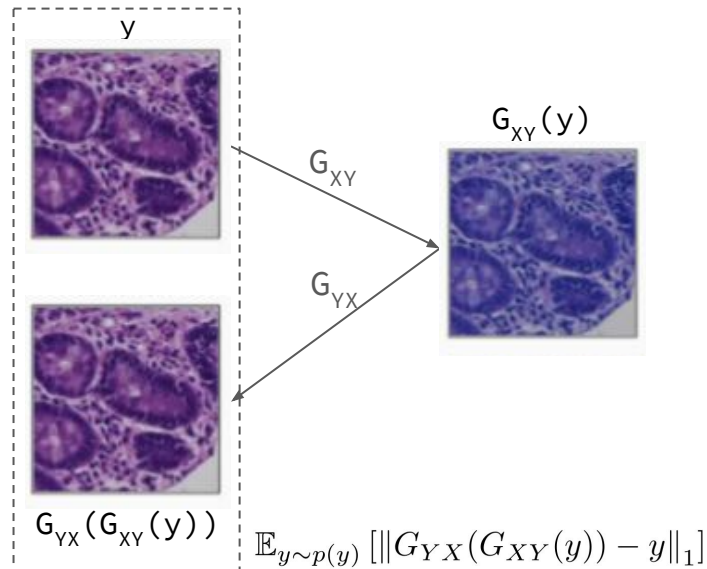
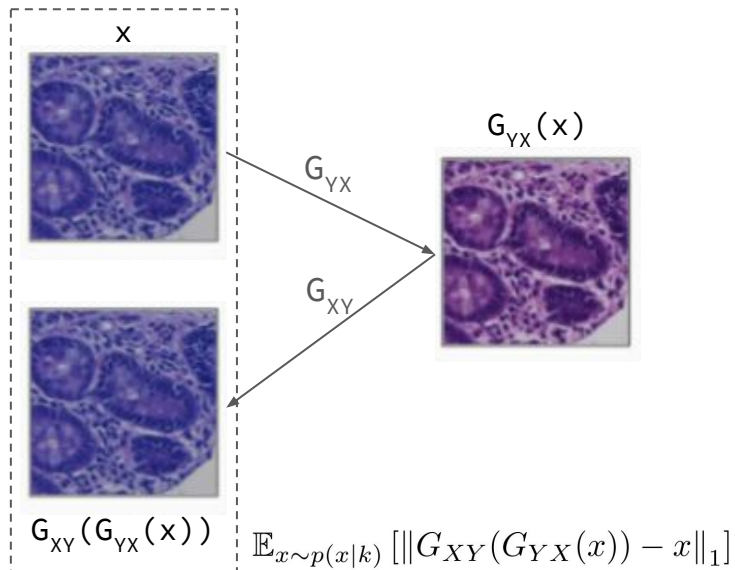
Objectives

Adversarial loss ensures that the stain distribution of the generated images matches the distribution of the real (ground truth) images in that domain



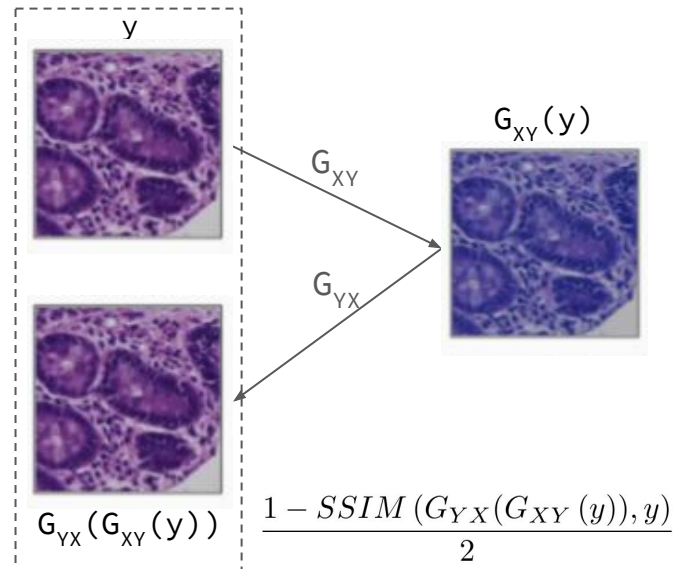
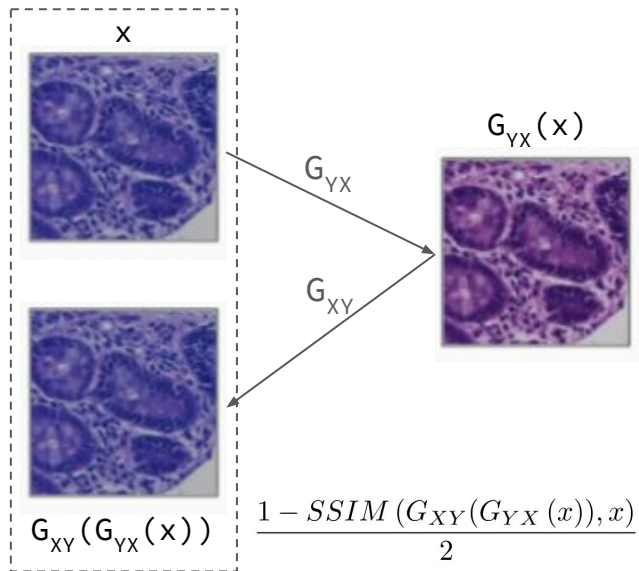
Objectives

