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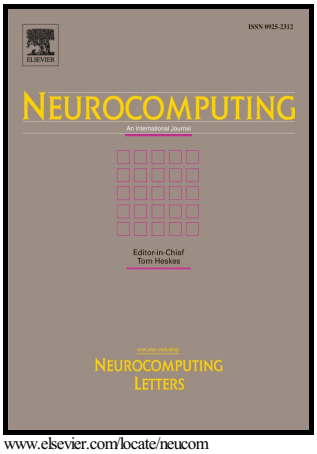

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Accurate segmentation of nuclei in pathological images via sparse reconstruction and deep convolutional networks

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Abstract

Automated cell segmentation is a critical step for computer assisted pathology related image analysis, such as automated grading of breast cancer tissue specimens. However, automated cell segmentation is complicated by (1) complexity of the data (possibly touching cells, stains, background clutters, and image artifacts) and (2) the variability in size, shape, appearance, and texture of the individual nuclei. Recently, there has been a growing interest in the application of "Deep Learning" strategies for the analysis of natural and pathological images. Histopathology, given its diversity and complexity, represents an excellent use case for application of deep learning strategies. In this paper, we put forward an automated nuclei segmentation method that works with hematoxylin and eosin (H&E) stained breast cancer histopathology images, which represent regions of whole digital slides. The procedure can be divided into three main stages. Initially, the sparse reconstruction method is employed to roughly remove the background and accentuate the nuclei of pathological images. Then, deep convolutional networks (DCN), cascaded by multi-layer convolution networks, are trained using gradient descent techniques to efficiently segment the cell nuclei from the background. In this stage, input patches and its corresponding labels are randomly sampled from the pathological images and fed to the training networks. The size of the sampled patches can be flexible, and the proposed method is robust when the times of sampling and the number of feature maps vary in a wide range. Finally, morphological operations and some prior knowledge are introduced to improve the segmentation performance and reduce the errors. Our method achieves about 92.45% pixel-wise segmentation accuracy and the *F1-measure* is 0.8393. This result leads to a promising segmentation performance, equivalent and sometimes surpassing recently published leading alternative segmentation methods with the same benchmark datasets.

Keywords

Nuclei segmentation, Deep convolutional networks, Histopathological images, Sparse reconstruction

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