Prostate Cancer Diagnosis and quantification using AI-enabled Software (SW)  
Wei Huang, MD1, Samuel Hubbard1, Parag Jain2 and Ramandeep Randhawa3  
1Department of Pathology and Laboratory Medicine, University of Wisconsin – Madison, 2PathomIQ, Inc, California

Background
Gleason scoring system is widely used in prostate cancer grading. Cancer volume is also known to predict patient’s outcome and is used for decision-making process [1] Accurate quantification of each Gleason Pattern (GP) is important and is demanded in pathology practice. [2,3] There are some challenges:  
- Evaluation of prostate biopsy slides is time-consuming  
- High inter-observer variability [4,5]  
- Discordance of diagnosing a minor component of GPs in prostate biopsy is reported at 48.7% between general pathologists and expert GU pathologists [6]

Our goal: Develop a universal and standardized platform for Gleason grading and GP quantification trained by GU pathologists to achieve accurate and reproducible diagnosis

Materials
1000 H&E prostate biopsy slides from the University of Wisconsin-Madison pathology archive were scanned with Aperio CS2 (Leica) at 40x.  
- Slides were split into training set (800) and test set (200).  
- Training slides were annotated by GU pathologist  
- Balanced dataset of varied morphologies, including GP3, GP4, GP5 cancer, high-grade prostatic intraepithelial neoplasia (HGPIN), perineural invasion (PNI), vessels and lymphocytes

Methods
- Deep Convolutional Neural Networks  
- Hybrid Architecture optimized for Grading  
- Combination of Classification and Segmentation Networks  
- Multiple nets:  
  - Gland segmentation, Epithelial detection, Gland-based and nuclei-based grading.  
  - Multi-scale model: multiple patch sizes at 5x to 40x resolution to capture nuclear detail as well as glandular context  
- Fine-Tuned Model  
- Sensitive to very small amount of high-grade cancer  
- Intelligent data selection for training  
- ensures balanced learning across various pattern types within and across imbalanced labels  
- Annotation Assistant: Pathologist only needs to review <5% of the data for annotations

Results

<table>
<thead>
<tr>
<th>Group</th>
<th>1 &lt;= 6</th>
<th>3-4</th>
<th>4-5</th>
<th>8</th>
<th>9-10</th>
</tr>
</thead>
<tbody>
<tr>
<td>Group 1</td>
<td>191 (95.5%)</td>
<td>Correct</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Group 2</td>
<td>5 (2.5%)</td>
<td>Under-graded by Software</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Group 3</td>
<td>4 (2%)</td>
<td>Over-graded by Software</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Deep learning enabled cancer-grading software offers objectivity, greater efficiency and precision in prostate cancer scoring and quantification  
Potential to help pathologists to minimize inter-observer variability and to increase efficiency and accuracy in their practice

Summary

- Deep learning enabled cancer-grading software offers objectivity, greater efficiency and precision in prostate cancer scoring and quantification  
- Potential to help pathologists to minimize inter-observer variability and to increase efficiency and accuracy in their practice

Disclosures
This research is sponsored by PathomIQ, Inc.

References