Short Abstract Presentations

Wednesday, May 8, 2019
8:00 am – 9:00 am

Locations:
Grand Ballroom 1
Kings Garden 1
Kings Garden 2/3
Brigade Room
<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:00am – 8:15am</td>
<td>Shivam Kalra</td>
<td>A Bunch of Barcodes for Identification of Histopathology Images</td>
</tr>
<tr>
<td>8:15am – 8:30am</td>
<td>Weijie Chen</td>
<td>Characterization and Assessment of Deep Learning Systems for Histopathology Whole Slide Imaging</td>
</tr>
<tr>
<td>8:30am – 8:45am</td>
<td>Marios A Gavrielides</td>
<td>Effect of Feature Information-Aided Review On Pathology Trainee Performance for Ovarian Cancer Subtyping: An Observer Study</td>
</tr>
<tr>
<td>8:45am – 9:00am</td>
<td>Richard Torres</td>
<td>Initial Clinical Validation of Clearing Histology with Multiphoton Microscopy (CHiMP) for Prostate Biopsy Diagnosis</td>
</tr>
</tbody>
</table>
A Bunch of Barcodes for Identification of Histopathology Images

Shivam Kalra (PhD candidate)\textsuperscript{1}, Charles Choi (BSc)\textsuperscript{2}, Wafik Moussa (MSc)\textsuperscript{2}, Liron Pantanowitz (MD)\textsuperscript{3} Hamid Tizhoosh (Professor)\textsuperscript{1} (hamid.tizhoosh@uwaterloo.ca)

\textsuperscript{1}University of Waterloo
\textsuperscript{2}Huron Digital Pathology
\textsuperscript{3}UPMC

Background
Content-based image retrieval deals with the identification of digital images using pixel values and their features. Digital pathology can benefit from image search in large archives of whole slide images as a dynamic and smart platform to exploit the information stored in evidently diagnosed cases.

Technology
The image search is based on a combination of supervised and unsupervised algorithms. Deep and handcrafted features are employed to characterize images. The search technology is inherently "unsupervised" as it works with raw data with no specific training for the search task.

Methods
We use a cohort of different algorithms including segmentation and clustering algorithms, deep networks and distance metrics for search and retrieval.

Results
The proposed image search platform is qualitatively tested with 300 WSIs. We achieved approximately 88% accuracy in predicting the correct class for a given query image using only the first search result (the best match). We also report validation results by the pathologist that resulted in 76% accuracy for the first match of the search. Additional statistics will be provided as well.

Conclusion
The initial results of this internal validation are quite encouraging. The visual similarity of retrieved cases is for most queries striking. We continue to improve the accuracy and the speed requirements of the search platform to make it feasible and useful for diagnostic, research and educational purposes.
Characterization and Assessment of Deep Learning Systems for Histopathology Whole Slide Imaging

Weijie Chen (weijie.chen@fda.hhs.gov)\(^1\), Weizhe Li\(^1\), Brandon Gallas\(^1\)

\(^1\)Division of Imaging, Diagnostics, and Software Reliability, OSEL/CDRH/FDA

**Background:** Development of deep learning (DL) algorithms for cancer diagnosis on histopathology whole slide images (WSI) is an active area of research. However, consensus is needed on approaches to characterize and assess such systems to assure quality and good science, and ultimately facilitate the deployment of such systems to the clinic.

**Technology** (optional): A deep learning algorithm usually has a complex architecture involving tens of millions of parameters. Its training, validation, and testing for cancer diagnosis in pathology relies on sufficient amount of WSI data with reliable annotations of abnormalities by expert pathologists. Color image processing technologies are usually used to augment the training data. Such algorithms are expected to be robust to variations from different scanners, tissue preparation and staining protocols, and other sources.

**Methods:** We surveyed relevant literature regarding algorithm characteristics and assessment methods. In the meantime, we implemented a deep learning system using the Camelyon16 dataset – WSI data for breast cancer nodal metastasis detection. Based upon these, we focus our investigations on three specific topics

- **Reproducibility:** identification of critical elements in algorithm descriptions such that the implementation is reproducible (if other researchers wish to) – a basic scientific requirement;
- **Quality and Robustness:** measures taken to assure quality of data, especially the reliability of ground truth; techniques to enhance robustness to variations in image acquisition procedures;
- **(Pre-)Clinical assessment:** types of DL output, interpretability and performance metrics; characterization of false positive and false negative errors by the algorithm.

**Results:** Not all published work in this area provided sufficient description to make their work reproducible. We have identified critical elements that should be included in algorithm descriptions. Color augmentation and normalization techniques have been shown to be useful in improving the performance of DL algorithms, although techniques vary, and further assessment would be useful. Assessment studies are mostly pre-clinical with both slide-based metrics and location-specific metrics. Further investigations are needed on appropriate clinical use, performance metrics, and design and execution of clinical studies for such DL algorithms.

