ePOSTER PRESENTATIONS GUIDE

October 16–18, 2026 · Manchester Grand Hyatt San Diego

54 poster presentations

Table of Contents

PathVisions26 ePoster Presentations

This year's poster session brings together 54 presentations spanning AI and computational pathology, image analysis, digital pathology operations, informatics, quality control, and more. Presenters from academic medical centers, health systems, and industry will be on hand to discuss their work and answer questions.

Posters are listed alphabetically by title beginning below. Use the "Browse by Topic" index or the table of contents to jump to areas of interest — many posters span more than one topic area. The name listed with each poster is its presenting author.

Dedicated ePoster Sessions

Dedicated poster sessions are scheduled throughout the conference to help attendees engage directly with presenters and facilitate discussion and networking. Specific poster board numbers will be shared closer to the conference.

Session 1: Friday, 5:00 PM – 6:00 PM (Reception)
Session 2: Friday, 6:00 PM – 7:00 PM (Reception)
Session 3: Saturday, 11:45 AM – 12:45 PM (Lunch)
Session 4: Saturday, 5:35 PM – 6:30 PM (Reception)

Times are subject to change; please confirm against the final conference schedule closer to the event.

Scientific Poster Competition

A panel of distinguished experts will judge participating posters, recognizing outstanding contributions across the following categories:

- Faculty/Staff (Non-Industry)
- Industry
- Trainee
- Technician/Technologist
- Patient-Focused

Browse by Topic

AI (36)

- A multi-scanner whole-slide image framework for detection of scanner-induced batch effects
- AI- assisted detection of signet ring cells in gastric carcinoma: a multi-reader crossover study
- AI-Assisted Grading of ACR and Prediction of Treatment Response in Liver Transplant Biopsies
- AI-Assisted Quantification of Intraepithelial Lymphocytes in Duodenal Biopsies
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging
- ATHENA: Augmented tissue histopathology evaluation and navigation assistant for digital pathology
- Automated whole-slide and hotspot Ki-67 quantification in gastrointestinal neuroendocrine neoplasms
- Autonomous multi-magnification AFB scan profile enhances the digital pathology workflow efficiency
- Beyond the black box: demonstrating granular reproducibility of AI-based HER2 IHC scoring
- Claudin 18.2 in Gastric Cancer Patients: Correlation Analysis and Artificial Intelligence Research
- Clinical validation of an AI-assisted tumor annotation workflow in molecular pathology
- Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.
- DAB-guided deep learning for robust automated mast cell quantification in gastrointestinal biopsies
- Do All Tissue Morphologies Have Prognostic Value in Colorectal Cancer? A Proof of Concept
- Feasibility of AI-assisted digital oral cytology for oral cancer screening and risk stratification
- From Diagnostic to Prognostic Risk Scores in GI Cancers: Using AI in H&E WSIs for Clinical Insights
- Functional Tissue Unit-based Whole-Slide Representation for Prostate Adenocarcinoma Histopathology
- Harness engineering for submission-ready pathology manuscripts with LLMs and AI tools
- Histology deep learning stratifies survival in trastuzumab deruxtecan HER2-negative breast cancer
- IHC membrane enrichment ratio (MER) depends on target localization and stain: analysis of IHCExplore
- In-line automated image quality control for scalable digital pathology workflows
- Interpretable Morphology-Driven Classification for Papillary versus Clear Cell Renal Cell Carcinoma
- Label-Free Missing Tissue Detection via Self-Supervised Learning
- Multi-hop patch graphs capture whole-slide architecture for lung cancer subtyping
- Perturbation fidelity for scanner-robust lung adenocarcinoma subtyping
- Predictive diagnostic safety using agentic artificial intelligence and failure mode analysis
- Standardizing digital pathology for AI development: an infrastructure for global clinical trials
- Subgroup-aware calibration for WSI survival models across institutions
- The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use
- The Zero-Keyboard Era in Pathology: From Report Standardization to Actionable Data Architecture
- Training-Free Tumor Region Identification in Breast Cancer Whole Slide Images
- Transfer learning and feature aggregation for renal cell carcinoma subtype classification
- UniScan-Ki67: Domain Normalization for Multi-Scanner Ki-67 Immunohistochemistry Using CycleGAN
- Virtual Staining from H&E WSIs for Rapid NSCLC Subtyping and Improved Diagnostic Workflow Efficiency
- Whole slide quality assurance via tile-level deep learning artifact detection in renal biopsies.

