ON USING CYTOPLASM AND STROMA FEATURES IN AUTOMATED CANCER DIAGNOSIS

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1. ABSTRACT

The utility of nuclear features for automated cancer diagnosis has been well established. Use of cytoplasm and stroma features, however, has not been addressed in an computer-aided diagnosis system, although there has been speculation about the possible use of such features. For example, stroma in pancreatic cancer has been noted as displaying distinctive growth patterns. It is likely that some characteristics of the cytoplasm and stroma are affecting the pathologist's perception of many histopathology slides. We have developed a system which extracts a variety of features from nuclei in histopathology imagery of breast cancer specimens, including size and shape, radiometric, texture, and chromatin-specific features. This system, however, can be used to extract these same features from any arbitrary image object. We investigate here the use of feature extraction and selection (via the new method of "grafting") for cytoplasm and stromal regions and the possible use of these features in an automated cancer diagnosis setting. We will provide an overview of the various features extracted, as well as the classifier used to discriminate cytoplasm and stroma in routine H&E stained histopathology imagery. In depth discussion will be focused on the feature selection for nuclei, cytoplasm, and stroma, and the intuitive explanations of these features. Additionally, we will present the differences in performance for classification of benign versus malignant imagery when cytoplasm and stroma features are included.