

# PathologyGAN: Learning deep representations of cancer tissue

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## Abstract

Histopathological images of tumors contain abundant information about how tumors grow and how they interact with their micro-environment. Better understanding of tissue phenotypes in these images could reveal novel determinants of pathological processes underlying cancer, and in turn improve diagnosis and treatment options. Advances of Deep learning makes it ideal to achieve those goals, however, its application is limited by the cost of high quality labels from patients data. Unsupervised learning, in particular, deep generative models with representation learning properties provides an alternative path to further understand cancer tissue phenotypes, capturing tissue morphologies.

In this paper, we develop a framework which allows Generative Adversarial Networks (GANs) to capture key tissue features and uses these characteristics to give structure to its latent space. To this end, we trained our model on two different datasets, an H&E colorectal cancer tissue from the National Center for Tumor diseases (NCT, Germany) and an H&E breast cancer tissue from the Netherlands Cancer Institute (NKI, Netherlands) and Vancouver General Hospital (VGH, Canada). Composed of 86 slide images and 576 tissue micro-arrays (TMAs) respectively.

We show that our model generates high quality images, with a Fréchet Inception Distance (FID) of 16.65 (breast cancer) and 32.05 (colorectal cancer). We further assess the quality of the images with cancer tissue characteristics (e.g. count of cancer, lymphocytes, or stromal cells), using quantitative information to calculate the FID and showing consistent performance of 9.86. Additionally, the latent space of our model shows an interpretable structure and allows semantic vector operations that translate into tissue feature transformations. Furthermore, ratings from two expert pathologists found no significant difference between our generated tissue images from real ones.

The code, generated images, and pretrained models are available at <https://github.com/AdalbertoCq/Pathology-GAN>

**Keywords:** Generative Adversarial Networks, Digital Pathology.

## 1. Introduction

Cancer is a disease with extensive heterogeneity, where malignant cells interact with immune cells, stromal cells, surrounding tissues and blood vessels. Histological images, such as haematoxylin and eosin (H&E) stained tissue microarrays (TMAs) or whole slide images (WSI), are a high-throughput imaging technology used to study such diversity. Despite be-

ing ubiquitous in clinical settings, analytical tools of H&E images remain primitive, making these valuable data largely under-explored. Consequently, cellular behaviours and the tumor microenvironment recorded in H&E images remain poorly understood. Increasing our understanding of such microenvironment interaction holds the key for improved diagnosis and treatment of cancer.

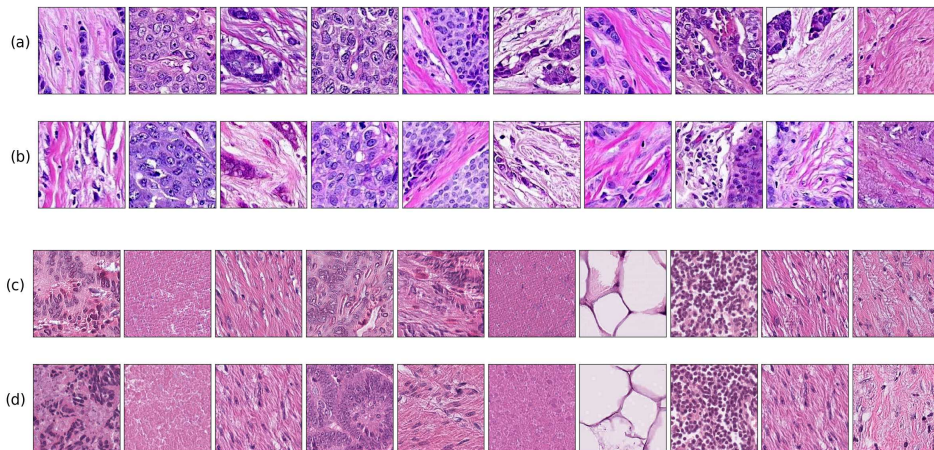


Figure 1: (a): Images ( $224 \times 224$ ) from PathologyGAN trained on H&E breast cancer tissue. (b): Real images, Inception-V1 closest neighbor to the generated above in (a). (c): Images ( $224 \times 224$ ) from PathologyGAN trained on H&E colorectal cancer tissue. (d) Real images, Inception-V1 closest neighbor to the generated above in (c).

The motivation for our work is to develop methods that could lead to a better understanding of phenotype diversity between/within tumors. We hypothesize that this diversity could be substantial given the highly diverse genomic and transcriptomic landscapes observed in large scale molecular profiling of tumors across multiple cancer types (Campbell et al., 2020). We argue that representation learning with GAN-based models is the most promising to achieve our goal for the two following reasons:

1. By being able to generate high fidelity images, a GAN could learn the most relevant descriptions of tissue phenotype.
2. The continuous latent representation learned by GANs could help us quantify differences in tissue architectures free from supervised information.

In this paper, we propose to use Generative Adversarial Networks (GANs) to learn representations of entire tissue architectures and define an interpretable latent space (e.g. colour, texture, spatial features of cancer and normal cells, and their interaction). To this end, we present the following contributions:

1. We propose PathologyGANs to generate high fidelity cancer tissue images from a structured latent space. The model combines BigGAN (Brock et al., 2019), StyleGAN

(Karras et al., 2019) and Relativistic Average Discriminator (Jolicoeur-Martineau, 2019).

2. We assess the quality of the generated images through two different methods: convolutional Inception-V1 features and prognostic features of the cancer tissue, such as counts and densities of different cell types (Beck et al., 2011; Yuan et al., 2012). Both features are benchmarked with the Fréchet Inception Distance (FID). The results show that the model captures pathologically meaningful representations, and when evaluated by expert pathologists, generated tissue images are not distinct from real tissue images.
3. We show that our model induces an ordered latent space based on tissue characteristics (e.g. cancer cell density or tissue type), this allows to perform linear vector operations that transfer into high level tissue image changes.

## 2. Related Works

Deep learning has been widely applied in digital pathology, from these we can differentiate between supervised and unsupervised learning approaches.

Supervised applications range from mitosis and cell detection (Tellez et al., 2018; Xu et al., 2019a; Zhang et al., 2019b), nuclei and tumor segmentation (Qu et al., 2019; Qaiser et al., 2019), histological subtype classification (Coudray et al., 2018; Wei et al., 2019), to survival and prognosis modeling (Katzman et al., 2018; Lee et al., 2018). Recently, there have been developments on relating phenotype to the molecular underpinning of tumors, in particular genomic characteristics (Coudray et al., 2018; Schmauch et al., 2020; Woerl et al., 2020; Fu et al., 2020; Coudray and Tsirigos, 2020; Kather et al., 2020), and spatial transcriptomics (Vickovic et al., 2019; He et al., 2020; Bergensträhle et al., 2020a; Schmauch et al., 2020; Wang et al., 2020; Bergensträhle et al., 2020b). Furthermore, previous traditional computer vision approaches (Beck et al., 2011; Yuan et al., 2012) already identified correlation between phenotype patterns and patient survival. These works highlight the importance and opportunities that building tissue phenotype representations bring, providing insight into survival or genomic information purely from tissue images such as TMA or WSIs.

Nevertheless, these methods require data labeling which is usually costly in time and effort, this is particularly the case for sequencing derived molecular labels. In addition, deep learning approaches have a lack of interpretability, which is also a major limiting factor in making a real impact in clinical practice.

Unsupervised learning applications mostly focus on nuclei (Xu et al., 2016; Mahmood et al., 2018), tissue (de Bel et al., 2018), or region-of-interest segmentation (Gadermayr et al., 2018, 2019), besides stain transformation (Rana et al., 2018; Xu et al., 2019b) and normalization (Zanjani et al., 2018). Within unsupervised learning, generative models have been briefly used for tissue generation (Levine et al., 2020), however this model lacks of representation learning properties. On the other hand, there has been some initial work on building cell and nuclei representations with models such as InfoGAN (Hu et al., 2019) and Sparse Auto-Encoders (Hou et al., 2019), although these models focus either on small sections of images or cells instead of larger tiles of tissue.

Building phenotype representations based on tissue architecture and cellular attributes remains a field to be further explored. Generative models offer the ability to create tissue representations without expensive labels and representations not only correlated with a predicted outcome (as in discriminative models), rather creating representations based on the similarities across the characteristics of tissue samples. Take a point mutation for example, it is now understood that mutations are frequently only shared in subpopulations of cancer cells within a tumor (Gerstung et al., 2020; Dentre et al., 2020). Therefore, it’s difficult to know if a point mutation is presented in the cells recorded in a image. Fundamentally, supervised approach is limited by the fact that molecular and clinical labels are often obtained from materials that are physically different from the ones in the images. The associations are therefore highly indirect and subject to many confounding factors

From generative models, Generative Adversarial Networks (GANs) have become increasingly popular, applied to different domains from imaging to signal processing. GANs (Goodfellow et al., 2014) are able to learn high fidelity and diverse data representations from a target distribution. This is done with a generator,  $G(z)$ , that maps random noise,  $z \sim p_z(z)$ , to samples that resemble the target data,  $\mathbf{x} \sim p_{\text{data}}(\mathbf{x})$ , and a discriminator,  $D(x)$ , whose goal is to distinguish between real and generated samples. The goal of a GAN is find the equilibrium in the min-max problem:

$$\min_G \max_D V(D, G) = \mathbb{E}_{\mathbf{x} \sim p_{\text{data}}(\mathbf{x})} [\log D(\mathbf{x})] + \mathbb{E}_{z \sim p_z(z)} [\log(1 - D(G(z)))]. \quad (1)$$

Since its introduction, modeling distributions of images has become the mainstream application for GANs, firstly introduced by Radford et al. (2015). State-of-the-art GANs such as BigGAN (Brock et al., 2019) and StyleGAN (Karras et al., 2019) have recently been use to generate impressive high-resolution images. Additionally, solutions like Spectral Normalization GANs (Miyato et al., 2018), Self-Attention GANs (Zhang et al., 2019a), and also BigGAN have achieved high diversity images in data sets like ImageNet (Deng et al., 2009), with 14 million images and 20 thousand different classes. At the same time, evaluating these models has been a challenging task. Many different metrics such as Inception Score (IS) (Salimans et al., 2016), Fréchet Inception Distance (FID) (Heusel et al., 2017), Maximum Mean Discrepancy (MMD) (Gretton et al., 2012), Kernel Inception Distance (KID) (Bińkowski et al., 2018), and 1-Nearest Neighbor classifier (1-NN) (Lopez-Paz and Oquab, 2016) have been proposed to do so, and thorough empirical studies (Huang et al., 2018; Barratt and Sharma, 2018) have shed some light on the advantages and disadvantages of each them. However, the selection of a feature space is crucial for using these metrics.

In our work we take a step towards developing a generative model that learns phenotypes through tissue architectures and cellular characteristics, introducing a GAN with representation learning properties and an interpretable latent space. We advocate that in the future these phenotype representations could give us insight about the diversity within/across cancer types and their relation to genomic, transcriptomic, and survival information; finally leading to better treatment and prognosis of the disease.

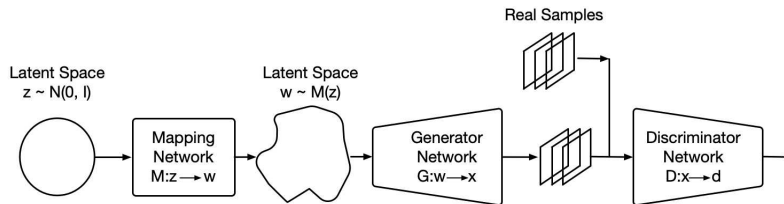


Figure 2: High level architecture of PathologyGAN. We include details of each module’s architecture in the Appendix K

### 3. Methods

#### 3.1 PathologyGAN

We used BigGAN (Brock et al., 2019) as a baseline architecture and introduced changes which empirically improved the Fréchet Inception Distance (FID) and the structure of the latent space.

BigGAN has been shown to be a successful GAN in replicating datasets with a diverse number of classes and large amounts of samples, such as ImageNet with approximately  $1M$  samples and  $20K$  classes. For this reason, we theorize that such model will be able to learn and replicate the diverse tissue phenotypes contained in whole slide images (WSI), being able to handle the large amount of tiles/patches resulting from diving the WSIs.

We followed the same architecture as BigGAN, employed Spectral Normalization in both generator and discriminator, self attention layers, and we also use orthogonal initialization and regularization as mentioned in the original paper.

We make use of the Relativistic Average Discriminator (Jolicoeur-Martineau, 2019), where the discriminator’s goal is to estimate the probability of the real data being more realistic than the fake. We take this approach instead of following the Hinge loss (Lim and Ye, 2017) as the GAN objective. We find that this change makes the model convergence faster and produce higher quality images. Images using the Hinge loss did not capture the morphological structure of the tissue (we provide examples of these results in the Appendix C). The discriminator, and generator loss function are formulated as in Equations 2 and 3, where  $\mathbb{P}$  is the distribution of real data,  $\mathbb{Q}$  is the distribution for the fake data, and  $C(x)$  is the non-transformed discriminator output or critic:

$$L_{Dis} = -\mathbb{E}_{x_r \sim \mathbb{P}} \left[ \log \left( \tilde{D}(x_r) \right) \right] - \mathbb{E}_{x_f \sim \mathbb{Q}} \left[ \log \left( 1 - \tilde{D}(x_f) \right) \right], \quad (2)$$

$$L_{Gen} = -\mathbb{E}_{x_f \sim \mathbb{Q}} \left[ \log \left( \tilde{D}(x_f) \right) \right] - \mathbb{E}_{x_r \sim \mathbb{P}} \left[ \log \left( 1 - \tilde{D}(x_r) \right) \right], \quad (3)$$

$$\tilde{D}(x_r) = \text{sigmoid} \left( C(x_r) - \mathbb{E}_{x_f \sim \mathbb{Q}} C(x_f) \right), \quad (4)$$

$$\tilde{D}(x_f) = \text{sigmoid} \left( C(x_f) - \mathbb{E}_{x_r \sim \mathbb{P}} C(x_r) \right). \quad (5)$$

Additionally, we introduce two elements from StyleGAN (Karras et al., 2019) with the purpose of allowing the generator to freely optimize the latent space and find high-level features of the cancer tissue. First, a mapping network  $M$  composed by four dense ResNet layers (He et al., 2016), placed after the latent vector  $z \sim \mathcal{N}(0, I)$ , with the purpose of

allowing the generator to find the latent space  $w \sim M(z)$  that better disentangles the latent factors of variation. Secondly, style mixing regularization, where two different latent vectors  $z_1$  and  $z_2$  are run into the mapping network and fed at the same time to the generator, randomly choosing a layer in the generator and providing  $w_1$  and  $w_2$  to the different halves of the generator (e.g. on a generator of ten layers and being six the randomly selected layer,  $w_1$  would feed layers one to six and  $w_2$  seven to ten). Style mixing regularization encourages the generator to localize the high level features of the images in the latent space. We also use adaptive instance normalization (AdaIN) on our models, providing the entire latent vectors.

We use the Adam optimizer (Kingma and Ba, 2014) with  $\beta_1 = 0.5$  and same learning rates of 0.0001 for both generator and discriminator, the discriminator takes 5 steps for each of the generator. Each model was trained on an NVIDIA Titan RTX 24 GB for approximately 72 hours.

### 3.2 Datasets

To train our model, we used two different datasets, an H&E colorectal cancer tissue from the National Center for Tumor diseases (NCT, Germany) (Kather et al., 2018) and an H&E breast cancer tissue from the Netherlands Cancer Institute (NKI, Netherlands) and Vancouver General Hospital (VGH, Canada) (Beck et al., 2011).

