Chapter 10
Algorithm Enhancements for Improvement of Localized Classification of Uterine Cervical Cancer Digital Histology Images

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ABSTRACT

In prior research, the authors introduced an automated, localized, fusion-based approach for classifying squamous epithelium into Normal, CIN1, CIN2, and CIN3 grades of cervical intraepithelial neoplasia (CIN) from digitized histology image analysis. The image analysis approach partitioned the epithelium along the medial axis into ten vertical segments. Texture, cellularity, nuclear characterization and distribution, and acellular features were computed from each vertical segment. The individual vertical

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segments were CIN classified, and the individual classifications were fused to generate an image-based CIN assessment. In this chapter, image analysis techniques are investigated to improve the execution time of the algorithms and the CIN classification accuracy of the baseline algorithms. For an experimental data set of 117 digitized histology images, execution time for exact grade CIN classification accuracy was improved by 32.32 seconds without loss of exact grade CIN classification accuracy (80.34% vs. 79.49% previously reported) for this same data set.

INTRODUCTION

There were 527,642 new invasive cervical cancer cases reported in 2012, with an estimated 265,672 deaths (Ferlay et al., 2012). Around 84% of the new cases were reported in less developed countries. Screening for cervical cancer and its precursor lesions is carried out using a Papanicolaou (Pap) test. Definitive evaluation requires histology slides of biopsied cervical tissue; interpretation of these slides is done by an expert pathologist (Jeronimo, Schiffman, Long, Neve, & Antani, 2004). Pathologists seek to detect cervical intraepithelial neoplasia (CIN), which is a pre-malignant condition for cervical cancer. A cervical biopsy is classified as normal (no CIN lesion) or one of three CIN grades: CIN1 (mild dysplasia), CIN2 (moderate dysplasia), or CIN3 (severe dysplasia) by identifying the atypical cells in the epithelium by the visual inspection of histology slides (Kumar, Abbas, Fausto, & Aster, 2014; Long, S, & G.R, 2011; Wang et al., 2009). Figure 1 shows examples of the CIN grades.

Delayed maturation with an increase in immature atypical cells from bottom to top of the epithelium has been observed as CIN increases in severity (Egner, 2010). As shown in Figure 1, atypical immature cells are often present in the bottom third of the epithelium for CIN1 (Figure 1b). The atypical immature cells commonly appear in the bottom two thirds of the epithelium for CIN2 (Figure 1c), and atypical immature cells are typically present in the full thickness of the epithelium for CIN3 (Figure 1d). In addition to analyzing the progressively increasing quantity of atypical cells from bottom to top of the epithelium, identification of nuclei atypia is also significant (Egner, 2010). Nuclei atypia is characterized by variation in nuclei shapes and sizes. Visual assessment of nuclei differences is challenging, contributing significantly to diagnostic inter- and intra-pathologist variation. Nuclei deformation characterization and atypical cell quantization play a critical role in identifying CIN grade (Kumar et al., 2014). Computer-assisted CIN diagnostic methods have been explored in other studies (Wang et al., 2009) (Guo et al., 2015) (De et al., 2013) (van der Marel et al., 2012) (Guillaud et al., 2005) (Keenan et al., 2000). These methods studied texture features (Guillaud et al., 2005), nuclei detection and Delaunay triangulation analysis (De et al., 2013)(Keenan et al., 2000), medial axis determination, and localized CIN grade assessment (Wang et al., 2009) (Guo et al., 2015) (De et al., 2013).

In previous research, we investigated a localized fusion-based approach to classify epithelium into four different CIN grades (Guo et al., 2015) (De et al., 2013) . The approach described in (Guo et al., 2015) yielded 88.5% accuracy for an image set of 61 digitized histology images. For this experimental dataset, the computation time was high, with an average feature extraction time of 36.18 seconds per image; some images took more than 200 seconds. Thus, it would be impractical to utilize those image analysis techniques in a semi-automated tool in a clinical setting to assist expert pathologists in their clinical assessment of digitized histology images