Advanced Imaging Technologies (10)

- A Multiplex Immunofluorescence Panel for Prognostic Assessment in Pancreatic Neuroendocrine Tumors
- AI-Assisted Grading of ACR and Prediction of Treatment Response in Liver Transplant Biopsies
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging
- Automated whole-slide and hotspot Ki-67 quantification in gastrointestinal neuroendocrine neoplasms
- Color management method validation for whole slide imaging scanners
- DAB-guided deep learning for robust automated mast cell quantification in gastrointestinal biopsies

- Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis
- Investigating Polychromatic Polarized Microscopy Signals in Hepatocellular Carcinoma
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality

Clinical Trials (2)

- Histology deep learning stratifies survival in trastuzumab deruxtecan HER2-negative breast cancer
- Standardizing digital pathology for AI development: an infrastructure for global clinical trials

Digital Pathology Operations (19)

- A low-cost, open-source digital pathology pipeline for translational pathology research
- ABMIL-RCT: rare-class tuning for bladder cancer molecular subtyping from whole-slide images
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- An Equity Tool: Integrating Medical Trainees into Academic Pathology in Puerto Rico and Caribbean
- Autonomous multi-magnification AFB scan profile enhances the digital pathology workflow efficiency
- Clinical validation of an AI-assisted tumor annotation workflow in molecular pathology
- Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.
- Digital pathology competency in resident training: Equipping physicians for tomorrow's opportunities
- Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis
- Fast WSI Downsampling for Sustainable Digital Pathology
- Histology deep learning stratifies survival in trastuzumab deruxtecan HER2-negative breast cancer
- In-line automated image quality control for scalable digital pathology workflows
- Label-Free Missing Tissue Detection via Self-Supervised Learning
- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation
- Planning scanner capacity and staffing in digital pathology: A trace-driven simulation framework
- Standardizing digital pathology for AI development: an infrastructure for global clinical trials
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality
- Virtual Staining from H&E WSIs for Rapid NSCLC Subtyping and Improved Diagnostic Workflow Efficiency

Enterprise Imaging (1)

- Lessons from a large regional transition to enterprise digital pathology

Fluorescence Microscopy (1)

- A Multiplex Immunofluorescence Panel for Prognostic Assessment in Pancreatic Neuroendocrine Tumors

Image Analysis (27)

- 3D pathology improves agreement and certainty of cribriform pattern diagnosis in prostate cancers
- A multi-scanner whole-slide image framework for detection of scanner-induced batch effects
- AI-Assisted Grading of ACR and Prediction of Treatment Response in Liver Transplant Biopsies
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging
- ATHENA: Augmented tissue histopathology evaluation and navigation assistant for digital pathology
- Automated whole-slide and hotspot Ki-67 quantification in gastrointestinal neuroendocrine neoplasms
- Autonomous multi-magnification AFB scan profile enhances the digital pathology workflow efficiency
- Beyond the black box: demonstrating granular reproducibility of AI-based HER2 IHC scoring
- Claudin 18.2 in Gastric Cancer Patients: Correlation Analysis and Artificial Intelligence Research
- Clinical validation of an AI-assisted tumor annotation workflow in molecular pathology
- Color management method validation for whole slide imaging scanners
- Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.

- DAB-guided deep learning for robust automated mast cell quantification in gastrointestinal biopsies
- Do All Tissue Morphologies Have Prognostic Value in Colorectal Cancer? A Proof of Concept
- Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis
- Feasibility of AI-assisted digital oral cytology for oral cancer screening and risk stratification
- Functional Tissue Unit-based Whole-Slide Representation for Prostate Adenocarcinoma Histopathology
- Histology deep learning stratifies survival in trastuzumab deruxtecan HER2-negative breast cancer
- Interpretable Morphology-Driven Classification for Papillary versus Clear Cell Renal Cell Carcinoma
- Multi-hop patch graphs capture whole-slide architecture for lung cancer subtyping
- The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use
- Training-Free Tumor Region Identification in Breast Cancer Whole Slide Images
- Transfer learning and feature aggregation for renal cell carcinoma subtype classification
- UniScan-Ki67: Domain Normalization for Multi-Scanner Ki-67 Immunohistochemistry Using CycleGAN
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality
- Virtual Staining from H&E WSIs for Rapid NSCLC Subtyping and Improved Diagnostic Workflow Efficiency