The H&E breast cancer dataset was built from the Netherlands Cancer Institute (NKI) cohort and the Vancouver General Hospital (VGH) cohort with 248 and 328 patients, respectively. Each of them include TMA images, along with clinical patient data such as survival time, and estrogen-receptor (ER) status. The original TMA images all have a resolution of  $1128 \times 720$  pixels, and we split each of the images into smaller patches of  $224 \times 224$ , and allowed them to overlap by 50%. We also performed data augmentation on these images, a rotation of  $90^\circ$ , and  $180^\circ$ , and vertical and horizontal inversion. We filtered out images in which the tissue covers less than 70% of the area. In total this yield to a training set of 249K images and a test set of 62K.

The H&E colorectal cancer dataset provides 100K tissue images of  $224 \times 224$  resolution, each image has an associated type of tissue label: adipose, background, debris, lymphocytes, mucus, smooth muscle, normal colon mucosa, cancer-associated stroma, and colorectal adenocarcinoma epithelium (tumor). This dataset is composed of 86 H&E stained human cancer tissue slides. In order to check the model’s flexibility and ability to work with different datasets, we decided not to apply any data augmentation and use the tiles as they are provided.

In both datasets, we perform the partition over the total tissue patches, not according to patients, since our goal is to verify the ability to learn tissue representations. We trained our model on the VGH/NKI and NCT datasets for 45 and 130 epochs, respectively.

In Appendix B we study the model’s capacity in capturing representations with small size datasets (5K, 10K, 20K) verifying its converge and ability to generalize.

### 3.3 Evaluation metric on PathologyGAN

The Fréchet Inception Distance (FID) (Heusel et al., 2017) is a common metric used to measure GANs performance, and it quantifies the GAN’s ability to learn and reproduce the

original data distribution. The goal of the FID score is to measure the similarity in quality and diversity between real  $p_{data}(x)$  and generated data  $p_g(x)$ .

Instead to measuring the distance between the real and generated distributions in the pixel space, it uses a pretrained ImageNet Inception Network (Szegedy et al., 2016) to extract features of each image, reducing the dimensionality of the samples and obtaining vision-relevant features. Feature samples are fitted into a multivariate Gaussian distribution obtaining real  $\mathcal{N}(\mu_{data}, \Sigma_{data})$  and generated  $\mathcal{N}(\mu_g, \Sigma_g)$  feature distributions. Finally, it uses the Fréchet distance (Fréchet, 1957) to measure the difference between the two distributions:

$$FID = d^2((\mu_{data}, \Sigma_{data}), (\mu_g, \Sigma_g)) = \|\mu_{data} - \mu_g\|_2^2 + Tr(\Sigma_{data} + \Sigma_g - 2(\Sigma_{data}\Sigma_g)^{1/2})$$

We evaluate our model by calculating the FID score from 10K generated images and randomly sampling 10K real images.

We focus on using FID as it is a common GAN evaluation method (Brock et al., 2019; Karras et al., 2019; Miyato et al., 2018; Zhang et al., 2019a) that reliably captures differences between the real and generated distributions. Additionally, we provide more details in Appendix I comparing FID to other metrics such as Kernel Inception Distance (KID) or 1-Nearest Neighbor (1-NN) in the context of digital pathology.

### 3.4 Quantification of cancer cells in generated images - Breast cancer tissue

In our results, we use the counts of cancer cells and other cellular information as a mean to measure the image quality and representation learning properties of our model. The motivation behind this approach is to ensure that our model capture meaningful and faithful representations of the tissue.

We use this information in two different ways, first as an alternative feature space for FID as each image is translated into a vector with cellular information in the tissue, and secondly to label each generated tissue image according to the cancer cell density, allowing us to visualize the representation learning properties of our model’s latent space.

The CRImage tool (Yuan et al., 2012) uses an SVM classifier to provide quantitative information about tumor cellular characteristics in tissue. This approach allows us to gather pathological information in the images, namely the number of cancer cells, the number of other types of cells (such as stromal or lymphocytes), and the ratio of tumorous cells per area. We limit the use of this information to breast cancer tissue, since the tool was developed for this specific case. Figure 3 displays an example of how the CRImage captures the different cells in the generated images, such as cancer cells, stromal cells, and lymphocytes.

Finally, we created 8 different classes that account for counts of cancer cells in the tissue image, and consecutively we label each generated image with the corresponding class, allowing us to more clearly visualize the relation between cancer cell density in generated images and the model’s latent space.

### 3.5 Tissue type assignation on generated images - Colorectal cancer tissue

The NCT colorectal cancer dataset provides a label along each  $224 \times 224$  tissue sample and we make use of this information to label each generated image with a type of tissue, assigning a label to each generated image according to the 10-nearest neighbors of real images in the Inception-V1 feature space.

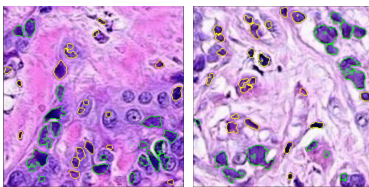


Figure 3: CRImage identifies different cell types in our generated images. Cancer cells are highlighted with a green color, while lymphocytes and stromal cells are highlighted in yellow.

In Figure 4 we show generated images on the left column and the nearest real neighbors on the remaining columns. We present the different tissue types: tumor (i), stroma (j), muscle (k), lymphocytes (l), debris (m), mucus (n), adipose (o), and background (p). From this example, we can conclude that distance in feature space gives a good reference to find the tissue type of generated images.

## 4. Results

### 4.1 Image quality analysis

We study the fidelity of the generated images and their distribution in relation to the original data in two different ways, through measures of FID metrics and by visualizing the closest neighbors between generated and real images.

We calculate Fréchet Inception Distance (FID) with two different approaches, with the usual convolutional features of a Inception-V1 network and with cellular information extracted from the CRImage cell classifier, as explained in Section 3.4. We restrict using CRImage to breast cancer tissue only since it was developed for that particular purpose.

Table 1 shows that our model is able to achieve an accurate characterization of the cancer tissue. Using the Inception feature space, FID shows a stable representation for all models with values similar to ImageNet models of BigGAN (Brock et al., 2019) and SAGAN (Zhang et al., 2019a), with FIDs of 7.4 and 18.65, respectively or StyleGAN (Karras et al., 2019) trained on FFHQ with FID of 4.40. Using the CRImage cellular information as feature space, FID shows again close representations to real tissue.

Additionally, in Figure 4 we present samples of generated images (first column) and its closest real neighbors in Inception-V1 feature space, the images are paired by rows. (a-h) correspond to different random samples of breast cancer tissue. In the case of colorectal cancer, we provide examples of different types of tissue: tumor (i), stroma (j), muscle (k), lymphocytes (l), debris (m), mucus (n), adipose (o), and background (p). We can see that generated and real images hold the same morphological characteristics.



Model	Inception FID Colorectal	Inception FID Breast	CRImage FID Breast
PathologyGAN	32.05±3	16.65±2.5	9.86±0.4

Table 1: Evaluation of PathologyGANs. Mean and standard deviations are computed over three different random initializations. The low FID scores in both feature space suggest consistent and accurate representations.

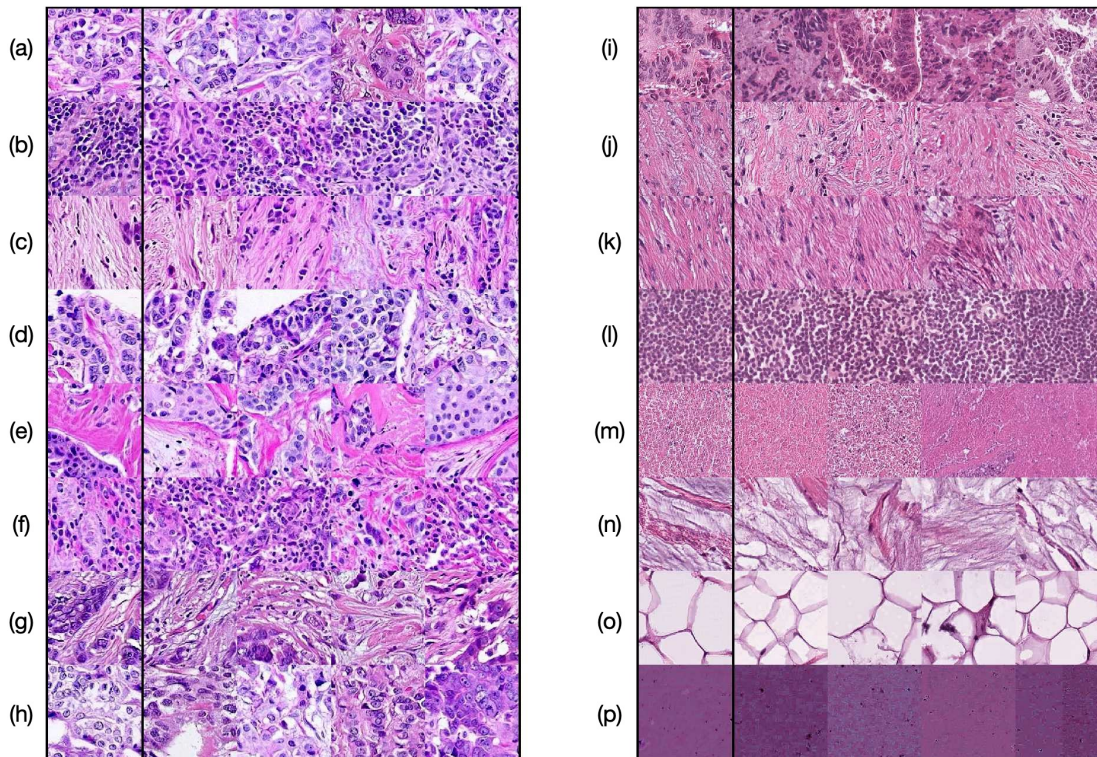


Figure 4: Nearest neighbors in Inception-V1 feature space for breast cancer (a-h) and colorectal cancer (i-p). For each row, first column images corresponds to a generated tissue samples from PathologyGAN, the remaining columns are the closest real images in feature space.

## 4.2 Analysis of latent representations

In this section we focus on the PathologyGAN’s latent space, exploring the impact of introducing a mapping network in the generator and using style mixing regularization. Here we will provide examples of its impact on linear interpolations and vector operations on the latent space  $w$ , as well as visualizations on the latent space  $w$ . We conclude that PathologyGAN holds representation learning properties over cancer tissue morphologies.

Figures 5 and 6 capture how the latent space  $w$  has a structure that shows direct relationship with tissue properties. To create this figures, we generated  $10K$  images and labeled them accordingly to Sections 3.4 and 3.5, along with each tissue image we also have the corresponding latent vector  $w$  and we used UMAP (McInnes et al., 2018) to project them to a two dimensional space.

Figure 5 reveals the relationship between number of cancer cells in the breast cancer tissue and regions of the latent space, low counts of cancer cells (class 0) are concentrated at quadrant *II* while they increase as we move to quadrant *IV* (class 7). Figure 6 displays how the distinct regions of the latent space generate different kinds of tissue. These examples provide evidence of a structured latent space according to tissue cellular characteristics and tissue type. We include a further detailed exploration with density and scatter plots in the Appendix E.

We also found that linear interpolations between two latent vectors  $w$  have better feature transformations when the mapping network and style mixing regularization are introduced. Figure 7 shows linear interpolations in latent space  $w$  between images with malignant tissue and benign tissue. (a, c) correspond to a model with a mapping network and style mixing regularization and (b, d) to a model without those features, we can see that transitions on (a, c) include an increasing population of cancer cells rather than the fading effect observed

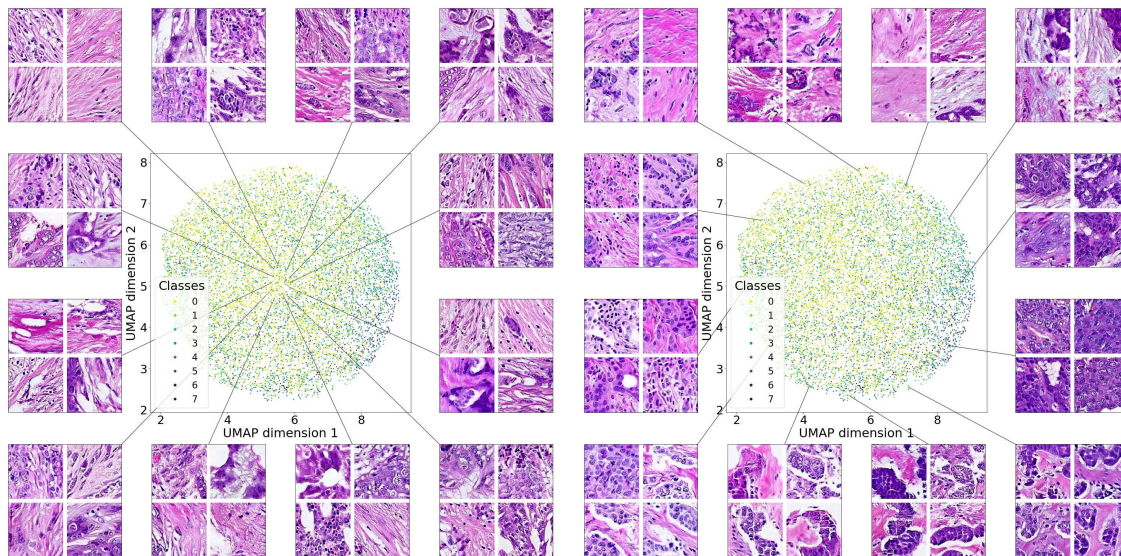


Figure 5: Latent space of PathologyGAN trained on breast cancer tissue from Netherlands Cancer Institute (NKI) and Vancouver General Hospital (VGH) dataset. Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples, each generated image is labeled with the density of cancer cells, class 0 for lowest and class 8 for highest. Moving from quadrant *II* to quadrant *IV* in the UMAP representation corresponds to increasing the density of cancer cells in the generated tissue.

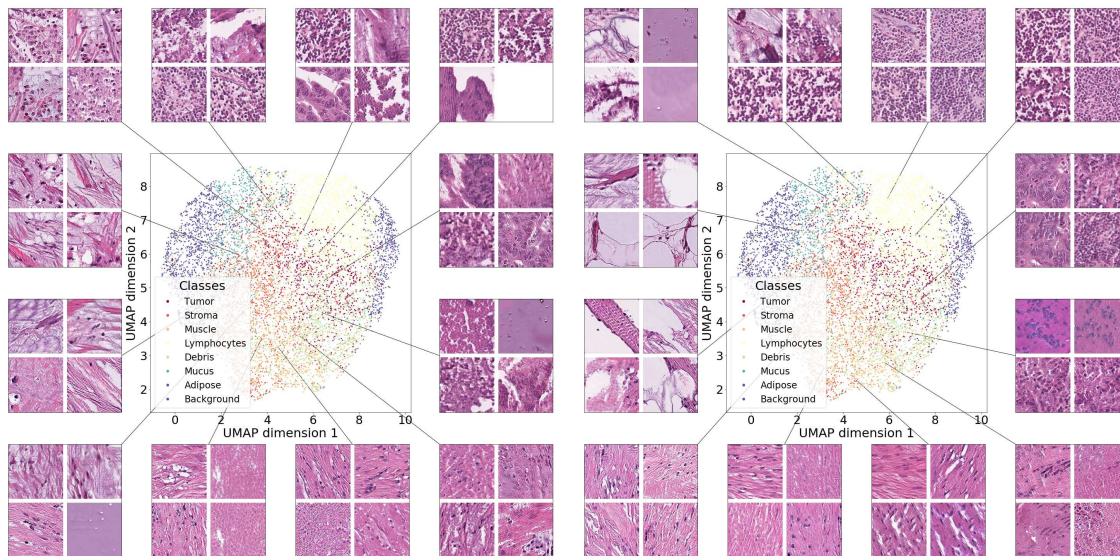


Figure 6: Latent space of PathologyGAN trained on colorectal cancer tissue from National Center for Tumor (NCT) dataset. Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples, each generated image is labeled with the type of tissue. Different regions of the latent space generate distinct kinds of tissue.

in images of (b, d). This result indicates that (a, c) better translates interpolations in the latent space, as real cells do not fade away.

