# Reimagining Singel-Cell Coloring Through Generative Modeling

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## Abstract

Generative modeling has been revolutionizing single-cell analysis. Cell coloring is an important step in visualizing individual cellular structures during the analysis of single cells. Traditional methods often lack efficiency and accuracy in representing distinct features. Our work employs generative models to enhance the fidelity of single-cell coloring, capturing intricate variations and preserving biologically relevant information. Our method has the potential to facilitate the process and better assist researchers in understanding cellular diversity, identifying rare cell types, and revealing hidden patterns in large-scale single-cell datasets.

## Introduction

Recent advancements in Generative AI have demonstrated great potential in the study of Single-Cell. Single-cell analysis techniques allow researchers to examine the gene expression, protein levels, and other molecular features of individual cells, enabling a deeper understanding of cell types, cellular diversity, developmental processes, disease mechanisms, and more. Recent studies have adopted Generative AI in modeling 3D single-cell organization (Donovan-Maiye et al. 2022), generating cell images(Goldsborough et al. 2017) through CrytoGAN and measuring single-cell transcriptomics(Lopez et al. 2018). However, there remains a noticeable gap in cell coloring, a critical step to understanding cellular structures. To address this gap, we present an approach that leverages generative AI models to facilitate the time-consuming cell coloring process, and further facilitate the analysis of single cells.

## Methodology

Due to the unavailability of datasets containing individual colored cell images from lab settings, we constructed our dataset by resorting to stable diffusion-based generation techniques. However, because of the lack of consistency among the generated images, we decided to build a connection between cell coloring technique and creative arts by adopting pre-existing art pieces as our dataset for simulating the cell coloring process. Particularly, we created a dataset consisting of 200 petri dish artworks from the artist Klari Reis'website using. The dataset is shown as Figure 1.




Figure 1: Petri Dish dataset

### Pix2pix

Pix2pix is a type of generative adversarial network (GAN) that focuses on image-to-image translations, where a generator network produces a colored version of the grayscale image, and a discriminator network is trained to tell the colored version from the real color image. Each original image is of size 256 x 512 containing two 256 x 256 images, so-called input and real image. The generator minimizes the adversarial loss as

$$\mathcal{L}_{\text{adv}}(G, D) = \mathbb{E}_{\text{real}}[\log D(\text{Real Image})] + \mathbb{E}_{\text{generated}}[\log(1 - D(G(\text{Input Image})))] \quad (1)$$

whereas the discriminator maximizes the adversarial loss as

$$\mathcal{L}_{\text{adv}}(G, D) = -\mathbb{E}_{\text{real}}[\log D(\text{Real Image})] - \mathbb{E}_{\text{generated}}[\log(1 - D(G(\text{Input Image})))] \quad (2)$$

### CycleGAN

CycleGAN is an extension of the GAN architecture that involves the simultaneous training of two generator models and two discriminator models.The main idea of CycleGAN is to utilize the power of unpaired data, i.e. the datasets in which the inputs and labels are not directly related. We took the advantage of CycleGAN without the need of pairing up the images.

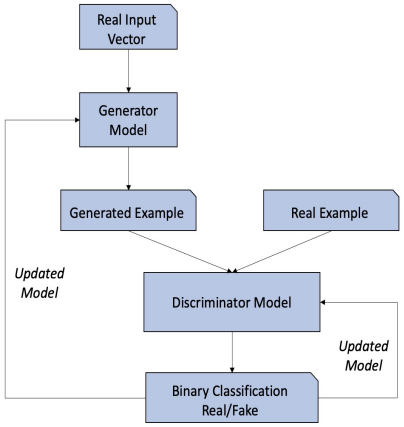


Figure 2: How CycleGAN works

### DeepDream

DeepDream visualizes the patterns learned by a deep neural network. It over-interprets and enhances the patterns it sees in an image by forwarding an image through the network, then calculating the gradient of the image with respect to the activations of a particular layer. The image is then modified to increase these activations, enhancing the patterns seen by the network, and resulting in a dream-like image.

## Results

### Data Preparation

We first transformed the colored cells to black and white version. This was achieved by conducting Canny Edge Detection. The black and white images in this way were just the extracted edges of the colored cells. Then we paired them up, so that each colored cell has its own black and white version. In this way, our dataset will have the {A1, B1} ...{An, Bn} pairs. Then we split the data into a train and test set and use the pairs to train our model to learn the coloring process.

### Modeling

We first fed our training set to the CycleGAN model and trained the images for 50 epochs. The results are shown on Figure 3.The style and color of each output image are very similar. This is consistent with the fact that CycleGan doesn't pair images up but treat them as two separate sets.

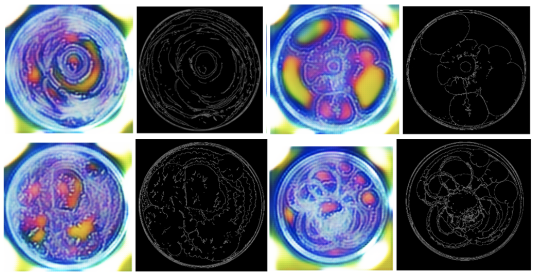

Figure 3: CycleGAN Results: Output - Input Pairs

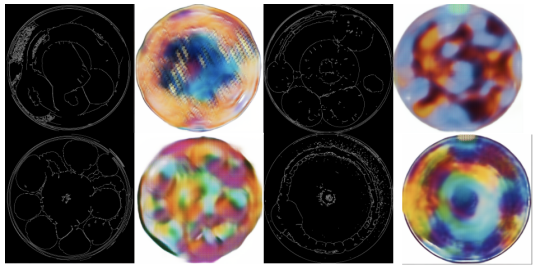

Figure 4: Pix2pix Results: Input - Output Pairs

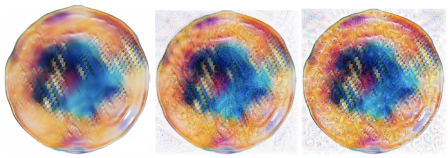

Figure 5: DeepDream Results

We then trained the model for 55 epochs with Pix2pixand tested the performance on the test set(10%of the dataset). Some selected output images are shown on Figure 4. Although the style and color are now different, the cell structures are blurred, so we adopted DeepDream algorithm to emphasize the cell structure. We maximized layer 6 and 8 of InceptionV3 to generate the images shown on Figure 5. Maximizing lower layers gives a messier texture.

## Conclusions

After training different models, we noticed that each component was distinctly colorized. Researchers are able to interpret cellular structures by the color. The models exhibit the potential to acquire the cell coloring pattern and apply it to each component based on specified cell coloring procedures.However, it became evident that there are still limitations. The emphasis on aesthetics appeared to compromise the accurate depiction of the physical cell structures. This underscores the need for continued refinement. Moreover, the application of colored cell artwork as a substitute for simulation necessitates further investigation to gain a comprehensive understanding of the models' performance when applied to authentic cellular imagery.

## References

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