Computer-assisted Histopathology: Experience with Neuroblastoma and Follicular Lymphoma

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We are developing algorithms for the computer-assisted prognosis of neuroblastoma, a childhood cancer and computer-assisted grading of follicular lymphoma, a cancer of the immune system. For both diseases, the clinical decision is reached by the pathologist after examining tumor samples under a microscope. However, this qualitative evaluation has high intra- and inter-reader variability. For example, the discrepancy between the institutional and central reviewers of neuroblastoma is 20%. Similarly, the agreement among experts for various grades of follicular lymphoma varies between 61% and 73%. By developing computer-assisted systems, we are aiming to make histopathological diagnosis of neuroblastoma and follicular lymphoma more accurate and reproducible, which can lead to more effective treatment and better outcome for patients.

In our approach, input images, digitized, whole-slide tumor samples, are segmented into distinct cytological components according to the color and texture characteristics using novel segmentation algorithms [1-2]. Then, clinically-motivated features are extracted to characterize the morphological characteristics [3-7]. The most relevant and discriminating features are automatically selected for statistical classification processes to label the images according to their content [3, 5, 7]. For instance, we have developed algorithms to classify neuroblastoma samples based on the Schwannian stromal development and grade of differentiation, and to separate high- and low-grade regions from follicular lymphoma slides.

The histopathological images are relatively large; therefore, our algorithms work on the images in a multi-resolution framework. We have tailored the classification algorithms to be compatible with this multi-resolution framework [3, 8, 9]. To increase the computational efficiency further, we have explored the use of general purpose graphical processor units (GPGPUs) and cell processors (Sony® Playstation 3) and successfully demonstrated significant performance improvements in the processing of histopathological images [10-11].

With our current neuroblastoma classification system, the whole-slide accuracy of classifying grade of differentiations is 87.9% and classifying Schwannian stromal development is 88.4%. Moreover, the follicular lymphoma classification method can differentiate high- and low-grade regions with perfect accuracy when tested on 17 slides. From the computational perspective, the multi-resolution approach introduces computational savings up to 60% on average. Additionally, the use of GPGPUs decreases the computation time more than 40 times so that processing of a relatively small whole-slide of size 50k × 50 k is reduced from 35 minutes to less than one minute. The relatively high accuracy of the algorithms coupled with feasible processing times using novel computational infrastructures are promising for the computer-aided analysis of whole-slide histopathological images.

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