In addition, we performed linear vector operations in  $w$ , that translated into semantic image features transformations. In Figure 8 we provide examples of three vector operations that result into feature alterations in the images. This evidence shows further support on the relation between a structured latent space and tissue characteristics.

Finally, we explored how linear interpolation and vector operations translate into the individual points in the latent space. In Figure 9 we provide examples of interpolations from stroma to tumor in colorectal cancer, and tumor to lymphocytes in breast cancer. Through the intermediate vectors we show that gradual transitions in the latent space translate into smooth feature transformations, in these cases increase/decrease of tumorous cells or increase of lymphocyte counts. Alternatively, Figure 10 shows how results from vector operations fall into regions of the latent space that correspond to the expected tissue type or a combination of features such as tumor and lymphocytes. With these figures we visualize the meaningful representations of cells and tissue types, and also the interpretability of the latent space. Appendix H contains additional examples of these visualizations.

### 4.3 Pathologists' results

To demonstrate that the generated images can sustain the scrutiny of clinical examination, we asked expert pathologists to take a test, setup as follows:

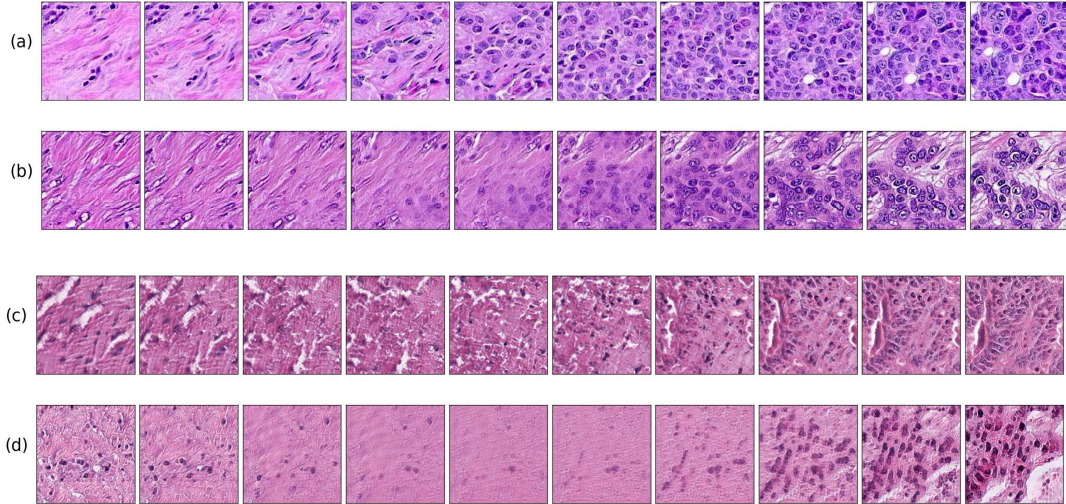


Figure 7: Linear interpolation in the latent space  $w$  from a benign (less cancer cells, left end) to a malignant tissue (more cancer cells, right end) on breast cancer (a, b) and colorectal cancer (c, d). (a, c) PathologyGAN model interpolations with a mapping network and style mixing regularization. (b, d) PathologyGAN model interpolations without a mapping network and style mixing regularization. (a, c) includes an increasing population of cancer cells rather than a fading effect from model (b, d), this shows that model (a, c) better translates high level features of images from latent space vectors.

- 50 Individual images - Pathologists were asked to rate all individual images from 1 to 5, where 5 meant the image appeared the most real.

We chose fake images in two ways, with half of them hand-selected and the other half with fake images that had the smallest Euclidean distance to real images in the convolutional feature space (Inception-V1). All the real images are randomly selected between the three closest neighbors of the fake images.

Figure 11 shows the test results in terms of false positive vs true positive for breast (a) and colorectal cancer tissue (b). We can see that pathologist classification is close to random. The pathologists mentioned that the usual procedure is to work with larger images with bigger resolution, but that the generated fake images were of a quality, that at the  $224 \times 224$  size used in this work, they were not able to differentiate between real and fake tissue.

## 5. Discussion

Our goal is to develop a generative model that is able to capture and create representations based tissue architectures and cellular characteristics that define phenotype, for this reason

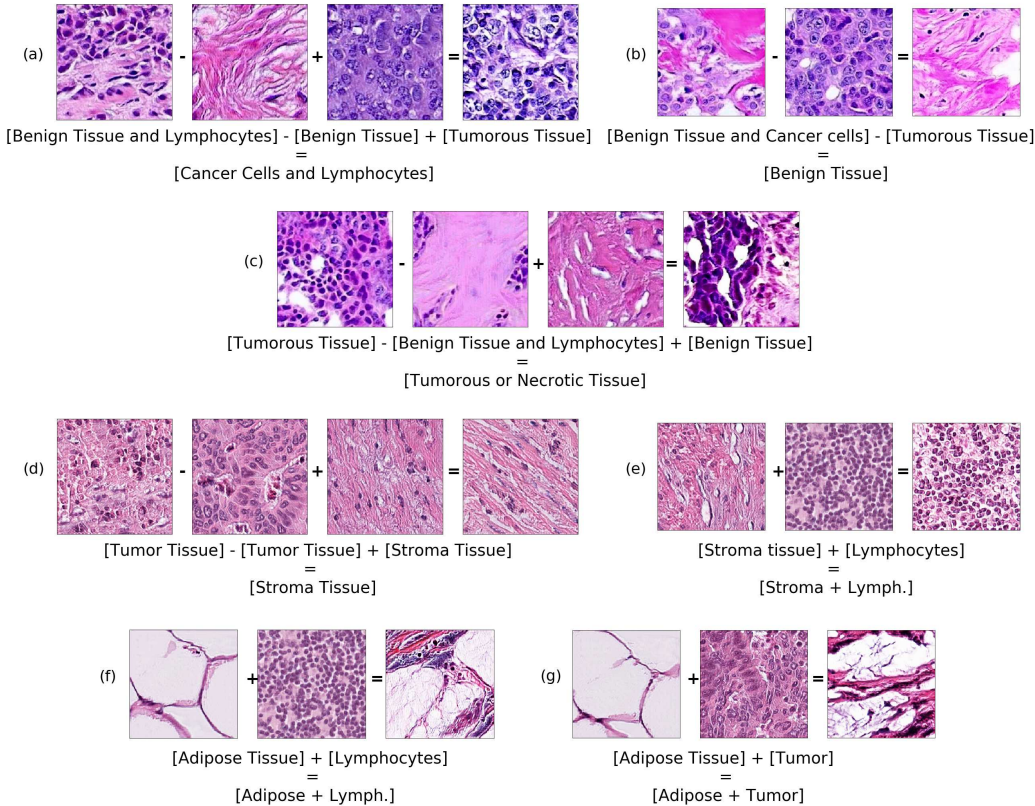


Figure 8: Linear vector operations on the latent space  $w$  translate into image feature transformations. We gather latent vectors that generate images with different high level features and perform linear operations on the vectors before we feed the generator, resulting into semantic translations of the characteristics of the images. We perform the arithmetic operations (a, b, and c) on breast cancer tissue and (d, e, f, and g) on colorectal cancer tissue.

our results are focused on testing two features of our model: Image quality of generated tissue and interpretability of representations/structure of the latent space.

Through image quality we tested the model’s ability to learn and reproduce the distribution of tissue and cellular information, we argue that by doing so it would have capture phenotypes. The FID results on Table 1 show that PathologyGAN does reproduce these distributions not only when it is judged by convolutional features (32.05/16.65) but also when we use an external tool to directly quantify cellular information in the tissue (9.86). We would like to highlight that the FID score measures the distribution difference between real and generated samples, and given the low values we argue that the model is also capturing the abundance or scarcity of different tissue patterns.

Figure 4 shows generated tissue samples and their closest real neighbors in the Inception-V1 convolutional space, allowing us to visually inspect the similarity between them. In the colorectal cancer samples we can see that the different types of tissue (from tumor (i) to background (p)) clearly resemble the real tissue. Breast cancer tissue samples (a-h) also

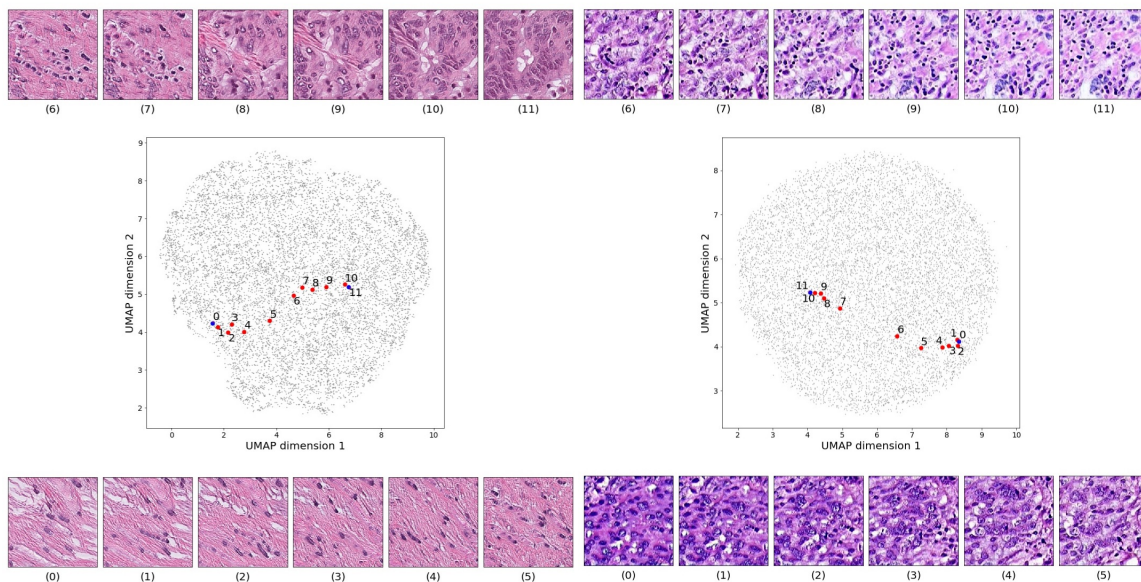


Figure 9: Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples where linear interpolations in the latent space are highlighted. Colorectal cancer (left) shows a transition between stroma and tumor, while Breast cancer (right) shows a transition between tumor and lymphocytes. Starting vectors are colored in blue while intermediate points of the interpolations are colored in red. Through the intermediate vectors we show that gradual transitions in the latent space translate into smooth feature transformations, increase/decrease of tumorous cells or increase of lymphocyte counts.

show the same result where the real and generated tissue present the same patterns and shapes.

As an additional image quality verification, we tested the generated images of our model against pathologists’ interpretation. We aimed to test that the generated tissues do not contain any artifacts that give them away as fake through the eyes of professionals. Given the near random classification between real/fake in Figure 11, we conclude that generated samples are realistic enough to pass as real through the examination of pathologists. We argue this is relevant because the model is able to reproduce tissue patterns to which pathologists are accustomed to.

With the previous results we conclude that the model is able to reproduce the detail and distribution of tissue, not only from the convolutional features or cellular characteristics perspective, but also by the interpretation of pathologists.

In relation to PathologyGAN’s latent space structure and interpretability of its representations, Figures 5 and 6 show how distinct regions of the latent space hold tissue and cellular information about the generated images. Figure 5 shows a clear relationship between regions of the latent space and the cancer cell density in the tissue, while Figure 6 directly links the region of the space with the different tissue types (e.g. tumor, stroma,

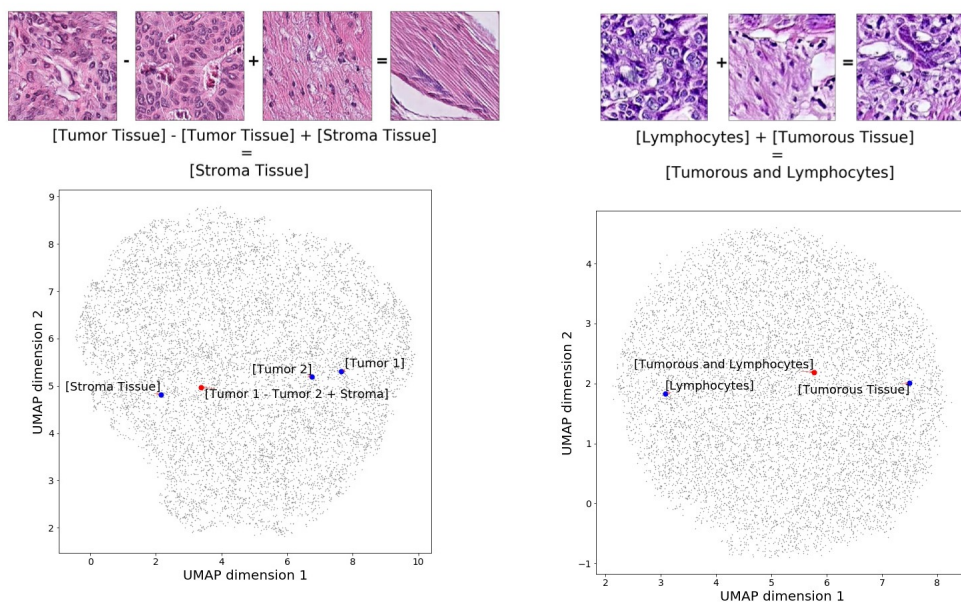


Figure 10: Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples where vectors involved in the linear vector operations are highlighted. Original vectors are colored in blue while the results are colored in red. We show colorectal cancer examples on the left and breast cancer examples on the right. After vector operations the results fall into regions of the latent space that correspond to the tissue type (left) or a combination of features, tumor and lymphocytes (right).

muscle, lymphocytes, debris, mucus, adipose, and background). In Figures 7 and 9 we relate linear interpolations between latent vectors and generated tissue attributes, showing that gradual transitions in the latent space transfer into smooth feature transformations, in these cases increase/decrease of tumorous cells or increase of lymphocyte counts. Finally, Figures 8 and 10 provide examples of linear vector operations and their translation into tissue characteristic changes, with different tissue changes. These results provide support on the representation learning properties of the model, not only holding meaningful information of cell and tissue types but also an interpretable insight to the representations themselves.

As future research, we consider that our model could be used in different settings. PathologyGAN could be extended to achieve higher resolutions such as  $1024 \times 1024$ , a level of resolution which could include complete TMAs which hold value for diagnosis and prognosis. In these cases, pathologists' insight will hold a higher value, since they are used to working at WSI or TMA level. In addition, the study with pathologists could be extended to include a larger number of experts and to use a random sample of generated images which would give a less biased result.

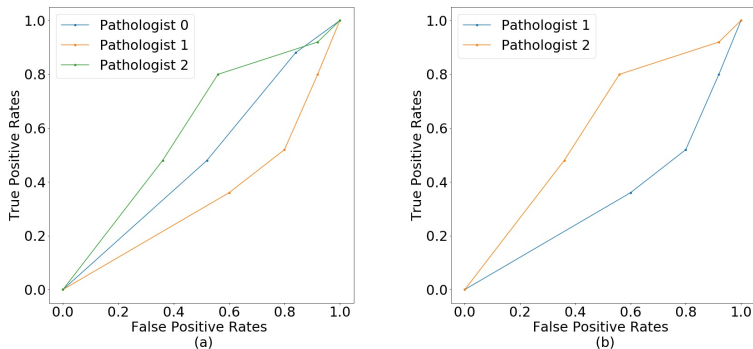


Figure 11: ROC curve of Pathologists’ real/fake classification for breast (a) and colorectal cancer tissue (b). The near random classification performance from both expert pathologists suggests that generated tissue images do not present artifacts that give away the tissue as generated.