**Conclusions:** Consensus development on technical characterization and clinical assessment methods will be very useful in translating DL technology to clinical use for cancer diagnosis.
Effect of Feature Information-Aided Review On Pathology Trainee Performance for Ovarian Cancer Subtyping: An Observer Study

Marios A Gavrielides, Ph.D.1, Meghan Miller, B.S.1-2, Ian S Hagemann, M.D., Ph.D.2,3, Heba Abdelal, MD.2, Zahra Alipour, M.D.2, Jie-Fu Chen, M.D.2, Behzad Salari, MD.2, Lulu Sun, M.D., Ph.D.2, Huifang Zhou, M.D., Ph.D.2, Jeffrey Seidman, M.D.4

1U.S. Food and Drug Administration, Center for Devices and Radiological Health, Office of Engineering and Science Laboratories, Silver Spring, Maryland
2Department of Pathology and Immunology, Washington University School of Medicine, St. Louis, Missouri
3Department of Obstetrics and Gynecology, Washington University School of Medicine, St. Louis, Missouri
4U.S. Food and Drug Administration, Center for Devices and Radiological Health, Office of In Vitro Diagnostics and Radiological Health, Silver Spring, Maryland

Background: Due to the potential for subtype-specific treatment of ovarian cancer, it is increasingly important for subtype to be diagnosed accurately and reproducibly. Pathologist performance for this task depends on the pathologist’s expertise. Informatics and computer-aided diagnosis tools may be useful in narrowing this knowledge gap. This study examines the effect of providing additional information regarding histological feature presence on the performance of pathology trainees for ovarian subtyping.

Technology (optional): Histological review was conducted on whole-slide images (WSI) using a single, calibrated monitor, and two different review modes: a) unaided, consisting of typical review of WSI images, and b) feature information-aided, or aided (see Figure 1), where in addition to reviewing WSI, observers were informed about which histologic features among {high-grade nuclear atypia, abundant mitoses, intra-cytoplasmic mucin, hyalinized stroma, clear cell architectural patterns, sarcomatous components, squamous differentiation, and endometriosis}, were identified previously by an expert in gynecological pathology on the same section.

Methods: Ninety WSI from 75 ovarian cancer patients were reviewed by six 2nd and 3rd year pathology residents using unaided and informatics-aided review modes with > 3-week washout period and order re-randomization between reviews. The reference standard on ovarian subtype consisted of majority consensus from a panel of 3 experts reading on a microscope. Concordance analysis was conducted between observers and the reference standard, across the unaided and aided review modes.

Results: Aided review improved pairwise concordance with the reference standard for five of six observers, by 3.3% to 17.8% (for 2 observers, increase was statistically significant). One observer had reduced concordance by 8.9%. Difference in concordance rate between aided and unaided reviews across subtypes was [+6.9%, +2.2%, +5.6%, +8.9%, -4.4%, +23.1%] for {high
grade serous, low grade serous, mucinous, clear cell, endometrioid, and carcinosarcomas} respectively.

**Conclusions:** Findings show the potential of information-aided review, focusing on the presence of pertinent histologic features, to improve concordance between trainees and expert pathologists for primary diagnosis tasks such as ovarian subtype classification. The observed improvement varied across trainees and histological subtypes. Future work will focus on computer-aided detection of histologic features in support of tumor classification.
Initial clinical validation of clearing histology with multiphoton microscopy (CHiMP) for prostate biopsy diagnosis

Richard Torrez, MD, MS1 (richard.torres@yale.edu) Eben Olson, PhD2, Sudhir Perincheri, MD, PhD2, Robert Homer, MD2, PhD, Michael J. Levene, PhD3, Darryl Martin, PhD4, Preston Sprenkle, MD, PhD4, Peter Humphrey, MD, PhD2
1 Dept of Laboratory Medicine, Yale School of Medicine
2 Dept of Pathology, Yale School of Medicine
3 Applikate Technologies LLC
4 Dept of Urology, Yale School of Medicine

Background. We have previously described the use of CHiMP, a direct-to-digital methodology capable of fast, easy, and cost-effective biopsy tissue processing and multi-level digital slide preparation without the need for the most technically challenging and time-consuming aspects of standard physical slide preparation. In this study we describe the first clinical validation study using this technique as applied to pathologist reads of human prostate tissue biopsies.

Methods. Single core biopsies from 20 consented individuals undergoing prostate biopsy for suspicion of prostate cancer were submitted for CHiMP imaging prior to standard histology processing. Three pathologists reviewed digital images for detailed diagnostic evaluation of all cases using web-based software, and separately reviewed physical H&E slides post CHiMP. A minimum 4-week washout period was used between review phases.

Technology. CHiMP employs a modified tissue processing protocol that includes formalin fixation with fluorescent staining during dehydration followed by optical clearing with optically matched clearing reagents for multiphoton microscopy, known as Clearing Histology with Multiphoton Microscopy (CHiMP). Most recently, we have described a specialized multiphoton microscope capable of imaging speeds comparable to whole slide imaging with high resolution and quality at depth without the need for wax embedding. Our customized web-based software for multi-level digital CHiMP images used for this evaluation is known as Stackstreamer.

Results. Specimens were received, processed, and imaged immediately post acquisition, enabling digital slide review within 3-6 hours post collection, much earlier than physical slides for the same cases were available. Concordance rates for diagnosis between digital slides and physical slides were similar to concordance rates between pathologists for physical slides alone or digital slides alone. No detrimental effects on physical slide preparation or evaluation were noted with the alternate pre-processing.