Informatics (13)

- A multi-scanner whole-slide image framework for detection of scanner-induced batch effects
- AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging
- Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.
- Do All Tissue Morphologies Have Prognostic Value in Colorectal Cancer? A Proof of Concept
- Efficiency of mobile video sharing application (Google Meet®) for real-time telepathology
- Ensuring data integrity at the source: advancing digital pathology through structured grossing
- Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis
- In-line automated image quality control for scalable digital pathology workflows
- Including Rare Tumor Mimics in AI datasets to improve Diagnostic Efficiency: A Case Report
- Interpretable Morphology-Driven Classification for Papillary versus Clear Cell Renal Cell Carcinoma
- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation
- Virtual Staining from H&E WSIs for Rapid NSCLC Subtyping and Improved Diagnostic Workflow Efficiency

Infrastructure (6)

- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation
- Planning scanner capacity and staffing in digital pathology: A trace-driven simulation framework
- Standardizing digital pathology for AI development: an infrastructure for global clinical trials
- The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality

Integration of AI (24)

- AI-Assisted Grading of ACR and Prediction of Treatment Response in Liver Transplant Biopsies
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging
- An Equity Tool: Integrating Medical Trainees into Academic Pathology in Puerto Rico and Caribbean
- ATHENA: Augmented tissue histopathology evaluation and navigation assistant for digital pathology
- Automated whole-slide and hotspot Ki-67 quantification in gastrointestinal neuroendocrine neoplasms
- Autonomous multi-magnification AFB scan profile enhances the digital pathology workflow efficiency
- Beyond the black box: demonstrating granular reproducibility of AI-based HER2 IHC scoring
- Clinical validation of an AI-assisted tumor annotation workflow in molecular pathology

- Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.
- Feasibility of AI-assisted digital oral cytology for oral cancer screening and risk stratification
- From Diagnostic to Prognostic Risk Scores in GI Cancers: Using AI in H&E WSIs for Clinical Insights
- Functional Tissue Unit-based Whole-Slide Representation for Prostate Adenocarcinoma Histopathology
- Harness engineering for submission-ready pathology manuscripts with LLMs and AI tools
- Histology deep learning stratifies survival in trastuzumab deruxtecan HER2-negative breast cancer
- In-line automated image quality control for scalable digital pathology workflows
- Including Rare Tumor Mimics in AI datasets to improve Diagnostic Efficiency: A Case Report
- Interpretable Morphology-Driven Classification for Papillary versus Clear Cell Renal Cell Carcinoma
- Label-Free Missing Tissue Detection via Self-Supervised Learning
- Perturbation fidelity for scanner-robust lung adenocarcinoma subtyping
- Predictive diagnostic safety using agentic artificial intelligence and failure mode analysis
- Subgroup-aware calibration for WSI survival models across institutions
- The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use
- The Zero-Keyboard Era in Pathology: From Report Standardization to Actionable Data Architecture

Integration of DP (17)

- A low-cost, open-source digital pathology pipeline for translational pathology research
- ABMIL-RCT: rare-class tuning for bladder cancer molecular subtyping from whole-slide images
- AI-Assisted Grading of ACR and Prediction of Treatment Response in Liver Transplant Biopsies
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging
- An Equity Tool: Integrating Medical Trainees into Academic Pathology in Puerto Rico and Caribbean
- Automated whole-slide and hotspot Ki-67 quantification in gastrointestinal neuroendocrine neoplasms
- Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.
- Ensuring data integrity at the source: advancing digital pathology through structured grossing
- Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis
- Including Rare Tumor Mimics in AI datasets to improve Diagnostic Efficiency: A Case Report
- Label-Free Missing Tissue Detection via Self-Supervised Learning
- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation
- The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use
- The Zero-Keyboard Era in Pathology: From Report Standardization to Actionable Data Architecture
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality

Logistics with WSI (10)

- A low-cost, open-source digital pathology pipeline for translational pathology research
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.
- Fast WSI Downsampling for Sustainable Digital Pathology
- Label-Free Missing Tissue Detection via Self-Supervised Learning
- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation
- Planning scanner capacity and staffing in digital pathology: A trace-driven simulation framework
- Standardizing digital pathology for AI development: an infrastructure for global clinical trials
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality

Monitors/Peripherals (input devices) (4)

- Color management method validation for whole slide imaging scanners
- Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis
- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation

Multiplex Technologies (2)

- A Multiplex Immunofluorescence Panel for Prognostic Assessment in Pancreatic Neuroendocrine Tumors
- Virtual Staining from H&E WSIs for Rapid NSCLC Subtyping and Improved Diagnostic Workflow Efficiency

Quality Control (16)

- 3D pathology improves agreement and certainty of cribriform pattern diagnosis in prostate cancers
- A multi-scanner whole-slide image framework for detection of scanner-induced batch effects
- AI-Assisted Grading of ACR and Prediction of Treatment Response in Liver Transplant Biopsies
- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- Color management method validation for whole slide imaging scanners
- Ensuring data integrity at the source: advancing digital pathology through structured grossing
- In-line automated image quality control for scalable digital pathology workflows
- Label-Free Missing Tissue Detection via Self-Supervised Learning
- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation
- Predictive diagnostic safety using agentic artificial intelligence and failure mode analysis
- Quality control issues affecting digital pathology workflows
- Standardizing digital pathology for AI development: an infrastructure for global clinical trials
- Training-Free Tumor Region Identification in Breast Cancer Whole Slide Images
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality
- Whole slide quality assurance via tile-level deep learning artifact detection in renal biopsies.

Regulatory Issues (2)

- Standardizing digital pathology for AI development: an infrastructure for global clinical trials
- The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use

Return on Investment (2)

- In-line automated image quality control for scalable digital pathology workflows
- Planning scanner capacity and staffing in digital pathology: A trace-driven simulation framework

Workflow (21)

- AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer
- AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging
- Autonomous multi-magnification AFB scan profile enhances the digital pathology workflow efficiency
- Clinical validation of an AI-assisted tumor annotation workflow in molecular pathology
- Color management method validation for whole slide imaging scanners
- Efficiency of mobile video sharing application (Google Meet®) for real-time telepathology
- Ensuring data integrity at the source: advancing digital pathology through structured grossing
- Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis
- Functional Tissue Unit-based Whole-Slide Representation for Prostate Adenocarcinoma Histopathology
- Histology deep learning stratifies survival in trastuzumab deruxtecan HER2-negative breast cancer
- In-line automated image quality control for scalable digital pathology workflows
- Lessons from a large regional transition to enterprise digital pathology
- More than Concordance: Lessons from Digital Pathology Scanner Validation

- Planning scanner capacity and staffing in digital pathology: A trace-driven simulation framework
- Predictive diagnostic safety using agentic artificial intelligence and failure mode analysis
- Standardizing digital pathology for AI development: an infrastructure for global clinical trials
- The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use
- The Zero-Keyboard Era in Pathology: From Report Standardization to Actionable Data Architecture
- Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality
- Virtual Staining from H&E WSIs for Rapid NSCLC Subtyping and Improved Diagnostic Workflow Efficiency
- Whole slide quality assurance via tile-level deep learning artifact detection in renal biopsies.

All Posters (A–Z)

The name listed with each poster is its presenting author.

1. 3D pathology improves agreement and certainty of cribriform pattern diagnosis in prostate cancers

Suet Ling Sarah Chow, MPhil — *Stanford University*

IMAGE ANALYSIS · QUALITY CONTROL

Prostate cancer (PCa) treatment decisions rely on glandular morphology defined by the Gleason grading system. Among Gleason pattern 4 subtypes, the cribriform variant is associated with worse prognosis and may influence management decisions. However, evaluation is currently based on 2D histologic sections, where cribriform structures may be sectioned at suboptimal levels, introducing ambiguity in interpretation. Slide-free 3D pathology enables volumetric assessment of intact specimens, overcoming sampling limitations and allowing visualization of complex tissue architecture in its native context. We hypothesize that access to localized 3D context can improve interobserver agreement and diagnostic certainty in cribriform diagnosis.Pathology datasets were generated from archival PCa specimens using H&E-analog staining imaged by open-top light-sheet microscopy. A curated set of 54 regions of interest (ROIs; 1 mm × 1 mm) with potential cribriform morphology was independently reviewed by 6 genitourinary pathologists in a 2D assessment phase, during which each ROI was classified as cribriform, not cribriform, or uncertain. ROIs labeled uncertain by each pathologist were re-evaluated in a targeted 3D review phase with limited depth context (1 mm × 1 mm × 40 µm; central plane matched to the original 2D image). Interobserver agreement improved from a mean weighted Cohen's kappa of 0.34 in the 2D phase to 0.46 after 3D review. Across 324 total annotations, 45 (14%) were initially uncertain; 32 of these (71%) were resolved after 3D review. We additionally present a qualitative morphologic atlas illustrating patterns that are ambiguous in 2D and clarified in 3D.These improvements suggest that restricted 3D context (40 µm) can reduce interpretive variability, with potential implications for PCa treatment decisions. The morphologic atlas highlights patterns where 3D evaluation is informative and may guide future studies, computational tool development, and 3D grading guidelines.