The representation learning properties of the model can also contribute as a educational tool, providing tissue samples with certain cellular characteristics that are rare, elucidating possible transitions of tissue (e.g. from tumor to high lymphocyte infiltration), or enabling the study of borderline cases (e.g. atypia) between generated images and pathologists interpretations.

Furthermore, the model could be used to generate synthetic samples to improve classifiers performance, helping to avoid overfitting and providing samples with rare tissue pathologies.

Finally, we consider the model can contribute to characterizing phenotype patterns, creating representations by cellular and tissue morphologies, this is where we think the tissue representation learning properties are key. Linking these phenotypes to patient related information such as genomic, transcriptomic information, or survival expectancy. Ultimately this could give insight to the tumor microenvironment recorded in the WSIs and a better understanding of the disease. In order to achieve this goal, it will require exploring the addition of an encoder to map real images into the GAN’s latent space (Quiros et al., 2020) and verify its converge when large amounts of samples are used, since WSIs in datasets like TCGA could amount to millions of tissue samples.

## 6. Conclusion

We presented a new approach to the use of machine learning in digital pathology, using GANs to learn cancer tissue representations. We assessed the quality of the generated images through the FID metric, using the convolutional features of a Inception-V1 network and quantitative cellular information of the tissue, both showed consistent state-of-the-art values for different kinds of tissue, breast and colorectal cancer. We showed that our model allows high level interpretation of its latent space, even performing linear operations that translate into feature tissue transformations. Finally, we demonstrate that the quality of



the generated images do not allow pathologists to reliably find differences between real and generated images.

With PathologyGAN we proposed a generative model that captures representations of entire tissue architectures and defines an interpretable latent space (e.g. colour, texture, spatial features of cancer and normal cells, and their interaction), contributing to generative models ability to capture phenotype representations.

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## Ethical Standards

The work follows appropriate ethical standards in conducting research and writing the manuscript. Our models were trained with publicly available data, for which no ethical approval was required.

## Conflicts of Interest

We declare we don't have conflicts of interest.

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## Appendix A. Code

We provide the code at this location: <https://github.com/AdalbertoCq/Pathology-GAN>

## Appendix B. Dataset size impact on representations.

To further understand PathologyGAN’s behavior with different dataset sizes and its ability to generalize, we sub-sample the NCT and created different dataset sizes of  $5K$ ,  $10K$ , and  $20K$  images.

We measure the ability to generalize and hold meaningful representations in two ways: by measuring the FID against the complete dataset of  $100K$  and by exploring the latent space, in order to check its structure.

Figure 12 shows that PathologyGAN’s latent space shows a structure regarding tissue types even for  $5K$  samples, although it is not able to reliably generalize the original dataset distribution. Table 2 shows how  $20K$  samples are enough to achieve a reasonable FID with 41.92.

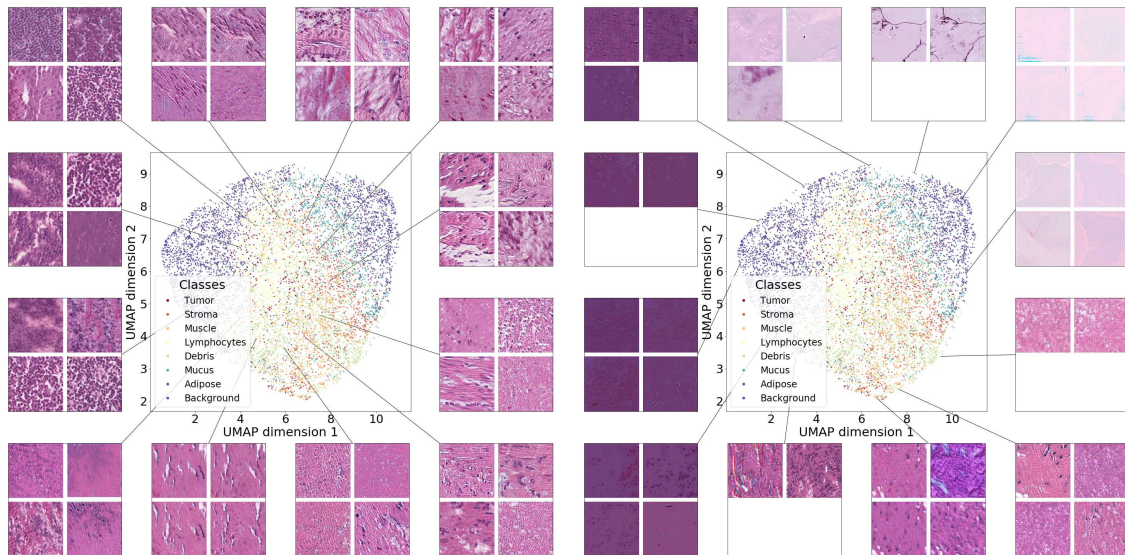


Figure 12: Latent space of PathologyGAN trained on colorectal cancer tissue from National Center for Tumor (NCT) dataset with  $5K$  samples. Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples, each generated image is labeled with the type of tissue. Even with  $5K$  samples, PathologyGAN holds an structured latent sapce where different regions of the latent space generate distinct kinds of tissue.



NCT Dataset Size	FID
5K	83.52
10K	56.03
20K	41.92
Complete 100K	32.05

Table 2: Evaluation of PathologyGANs for different dataset sizes.

### Appendix C. Hinge vs Relativistic Average Discriminator

In this section we show corresponding generated images and loss function plots for Relativistic Average Discriminator model and Hinge Loss model.

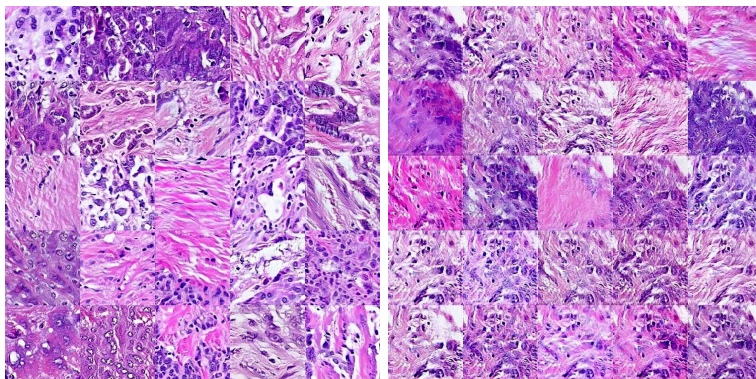


Figure 13: Left grid images correspond to Relativistic Average Discriminator model vs right grid images from the Hinge loss model. We can see that the Relativistic Average model is able to reproduce cancer tissue characteristics compared to Hinge loss, which does not.

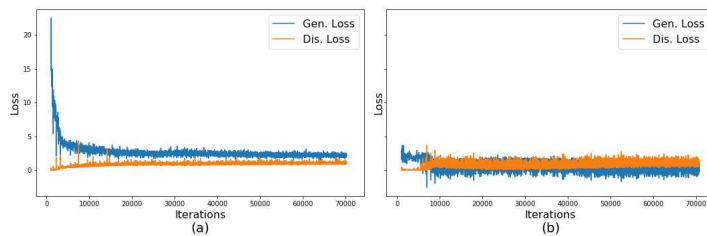


Figure 14: (a) Generator and Discriminator loss functions of the Relativistic Average Discriminator model, (b) Generator and Discriminator loss functions from the Hinge loss model. Here we capture the corresponding loss functions to the images in Figure 13, both of them converge but only Relativistic Average Discriminator produces meaningful images.

## Appendix D. Nearest Neighbors Additional Samples

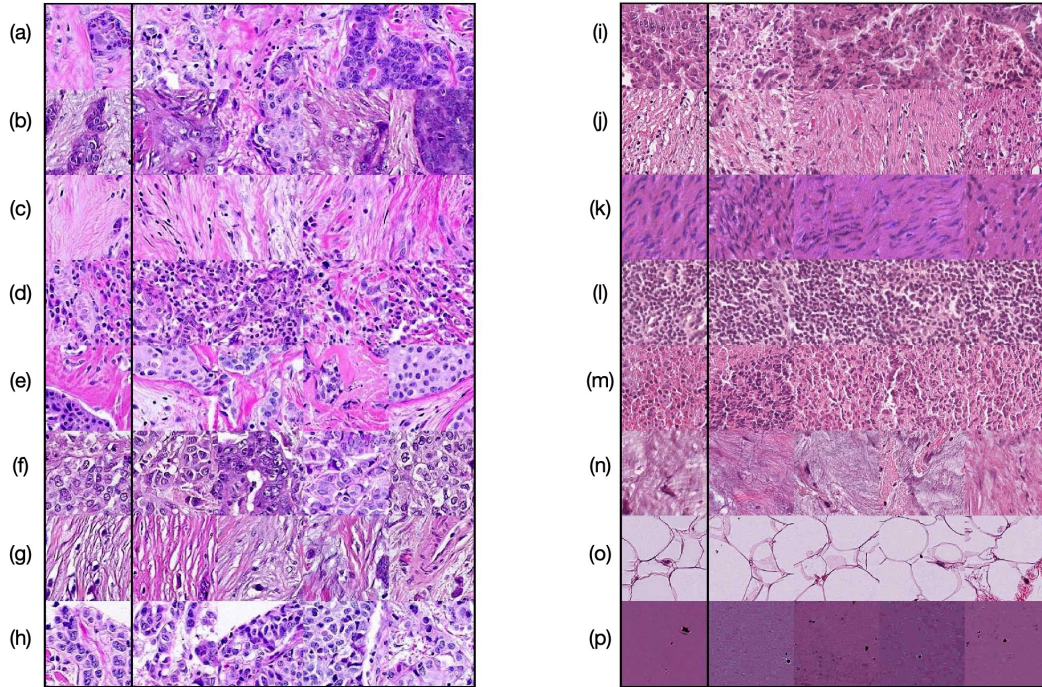


Figure 15: Nearest neighbors in Inception-V1 feature space for breast cancer (a-h) and colorectal cancer (i-p). For each row, first column images corresponds to a generated tissue samples from PathologyGAN, the remaining columns are the closest real images in feature space.

## Appendix E. Mapping Network and Style Mixing Regularization Comparison

To measure the impact of introducing a mapping network and using style mixing regularization during training, we provide different figures of the latent space  $w$  for two PathologyGANs, one using these features and another one without them. We include both datasets, breast and colorectal cancer tissue.

Figures 16, 17, 18, and 19 capture the clear difference in the latent space ordering with respect to the counts of cancer cells and types of tissue in the image. Without a mapping network and style mixing regularization the latent space  $w$  shows a random placement of the vectors subject to the tissue characteristics, when these two elements are introduced different regions of the latent space produce images with distinct characteristics.

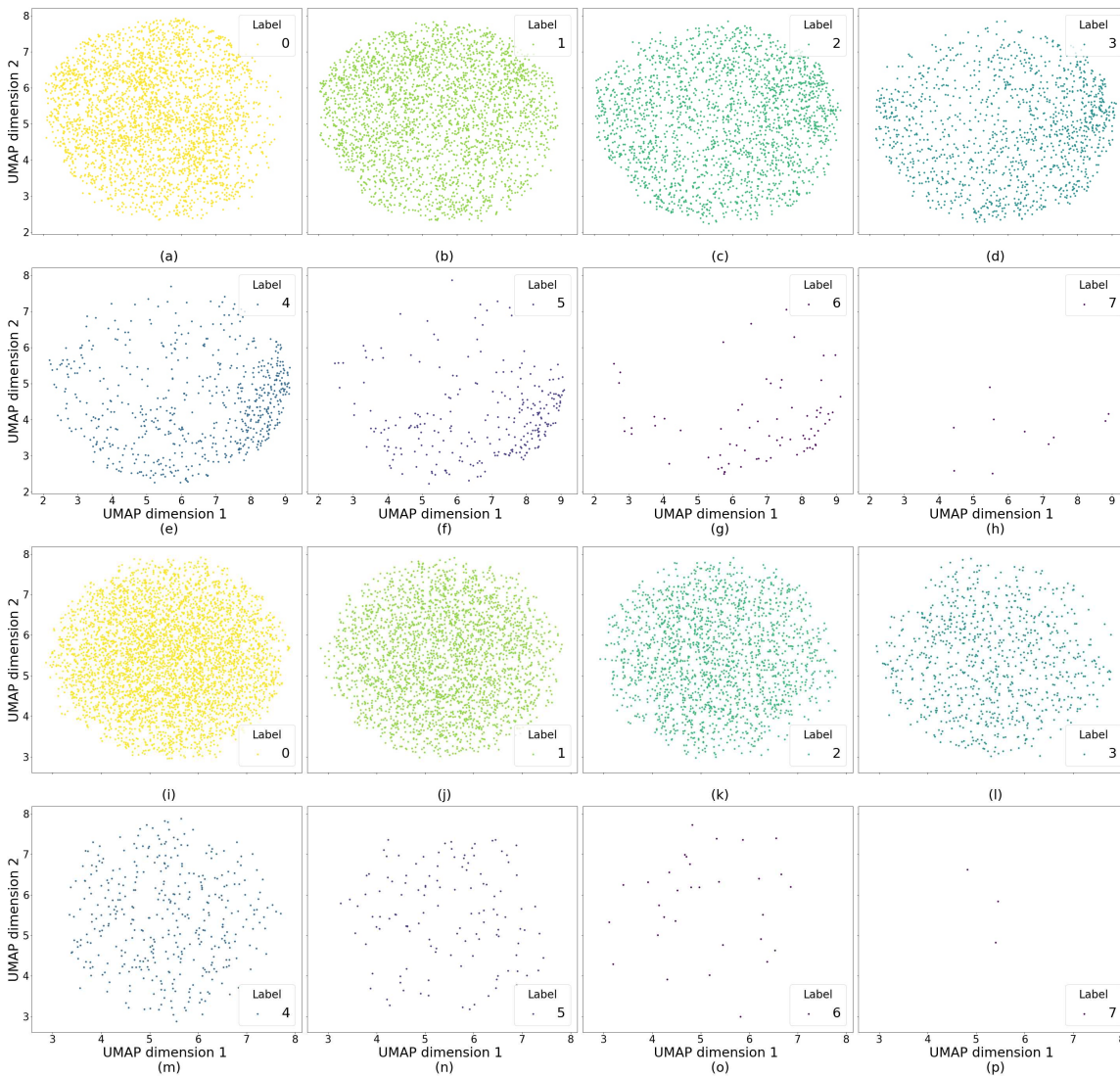


Figure 16: Breast cancer tissue: Comparison of the latent space  $w$  for two different PathologyGAN models, (a-h) include a mapping network and style mixing regularization, and (i-p) do not include them. Each sub-figure shows datapoints only related to one of the classes, and each class is subject to the count of cancer cells in the tissue image, (a) and (i) [class 0] are associated to images with the lowest number of cancer cells, (h) and (p) [class 8] with the largest. In the model (a-h) images with increasing number of cancer cells correspond to proportionally moving to quadrant *IV* in the 2 dimensional space, where (i-p) are randomly placed. This figure shows how including the mapping network and style mixing regularization introduces representation learning properties.