Cycle consistency loss is implemented to reconcile with the unpaired nature of the task. The reconstructed image is compared to the original source image



Objectives

Structural cycle consistency loss uses a color agnostic structural dissimilarity loss based on the Structural Similarity (SSIM) index

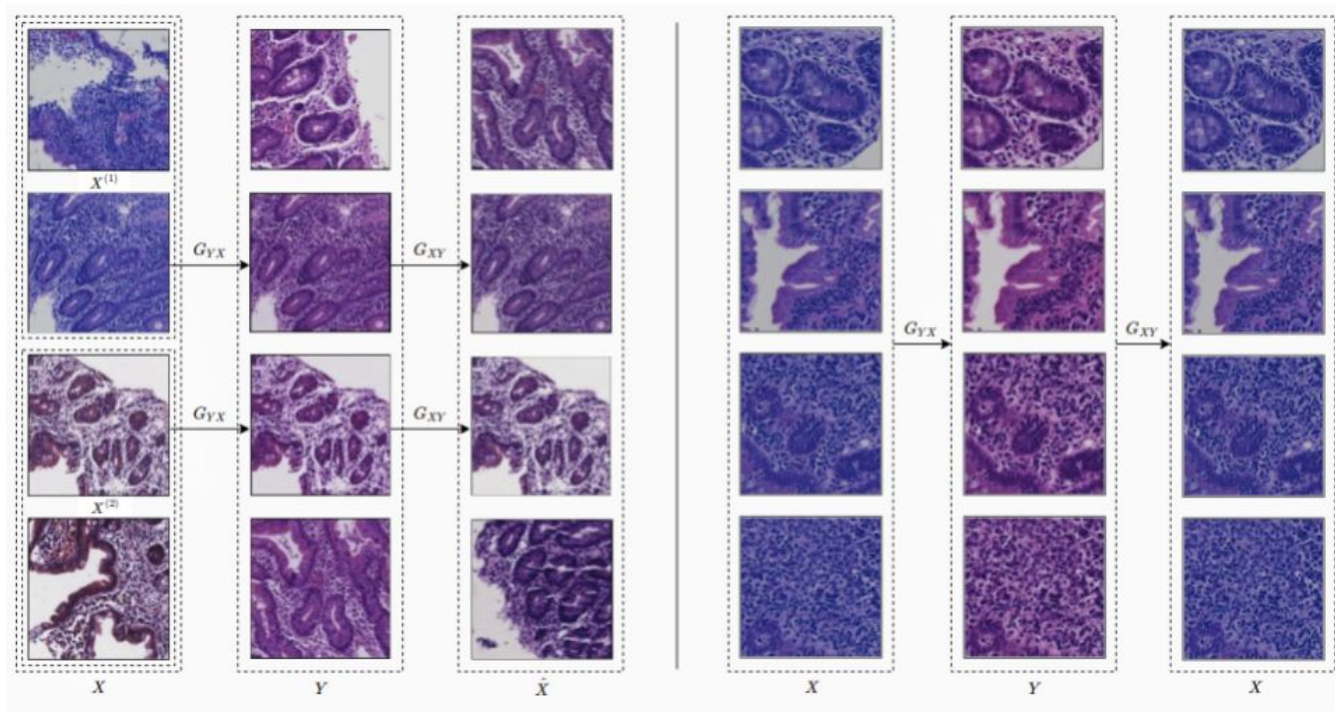


Network Architecture details

- Both the generators are U-Nets
- The discriminator is a 4 block CNN
- **Self-attention layers** were added after every convolutional block in both the generator and the discriminator network.

The self-attention mechanism leverages long range dependencies across image regions to synthesize images with finer details in regions based on a different spatial region in the image.

Results



Mapping was done from two sub-domains of X to Y.

