AI in Nephropathology Workshop Amsterdam 2021

12th of March 2021 web conference via WebEx

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Schedule is Amsterdam local time (GMT+1)

Committee:
Pinaki Sarder, Joris J. Roelofs, Marian Clahsen-van Groningen, Hien. V. Nguyen, Jesper Kers, Jan U. Becker

14:00-15:00 Technical aspects
Chairs: Pinaki Sarder, Hien V. Nguyen

14:00-14:20 Development of AI for transplant nephropathology (Jeroen van der Laak, Meyke Hermsen)
14:20-14:40 Artificial intelligence in nephropathology: preliminary data and remaining challenges (Hien V. Nguyen)
14:40-15:00 Integration of omics data with image features (Ulysses Balis, Jeff Hodgin)

15:00-15:10 Break

15:10-16:10 Applications in native kidney pathology
Chairs: John Tomaszewski, Avi Rosenberg

15:10-15:30 AI in diabetic nephropathy (Pinaki Sarder)
15:30-15:50 AI in GN (Pietro A. Cicalese)
15:50-16:10 Computational pathology and experimental models of glomerular disease (Avi Z. Rosenberg)

16:10-17:00 Break

17:00-18:00 **Oral abstracts**
Chairs: Joris J. Roelofs, Marian Clahsen-van Groningen

17:00-17:15 Glomerular volume, density, and % global sclerosis by deep learning in living kidney donor implantation biopsies (Darryl E. Wright et al. Rochester, MN, USA)

17:15-17:30 Computer aided diagnosis of glomerulosclerosis using IBM Watson and feature based models (Francesco Pesce et al. Bari, Italy)

17:30-17:45 Quantification of renal fibrosis on pathology images using deep learning on local and global representations (Vijaya B. Kolachalama et al. Boston, MA, USA)

17:45-18:00 MorphSet: improving case assessment for antibody-mediated rejection through learned prognostic vectors (Syed Rizvi et al. Houston, TX, USA)

18:00-18:10 Break

18:10-19:30 Applications in transplant kidney pathology
Chairs: Mark Stegall, Jesper Kers

18:10-18:30 Deep Learning-based classification of kidney transplant pathology (Roman D. Bülow)

18:30-18:50 Data-driven derivation and validation of novel phenotypes for transplant rejection using semi-supervised clustering (Maarten Naesens)

18:50-19:10 Banff Digital Pathology Working Group (DPWG) update (Alton "Brad" Farris)

19:10-19:30 The path to automated reading of renal allograft biopsies—manual morphometry and deep learning (Mark Stegall)

19:30-20:00 Transatlantic funding
Chair: Jan U. Becker
The US perspective (Daniel Gossett)
The EU perspective (Sabine Steiner-Lange)

Summary and closing remarks (organising committee)

Faculty:
Ulysses Balis, Michigan, MI, USA
Jan U. Becker, Cologne, Germany
Marian Clahsen-van Groningen, Rotterdam, The Netherlands
Roman D. Bülow, Aachen, Germany

Pietro A. Cicalese, Houston, TX, USA
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Mark Stegall, Rochester, MN, USA
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Abstracts

Glomerular volume, density, and % global sclerosis by deep learning in living kidney donor implantation biopsies

D. E. Wright [Rochester], A. Denic [Rochester], M. P. Alexander [Rochester], L.Barisoni [Durham], B. J. Erickson [Rochester], T. L. Kline [Rochester], A. D. Rule [Rochester]

Background:
Glomerular volume and density are important indicators of overall kidney health, but an automated approach for quantifying on biopsy is needed.
Materials and Methods:
Whole slide images of kidney cortex stained for periodic acid–Schiff from 1150 living kidney donors were studied. Slides were manually segmented for cortex and each non-sclerosed glomerular (NSG) and globally-sclerosed glomerular (GSG) profile. The segmented regions were cropped, down-sampled by factor 4, and resized to 2048-by-1024 pixels. A U-Net was trained with the weighted dice loss (parenchyma:NSG:GSG ratio of 1:5:10) on 564 donors and validated on 291 donors. Analyses used an independent test set of 295 donors. The Weibel-Gomez stereological model estimated glomerular volume and density from profiles.
Results: The final network had a dice coefficient of 0.909 for NSG, 0.570 for GSG and 0.952 for cortex profiles. Manual versus automated mean values and correlations were compared: non-sclerosed glomerular volume (.0027mm3

versus .0027mm3 [p=.77], r=.72); NSG density per mm2 (19.3 versus 17.2 [p<.001], r=.78); and %GSG (2.7% versus 5.1% [p<.001], r=.47). Manual versus automated correlations with clinical characteristics were compared: non-sclerosed glomerular volume with BMI(.27 versus .17), GFR(.22 versus .21), 24h-urine albumin(.15 versus .15), and cortical volume(.31 versus .27); glomerular density with BMI(-.26 versus -.23), hypertension(-.17 versus -.17), 24-urine albumin(-.18 vs -.13), and cortical volume(-.20 versus -.17); and %GSG with age(.34 versus .30), GFR(-.18 versus -.13), hypertension(.12 versus .10), and cortical volume(-.12 versus -.09).
Conclusion:
Automated determination of glomerular volume and density and % global sclerosis is feasible and clinically relevant in donor biopsies.

