University of Basel

Department of
Biomedical Engineering

University of Basel, Department of Biomedical Engineering, Hegenheimermattweg 167c, 4123 Allschwil

Master of Science – Biomedical Engineering
Thesis Proposal

Diffusion models for Batch Style Transfer of Histology Images

Staining plays a pivotal role in the initial stages of preparing tissue samples for histological examination. However, there exists notable divergence in staining techniques across various laboratory settings and institutions. These differences may stem from variations in staining agents, methodologies, or procedures employed by different pathologists or digital imaging systems. Such discrepancies in staining can result in a substantial decline in the precision and replicability of deep learning algorithms utilized in histological analysis.

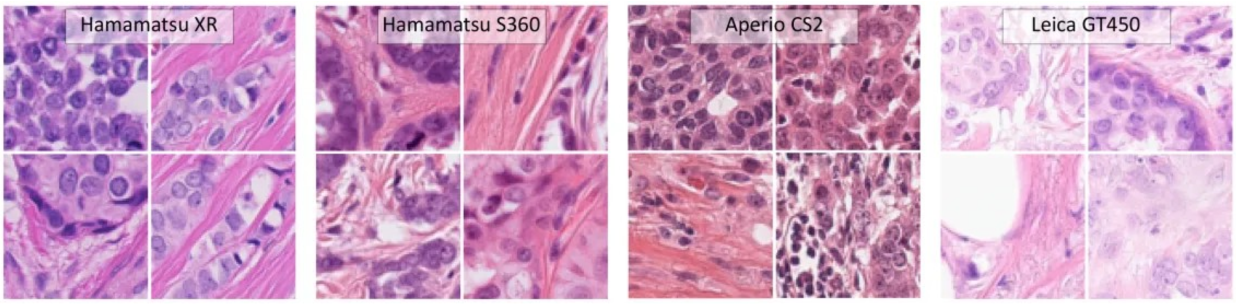

Fig 1: Image variations, induced by different scanners.

To mitigate the challenge posed by stain variations across disparate domains, the concept of stain style transfer has emerged. Among contemporary techniques, Diffusion Denoising Probabilistic Models (DDPM) stand out as state-of-the-art solutions for tasks such as image generation, inpainting, and super-resolution, making them particularly relevant to our objective. Notably, they exhibit superiority over Generative Adversarial Networks (GANs) or AutoEncoders (AE) for our specific application. However, diffusion models take a lot of time to compute because of number of computational steps during the inference process. A common strategy to address this inefficiency is the adoption of Diffusion Denoising Implicit Models (DDIM) with non-stochastic sampling, enabling the skipping of numerous inference steps.

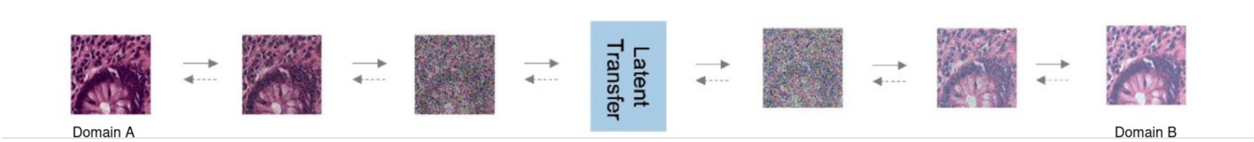

Fig 2: Scheme of domain style transfer using diffusion process.

The primary objective of this master thesis is to develop a deep learning model based on DDIM capable of accurately converting histology images from one domain to another. Our investigation will utilize openly accessible datasets such as the MITOS-ATYPIA 14 Challenge and The Cancer Genome Atlas (TCGA). Additionally, we will explore the potential of the Latent Diffusion Model, which involves pre-training an AE model followed by training a diffusion model within a low-dimensional latent space.

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Nature of the Thesis

- Programming: 80%
- Documentation: 20%

Specific Requirements

- Programming skills: Python, Pytorch
- Experience in deep learning

Group Leader / Supervisor

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