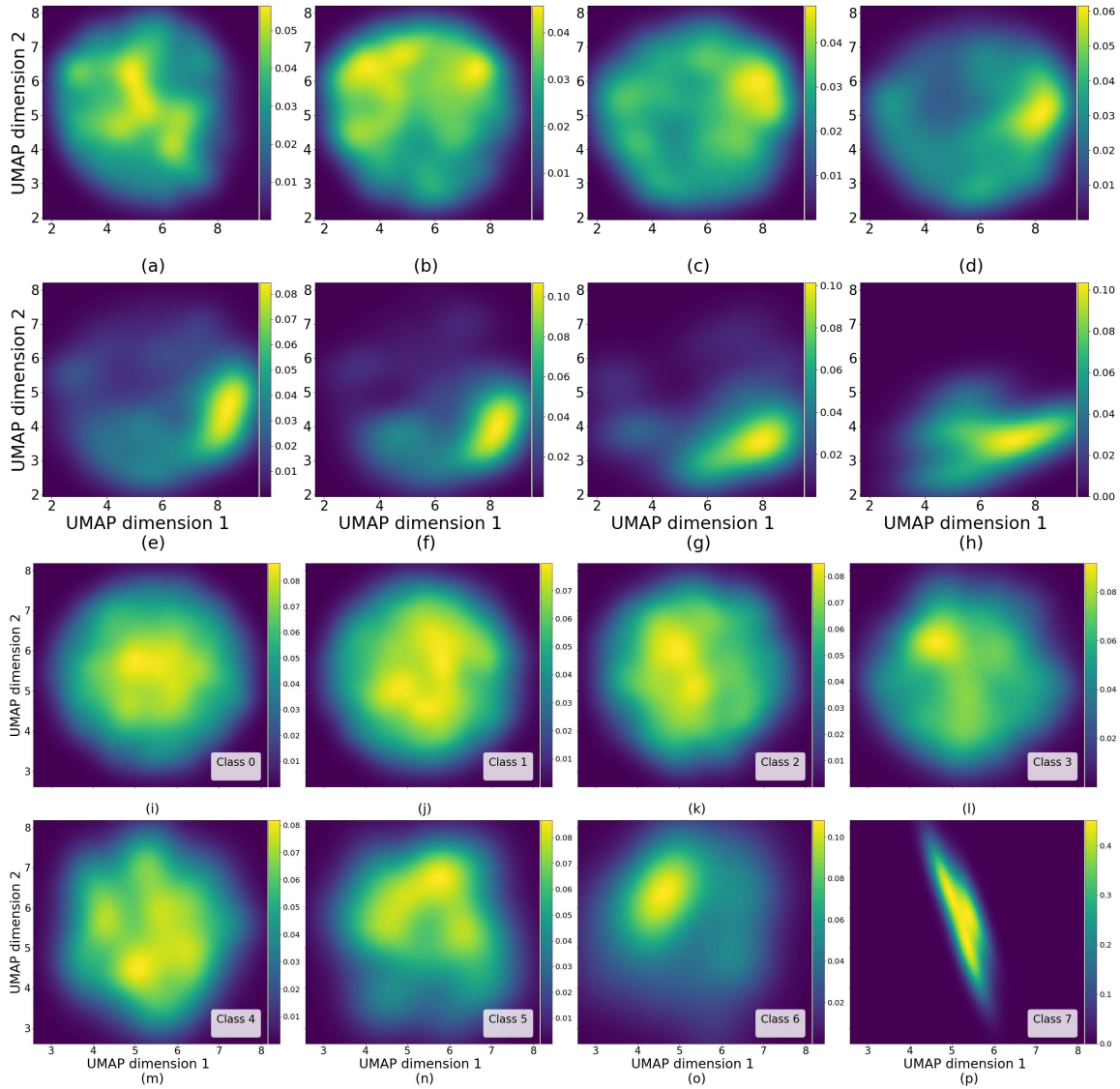


Figure 17: Breast cancer tissue: Comparison of the latent space  $w$  for two different PathologyGAN models, (a-h) include a mapping network and style mixing regularization, and (i-p) do not include them. Each sub-figure shows the density of datapoints only related to one of the classes, and each class is subject to the count of cancer cells in the tissue image, (a) and (i) [class 0] are associated to images with the lowest number of cancer cells, (h) and (p) [class] with the largest. In the model (a-h) images with increasing number of cancer cells correspond to proportionally moving to quadrant *IV* in the 2 dimensional space, where (i-p) are randomly placed. This figure shows how including the mapping network and style mixing regularization introduces representation learning properties.

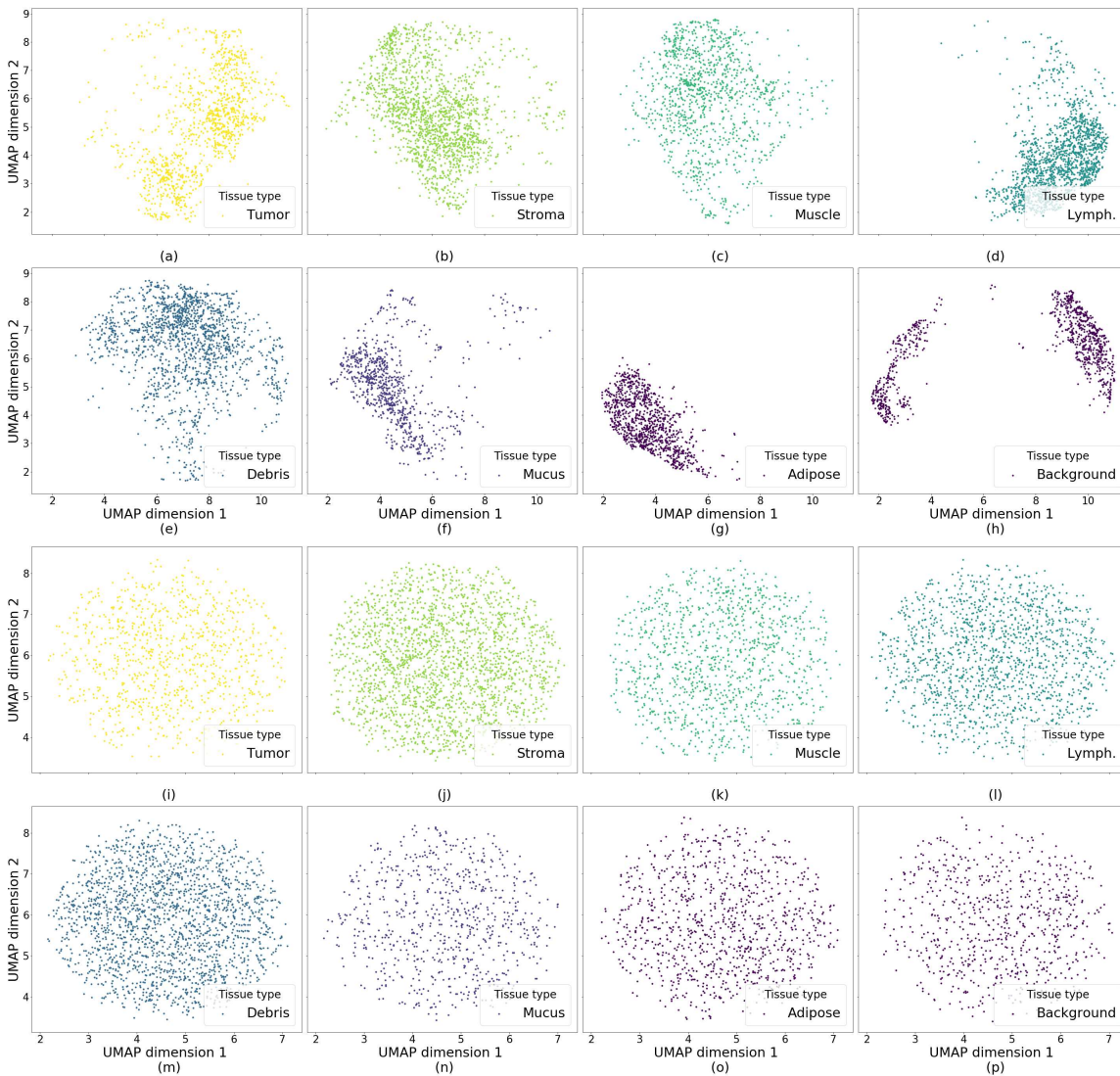


Figure 18: Colorectal cancer tissue: Comparison of the latent space  $w$  for two different PathologyGAN models, (a-h) include a mapping network and style mixing regularization, and (i-p) do not include them. Each sub-figure shows datapoints only related to to one type of tissue. In the model (a-h) distinct regions of the latent space correspond to different tissue types, while in model (i-p) they are randomly placed. This figure shows how including the mapping network and style mixing regularization introduces representation learning properties.

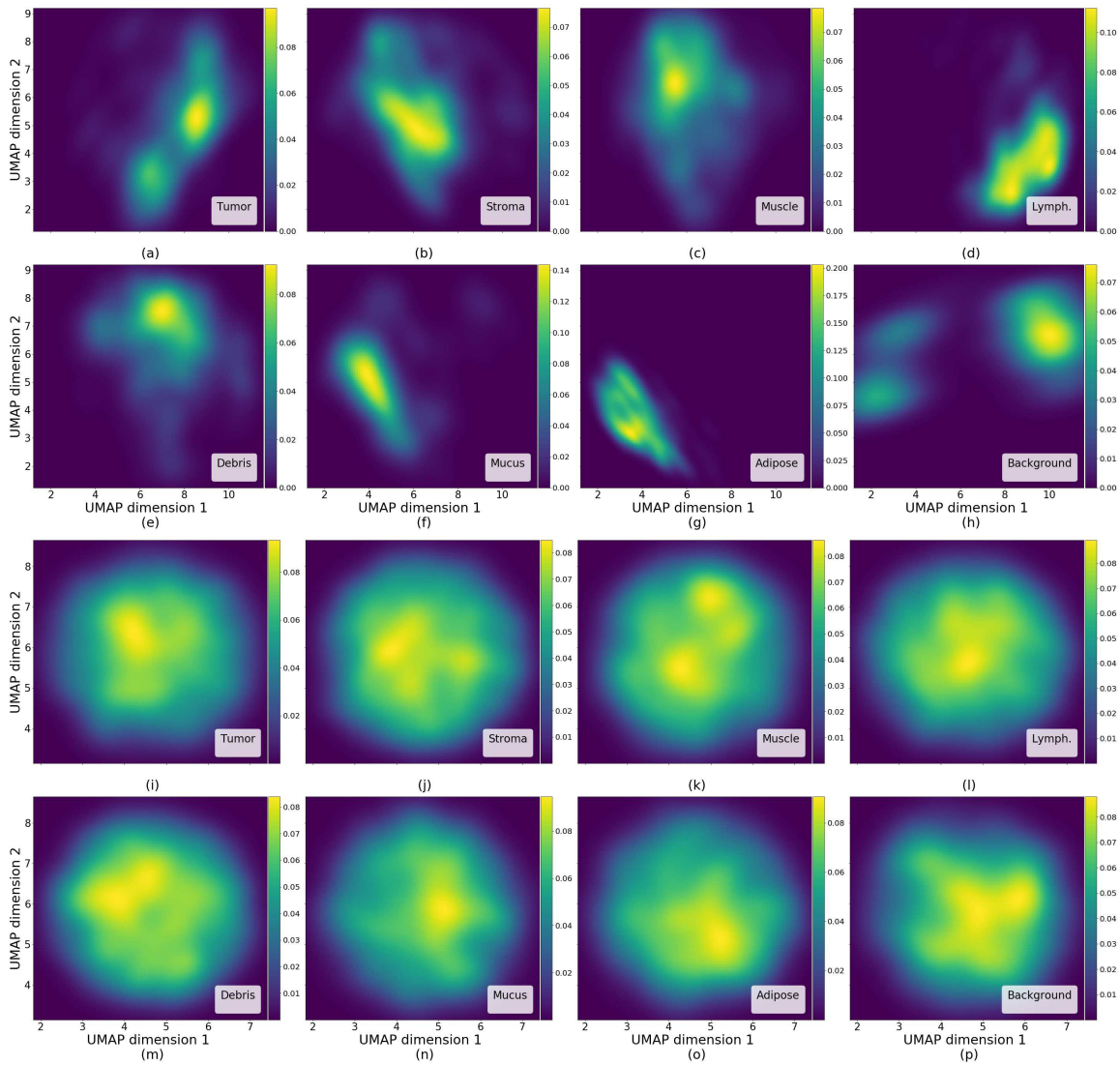


Figure 19: Colorectal cancer tissue: Comparison of the latent space  $w$  for two different PathologyGAN models, (a-h) include a mapping network and style mixing regularization, and (i-p) do not include them. Each sub-figure shows the density of datapoints only related to one type of tissue. In the model (a-h) distinct regions of the latent space correspond to different tissue types, while in model (i-p) they are randomly placed. This figure shows how including the mapping network and style mixing regularization introduces representation learning properties.

## Appendix F. Vector Operation Samples

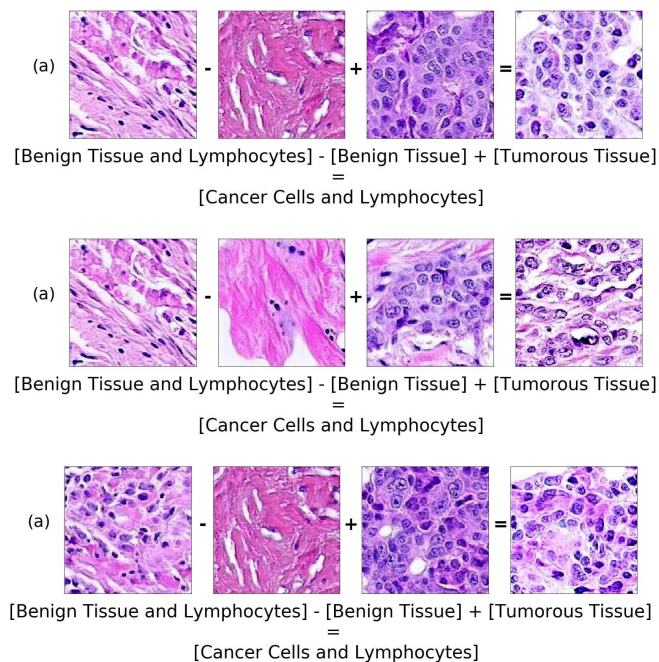


Figure 20: Breast cancer: samples of vector operations with different images, all operations correspond to: Benign tissue and lymphocytes- benign tissue + tumorous tissue = cancer cells and lymphocytes.

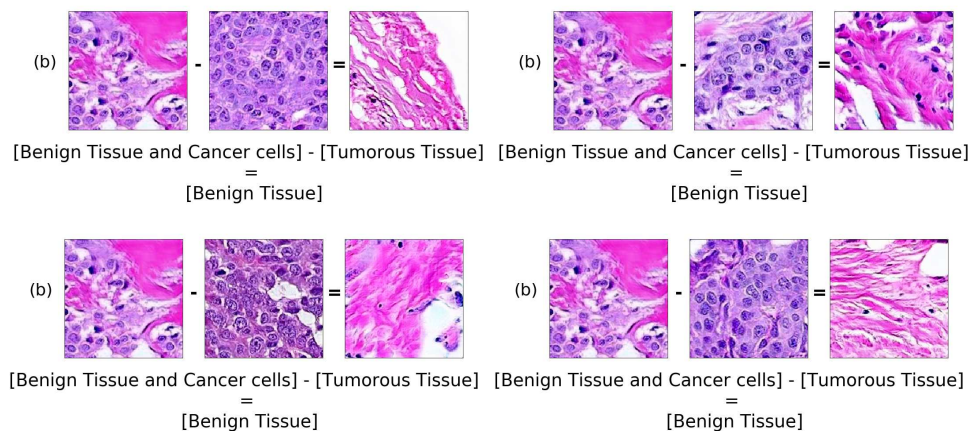


Figure 21: Breast cancer: samples of vector operations with different images, all operations correspond to: Benign tissue with patches of cancer cells - tumorous = benign tissue.

