Cell nuclei detection for computerized cancer diagnosis based on stochastic geometry and deep learning

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A modern cancer diagnostic is based heavily on cytological tests. Unfortunately, experienced pathologists need a lot of time to inspect cell nuclei coming from the tissue sample. Such a diagnosis can be facilitated and speeded up by using automatic image segmentation and analysis methods. But, we have to take into account the fact that a cytological image is a hard problem for computer vision because tissue samples are composed of complex cellular structures. Classical segmentation methods such as thresholding, active contours or watershed transform are effective only for simple cases where nuclei are well isolated from each other. In case of cytological material, this requirement is very rarely fulfilled. To tackle this problem a hybrid approach based on convolutional neural network (CNN) and stochastic geometry is proposed for automated detection of nuclei. We can observe that more and more nuclei segmentation and detection approaches are based on CNN. The main advantage of this approach is that CNN learns from training data a hierarchy of filters to extract invariant features to segment images. This approach has proven to be more accurate for semantic segmentation than methods based on features engineered by hand. However, cytological images are specific in this sense that nuclei usually are clumped, and therefore occlusions are very frequent. Consequently, we typically need to detect nuclei which are only partially visible. To overcome this problem, results of semantic segmentation are post-processed with the help of stochastic geometry to extract nuclei from clusters which CNN missed to detect. Nuclei distribution is modeled by the stochastic process, and then Besag's iterated conditional modes approach is applied to find the configuration of nuclei models that fit the input image best. The method is tuned to detect cell nuclei that are partially occluded or create dense clusters. To test the effectiveness of the proposed method, it was applied to detect nuclei in breast cancer cytological images. Detection accuracy was determined concerning reference results obtained by manual segmentation of cell nuclei. The proposed approach has led to better results than the marker-controlled watershed both in the number of correctly detected nuclei and in the number of false detections.