2. A low-cost, open-source digital pathology pipeline for translational pathology research

Joseph Stenberg, DO — *University of New Mexico*

DIGITAL PATHOLOGY OPERATIONS · INTEGRATION OF DP · LOGISTICS WITH WSI

Digital pathology (DP) adoption remains limited in many small- and mid-sized laboratories due to high instrumentation costs and workflow implementation barriers. In this project, we developed and evaluated a low-cost, end-to-end digital pathology pipeline using repurposed computer and microscopy hardware and open-source software for use in translational pathology research. Our DP pipeline features a readily available microscope in our pathology lab (Olympus BX41) with a commercial, full-frame camera (Canon D6) for image acquisition. The remaining computer, microscope, and camera components necessary for the pipeline were purchased used from various third-party vendors. Bone marrow biopsy specimens, including those with myelodysplastic syndrome (MDS) and those without significant abnormality, were used as test-cases and digitized using a manual image capture method. This was followed by image stitching using an open-source software (Fiji). The digitized histology images were stored on a remote Ubuntu 22.04 server, backed up to a network-attached storage (NAS). The whole slide images (WSIs) were managed using an open-source image management system (OMERO v5.a6.4). Remote asynchronous review was performed by pathologists (n=7) with varied subspecialty training located in Albuquerque, NM; Salt Lake City, UT; and Palo Alto, CA. The DP pipeline's usability was assessed using a 23-question survey questionnaire. Our DP workflow achieved a high diagnostic concordance (84%) and was consistently rated as robust, user-friendly, and suitable for small-scale translational pathology research activities. While not intended as a clinical platform, our work demonstrates the feasibility of scalable, open-source, budget-friendly DP solutions that expand access to slide imaging workflows in academic and translational research settings. Furthermore, such platforms serve as excellent educational tools for resident education in digital pathology.

3. A multi-scanner whole-slide image framework for detection of scanner-induced batch effects

Lina Takemaru, MPS — *University of Pennsylvania*

AI · IMAGE ANALYSIS · INFORMATICS · QUALITY CONTROL

Introduction: Pathology foundation models (PFMs) learn morphological features from whole-slide images (WSIs) and achieve strong performance in diagnosis, prognosis, and biomarker discovery. However, the robustness of PFMs to technical variation across slide scanners is poorly understood.

Methods: We evaluated scanner-induced batch effects using 109 normal tissue WSIs scanned on four platforms: Aperio AT2, Aperio GT450, Aperio VERSA 8, and Akoya PhenoCycler-Fusion. Features were extracted from 19 patch-level PFMs. We quantified scanner signal using logistic regression, assessed stain normalization and batch correction methods, evaluated supervised tissue classification under cross-scanner settings, and performed unsupervised clustering and attention-based multiple instance learning (ABMIL).

Results: Scanner identity was strongly encoded in PFM features. Cosine similarity between embeddings of identical patches across scanners and PFMs ranged from 0.20 to 0.97 (median: 0.66), indicating distortion of biological signal. Scanner prediction exceeded 97% accuracy across PFMs. Stain normalization had minimal impact, suggesting batch effects extend beyond color variation. In supervised tissue classification, performance dropped by an average of 14.66% +/- 2.44% under cross-scanner confounding compared to balanced training. In unsupervised analyses, scanner-driven structure dominated, separating identical patches by scanner and obscuring biological patterns. ABMIL highlighted different tissue regions depending on scanner (Fig. 1). PCA revealed heterogeneous batch effects with both linear and non-linear variation across PFMs. Methods such as ComBat and Harmony reduced scanner signal but degraded biological information.