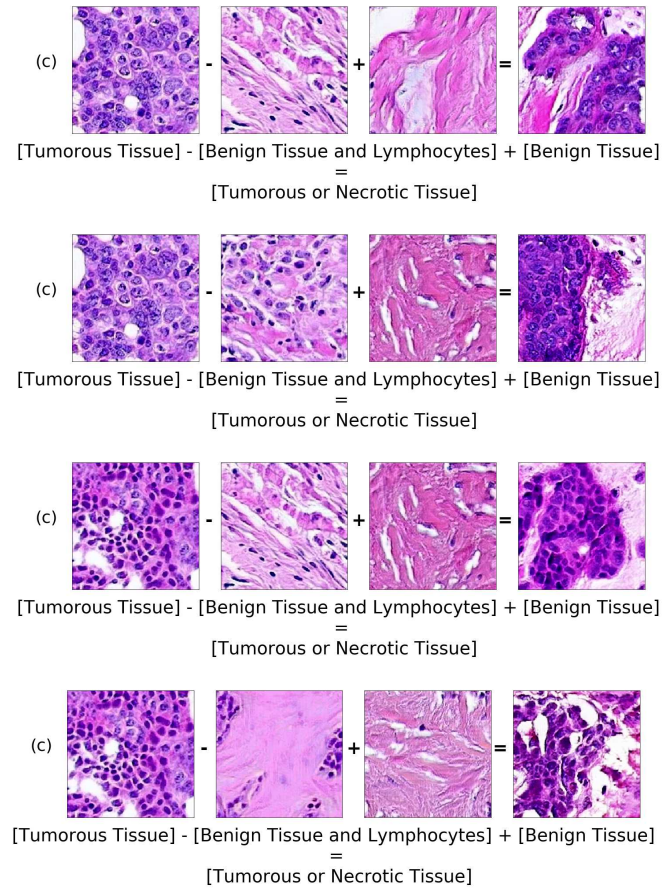


Figure 22: Breast cancer: samples of vector operations with different images, all operations correspond to: Tumorous tissue with lymphocytes - benign tissue with lymphocytes + benign tissue = tumorous or necrotic tissue.



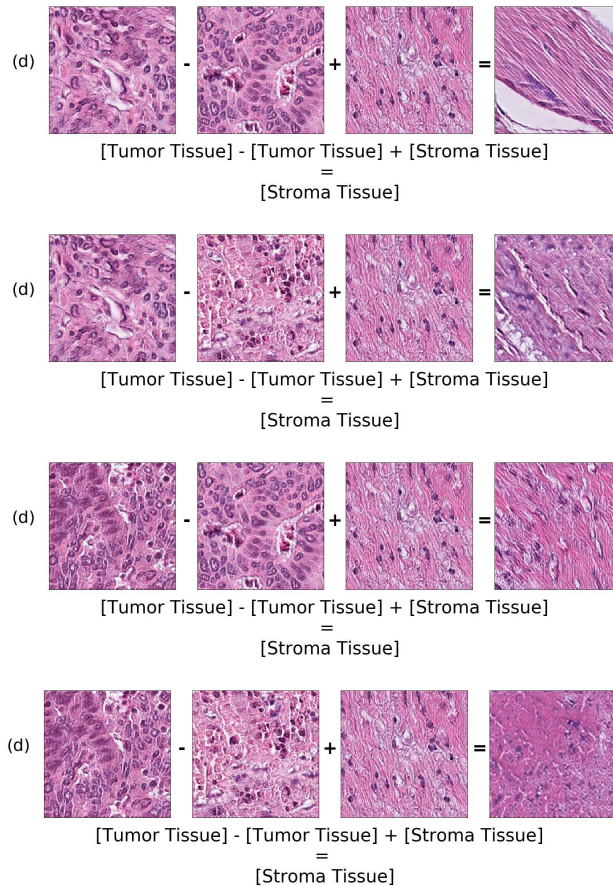


Figure 23: Colorectal cancer: samples of vector operations with different images, all operations correspond to: Tumor tissue - Tumor tissue + Stroma tissue = Stroma Tissue.

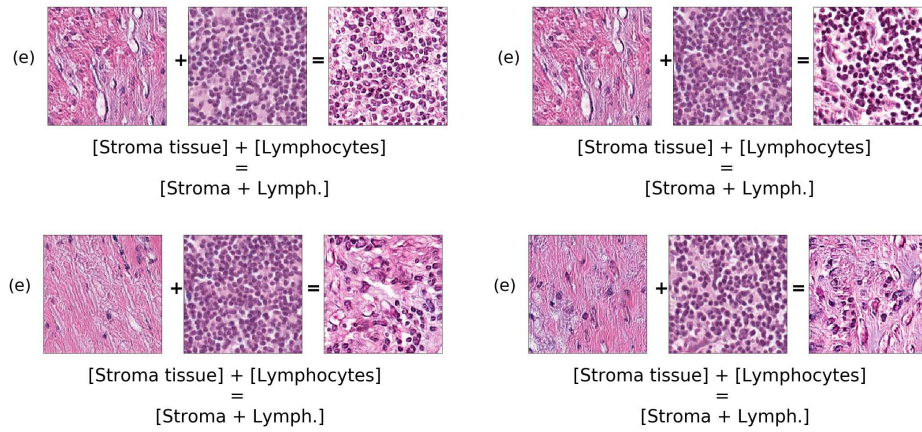


Figure 24: Colorectal cancer: samples of vector operations with different images, all operations correspond to: Stroma tissue + Lymphocytes = Stroma and Lymphocytes.

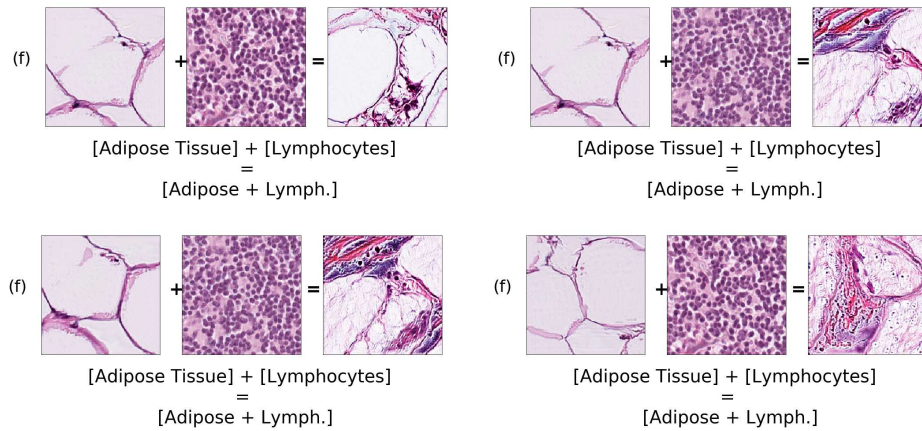


Figure 25: Colorectal cancer: samples of vector operations with different images, all operations correspond to: Adipose tissue + Lymphocytes = Adipose and Lymphocytes.

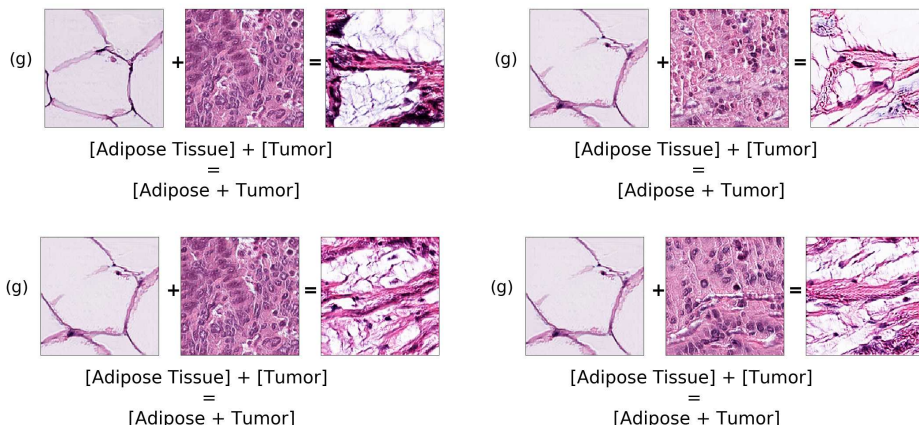


Figure 26: Colorectal cancer: samples of vector operations with different images, all operations correspond to: Adipose tissue + Tumor tissue = Adipose and Tumor.

## Appendix G. PathologyGAN at 448x448

We include in this section experimental results of a  $448 \times 448$  image resolution model. We trained this model for 90 epochs over approximately five days, using four NVIDIA Titan RTX 24 GB.

Over one model the results of Inception FID and CRImage FID were 29.53 and 203 respectively. We found that CRImage FID is highly sensitive to changes in the images since it looks for morphological shapes of cancer cells, lymphocytes, and stroma in the tissue, at this resolution the generated tissue images don't hold the same high quality as in the  $224 \times 224$  case. As we capture in the **Conclusion** section, this is an opportunity to improve the detail in the generated image at high resolutions.

Figure 27 show three examples of comparisons between (a) PathologyGAN images and (b) real images. Additionally, the representation learning properties are still preserved in the latent space. Figure 28 captures the density of cancer cells in the  $448 \times 448$  tissue images as previously presented for the  $224 \times 224$  case in **Appendix C**.

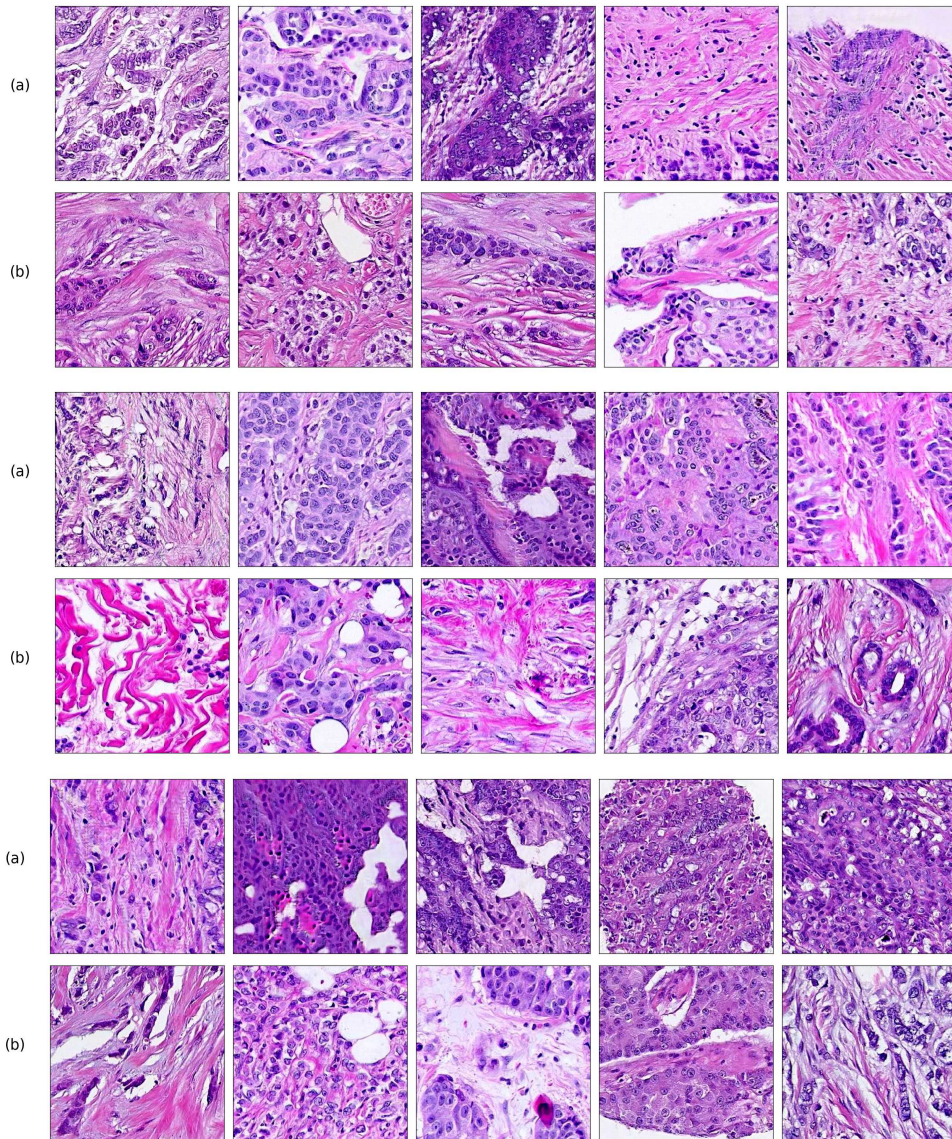


Figure 27: (a): Images ( $448 \times 448$ ) from PathologyGAN trained on H&E breast cancer tissue. (b): Real images.

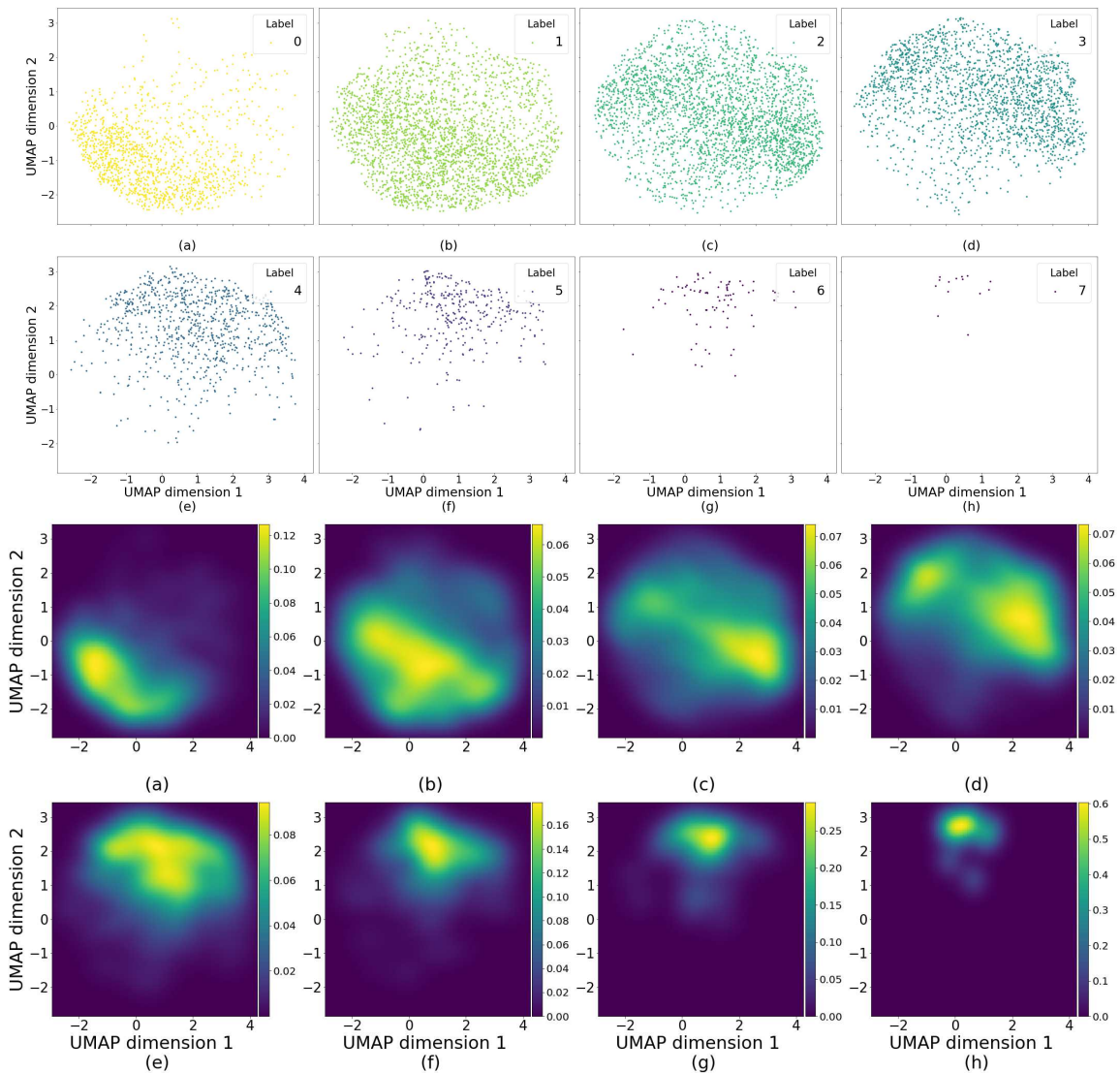


Figure 28: Scatter and density plots of  $448 \times 448$  samples on the UMAP reduced representation of the latent space  $w$ . Each subfigure (a-h) belongs to samples of only one class, where each class represents a range of counts of cancer cells in the tissue image. (a) accounts for images with the lowest number of cancer cells and (h) corresponds to images with the largest count, subfigures from (a) to (h) belong to increasing number of cancer cells. As previously shown in Figure 16 and 17 for the  $224 \times 224$  resolution, representation learning properties are still held at  $448 \times 448$ .