Comparison with traditional methods

Many-to-one setup

Method	$X^{(1)}$ to Y	$X^{(2)}$ to Y	Y to $X^{(1)}$
Vahadane	0.861 ± 0.108	0.919 ± 0.029	0.932 ± 0.033
Macenko	0.942 ± 0.033	0.934 ± 0.022	0.941 ± 0.020
StainGAN	0.927 ± 0.011	0.943 ± 0.027	0.929 ± 0.021
SAASN	0.977 ± 0.007	0.989 ± 0.002	0.981 ± 0.004

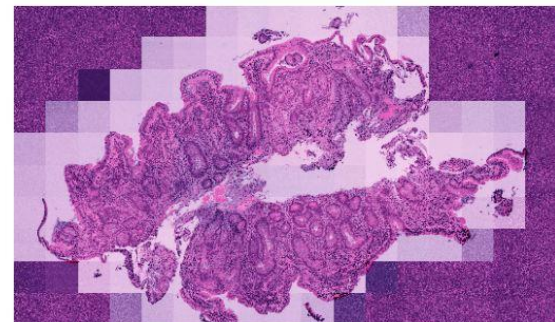
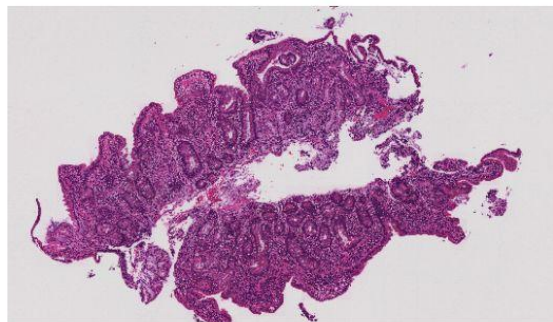
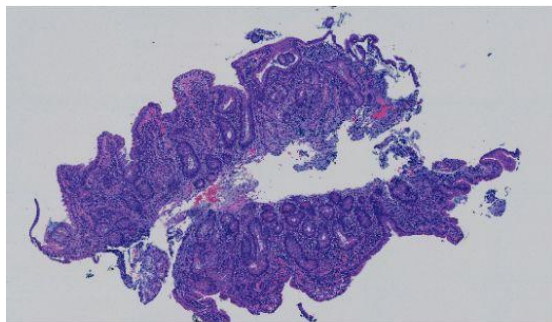
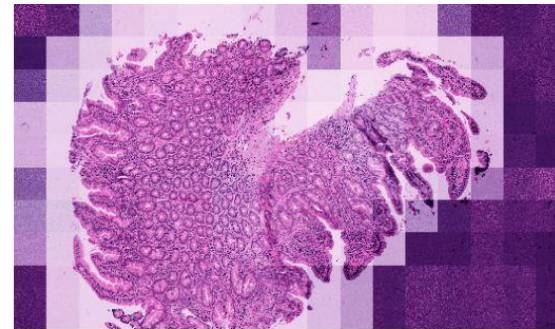
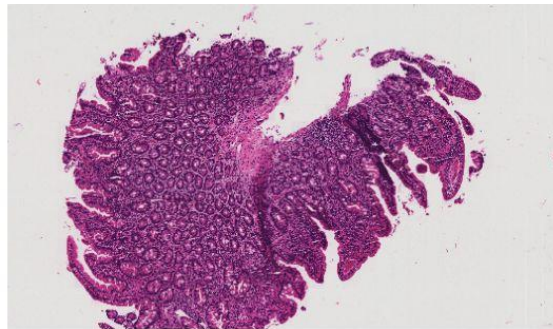
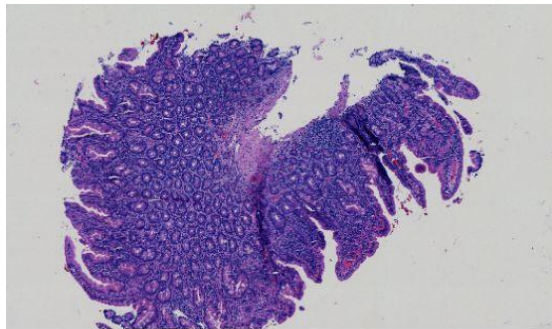
Table 1. Mean \pm Standard deviation of the SSIM index values for normalization across domains. For StainGAN and SAASN all values are computed for a *many-to-one* setup on the first dataset.

One-to-one setup

Method	Aperio to Hamamatsu	Hamamatsu to Aperio
Vahadane	0.971 ± 0.031	0.955 ± 0.038
Macenko	0.968 ± 0.034	0.956 ± 0.039
StainGAN	0.967 ± 0.009	0.947 ± 0.032
SAASN	0.995 ± 0.001	0.996 ± 0.001

Table 2. Mean \pm Standard deviation of the SSIM index values for normalization across domains. For StainGAN and SAASN all values are computed for the *one-to-one* setup on the second dataset.

Comparison with traditional methods



Original

SAASN

Macenko

Questions?