Computational Quantification of Interstitial Fibrosis and Tubular Atrophy (IFTA) for CKD Cases of the Kidney Precision Medicine Project

Session Information

 Molecular Pathology, Pathogenesis, and Animal Models: A Correlative Approach to Kidney Diseases

November 05, 2021 | Location: Simulive, Virtual Only

Abstract Time: 04:30 PM - 06:00 PM

Category: Bioengineering

• 300 Bioengineering

Authors

- Lutnick, Brendon, University at Buffalo, Buffalo, New York, United States
- Rosenberg, Avi Z., University of Michigan, Ann Arbor, Michigan, United States
- Barisoni, Laura, Duke University, Durham, North Carolina, United States
- Alpers, Charles E., University of Washington, Seattle, Washington, United States
- Chen, Yijiang, Case Western Reserve University, Cleveland, Ohio, United States
- Janowczyk, Andrew, Case Western Reserve University, Cleveland, Ohio, United States
- Madabhushi, Anant, Case Western Reserve University, Cleveland, Ohio, United States
- Torrealba, Jose, The University of Texas Southwestern Medical Center, Dallas, Texas, United States
- Weins, Astrid, Brigham and Women's Hospital, Boston, Massachusetts, United States
- Stillman, Isaac Ely, Harvard University, Cambridge, Massachusetts, United States
- Herlitz, Leal C., Cleveland Clinic, Cleveland, Ohio, United States
- Rodrigues, Luis, Universidade de Coimbra, Coimbra, Coimbra, Portugal
- Zuckerman, Jonathan E., University of California Los Angeles, Los Angeles, California, United States
- Jain, Sanjay, Washington University in St Louis, St Louis, Missouri, United States
- Balis, Ulysses G. J., University of Michigan, Ann Arbor, Michigan, United States
- Jen, Kuang-Yu, University of California Davis, Davis, California, United States
- Sarder, Pinaki, University at Buffalo, Buffalo, New York, United States

Group or Team Name

• Kidney Precision Medicine Project

Quantification of interstitial fibrosis and tubular atrophy (IFTA) is critical in the evaluation of kidney diseases. In this study, our previously developed computational IFTA segmentation model was tested on an independent dataset of renal biopsy whole slide images (WSI) from Kidney Precision Medicine Project (KPMP) and compared to visual assessment.

Methods

A computational model for the IFTA segmentation was trained using 48 PAS stained WSIs from kidney biopsies obtained at three non-KPMP institutions. Twenty-six PAS WSIs from the KPMP chronic kidney disease (CKD) cohort were used as independent testing dataset. Quality control (QC) of the KPMP WSIs was performed using HistoQC, a previously developed QC tool for digital pathology images. Computationally derived percent IFTA scores were calculated using morphological processing to segment IFTA tissue regions in WSIs. Three KPMP pathologists independently estimated the percent IFTA on the same KPMP dataset. The pathologists' estimates and the computationally predicted percent IFTA values were compared pairwise using Pearson correlation.

Results

Computationally derived IFTA segmentations from select cases are shown in *Fig. 1a*. The Pearson correlation showed a high degree of agreement between both pathologists and the computational model. The pairwise correlations are shown in the confusion matrix in *Fig. 1b*.

Conclusion

Computational segmentation of IFTA has the potential to add enhanced reproducibility, precision, and efficiency to clinical tasks such as the estimation of percent IFTA.

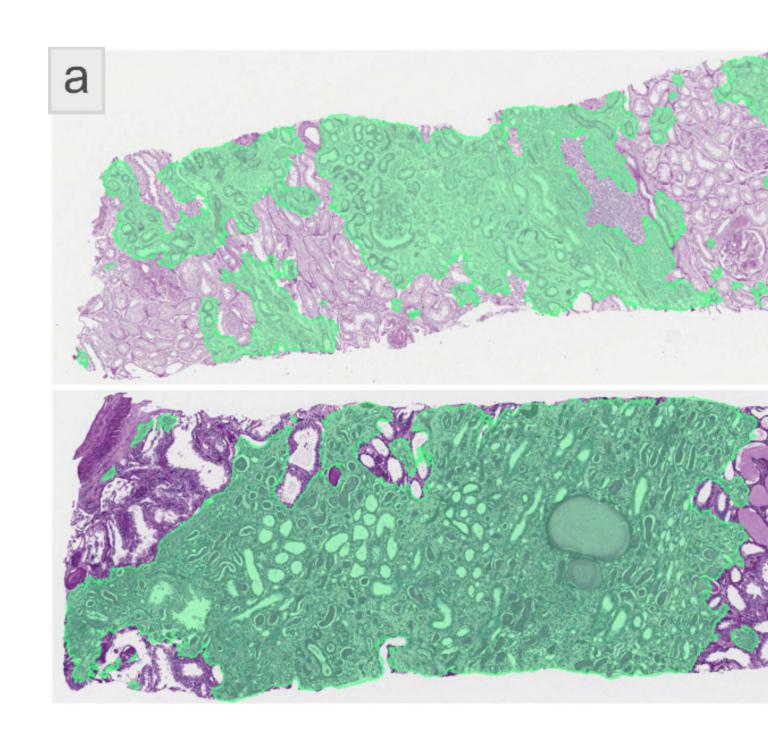


Figure 1. IFTA quantification results for KF segmented IFTA region in green overlaid or correlation measures comparing pathologists' IFTA scores.

Funding

• NIDDK Support