Classification of Subtle Morphological Features for Individual Nuclei in Stained Glioma Tissue Slides

Singh, Kunal

Gliomas are one of the most complex, deadly types of brain cancers that affect millions of people globally. Pathologists diagnose different types of glioma by analyzing the visual features of nuclei in stained tissue samples from biopsies. However, due to the high number of nuclei present on a whole slide image, it is difficult to characterize all of the nuclei manually. This project presents a novel framework for the automatic classification of shapes and multiple attributes for individual nuclei in glioma tissue slides. Six classes based on shape and nine classes based on attributes were established. 1650 separate images of nuclei from both low and high-grade glioma tissue slides were annotated with a single shape class and multiple attribute classes. Nuclei images were segmented using color deconvolution and enhancement, and Local Binary Patterns and Gabor filter responses were extracted as representative features. Multiple shape and attribute Support Vector Machine (SVM) models were trained with subsets of the feature sets using an RBF-kernel and optimized parameters with 5-fold cross validations. The shape SVM models were designed to predict a single shape class for a given image while the attribute models were designed to predict multiple attribute classes. The average weighted classification precision for shapes was 71.18% and the jaccard similarity score for attributes was 74.90% for a 200-image test set. This work is the first to classify two types of subtle morphological nuclei features in a separate manner. The framework is generic and can be applied to other pathology image classifications. With a framework to automatically classify both shapes and attributes separately, pathologists will have richer information to make more informed and efficient diagnoses.

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