Predicting the Presence of Clinically Significant Prostate Cancer Using Multiparametric MRI and MR-US Fusion Biopsy

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Prostate cancer (PCa)

- Most common newly diagnosed cancer in US men and second deadliest.
- Gold standard diagnosis is biopsy, but this has substantial limitations.
- Both biopsy and surgical resection have associated morbidity and mortality.
- Making treatment decisions can be difficult.
Research goal

This R21:

- [SA-1] To develop a deep learning architecture that produces voxel-level detection of aggressive cancer (Gleason grade > 3) based on mp-MRI data using digital pathology information as the ground truth.
- [SA-2] To integrate voxel-level predictions with clinical variables in a multimodal predictive nomogram for risk stratification of prostate cancer patients.

Long term:

- Combine radiology + pathology + omic features into quantitative nomograms for predicting cancer aggression.
Potential impact

- Improve the quality of mp-MRI ROIs for targeted biopsy.
- Make a useful estimate of risk in regions that are difficult to biopsy.
- Create a quantitative imaging biomarker that would improve the efficacy of active surveillance.
- In combination with clinical features, produce an overall prediction of the likelihood of clinically significant prostate cancer that could allow for deferral of biopsies in some patients.
Prostate MR imaging

- T2
- ADC
- Ktrans
- Kep
Radiologist annotation
Prostate MR/US fusion biopsy
Whole mount histology
Gold standard

Inherent challenges:

- Radiologist underestimates tumor volume.
- Some biopsy cores taken through target are normal, illustrating risk of undergrading.

Light blue: Prostate capsule
Green: ROI generated by radiologist
Red: Cancer segmentation generated after surgery using wholemount pathology slides
Dark blue: Negative biopsies (needle path in MR space)
Orange: Positive Biopsies
Classifying PCa from whole mount

- T2, ADC, Kep, Ktrans, and 3D T2 ROIs from 132 whole mount patients.
- T2, ADC, and the ensemble of Kep and Ktrans were registered using a mutual information-based method.
- A four-layer CNN was trained using eight-fold patient-level cross-validation.
Results

ROC curve for each fold (Epoch 25)

Red: predictions
Green: ROI
Classifying PCa from biopsies

- Can we classifying voxel cores (i.e., imaging biopsy) into > 3+3?
- Generate cores and their features.
- 9,384 cores.
- 537 patients in 8-fold train
- 138 patients in test
- SVM classifier
- Test AUC 0.72
Multi-instance learning framework

- Incorporate biopsies as weakly labeled data (>1000 cases).
- We know there is (or isn’t) cancer in the core, but we are not certain which voxels are involved.
- Add MIL layer that aggregates patch-level predictions into core level predictions.
Whole slide imaging

110k x 50k = 5.5 billion pixels

Prostate T2

CIFAR-10
Deep learning for cancer grading

- U-Net architecture combines features from shallower layers with those from deeper layers.
- Information from patches of three different scales is used to generate a segmentation mask for the centered patch.
Integrated reporting with image analysis
Questions

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