Conclusion: Scanner variation is a major source of technical batch effects learned by PFMs, impacting both supervised and unsupervised analyses. Addressing scanner variation is critical to improving robustness of PFMs for research settings and clinical deployment.

4. A Multiplex Immunofluorescence Panel for Prognostic Assessment in Pancreatic Neuroendocrine Tumors

Michelle A. Wood-Trageser, Dr., PhD — *University of Pittsburgh/UPMC*

ADVANCED IMAGING TECHNOLOGIES · FLUORESCENCE MICROSCOPY · MULTIPLEX TECHNOLOGIES

Introduction: Pancreatic neuroendocrine tumors (PanNETs) exhibit variable clinical behavior, and accurate prognostic stratification requires evaluation of multiple biomarkers. Loss of ATRX, DAXX, or Menin protein expression identifies primary PanNETs at elevated risk for early recurrence and distant metastasis; synaptophysin and chromogranin A confirm neuroendocrine lineage. Sequential immunohistochemistry (IHC) on small biopsies and cytology specimens is tissue-intensive, limiting the scope of prognostic assessment. Multiplex immunofluorescence (mIF) enables simultaneous interrogation of multiple markers on one tissue section, preserving material for parallel molecular testing.

Design: A laboratory developed test (LDT) incorporating ATRX, DAXX, Menin, synaptophysin, and chromogranin A was optimized on normal pancreas and PanNETs using clinically validated antibodies on Ventana Discovery Ultra, for parameters including antigen retrieval conditions, antibody staining order, tyramide signal amplification, and fluorophore intensity. A validation cohort of 26 PanNETs underwent parallel mIF and IHC with imaging on a Quanterix PhenoImager HT 2.0; all markers were scored as preserved or loss of expression.

Results: Concordance between mIF and IHC was 93.8%. Marker-specific concordance was 100% for synaptophysin and ATRX, 92.3% for chromogranin A, 90% for DAXX, and 84.6% for Menin. Discordant results were due to autofluorescence interference with chromogranin A during spectral unmixing, increased sensitivity of IF for DAXX, and indeterminate Menin staining by mIF.

Conclusion: This validated mIF LDT enables concurrent prognostic biomarker profiling of PanNETs on one tissue section, reducing tissue usage and providing complete assessment of recurrence-associated alterations. Clinical deployment of this LDT expands access to prognostic biomarker testing on small biopsies and cytology specimens, directly informing surveillance intensity and therapeutic planning for patients with PanNETs.

5. ABMIL-RCT: rare-class tuning for bladder cancer molecular subtyping from whole-slide images

Jiun-I Lai — *National Yang Ming Chiao Tung University*

DIGITAL PATHOLOGY OPERATIONS · INTEGRATION OF DP

Background: Molecular subtyping of muscle-invasive bladder cancer informs prognosis and therapeutic selection, yet RNA-based assays remain costly and inaccessible in many settings. Computational pathology offers a scalable alternative through attention-based multiple instance learning (ABMIL) applied to whole-slide images (WSIs). However, severe class imbalance in the Cancer Genome Atlas Urothelial Carcinoma (TCGA-BLCA) cohort, in which the luminal and neuronal-like subtypes collectively represent under 12% of cases, frequently drives deep learning models into complete class collapse and precludes minority-class prediction.

Methods: An ABMIL rare-class tuning protocol (ABMIL-RCT) was developed, integrating bag-level oversampling (neuronal-like 3x, luminal 2x), cosine annealing with warm restarts, and post-hoc threshold calibration. Training was performed on TCGA-BLCA (n=377) under 5-fold cross-validation, with tile-level features extracted by the UNI2-h Vision Transformer (ViT-H/14, 1,536-dimensional). External validation used an independent Taipei Veterans General Hospital (TVGH) cohort of 177 Philips IntelliSite WSIs from 160 bladder cancer patients (3.6 million patches).

Results: ABMIL-RCT improved mean macro AUROC from 0.865 to 0.882 and balanced accuracy from 44.7% to 54.2%. Class collapse for the two rarest subtypes was resolved, with recall recovered from 0.0% to 24.0% for luminal and from 0.0% to 31.6% for neuronal-like. On TVGH validation, the baseline predicted no neuronal-like slides (0 of 177), whereas ABMIL-RCT predicted 7.9%, matching the 5-7% prevalence reported in prior classification studies. Intra-patient subtype concordance reached 86.7% across multi-slide cases.