Conclusions. No significant limitations for primary diagnosis using CHiMP with prostate biopsy specimens were identified in this initial validation. There were no identifiable risks for subsequent physical slide prostate biopsy diagnosis in prostate biopsy samples previously processed by CHiMP. Next phase validation can proceed for clinical implementation of CHiMP for prostate diagnosis.
Computational Pathology
King’s Garden 1

8:00am – 8:15am  Hossain Md Shakhawat  Assessment of HER2 amplification in invasive breast cancer from CISH using digital and computational pathology

8:15am – 8:30am  Hsiang-Sheng Wang  Automatic Mycobacterium tuberculosis detection using simple image processing with artificial intelligence(AI)

8:30am – 8:45am  Paul Christensen  Java versus Data Analysis Expressions (DAX): A Comparison of Programming Effort

8:45am – 9:00am  Mahdi S. Hosseini  From Patch-Level into Pixel-Level Annotation: Semantic Segmentation of Whole Slide Images by Histological Tissue Type
Assessment of HER2 Amplification in Invasive Breast Cancer from Chromogenic in Situ Hybridization Using Digital and Computational Pathology

Hossain Md Shakhawat1,2(∗mshimul86@gmail.com); Tomoya Nakamura1; Matthew Hanna2; Noahiro Uraoka2; Dara S. Ross2; Meera R. Hameed2; Masahiro Yamaguchi1; Yukako Yagi2

1Tokyo Institute of Technology, School of Engineering, Yokohama, Japan
2Memorial Sloan Kettering Cancer Center, Department of Pathology, New York, USA

Background
HER2 gene amplification is seen in up to 20% of breast cancer and has prognostic and therapeutic indications. Fluorescent in situ hybridization (FISH) and chromogenic in situ hybridization (CISH) are the standard assays to determine the HER2 amplification status, the latter utilizing a bright-field microscope. CISH is evaluated by counting at least 20 cancer nuclei manually according to the American Society of Clinical Oncology (ASCO)/College of American Pathologists (CAP) guidelines. However, this process is time prohibitive. The purpose of this study is to develop an automated system to quantify the HER2 amplification status by CISH whole slide images (WSI), utilizing digital image analysis techniques.

Technology
A model was created to mirror the ASCO/CAP HER2 guidelines. It detected singular (non-overlapping) nuclei and identified HER2 and chromosome enumeration probe 17 (CEP17) signals per nuclei from the annotated regions. The method utilized color unmixing and machine learning techniques for nuclei detection. HER2 and CEP17 signals were detected based on RGB intensity and counted for each nucleus where CEP17≥2 and HER2>CEP17.

Methods
Patient specimens diagnosed with invasive breast carcinoma with prior immunohistochemistry (IHC) and FISH analysis were randomly selected. Subsequent manual assessment of CISH was performed. CISH whole slide images were generated at 40x (0.13 um/pixel) by the P250 3DHistech scanner. Subspecialty breast pathologists annotated regions containing invasive tumor cells. Then, the developed model quantified 20 nuclei with the highest differentiation values (HER2-CEP17). Finally, HER2 status was determined based on the HER2/CEP17 ratio as

\[
\text{HER2 Status} = \begin{cases} 
\text{amplified, if ratio } \geq 2.0 \\
\text{non - amplified, if ratio } < 2.0 
\end{cases}
\]

(1)

Additionally, another 20 nuclei were quantified if the ratio was =>1.8 and <=2.2.

Results
The proposed method was compared with manual CISH counting in terms of HER2/CEP17 ratio for 13 cases. The correlation coefficient was 0.97, which indicates the efficacy of the proposed method to quantify HER2 amplification automatically. Table 1 (next page) shows the HER2 status of 9 positive and 4 negative cases by IHC, FISH, manual CISH, and automatic CISH quantification.

Conclusions
The proposed methodology has a high concordance with manual quantification. In the future, cancer regions will be detected automatically using deep learning. The final system will enable automatic cancer detection followed by the automatic quantification of HER2 amplification.
Table 1. Results for 13 cases in immunohistochemistry (IHC), FISH, manual CISHER and proposed automatic CISHER quantification

<table>
<thead>
<tr>
<th>Case</th>
<th>IHC</th>
<th>FISH ratio</th>
<th>Manual CISHER ratio</th>
<th>Automatic CISHER ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1-2+</td>
<td>2.1</td>
<td>2.68</td>
<td>3.17</td>
</tr>
<tr>
<td>2</td>
<td>2+</td>
<td>6.6</td>
<td>6.39</td>
<td>6.46</td>
</tr>
<tr>
<td>3</td>
<td>1-2+</td>
<td>1.0</td>
<td>0.89</td>
<td>0.84</td>
</tr>
<tr>
<td>4</td>
<td>2-3+</td>
<td>5.1</td>
<td>6.78</td>
<td>5.91</td>
</tr>
<tr>
<td>5</td>
<td>3+</td>
<td>N/A</td>
<td>2.82</td>
<td>2.41</td>
</tr>
<tr>
<td>6</td>
<td>N/A</td>
<td>2.3</td>
<td>2.29</td>
<td>2.35</td>
</tr>
<tr>
<td>7</td>
<td>1-2+</td>
<td>2.1</td>
<td>1.97</td>
<td>1.72</td>
</tr>
<tr>
<td>8</td>
<td>1-2+</td>
<td>1.4</td>
<td>1.41</td>
<td>1.45</td>
</tr>
<tr>
<td>9</td>
<td>2+</td>
<td>1.4</td>
<td>1.22</td>
<td>1.79</td>
</tr>
<tr>
<td>10</td>
<td>2+</td>
<td>2.3</td>
<td>1.96</td>
<td>1.61</td>
</tr>
<tr>
<td>11</td>
<td>2+</td>
<td>1.1</td>
<td>1.11</td>
<td>0.63</td>
</tr>
<tr>
<td>12</td>
<td>3+</td>
<td>2.6</td>
<td>2.71</td>
<td>2.57</td>
</tr>
<tr>
<td>13</td>
<td>2+</td>
<td>3.1</td>
<td>3.13</td>
<td>3.62</td>
</tr>
</tbody>
</table>

