Chapter 21
Texture-Based Evolutionary Method for Cancer Classification in Histopathology

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ABSTRACT

Real-world histology tissue textures owing to non-homogeneous nature and unorganized spatial intensity variations are complex to analyze and classify. The major challenge in solving pathological problems is inherent complexity due to high intra-class variability and low inter-class variation in texture of histology samples. The development of computational methods to assists pathologists in characterization of these tissue samples would have great diagnostic and prognostic value. In this chapter, an optimized texture-based evolutionary framework is proposed to provide assistance to pathologists for classification of benign and pre-malignant tumors. The proposed framework investigates the imperative role of RGB color channels for discrimination of cancer grades or subtypes, explores higher-order statistical features at image-level, and implements an evolution-based optimization scheme for feature selection and classification. The highest classification accuracy of 99.06% is achieved on meningioma dataset and 90% on breast cancer dataset through Quadratic SVM classifier.

INTRODUCTION

Real-world histology textures are much different from synthetic textures acquired in a controlled environment. The histology tissue textures have inherent non-stationary, heterogeneous and unorganized spatial intensity variations where different image regions can have different textural characteristics including scale, orientation, contrast or visual appearance. For this reason, adaptive approaches with quantitative methods for Computer-Aided Diagnosis (CAD) were employed in the past for the accurate diagnosis of

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cancers (Dundar et al., 2011), (Niwas, Palanisamy, Chibbar, & Zhang, 2012), (Irshad, Gouaillard, Roux, & Racoceanu, 2014). Major issues that need to be addressed regarding such challenging pathological problems include capturing the cellular architecture differences, removal of image artifacts and noise that arises in the tissue fixation, slide preparation and staining procedures. Diverse computer-aided techniques have been employed in the past with a varying degree of success for the solution of complex histopathological problems. Recent years have witnessed a significant growth of quantitative research studies on applications of digital pathology (Irshad et al., 2014), (Huang and Lai, 2010), (Al-Kadi, 2015) as a result of current progress in high-throughput whole-slide tissue scanning technology.

In almost all the types of cancer diagnosis, the classification system proposed for a specific type fails on other types. This is due to the variation in tissue architecture and structures. Therefore, unsupervised identification and analysis of these variations is essential for designing a generic classifier. Such a process can be designed by proposing tolerant methods for structure segmentation, feature extraction, feature selection and classification. This work is an attempt in this direction.

The morphometric analysis at the nuclei level has found wide application in histological image analysis (Dundar et al., 2011), (Irshad et al., 2014), (Huang et al., 2010). The morphometric characteristics of nuclei components are likely to present dominant role in the discrimination process of cancer grades and subtypes. However, the precise segmentation of the nuclei from biopsy images is found a complex and challenging task. Segmentation methods like thresholding, region growing, watershed, and active contours detect imprecise contours for the nuclei with heterogeneous texture, non-crisp boundaries, touching, and overlapping (Gurcan et al., 2009), (Irshad, Veillard, Roux, & Racoceanu, 2014). Segmentation may not suit the histological classification problems where the cancer types or subtypes have high intra-class and low inter-class variations in nuclei shapes, nuclei characterizing different tumor subtypes present in an image, and large number of overlapping and touching nuclei.

Histology texture classification problems are challenging to solve owing to inherent complexities of tissue textures including the non-homogeneous nature and the high intra-class variability and low inter-class differences in the texture of tumor samples. The textural analysis scans the image as a whole rather than its constituents and captures the variations among the texture patterns to classify images. Hence, the holistic approach of texture analysis may suit more for the classification of cancer types or subtypes which possess some distinguishing textural patterns. Histology texture classification primarily involves following main steps as: extraction of most representative features to maximally capture and portray the intrinsic tissue texture, selection of highly distinguishing and predictive features that are robust with respect to noise present in histology slides, and selection of an optimal classifier to recognize patterns even in the presence of large variations in the data and weak descriptors.

In this chapter, a texture-based optimized evolutionary abstract feature selection and classification framework is proposed and tested on the pathological classification of grade-I benign meningioma and intraductal proliferative breast lesions with significantly high accuracy. The proposed framework exploits higher-order textural statistics, classifier-based optimal selection of texture features, and classification through the best SVM kernel. This research work answers some very pertinent questions. They are:

- Is the texture analysis at image level more appropriate than morphometric analysis at nuclei level to discriminate cancer grades or subtypes?
- Is the combination of three color channels more informative than a single color channel?