## Appendix H. Visualization of linear interpolations and vector operations in the latent space.

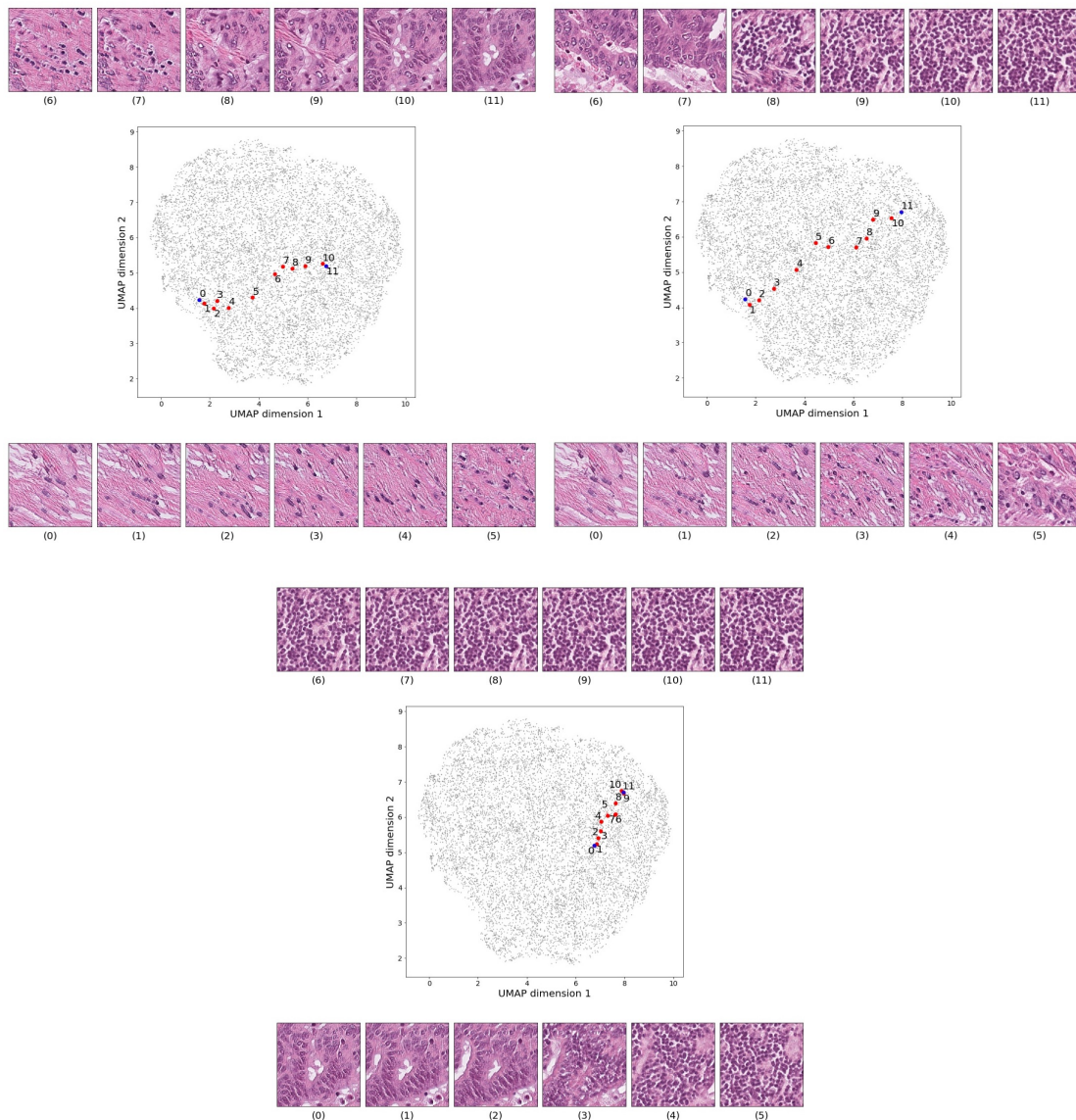


Figure 29: Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples where linear interpolations in the latent space are highlighted. We present colorectal cancer transition from stroma to tumor, stroma to lymphocytes, and tumor to lymphocytes. Starting vectors are colored as blue while intermediate points of the interpolations are colored as red. Through the intermediate vectors we show that gradual transitions in the latent space translate into smooth feature transformations, increase/decrease of tumorous cells or increase of lymphocyte counts.

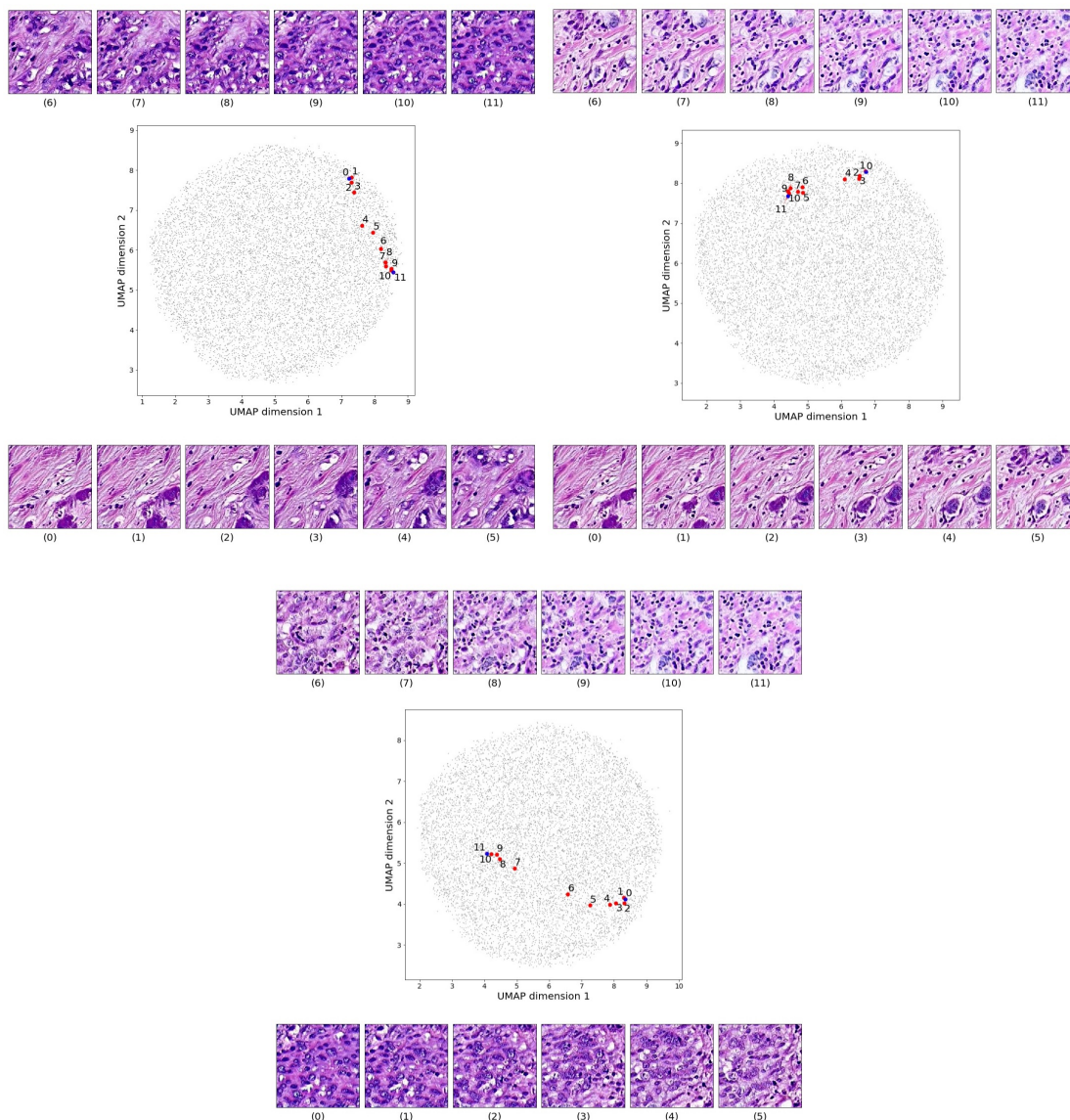


Figure 30: Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples where linear interpolations in the latent space are highlighted. We present breast cancer transition from stroma to tumor, stroma to lymphocytes, and tumor to lymphocytes. Starting vectors are colored as blue while intermediate points of the interpolations are colored as red. Through the intermediate vectors we show that gradual transitions in the latent space translate into smooth feature transformations, increase/decrease of tumorous cells or increase of lymphocyte counts.

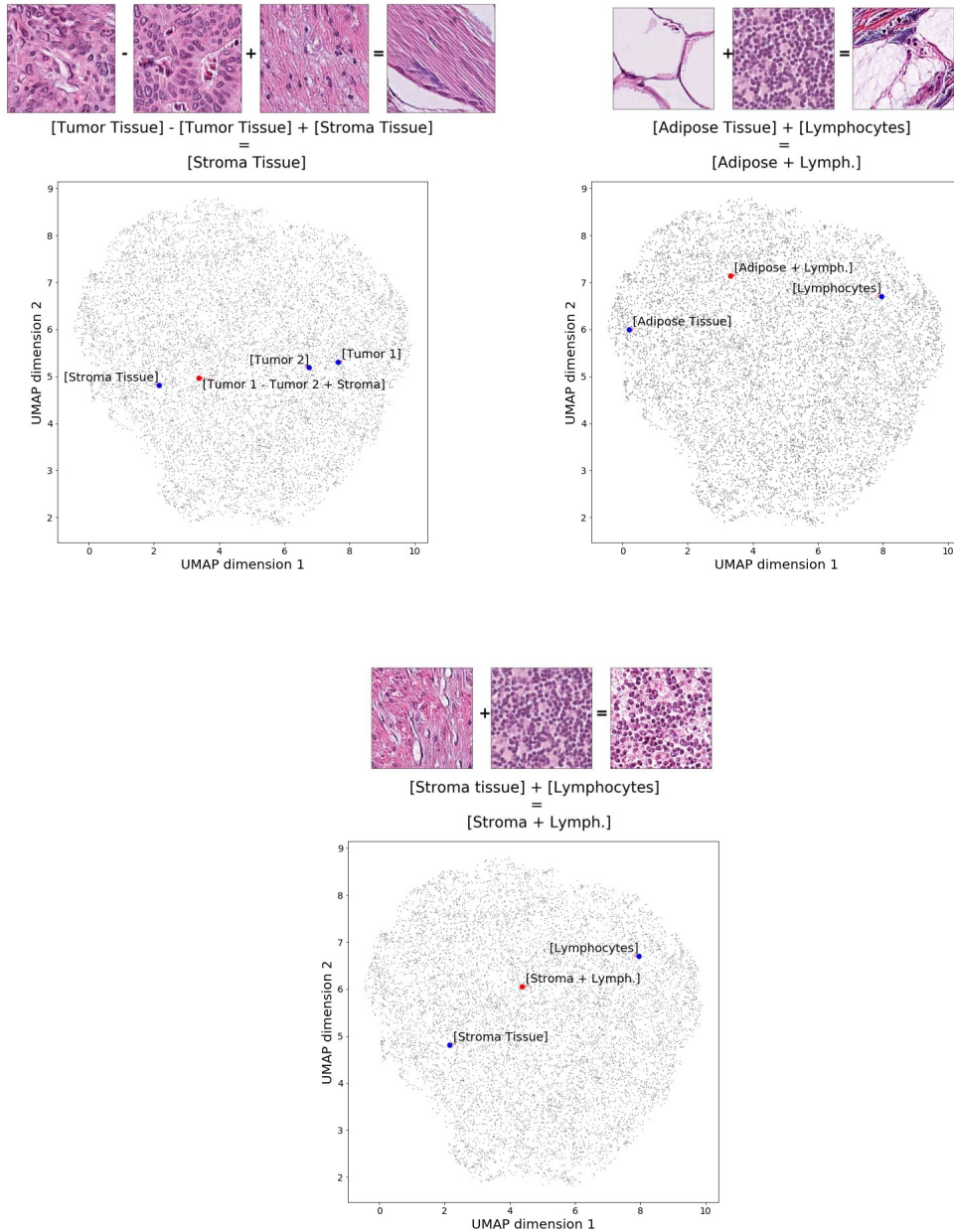


Figure 31: Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples where vectors involved in the linear vector operations are highlighted. Original vectors are colored in blue while the results are colored in red. We show colorectal cancer examples where after vector operations the results fall into regions of the latent space that correspond to the tissue type.