N/A: Not available, ratio: HER2/CEP17
Automatic Mycobacterium tuberculosis detection using simple image processing with artificial intelligence (AI)

Hsiang-Sheng Wang, MD (wanghsiang1@gmail.com), Wen-Yih Liang, MD, MS

Department of Pathology, Taipei Veterans General Hospital, Taiwan

Background:
Tuberculosis (TB) infection is a major public health issue in Taiwan for a long period of time. During clinical practice, pathologist is one of the most important members for diagnosis. The acid-fast stain (AFS) is a special stain for identifying pathogen like Mycobacterium. However, it is a time-consuming and exhausted work for identifying small micro-organism positive in AFS even by an experienced pathologists. Due to the special feature of TB in AFS, we generate an image filter processing then combined with convolutional neural network (CNN) to detect TB automatically in virtual slides.

Methods:
We first create a six-filtered method for image processing and pick up candidate by color, size, shape, color saturation, background correction and edge. The candidate image is cropped into 40 x 40 pixel small image and piping into CNN for recognition. We use tensorflow and keras as our CNN backend. The CNN structure is generated by multiple paired layers of conv2d network and maxpooling layer following 2 dense layers. The training set contains 52 positive samples where TB are labeled by experienced pathologist. Another 50 samples (All TB PCR positive but only 22 cases are TB positive by pathologist-confirmed AFS in final report) are also collected for validation.

Results:
The 50 validation cases are 22 AFS positive in pathologist’s final report. Our AI take total 1~27 minutes go through each case with average around 10 minutes. AI finally picks up 47 cases positive within all 50 validation cases and return the location of AFS positive area in each slide. We re-confirmed all these area and surprisingly find that only 3 of these 47 cases are false positive. The rest of 44 cases are all true positive. There is no case diagnosed TB positive missed by AI.

Conclusions:
The AI system we build can work pretty well on detecting highly possible candidate within AFS. Our result also shows that AI can assist pathologist to recognized TB even in very small amount of bacilli.
Java versus Data Analysis Expressions (DAX): A Comparison of Programming Effort

Paul Christensen, MD¹ (pachristensen@houstonmethodist.org), S. Wesley Long, MD, PhD¹

¹ Department of Pathology and Genomic Medicine, Houston Methodist Hospital

Background: Analytics tools include spreadsheets with formulas, databases with aggregation functions, programming languages, and vendor software solutions. Each tool varies in its ability to support the spectrum of novice to highly-technical users in basic and complex analyses. The aim of this work was to quantitate the programming effort to perform an identical analysis in Java versus DAX (library of Excel Power Pivot functions).

Technology: Java, Microsoft Excel, Power Query, Power Pivot, DAX

Methods: An algorithm to quantitate the impact of an HPV-reflex testing strategy from a database containing 21279 HPV tests and 59713 associated cervical biopsies was implemented in both Java and DAX. Programming time and number of lines of code were compared for both methods. Package import statements, closing curly braces and empty lines were excluded from the count.

Results: The Java solution required more programming time (2 hours versus 1 hour) and more lines of code than the DAX solution (292 versus 34 lines total, with 63 versus 16 for input/output, 181 versus 0 for the data model, and 58 versus 18 for the analysis). The DAX data model is stored in tables and requires no additional code.

Conclusions: Data analysis performed in Excel, when coupled with Power Query, Power Pivot and DAX, required less programmatic effort than the Java solution. Microsoft Office is ubiquitous in the United States workplace, and most pathologists have access to Excel. The learning curve to create Calculated Columns and Measures in DAX is lower for the average pathology resident when compared with learning how to write programming code. DAX is capable of handling complex analyses, including data with one-to-many relationships, time intelligence calculations, and analyses requiring local minimums or maximums grouped on common fields (such as a patient identifiers). Shortcomings of DAX include no built-in statistical tests or machine-learning features. Although programming languages such as Java, Python, and R are highly expressive for complicated algorithms, Microsoft Excel and its extensions may be one of the most accessible and useful data analysis tools for pathologists to learn. Training pathologists with these tools saves time in calculations and reduces manual mistakes.
From Patch-Level into Pixel-Level Annotation: Semantic Segmentation of Whole Slide Images by Histological Tissue Type

