TECHNISCHE UNIVERSITÄT DARMSTADT

Virtually stain-to-stain transformation of histopathological images

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In computational pathology, reliable analysis via a stained tissue sample digitized by a whole-slide image (WSI) scanner plays a vital role in pathological evaluation. Histological staining of the tissue sample provides precise information about the relationships between tissue components via chromatic distinction. The most commonly used stain is hematoxylin and eosin (H&E), which has become standard in almost every case and provides information about the morphological structure of the tissue sample [1]. Besides H&E, immunohistochemical (IHC) stains for colorectal adenocarcinoma are also available to indicate different tissue components or connections, such as cytokeratin (CK) 20, CK7, and CDX2 [2]. The use of immunohistochemistry (IHC) staining [3] in addition to H&E staining to detect the density of immune cells in the cancerous region [4] in colon cancer cases can be shown as an ideal example of such a situation.

The conventional laboratory staining workflow, which requires an expensive laboratory infrastructure, is time-consuming, complex, and tedious. In this method, tissue samples taken from the patient are sliced into approximately 5μm slices and fixed on a glass slide, followed by staining. Moreover, the process becomes even more complex and unmanageable when multiple staining is required. The bleaching and washing processes carried out in the restaining method of the tissue sample will cause the tissue to deform, resulting in loss of information. Moreover, repeating the restaining process for each specific stain will increase the diagnostic time and cost.

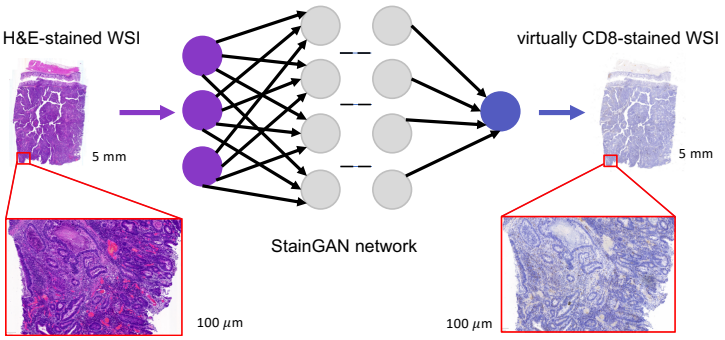

Figure 1: Overview of self-attention aided contrastive learning-based H&E stain to CD8 stain transformation network. Sample tissue stained with H&E dye in the laboratory is virtually restained with the CD8 dye.

In this study, a previously developed deep neural network–based restaining method will be improved by leveraging diffusion models [5] as well as extending the dataset.

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