Conclusion: ABMIL-RCT resolves rare-class collapse in bladder cancer molecular subtyping and generalizes across scanner platforms without fine-tuning, supporting WSI-based subtyping as a scalable alternative to transcriptomic assays in community laboratories.

6. AI- assisted detection of signet ring cells in gastric carcinoma: a multi-reader crossover study

Akansha Deshwal — *The Ohio State University*

AI

INTRODUCTIONGastric signet ring cell carcinoma is a rare, aggressive adenocarcinoma subtype. Identification in endoscopic biopsies is challenging due to subtle morphology and sparse distribution, particularly in CDH1 mutated tumors with inconspicuous growth pattern. Early diagnosis is critical given the propensity for diffuse infiltration and early metastasis. METHODSA retrospective, multi-reader, multi-case crossover study evaluated 41 gastric biopsies from patients with monoallelic CDH1 mutation (8 positive, 33 negative), each treated as an independent case, for the presence or absence of signet ring cells. Four experienced pathologists were divided into two groups. One group reviewed hematoxylin and eosin (H&E) slides with AI assistance (Ibex Analytics, Jerusalem, Israel), while the other evaluated digital H&E slides without AI. After a two-week washout, groups crossed over. Endpoints included diagnostic accuracy, time to diagnosis, immunohistochemistry (IHC) requirement, and AI heatmap interpretation. The original diagnosis served as the reference standard.RESULTSAI assistance achieved 100% pooled sensitivity (32/32) versus 93.8% (30/32) for H&E alone; 2 false negatives occurred exclusively in the unassisted arm. Pooled specificity was 87.1% (115/132) with AI versus 97.0% (128/132) with H&E alone. Mean time to diagnosis on positive cases decreased 61% (9.1s vs 23.4s); overall mean time decreased 21% (44.7s vs 56.3s). The AI heatmap flagged all 8 positive cases (5 high-confidence, 3 intermediate signals), with 4 intermediate signals among 33 true negatives (Table 1).CONCLUSIONAI assistance improved sensitivity and reduced time to diagnosis for signet ring cell identification, most markedly on positive cases. Reader-level variability in specificity underscores the importance of heatmap calibration and structured reader training. These findings support the clinical utility of AI-assisted digital pathology in this diagnostically challenging entity.

7. AI-Assisted Grading of ACR and Prediction of Treatment Response in Liver Transplant Biopsies

Haider A. Mejbel — *Emory University*

ADVANCED IMAGING TECHNOLOGIES · AI · IMAGE ANALYSIS · INTEGRATION OF AI · INTEGRATION OF DP · QUALITY CONTROL

Introduction: Acute cellular rejection (ACR) represents a common complication in the post-liver transplant setting, affecting 15-40% of recipients. Although the Banff grading is a standard method for assigning ACR, it is associated with interobserver variability. Thus, we developed an AI-assisted model to objectively quantify the ACR score and predict the response to initial corticosteroid therapy.Methods: 234 biopsy-confirmed ACR patients with at least 6 months of follow-up (2020-2023) were identified. A deep learning model analyzed H&E whole-slide images to identify and assess the Banff grading components, including portal tract inflammation, bile duct damage, and venous endothelial inflammation. In conjunction with clinical

variables, we tested the trained models for ACR grading as well as for steroid therapy response on a separate test set of 70 patients.

Results: Our cohort encompasses 234 patients (mean age 54 years; 68% males) with mild (42.3%), moderate (35.5%), and severe (19.2%) ACR, respectively, including 70.1% patients who had a durable response to initial therapy. AI-assisted grading shows comparable results to hepatopathologists' review (Kappa 0.81 vs. 0.48, respectively). On the test set, the AI-assisted model had an AUROC of 0.91 (95% CI 0.86-0.95) with 89.2% sensitivity and 83.4% specificity. Several factors are associated with low response to therapy. These included grade of portal tract inflammation (OR 3.1; p60 years (OR 1.71; p=0.02).

Conclusions: AI-assisted model can be used as an augmented tool to objectively assess liver transplant biopsies for ACR and predict response to therapy. A larger-scale prospective study with external validation is necessary.