Mahdi S. Hosseini\textsuperscript{1,4} (mahdi.hosseini@mail.utoronto.ca), Lyndon Chan\textsuperscript{1}, Corwyn Rowsell\textsuperscript{2,3}, Konstantinos N. Plataniotis\textsuperscript{1}, Savvas Damaskinos\textsuperscript{3}

\textsuperscript{1}Multimedia Lab, University of Toronto, Canada
\textsuperscript{2}Division of Pathology, St. Michaels Hospital, Toronto, Canada
\textsuperscript{3}Department of Laboratory Medicine and Pathobiology, University of Toronto, Canada
\textsuperscript{4}Huron Digital Pathology, Waterloo, ON, Canada

Content
The gold standard for digitized histopathological diagnosis is to first identify relevant tissues in Whole Slide Images (WSI) known as regions of interest, or ROIs, and then examine these to diagnose for disease. Normally, developing an assistive computational tool to segment the WSI by tissue type would require pixel-level annotation of histological tissue type (HTT). However, pixel-level annotation is impractical considering the huge time cost and effort required by pathologists. We have sought to address this problem by training an automated segmentation tool from patch-level annotations to predict HTTs at the pixel level, assisting pathologists in identifying ROIs for diagnosis.

Technology
The Atlas of Digital Pathology (ADP) database is used to develop a weakly-supervised semantic segmentation pipeline. The ADP database is comprised of 17,688 labeled image patches extracted from 100 tissue slides (mainly H&E) across different body organs and digitized using Huron TissueScope LE1.2 WSI scanner at 40X magnification (0.25um/pixel resolution). Each patch is 1088x1088 pixels and is labeled with multi-class of Histological Tissue Types (HTT).

Methods
The semantic segmentation tool is composed of four main steps as follows. First, a patch-level HTT classifier is developed by training a Convolutional Neural Network (CNN) on the ADP database. A pixel-level HTT segmentation utility is developed next using the Gradient-weighted Class Activation Map (Grad-CAM) technique based on the class prediction. Proper adjustments are applied on the Grad-CAM features to address different characteristics of the morphological and functional HTTs. Finally, a post-processing technique is adopted to enhance the Grad-CAM segmentations to conform to the tissue contours.

Results
Figure 1 demonstrates the semantic segmentation pipeline discussed above. An image patch example of exocrine glands is fed into the pipeline to segment both morphological (predominantly loose connective, simple columnar, and leukocytes) and functional tissues (predominantly exocrine glands and transport vessels).
Conclusions

The pixel-level segmentation of a WSI by histological tissue type can be achieved by training a weakly-supervised semantic segmentation algorithm on the ADP database that is labeled on the patch-level. The results suggest that the segmentation utility can be adopted by pathologists as an assistive tool to identify different ROIs on a WSI.
<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:00am – 8:15am</td>
<td>Orly Ardon</td>
<td>Digitally Tracking Manual Microscopy Slide Reading for Digital Workflow Development</td>
</tr>
<tr>
<td>8:15am – 8:30am</td>
<td>Cathy Chen</td>
<td>Improving medical students’ understanding of pediatric diseases through Philips Pathology Tutor (formerly PathXL)</td>
</tr>
<tr>
<td>8:30am – 8:45am</td>
<td>Veronica Klepeis</td>
<td>Analysis of Free-Text Comments Made by Pathologists in Cancer Synoptic Reports</td>
</tr>
<tr>
<td>8:45am – 9:00am</td>
<td>Alexander Turchin</td>
<td>Canary - a Natural Language Processing Platform for Clinicians and Researchers</td>
</tr>
</tbody>
</table>
Digitally Tracking Manual Microscopy Slide Reading for Digital Workflow Development

Kohan, JL1 (jessica.l.kohan@aruplab.com); Lobell N1; Mathison B1; Couturier MR1,2; Ardon O1,2

1 ARUP Institute for Clinical and Experimental Pathology, Salt Lake City, UT
2 Department of Pathology, University of Utah, Salt Lake City, UT

Background
The development of new digital workflows requires an understanding of current proven laboratory workflows. Microscopy usage metrics including slide reading time, technique, and area covered by technologists are needed in order to capture the standard manual workflow to establish a comparable digital workflow. The novel development of a deep learning screening tool for a high volume, high complexity infectious disease lab test initiated a quantitative and qualitative study to capture the current manual workflow.

Methods
A video camera placed in close proximity to a clinical lab microscope filmed eight different technologists’ hand movements during typical daily runs of 30 slides. The hand movement footage was analyzed using Adobe Premier for read time and number of fields of view examined on each slide. An augmented reality device capable of tracking microscope stage movements was then used as a comparison to the video recordings study. The device generated additional data including the time spent in each field of view, accurate spatial locations on the slide, and measurements of reading time spent per slide. Data was analyzed and compared to perceived microscope usage as well as video camera captured data.

Results
The mean time analyzed using the video camera recordings varied greatly between individual technologists, ranging from 26.4 - 147.5 seconds/slide. Similarly, the mean fields of view ranged from 45-196.3/slide. Additional data obtained from the augmented reality device illustrated significant variability between technologists’ unique reading patterns and area covered on a slide. The results were used to determine metrics for a new machine learning tool as well as training in the lab.

