Synthesizing Skin Tissue Images from Single-Cell Gene Expression Data Using a Generative Adversarial Network

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Introduction

The diagnosis and treatment of skin diseases have traditionally relied on whole slide images (WSIs) and molecular analysis techniques. While WSIs provide detailed tissue samples, their resolution is limited by imaging constraints, which impeded the ability to capture complex spatial organization and heterogeneity of skin tissues. The limitation often results in incomplete or inaccurate characterization of skin pathologies.

Objective

This project utilized single-cell gene expression data and whole slide images to generate high-resolution images of the skin through a cGAN. The gene-expression data was spatially resolved with Visium ST.

Keywords

Bioinformatics, Conditional Generative Adversarial Networks (cGAN), Deep Learning, scRNA-seq, Single-Cell Gene Expression, Tensorflow, Tissue Morphology, Visium ST

Methods

- Data Collection
  - Single-Cell RNA sequencing data and whole slide images from Dartmouth Hitchcock Medical Center
- Model Architecture
  - Encoder-Decoder Network: This network maps scRNA-seq data to a latent space that captures cellular features and tissue structure
  - Image Generation Network: Takes latent space representations and generates synthetic skin tissue images
- Training and Evaluation
  - Trained with scRNA-seq, Visium ST data, and WSIs
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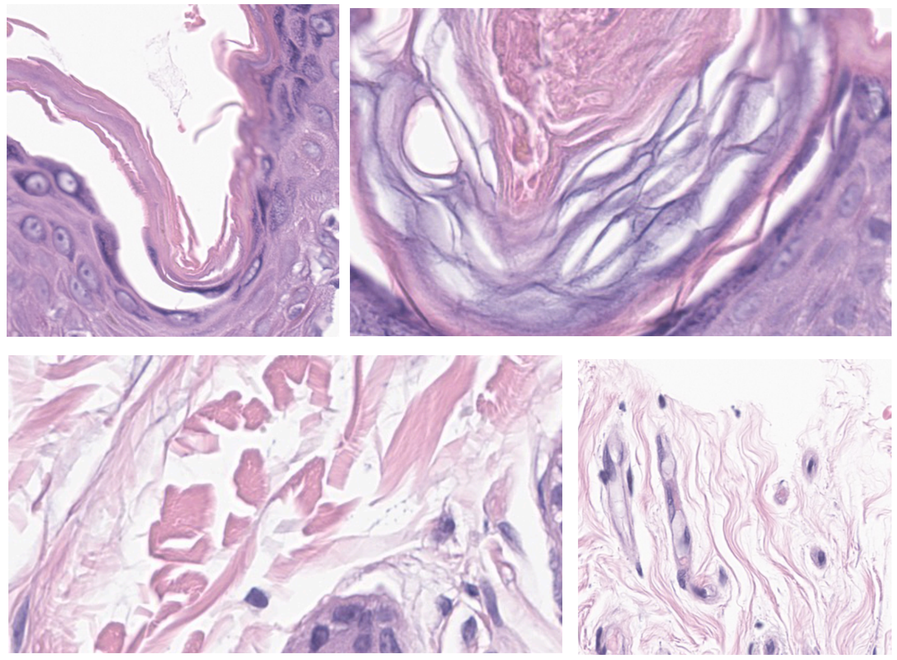
Results

Original WSIs



GAN Generated Images

Discussion

There were more than 30,000+ pre-processed files in the dataset. Due to time-constraints as well as the magnitude of the data, only 9 patches were used to train the GAN. Due to this, future work will focus on refining the GAN architecture, incorporating a larger sub-section of the pre-processed data, exploring applications to other tissues, and validating the approach in clinical settings.

References

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