Computer aided diagnosis of glomerulosclerosis using iBM Watson and feature-based models

F. Pesce1, F. Albanese1, D. Mallardi1, M. Rossini1, P. Suavo-Bulzis1, G. Pasculli1,4, F.S. Debitonto2, R. Lemma2, A. Brunetti3, G.D. Cascarano3, V. Bevilacqua3, L. Gesualdo1 1 Nephrology, Dialysis, and Transplantation Unit, Department of Emergency and Organ Transplantation, University of Bari Aldo Moro, Bari, Italy; 2 IBM Client Innovation Center, Italy; 3 Department of Electrical and Information Engineering (DEI), Polytechnic University of Bari, Italy, Via Edoardo Orabona, 4, Bari, 70125, Italy. 4 Department Computer, Control and Management Engineering Antonio Ruberti (DIAG), La Sapienza University, Rome, Italy.

Background:
On a histological level, advanced stages of various renal diseases display glomerular sclerosis, which can be observed using light microscopy on tissue samples collected during kidney biopsy. Computer-Aided Diagnosis (CAD) systems take advantage of artificial intelligence's (AI) ability in healthcare to assist physicians with diagnosis.
Methods:
We propose a new CAD method that analyses histological images and distinguishes between sclerotic and non-sclerotic glomeruli. We developed, tested, and compared two Artificial Neural Network (ANN) classifiers to achieve this aim. The former uses image-processing procedures to identify hand-crafted features derived from Regions of Interest (ROIs) using a shallow ANN. Instead, the IBM Watson Visual Recognition System employs a deep ANN to make decisions based on the images as input data, hence eliminating the need to

design any procedure for representing images with features. The input dataset included 428 sclerotic glomeruli and 2344 non-sclerotic glomeruli derived from Aperio ScanScope System images of kidney biopsies.
Results:
Both AI approaches were able to distinguish between sclerotic and non-sclerotic glomeruli with high accuracy (mean MCC = 0.95 and mean Accuracy = 0.99). The approach based on feature extraction and classification would allow clinicians to gain information on the most discriminating features, despite the systems appearing to be comparable. In fact, by analysing which subset of features had the greatest impact on the final decision, we could better explain the classifier's decision.
Conclusions. Our support system can help renal pathologists to work more efficiently in both clinical and research settings.

Quantification of renal fibrosis on pathology images using deep learning on local and global representations

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Background:
Interstitial fibrosis and tubular atrophy (IFTA) on a renal biopsy are strong indicators of disease chronicity and prognosis. Techniques that are typically used for IFTA grading remain manual, leading to variability among pathologists.

Accurate IFTA estimation using computational techniques can reduce this variability and provide quantitative assessment by capturing the overall pathologic features.
Methods:
Using trichrome-stained whole slide images (WSIs) processed from human renal biopsies, we developed a deep learning framework that captured local pathology and finer pathological structures at high resolution as well as the WSI-level global context to predict IFTA grade. WSIs (n=67) were obtained from The Ohio State University Wexner Medical Center (OSUWMC) and reviewed by five nephropathologists, who independently provided IFTA grades: <=10% (None or minimal), 11-25% (Mild), 26-50% (Moderate), and >50% (Severe). The model was developed by associating the WSIs with the pathologist grade determined by majority voting (ground truth). Model performance was evaluated on WSIs (n=28) obtained from the Kidney Precision Medicine Project (KPMP).
Results:
There was a substantial agreement on the IFTA grading between the pathologists and the ground truth (Kappa=0.622±0.071). The model accurately captured the IFTA grade on both datasets (Accuracy=71.8±5.3% on OSUWMC, 65.0±4.2% on KPMP). Identification of salient regions by combining local and global pathological features yielded visual representations that were consistent with the pathologist-based IFTA grading.
Conclusion:
Our approach to analyzing local- and WSI-level changes in renal biopsies attempts to mimic the pathologist and provides a regional and contextual estimation of IFTA. Such methods can potentially assist clinicopathologic diagnosis.

MorphSet: Diagnosing Antibody-Mediated Rejection Through Learned Diagnostic Vectors

Pietro A. Cicalese, Syed Rivzi, Ibrahim Batal, Candice Roufosse, Marian Clahsen-van Groningen, Chandra Mohan, Hien V. Nguyen, Jan U. Becker

Introduction:
Computer-aided diagnostic systems hold great promise for improving the accuracy and reproducibility of renal transplant pathology diagnostics. Common approaches for training Deep Neural Networks (DNNs) to predict Antibody-Mediated Rejection (AMR) in glomeruli currently involves the replication of costly expert nephropathologists assessment of a large number of individual glomeruli samples. We chose to explore an alternative approach.

Methods:
This approach, called MorphSet, is a DNN architecture inspired by set transformers that processes encoded representations of Monte Carlo (MC)-sampled glomerular compartment crops to produce biopsy-level predictions (AMR or no-AMR). This method bypasses the need for costly fine-grained expert annotations. We tested this approach on a set of n=89 randomly selected biopsies from our archive (n=51 chronic-active, chronic or active AMR; and n=38 without AMR). All 1,655 open glomeruli on two PAS level sections were included as manual crops from micrographs taken with a x40 objective. As a baseline we trained an EfficientNet-B3 encoder using a consensus-label approach, and comparisons were done using ROC curve metrics.
Results:
The EfficientNet-B3 baseline yielded an AUC of 0.962, MorphSet outperforming it with 0.999 on case level predictions. In addition, MorphSet displayed higher confidence and point estimates in its AMR diagnoses in the confidence visualizations.
Conclusion:
MorphSet outperformed a state-of-the-art DNN architecture on our dataset for the diagnosis of AMR. We note that MorphSet does not require fine-grained assessments, instead relying on learned understandings of discriminative features in its predictions. MorphSet-based diagnostic systems for AMR could be easily expanded with additional training sets from trusted institutions.