Conclusions
Slide reading techniques vary greatly across different microscopy users in the infectious disease setting. These metrics are useful for machine learning based diagnostic tool development. The methods developed will be used for additional studies in different areas of the lab as digital workflows are introduced.
Improving medical students’ understanding of pediatric diseases through Philips Pathology Tutor (formerly PathXL)

Cathy P. Chen¹(chen.cathy@medstudent.pitt.edu); Bradley Clifford²; Matthew O’Leary²; Douglas J. Hartman¹,³; Jennifer Picarsic¹,⁴

¹University of Pittsburgh School of Medicine
²Pathology Informatics, Enterprise Pathology
³Department of Pathology, University of Pittsburgh Medical Center
⁴Department of Pathology, University of Pittsburgh Medical Center Children’s Hospital of Pittsburgh, Pittsburgh, PA, USA

Background: Online case-based modules have been increasingly integrated into medical education to optimize learning. Medical students may have access to online clinical-based modules during their clinical rotations, but they often lack information about the histopathology correlates of diseases and minimal time is devoted to pathology teaching. To address this gap, we created histopathology case-based e-modules to complement the pediatric clerkship curriculum in order to enhance medical students’ understanding of pediatric diseases.

Technology: Tutor (Philips Pathology, Amsterdam, Netherlands), formerly PathXL, is an interactive web-based program licensed through the University of Pittsburgh School of Medicine Department of Pathology.

Methods: Five histopathology case-based e-modules with pre/post-tests were developed in Tutor. Each module contains a clinical vignette, digital microscopy with detailed explanation of disease process, a supplementary image, and links to additional resources. Slide annotations direct users to areas of interest. Five pre/post-test questions related to the modules were also developed in Tutor. Topics were selected based on established learning objectives for pediatric clerkships. Pre/Post-tests were administered at the beginning and end of each rotation. Test group had access to the Tutor modules, whereas control group did not. Both groups completed the pre/post-tests. Post-test was followed by a voluntary feedback survey.

Results: Twenty-two students completed the study (control group n=9, test group n=13). Test group improved their post-test scores from their pre-test scores by about one point; control group did not (Table 1). Students responded that test questions were helpful in assessing their knowledge of the pediatric pathology (90%) and expressed relative ease of use with the Tutor program (80%).

Table 1. Comparison of mean pre-test and post-test scores

<table>
<thead>
<tr>
<th></th>
<th>Pre-test</th>
<th>Post-test</th>
<th>Differences</th>
<th>P^a</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control Group</td>
<td>3.78</td>
<td>3.78</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>Test Group</td>
<td>3.38</td>
<td>4.31</td>
<td>0.92</td>
<td>0.01</td>
</tr>
</tbody>
</table>
P values determined by using paired t test.

Conclusions: Medical students with access to the Tutor modules had improved post-test scores compared to those without access to the modules. Students responded favorably to the new technology. Incorporating histopathology case-based online modules into the pediatric clerkship curriculum may heighten medical students' understanding of important pediatric diseases. Our model may serve as a pilot for introduction into other medical education platforms.
Analysis of Free-Text Comments Made by Pathologists in Cancer Synoptic Reports

Veronica Klepeis, MD (vklepeis@mgh.harvard.edu), PhD, Emilio Madrigal, D.O.

Massachusetts General Hospital

Background
The benefits of presenting cancer diagnoses in a synoptic report are well-recognized. However, an often-cited drawback of electronic synoptic reporting is the rigid format. A modified version of the College of American Pathologists electronic cancer checklists was implemented at our institution in which more free-text entry comment fields were included to help alleviate this issue. The goal of this study was to review all free-text entries in signed-out synoptic reports to reveal potential deficiencies and ultimately optimize synoptic templates.

Methods
All cases signed out in our laboratory information system, Sunquest CoPath Plus, between January 1, 2017 and December 31, 2018 that contained a synoptic report entered using the integrated mTuitive xPert software were exported for analysis. Each synoptic report was categorized by organ/location type. We initially focused on one of the most commonly used synoptics, namely invasive breast carcinoma (IBC). For each IBC synoptic, all free-text entries were noted and categorized by type.

Results
A total of 6501 synoptic reports were signed out over the two-year period and, of those, 23% (1524) were IBC synoptics. 68% of IBC synoptics contained one or more free-text entries. More specifically, 7% of IBC reports contained free-text entries in the header section, 55% in the invasive carcinoma section, 15% in the DCIS section, 22% in the margin sections, 13% in the lymph node section and 24% in the ancillary studies section. In the tumor section, comments on tumor size (17%), tumor grade (11%) and tumor focality (8%) were most common, followed by lymphovascular invasion (6%). Location of DCIS often required free-text comment (10%), while a lymph node comment field was used 10% of the time. In contrast, a general comment section at the end of the report was only used in 0.5% of cases.

Conclusions
Free-text entry fields in synoptic reports provide a place for pathologists to explain complexities and unique features of cancer diagnoses. Furthermore, by monitoring types of comments, synoptic templates can be optimized to include more relevant answer choices with the goal of streamlining data entry.
Canary - a Natural Language Processing Platform for Clinicians and Researchers

Alexander Turchin, MD, MS (aturchin@bwh.harvard.edu)

Brigham and Women's Hospital, Boston, MA

Background
A large fraction of information in Pathology medical records is contained in narrative documents, as many nuances of tissue characterization cannot be reflected in coding terminologies. While historically narrative data were analyzed using manual chart review, recently natural language processing (NLP) technology has been increasingly used to obtain information from narrative medical documents. However, many NLP tools either require computer science training to use or are expensive. A low-cost solution accessible to users without software engineering expertise is therefore needed.

