A Deep Learning Model for Detection of PCa in Cores with Noisy Labels

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Introduction, and Rationale: A key challenge for building Computer Aided Diagnosis (CADx) models for prostate cancer is that the histopathology data used as ground truth for training such models is not finely annotated. Here, we propose a solution to alleviate this challenge as part of an ultrasound-guided system for detecting significant prostate cancer. Specifically, we develop a machine learning approach, robust to uncertainty and noise in labeled data, to train a CADx model that uses Temporal Enhanced Ultrasound (TeUS) \cite{1}. TeUS is a new paradigm in prostate cancer detection proposed by our group which enables the depiction of patient-specific cancer maps overlaid on ultrasound images during biopsy.

Specific Aim: Our aim is to devise a solution for handling ambiguous labels of histopathology data in training a CADx model for detection of significant prostate cancer using TeUS.

Materials and Method: TeUS data was acquired from 255 biopsy cores of 158 patients during MR-TRUS fusion prostate biopsy. Prior to firing the biopsy gun, the ultrasound transducer was held steady for about 5 seconds to acquire 100 frames of ultrasound data in the plane of the biopsy. The pathology of the data is as follows: 83 cancerous cores with Gleason Score (GS) 3+3 or higher and 172 non-cancerous cores of chronic inflammation, fibro-muscular tissue, atrophy and prostatic intraepithelial neoplasia (PIN). An area of 2 \times 10 \text{mm}^2 (divided to 80 equally-sized Regions of Interest, ROI, of 0.5 \times 0.5 \text{mm}) along the projected needle path was analyzed for each biopsy core.

The proposed model consisted of two steps. First, a Long Short-Term Memory (LSTM) network was trained with TeUS data from ROIs of cores with at least 7 \text{mm} of cancer (32 cores), where the core is more homogeneous and the labeling less noisy. LSTMs are capable of handling long-term dependencies which allows us to learn the shared underlying information between TeUS sequences in cancerous and normal ROIs. Next, an ensemble model was utilized to make a final decision of cancerous or benign for the entire biopsy core, given what the model learned from individual ROIs. The final model was evaluated on biopsy cores with at least 3 \text{mm} of cancer, where the labeling is noisy and the core heterogeneous.

Results: The proposed two-stage model is able to predict the labels for the biopsy cores where detailed annotation are not available (noisy labels). For a test dataset of 193 cores, we achieved AUC of 0.79 and 0.93 for predicting labels of all cores and cores with high-MR suspicious levels, respectively.

Discussion and Conclusion: The problem of inaccurate labeling for medical data is inevitable and needs to be addressed in order to build a high performing CADx model. Building such models using biopsy data (often the case in prostate cancer) is even more challenging since the ground truth is not finely annotated. By modeling the biopsy data in two stages, first at ROI level and then at core level, we enable an automated approach for setting the threshold for determining the ROI labels, and consecutively the label for a core. This approach can have an impact on building more accurate CADx systems.