

A Computational Pipeline for Segmentation and Classification of Tubules

Session Information

- [Pathology and Lab Medicine](#)

November 03, 2022 | Location: Exhibit Hall, Orange County Convention Center, West Building

Abstract Time: 10:00 AM - 12:00 PM

Category: Pathology and Lab Medicine

- 1700 Pathology and Lab Medicine

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Background

The highly repetitive kidney structure is well-suited for high-throughput segmentation using unsupervised methods. Herein, we combined image-based, machine learning (ML) tools to realize an computational pipeline for image curation, segmentation, and classification.

Methods

25 chronic kidney disease and 10 healthy reference tissue were first curated using HistoQC, an open source tool for qualification of whole slide images (WSIs), for histology and imaging artifacts in WSIs that would interfere with ML techniques. WSIs were then processed by the

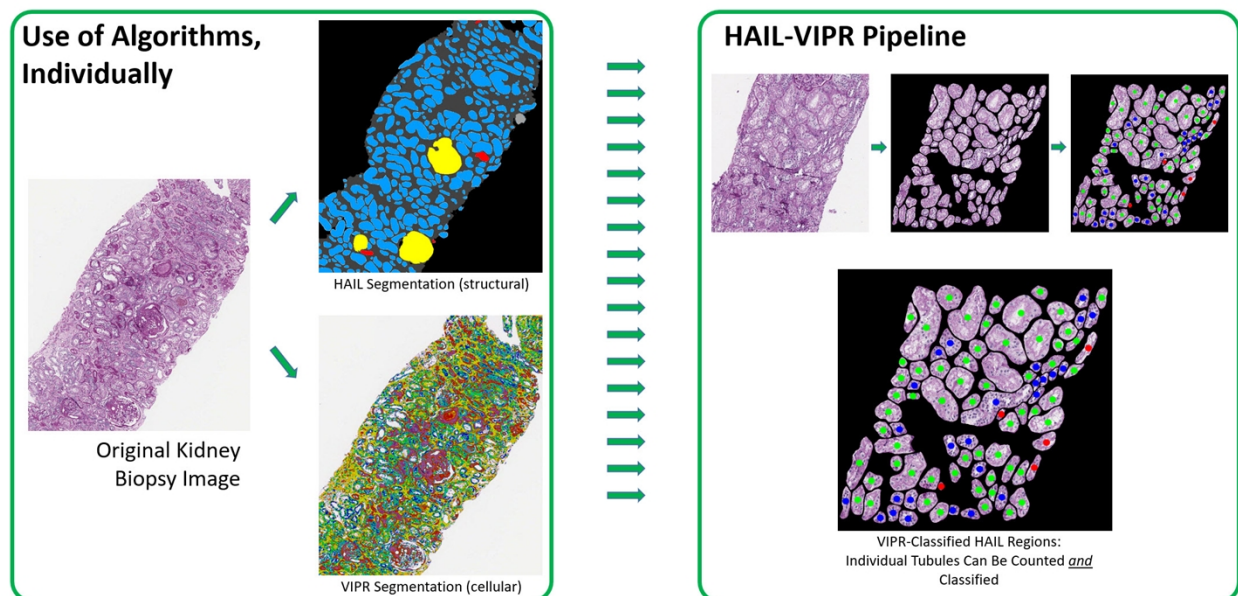
Human-AI-Loop pipeline, a deep-learning-based supervised image segmentation tool, to generate binary masks of all tubules. Segmented tubules were then extracted and processed at the pixel level by the spatially invariant vector quantization (SIVQ) algorithm, which is prepackaged as the validated identification of pre-qualified regions algorithm (VIPR). SIVQ mines a composite vector of biological content inherent in single pixel domains by extracting local kernel goodness-of-fit to a library of pre-selected Fourier signatures of histological primitives. Renal pathologists manually labeled each segmented tubules as normal and abnormal proximal, normal and abnormal distal, and abnormal indeterminate.

Results

3 machine learning-based tubular classes (1-3) were identified by VIPR. There was >95% correlation between manual scoring of proximal tubules (normal and abnormal) and class 1, manual scoring of distal tubules (normal and abnormal) vs. class 2, and for normal vs. abnormal tubular morphology.

Conclusion

Our tools will enable development of large scale feature extraction and statistical quantification of different sub-classes of tubules from giga-pixel size kidney WSIs. This pipeline unleashes the power of artificial intelligence in precision nephrology with the promise of deriving novel digital image biomarkers that can potentially inform disease progression or alignment with molecular markers for theragnostic discoveries.



Pre-segmentation of tubules by initial use of HAIL allows for subsequent classification of biological tubule context of with VIPR, yielding much higher classification fidelity, owing to the exclusion of other nephron structures from the unsupervised pool of pixels under interrogation. Reduction of the background pixels from foreground areas increases classification performance.

Funding

- NIDDK Support