Technology
To meet these needs we developed Canary – an open source NLP platform that is aimed at clinicians, researchers and analysts without computer science expertise that is publicly available at http://canary.bwh.harvard.edu/.

Methods
Canary is a graphic user interface-based platform that allows users to create their own NLP tools using a combination of user-developed lexicons and detection criteria, ranging from simple to complex. Canary supports a number of advanced NLP functionalities, including: a) detection of concept-value pairs (e.g. tumor grade or TNM stage); b) identification of concepts distributed over multiple sentences (e.g. The specimen consists of an intact gallbladder. In the lumen there is an irregular shaped mass.); c) extraction of concept components that can be at varying distance from each other; and d) parallel processing. All Canary NLP tools are portable to any Canary installation; it has both a graphic user interface and a command-line interface for batch processing.

Results
Canary has been successfully used for development of a range of NLP tools, including diagnosis identification, medication management and analysis of imaging reports. Sensitivity and positive predictive value of NLP tools developed using Canary platform has ranged between 80-95% and it has reached speeds of text processing at 1 MB / minute / CPU core. A number of NLP tools developed for the Canary platform are publicly available in the Canary NLP Tool Library (http://canary.bwh.harvard.edu/library/).

Conclusions
Canary is a versatile NLP platform that can be effectively used by clinicians and researchers to extract information from electronic medical records. It is particularly promising for applications in specialties, like Pathology, where a large fraction of data is contained in narrative reports.
<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker(s)</th>
<th>Topic</th>
</tr>
</thead>
<tbody>
<tr>
<td>8:00am – 8:15am</td>
<td>Edward Klatt</td>
<td>Cognitive Informatics</td>
</tr>
<tr>
<td>8:15am – 8:30am</td>
<td>Mehrvash Haghighi</td>
<td>From Value Stream Mapping to Value-Based Health Care</td>
</tr>
<tr>
<td>8:30am – 8:45am</td>
<td>Aryeh Stock</td>
<td>Converting the Narrative to Analytics: Unlock the Value of Your Data</td>
</tr>
<tr>
<td>8:45am – 9:00am</td>
<td>Yonah Ziemba &amp; Vanesa Bijol</td>
<td>Informatics Education in Pathology Residency Programs: A Successful Team-Based Approach</td>
</tr>
</tbody>
</table>
Cognitive Informatics

Edward Klatt, MD (klatt_ec@mercer.edu)

Mercer University School of Medicine, Pathology

**Background**
Cognitive informatics combines cognitive, behavioral, and information sciences to inform design of health information technology through analysis of human information processing and collaborative requirements of work being done by end users. People are the ultimate users of biomedical information.

**Methods**
A literature review regarding human cognition informs refinements for providing information to the healthcare team. Informaticians can recognize limitations of human cognition and draw upon cognitive science to inform the design and evaluation of technical solutions for information management and interface with the healthcare team.

**Results**
The human brain has a finite capacity for processing new information because neuronal synapse formation is a rate-limited process, called long-term potentiation. Short-term working memory may be limited to no more than 4 separate informational items processed simultaneously. Cognitive load is reduced by breaking down complex tasks into a series of simplified tasks. Long-term memory supplies immediate access to multiple informational items simultaneously. Visual long-term memories can be extensive and detailed, so use of imaging is effective for providing information. Attention span may be task dependent and highly variable among persons. Effective attention span for learning may not exceed 20 minutes. Attention requires control over distracting information. Noise is most distracting when it more closely resembles recognizable human speech. Multitasking is multisequencing, and adding tasks leads to performing each in shorter sequences, because tasks compete for working memory, reducing the effectiveness of working memory applied to each task. Workplace stress with emotional arousal adversely impacts memory storage and function when too high.

**Conclusions**
Solutions applying cognitive informatics include methods to address cognitive load. Medicine is data-rich, but the data are complex. Visual analytics is a means to provide advanced interactive visual interfaces to aid reasoning over, and interpretation of, complex data to avoid information overload. Deep learning describes machine learning algorithms capable of combining many raw inputs into layers of intermediate features. Deep learning has the potential to address problems of cognitive load and constraints of human information processing. Application of deep learning to imaging informatics includes repurposing features extracted from natural images for training, then applying the model to real-world problems.
From Value Stream Mapping to Value-Based Health Care

Mehrvash Haghighi, MD (Mehrvash.Haghighi@mountsinai.org)

Mount Sinai Health System

Background
Health care organizations, due to the transition from fee-for-service to value-based systems, started to embrace lean methodology as a business strategy to achieve better operational efficiency and cost reduction. Educating resident competence in understanding, developing, and implementing successful QI projects is essential for their future success as a pathologist in the value-based era.

Methods
We adopted the Juran principle as the foundation of our QI curriculum with a strong emphasis on value stream mapping. Residents were divided into six groups with relatively balanced gender composition and level of training. The program contained four lectures (proof of need, project identification, diagnostic journey, and remedial journey) with associated activities/games, a case study session, and performance of a mentored QI project. In the case study session, a real business manufacturing case was presented to the residents, and they were asked to perform workflow analysis, draw value stream mapping, propose a solution, and calculate the improvement in performance indexes.

