Title: Automatic cancer detection and localization on prostatectomy histopathology images

Trainee Name: Wenchao Han

Supervisor(s): Dr. Aaron Ward

Structured Abstract:

Introduction: Quantitative, graphical pathology reporting from radical prostatectomy specimens for prostate cancer would benefit prognosis and post-surgical therapy related to tumour volumes and their Gleason grades [1,2] as well as research studies involving validation of in vivo imaging against gold-standard histopathology [3]. Our goal is to develop a fully automatic software system for tumour delineation on histopathology that is robust to staining variability and fast and accurate to integrate into future digital pathology workflows.
Methods: We obtained 199 whole-slide images (WSIs) of hematoxylin and eosin (H&E)-stained tissue sections from 49 radical prostatectomy patients. The tissue sections were scanned with two different scanners: Aperio ScanScope GL (Leica Biosystems, Wetzlar, Germany) and Aperio ScanScopeAT Turbo (Leica Biosystems, Wetzlar, Germany). All computations were independently performed on 480μm×480μm sub-images fully covering each WSI. Our method consists of the following steps. (1) Segment each sub-image into nuclei, lumen and stroma/other tissue components by color deconvolution and adaptive thresholding. (2) Extract first and second order statistical features of segmented tissue components and select the top-ranked 13 features using backward feature selection. (3) Classify cancer vs. non-cancer sub-images using supervised machine learning. (4) Perform leave-one-patient-out, 2-fold, and 5 fold cross-validation using fisher, logistic, and support vector machine (SVM) classifiers to estimate the system performance. Our implementation used Matlab 2017a (The Mathworks, Natick, MA), OpenCV 3.1 for SVM implementation, and PRtools 5.0 (Delft Pattern Recognition Research, Delft, The Netherlands) for implementation of all other machine learning algorithms.
Results: Tissue component maps generated from step (1) of the algorithm were qualitatively accurate. Cancer vs. non-cancer classification performed in steps (2-4) yielded 89.4%±4.7% accuracy and an area under the receiver operating characteristic curve of 0.94±0.042 using the SVM classifier with leave-one-patient-out cross-validation. Similar results were obtained using the other classifiers and validation methods.
Conclusion: Our proposed adaptive thresholding compensated for staining variability after color deconvolution for tissue component segmentation. Tissue component-based texture features yielded good discrimination capability for cancer vs. non-cancer segmentation. Our on-going work involves adapting our method for cancer grading.
References: [1] L. Egevad et al, Modern Pathology 24(1), 1–5, 2011; [2] T. H. van der Kwast et al, Modern Pathology 24(1), 16–25, 2011; 2Croke et al. Radiat Oncol (2014) 9:303; [3] E. Gibson et al., Int J Radiat Oncol Biol Phys 96(1), 188-96, 2016