

Deep learning assisted histological image generation

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Abstract

Histological assessment of tissue samples comprises the most critical step for treatment planning and patient management for pathologies such as cancer [1, 2]. Inspection of tissue material might reveal significant information regarding the grade, the stage, the progression and the biological continuity of the disease, among others, which are crucial elements for disease prognosis. However, the evaluation of tissue sections is prone to misinterpretations due to many factors, one of them being inadequate sampling, or sampling errors. Ideally tissue samples should be removed from the most representative area of the pathology, and the full extent of the removed tissue sample needs to be evaluated by the expert histopathologist. However, on routine conditions, only a part of the removed biopsy material is prepared for microscopy viewing, on average five sections per patient/case. This adds a second type of sampling error to the process, since the important information might be found at a part of the tissue that has not been placed on the microscopy slide.

In this study, we present a method for reviewing the full extent of removed biopsy material and we illustrate that the important information may appear in any part/section of removed sample, highlighting the need to establish protocols that will enable effective viewing of the full extent of the removed sample. The proposed method relies on using deep learning for producing high resolution tissue images [3]. Data from inflammation, benign and cancer cases breast carcinoma were collected from the Department of Pathology of the General Hospital of Athens "Hippocraton", Greece following the approval of the Scientific Council of the Hospital (Approval number 65/8-11-2021) and the Research Ethics Committee of the University of West Attica, Greece (Approval number 108080/30-11-2021). Using a light microscopy imaging system consisting of a Leica DM 2500 microscope and a Leica DFC 420 C camera, images were digitized from H&E-stained tissue sections that were cut consecutively. The 2D digitized images were combined using a Convolution Neural Network (CNN) [3], which was designed to create different image planes (xy, xz or yz) of the sample. According to the expert evaluation (E.K.), additional features of the pathology, not identifiable on the standard xy images, emerged when viewing all image planes. The proposed methodology highlights the need to upgrade standard conventional 2D tissue biopsy evaluation into 3D volume visualization, since in this way, additional information, that might be proven crucial for the characterization of the samples, may emerge.

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