Results
The average attendance rate was 90%. The junior residents in the order of first- and second-year residents showed the highest level of engagement in weekly assignments. There were no significant differences in performance based on gender/age. The results indicated that residents had increased their knowledge in QI methodologies. Four out of six teams (66%) delivered all phases of the project performance (quality planning, control and improvement) with a perfect score. One of the completed projects addressed an issue related to the autopsy department at the organizational level which resulted in 50% improvement in performance in the early stages of implementation. For this specific project, a combination of different strategies including repair, renovation, and reinvention were deployed. In other three projects, quality improvement was achieved through advancement of technologies. One of the team submitted the project end-result as an innovation proposal for grant approval.

Conclusion
The objectives of this program included educating residents to identify a problem/defect, illustrating the issue using value stream mapping, selecting the best solution using different methods and techniques, defining a project to solve the problem. We consider the successful implementation of the QI projects to be the evidence of an effective learning mechanism for advancing resident education in quality improvement and project management.
Converting the Narrative to Analytics: Unlock the Value of Your Data

Aryeh Stock, MD (aryeh.stock@mountsinai.org); Brandon Veremis, DDS; Mehrvash Haghighi, MD

Icahn School of Medicine at Mount Sinai

BACKGROUND
Currently, surgical pathology reports are stored as a free-text variable character field. This means that a huge amount of time is spent on hunting and gathering rather than understanding and interpreting data and creating valuable prognostic metrics. The developed program can navigate the narrative diagnostic text and automatically parse it to the part type and corresponding diagnosis in an Excel (Microsoft) spreadsheet. This program opens the door to readily available quantifiable data on a wide range of clinical outcomes. Examples include the ability to track changes in the progress of disease over time, the ability to correlate various surgical techniques with an adverse event timeline (e.g., complications, severity of complication). Mount Sinai has vast amounts of clinical data that are being underutilized, simply because it is saved in a format that is not “analysis-friendly.”

TECHNOLOGY
Scripts were written in Google Docs and Python (3.27.2) with NumPy (1.15.4) and pandas (0.23.4) libraries.

METHODS
Utilizing rule-based natural language processing and syntax recognition, scripts in Google Docs and Python were written to parse narrative surgical pathology reports and generate database-ready spreadsheets.

RESULTS
This script can rapidly identify, sort and assign numerical values to the findings of a narrative-based pathology report. A proof-of-concept script was written that can navigate colon biopsy reports and generates a heat map of the severity of inflammation throughout the colon.

CONCLUSIONS
Short-term applications allow for the integration of heat maps on colonoscopy reports to show how the severity of IBD changes throughout a patient’s colon and over time. Broader applications include the potential to extract quantifiable data from a variety of pathology reports for use in research and value-based care. This application is best-suited to divisions that use pre-formatted codes to write their reports. Future directions include incorporating statistical natural language processing to extract data from reports written with less consistent use of language.
Informatics Education in Pathology Residency Programs: A Successful Team-Based Approach

Yonah Ziemba¹ (yonah.ziemba@gmail.com), Tarush Kothari¹, Vanesa Bijol¹, Kalpana Reddy¹, Michael Esposito¹

¹Zucker School of Medicine at Hofstra/Northwell

Background
Training gaps in pathology residency curriculum have recently become well-recognized, and surveys show that newly-employed pathologists identify informatics as an area where training is insufficient for successful practice. This is partly because informatics is not amenable to the common training model in which residents rotate on clinical services to assist attendings in their daily work. Herein, we describe a successful team-based learning (TBL) approach implemented at our residency program that does not require dedicated faculty. This has been implemented for two years with remarkable success and is accessible to any program.

Methods
TBL sessions that correspond to topics in the Pathology Informatics Essential for Residents (PIER) Resource Toolkit were attended monthly by 16 residents. Preparation for the session consists of PIER’s recommended resources and practice exercises. The discussion focuses on each resident’s implementation of the practice exercises, or on scenarios that mirrored the PIER learning objectives. Faculty merely function as moderators, and the content is driven by the residents.

Results
To quantify effectiveness, we reviewed studies that assess TBL models similar to ours. Studies measured one of three outcomes: engagement, satisfaction, and examination scores. Kelly et al reported that students were significantly more engaged during TBL than during lecture, as measured by the STROBE tool. Balwan et al found that TBL was associated with increased satisfaction among faculty and residents when implemented at an Internal Medicine Residency Program. Koles et al reported that TBL was associated with higher scores on medical school examinations. In addition, authors note that advantages to TBLs compared to lecture include development of creativity, critical thinking and interpersonal skills.

Conclusions
Active learning in TBL is more effective than passive learning in lecture, and TBLs in pathology informatics are accessible and easy to implement. The resources provided by PIER are flexible and can be adapted to a team-based approach for a large group, or a project-based approach for a single resident on an Informatics rotation. Strengths of PIER include that it is free to all pathology residency programs, it can be adapted to fit a variety of curriculum structures and can be implemented without the benefit of dedicated informatics faculty.