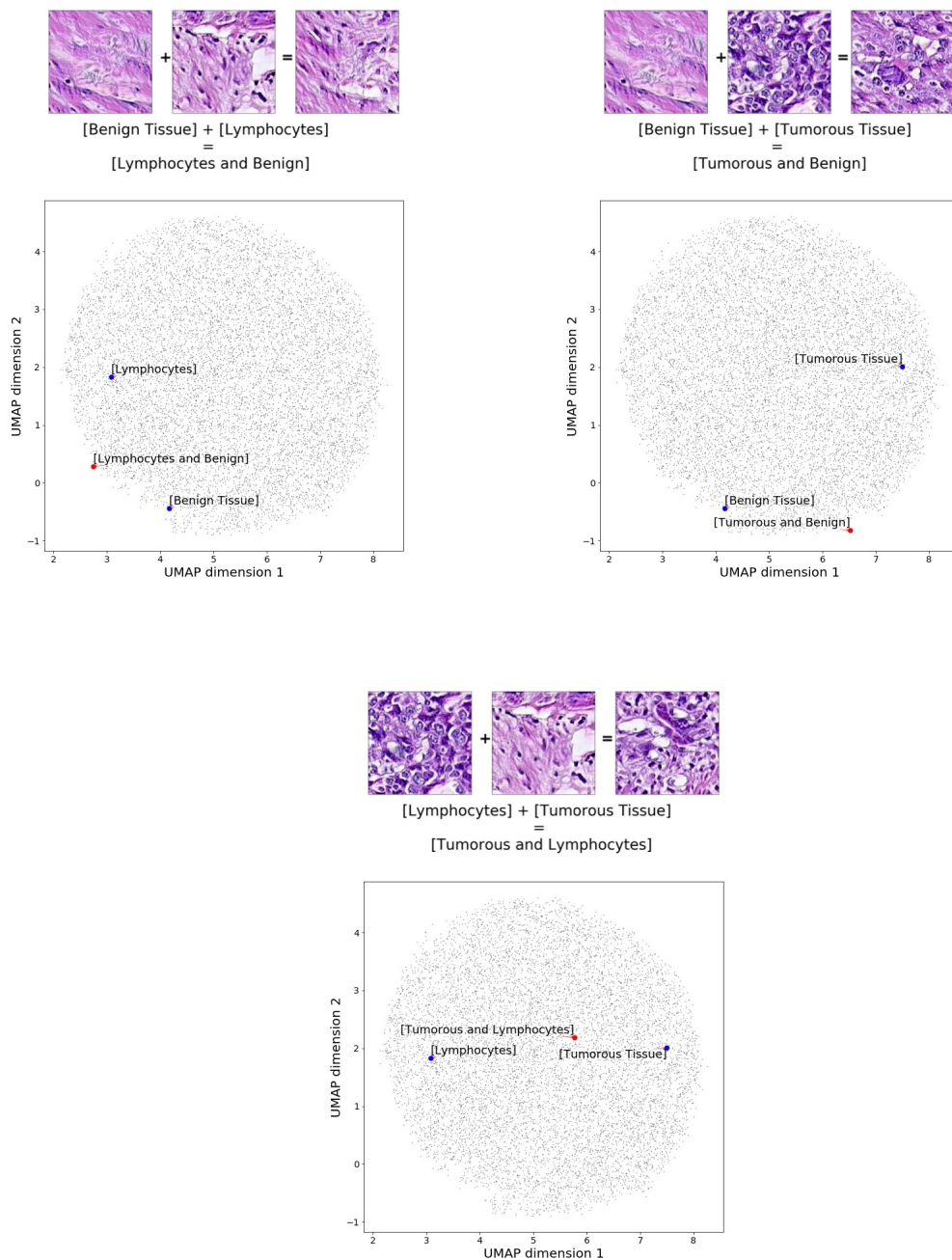


Figure 32: Uniform Manifold Approximation and Projection (UMAP) representations of generated tissue samples where vectors involved in the linear vector operations are highlighted. Original vectors are colored in blue while the results are colored in red. We show breast cancer examples where after vector operations the results combination of different features such as tumor, benign tissue, or lymphocytes.

## Appendix I. GAN evaluation metrics for digital pathology

In this section, we investigate how relevant GAN evaluation metrics perform on distinguishing differences in cancer tissue distributions. We center our attention on metrics that are model agnostic and work with a set of generated images. We focus on Fréchet Inception distance (FID), Kernel Inception Distance (KID), and 1-Nearest Neighbor classifier (1-NN) as common metrics to evaluate GANs. We do not include Inception Score and Mode Score because they do not compare to real data directly, they require a classification network on survival times and estrogen-receptor (ER), and they have also showed lower performance when evaluating GANs (Barratt and Sharma, 2018; Xu et al., 2018).

Xu et al. (2018) reported that the choice of feature space is critical for evaluation metrics, so we follow these results by using the 'pool\_3' layer from an ImageNet trained Inception-V1 as a convolutional feature space.

We set up two experiments to test how the evaluation metrics capture:

- Artificial contamination from different staining markers and cancer types.
- Consistency when two sample distributions of the same database are compared.

### I.1 Detecting changes in markers and cancer tissue features

We used multiple cancer types and markers to account for alterations of color and shapes in the tissue. Markers highlight parts of the tissue with different colors, and cancer types have distinct tissues structures. Examples of these changes are displayed in Figure 33.

We constructed one reference image set with 5000 H&E breast cancer images from our data sets of NKI and VGH, and compared it against another set of 5000 H&E breast cancer images contaminated with other markers and cancer types. We used three types of marker-cancer combinations for contamination, all from the Stanford TMA Database (Marinelli et al., 2008): H&E - Bladder cancer, Cathepsin-L - Breast cancer, and CD137 - Lymph/Colon/Liver cancer.

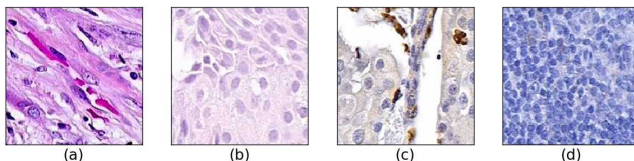


Figure 33: Different cancer types and markers. (a) H&E Breast cancer, (b) H&E Bladder cancer, (c) Capthepsin-L Breast cancer, and (d) CD137 Bone marrow cancer. We can see different coloring per marker, and tissue architecture per cancer type.

Each set of images was constructed by randomly sampling from the respective marker-cancer type data set, which is done to minimize the overlap between the clean and contaminated sets.

Figure 34 shows how (a) FID, (b) KID, (c) 1-NN behave when the reference H&E breast cancer set is measured against multiple percentage of contaminated H&E breast cancer sets. Marker types have a large impact due to color change and all metrics capture this except for

1-NN. Cathepsin-L highlights parts of the tissue with brown colors and CD137 has similar color to necrotic tissue on H&E breast cancer, but still far from the characteristic pink color of H&E. Accordingly, H&E-Bladder has a better score in all metrics due to the color stain, again expect for 1-NN. Cancer tissue type differences are captured by all the metrics, which shows a marker predominance, but we can see that on the H&E marker the differences between breast and bladder types are still captured.

In this experiment, we find that FID and KID have a gradual response distinguishing between markers and cancer tissue types, however 1-NN is not able to give a measure that clearly defines these changes.

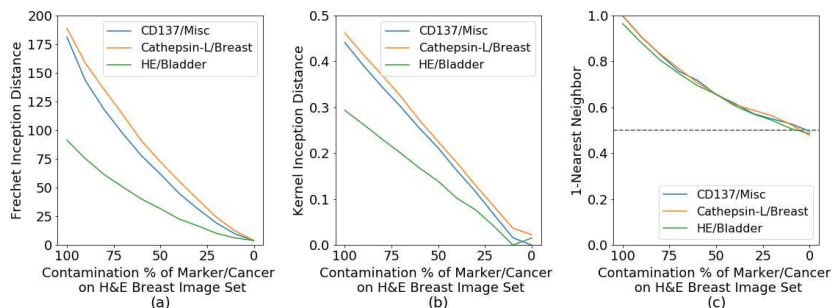


Figure 34: Distinguishing a set H&E Breast cancer images against different contamination of markers and cancer types. For a metric to be optimal, the value should decrease along with the contamination. (a) corresponds to FID, (b) KID, (c) 1-NN. FID and KID gradually define changes in marker and tissue type, 1-NN does not provide a clear measure of the changes.

## 1.2 Reliability on evaluation metrics

Another evaluation we performed was to study which metrics are consistent when two independent sample distributions with the same contamination percentage are compared. To construct this test, for each contamination percentage, we create two independent sample sets of 5000 images and compare them against each other. Again, we constructed these image sets by randomly selecting images for each of the marker-cancer databases. We do this to ensure there are no overlapping images between the distributions.

In Figure 35 we show that (a) FID has a stable performance, compared to (b) KID, and especially (c) 1-NN. The metrics should show a close to zero distance for each of the contamination rates since we are comparing two sample-distributions from the same data set. This shows that only FID has a close to zero constant behavior across different data sets when comparing the same tissue image distributions.

Based on these two experiments, we argue that 1-NN does not clearly represent changes in the cancer types and marker, and both KID and 1-NN do not give a constant reliable measure across different markers and cancer types. Therefore we focused on FID as the most promising evaluation metrics.

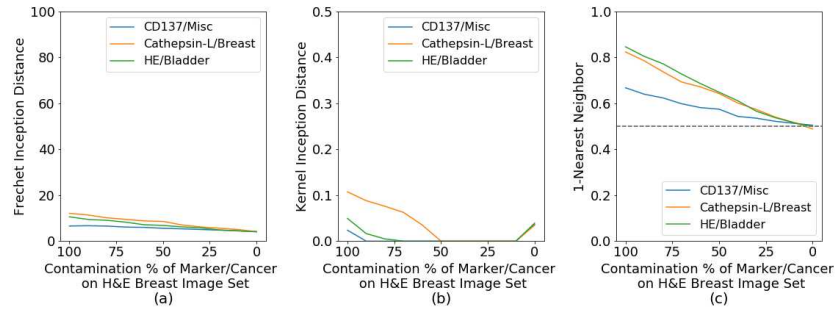


Figure 35: Consistency of metrics when two independent sets of images with the same contamination are compared. Consistent metrics should be close to zero for each of the contamination rates. (a) FID, (b) KID, and (c) 1-NN, we can see that FID is the metric that shows a close to zero constant measure.

## Appendix J. Pathologists Tests

We provide in here examples of the tests taken by the pathologists:

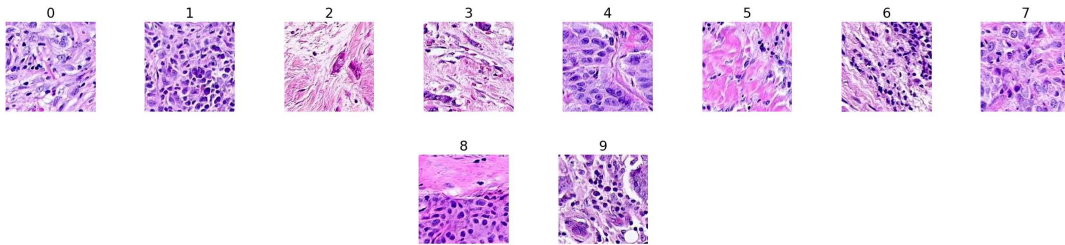


Figure 36: Individual images for breast cancer tissue.

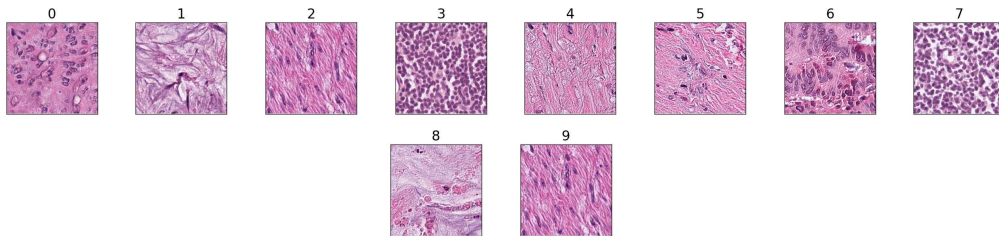


Figure 37: Individual images for colorectal cancer tissue.

## Appendix K. Model Architecture

Generator Network $G : w \rightarrow x$	
Dense Layer, adaptive instance normalization (AdaIN), and leakyReLU	200 $\rightarrow$ 1024
Dense Layer, AdaIN, and leakyReLU	1024 $\rightarrow$ 12544
Reshape	$7 \times 7 \times 256$
ResNet Conv2D Layer, 3x3, stride 1, pad same, AdaIN, and leakyReLU 0.2	$7 \times 7 \times 256 \rightarrow 7 \times 7 \times 256$
ConvTranspose2D Layer, 2x2, stride 2, pad upscale, AdaIN, and leakyReLU 0.2	$7 \times 7 \times 256 \rightarrow 14 \times 14 \times 512$
ResNet Conv2D Layer, 3x3, stride 1, pad same, AdaIN, and leakyReLU 0.2	$14 \times 14 \times 512 \rightarrow 14 \times 14 \times 512$
ConvTranspose2D Layer, 2x2, stride 2, pad upscale, AdaIN, and leakyReLU 0.2	$14 \times 14 \times 512 \rightarrow 28 \times 28 \times 256$
ResNet Conv2D Layer, 3x3, stride 1, pad same, AdaIN, and leakyReLU 0.2	$28 \times 28 \times 256 \rightarrow 28 \times 28 \times 256$
Attention Layer	at $28 \times 28 \times 256$
ConvTranspose2D Layer, 2x2, stride 2, pad upscale, AdaIN, and leakyReLU 0.2	$28 \times 28 \times 256 \rightarrow 56 \times 56 \times 128$
ResNet Conv2D Layer, 3x3, stride 1, pad same, AdaIN, and leakyReLU 0.2	$56 \times 56 \times 128 \rightarrow 56 \times 56 \times 128$
ConvTranspose2D Layer, 2x2, stride 2, pad upscale, AdaIN, and leakyReLU 0.2	$56 \times 56 \times 128 \rightarrow 112 \times 112 \times 64$
ResNet Conv2D Layer, 3x3, stride 1, pad same, AdaIN, and leakyReLU 0.2	$112 \times 112 \times 64 \rightarrow 112 \times 112 \times 64$
ConvTranspose2D Layer, 2x2, stride 2, pad upscale, AdaIN, and leakyReLU 0.2	$112 \times 112 \times 64 \rightarrow 224 \times 224 \times 32$
Conv2D Layer, 3x3, stride 1, pad same, 32 $\rightarrow$ 3	$224 \times 224 \times 32 \rightarrow 224 \times 224 \times 3$
Sigmoid	

Table 3: Generator Network Architecture details of PathologyGAN model.

Discriminator Network $C : x \rightarrow d$	
$x \in \mathbb{R}^{224 \times 224 \times 3}$	
ResNet Conv2D Layer, 3x3, stride 1, pad same, and leakyReLU 0.2	$224 \times 224 \times 3 \rightarrow 224 \times 224 \times 3$
Conv2D Layer, 2x2, stride 2, pad downscale, and leakyReLU 0.2	$224 \times 224 \times 3 \rightarrow 122 \times 122 \times 32$
ResNet Conv2D Layer, 3x3, stride 1, pad same, and leakyReLU 0.2	$122 \times 122 \times 32 \rightarrow 122 \times 122 \times 32$
Conv2D Layer, 2x2, stride 2, pad downscale, and leakyReLU 0.2	$122 \times 122 \times 32 \rightarrow 56 \times 56 \times 64$
ResNet Conv2D Layer, 3x3, stride 1, pad same, and leakyReLU 0.2	$56 \times 56 \times 64 \rightarrow 56 \times 56 \times 64$
Conv2D Layer, 2x2, stride 2, pad downscale, and leakyReLU 0.2	$56 \times 56 \times 64 \rightarrow 28 \times 28 \times 128$
ResNet Conv2D Layer, 3x3, stride 1, pad same, and leakyReLU 0.2	$28 \times 28 \times 128 \rightarrow 28 \times 28 \times 128$
Attention Layer at $28 \times 28 \times 128$	
Conv2D Layer, 2x2, stride 2, pad downscale, and leakyReLU 0.2	$28 \times 28 \times 128 \rightarrow 14 \times 14 \times 256$
ResNet Conv2D Layer, 3x3, stride 1, pad same, and leakyReLU 0.2	$14 \times 14 \times 256 \rightarrow 14 \times 14 \times 256$
Conv2D Layer, 2x2, stride 2, pad downscale, and leakyReLU 0.2	$14 \times 14 \times 256 \rightarrow 7 \times 7 \times 512$
Flatten $7 \times 7 \times 512 \rightarrow 25088$	
Dense Layer and leakyReLU, $25088 \rightarrow 1024$	
Dense Layer and leakyReLU, $1024 \rightarrow 1$	

Table 4: Discriminator Network Architecture details of PathologyGAN model.

Mapping Network $M : z \rightarrow w$
$z \in \sim \mathbb{R}^{200} \sim \mathcal{N}(0, I)$
ResNet Dense Layer and ReLU, $200 \rightarrow 200$
ResNet Dense Layer and ReLU, $200 \rightarrow 200$
ResNet Dense Layer and ReLU, $200 \rightarrow 200$
ResNet Dense Layer and ReLU, $200 \rightarrow 200$
Dense Layer, $200 \rightarrow 200$

Table 5: Mapping Network Architecture details of PathologyGAN model.