8. AI-Assisted Quantification of Intraepithelial Lymphocytes in Duodenal Biopsies

Jiayi Zhao — *Fulgent Genetics*

AI

Abstract: Duodenal Intraepithelial Lymphocytosis (DIL) diagnosis requires quantifying intraepithelial lymphocytes relative to epithelial cells in duodenal villi, a labor-intensive task. We propose an AI-assisted solution to improve efficiency and consistency, reducing review time by ~15% while maintaining human validation and reproducibility.

Introduction: DIL diagnosis requires identifying well-oriented villi and manually counting IELs relative to epithelial cells, typically at the villus tip. We propose an AI-assisted approach that automates this process using segmentation to identify well-preserved villi and detection to identify lymphocytes and epithelial cells. The system computes ratios and provides visual and quantitative outputs to support pathologist review. Method: The AI pipeline was developed using expert annotations on 10 whole slide images, labeling lymphocytes, epithelial cells, and villus regions. It includes a detection model to identify lymphocytes (small, round nuclei) and epithelial cells (elongated nuclei), and a segmentation model to delineate well-preserved villi and countable epithelial regions. Segmentation restricts analysis to relevant areas. Within these regions, detected cells are counted to compute the lymphocyte-to-epithelial cell ratio. The system highlights high-density regions and provides visual and quantitative outputs for review.

Results: Tile-level predictions align well with ground truth (Fig. 1), with minor errors in challenging regions. High accuracy (~95%, Fig. 2) is observed, with background errors mitigated by segmentation. Strong performance is shown, supporting reliable IEL quantification.

Conclusion: This work presents an AI-based solution to support DIL diagnosis. By combining detection and segmentation, it improves efficiency and reduces variability in IEL quantification while maintaining human oversight. Future work will focus on validation, IEL distribution modeling, and integration with clinical data.

9. AI-Driven Digital Image Analysis Improves Reproducibility and Precision in HER2-Low Breast Cancer

Wenfang Liu, MD, PhD — *The Ohio State Univerisity*

ADVANCED IMAGING TECHNOLOGIES · AI · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INTEGRATION OF AI · INTEGRATION OF DP · LOGISTICS WITH WSI · QUALITY CONTROL · WORKFLOW

Background: Distinguishing HER2 IHC score 0 from low expression (1+ or 2+/ISH−) is clinically important with the advent of HER2-targeted therapies, yet remains subjective with substantial interobserver variability. The relationship between routine IHC classification and underlying tumor biology is also incompletely defined. AI-assisted digital image analysis (DIA) may improve both reproducibility and biological relevance.

Design: A total of 376 HER2-negative breast cancer cases (IHC 0, 1+, or 2+/ISH−) from 2021-2022 were analyzed. Pathologist interpretation was based on original clinical diagnoses and compared with AI-assisted DIA using the Visiopharm HER2 application on whole slide images. Correlation with HER2 fluorescence in situ hybridization (FISH) copy number and HER2/CEP17 ratio was assessed.As discordance was greatest at the HER2 0 versus 1+ boundary, a focused cohort of 32 HER2-negative cases (IHC 0 or 1+) was selected to evaluate interobserver variability. These cases were independently reviewed by two pathologists and with DIA, and agreement was assessed using Cohen's kappa.

Results: In the larger cohort, DIA showed strong concordance with original pathologist interpretation, with discrepancies mainly between adjacent categories. Both DIA- and pathologist-defined HER2-low groups demonstrated significantly higher HER2 FISH copy number and HER2/CEP17 ratio compared to HER2 0 tumors ($p < 0.001$). DIA achieved slightly greater separation between HER2 0 and HER2-low groups (mean copy number 2.57 vs 3.25) than pathologist assessment (2.58 vs 3.22).In the focused cohort, interobserver agreement between two pathologists was fair ($\kappa = 0.39$). DIA improved concordance, achieving moderate agreement ($\kappa = 0.50$ with one pathologist).

Conclusion: AI-assisted DIA using the Visiopharm HER2 application improves reproducibility and correlates with molecular measures of HER2 expression.Variability at the HER2 0 versus 1+ boundary can be partially mitigated by AI.

10. AI-guided 3D reconstruction of human lymphoid architecture from whole-slide pathology imaging

Yutong Zhu, MS — *University of Pennsylvania*

ADVANCED IMAGING TECHNOLOGIES · AI · IMAGE ANALYSIS · INFORMATICS · INTEGRATION OF AI · INTEGRATION OF DP · WORKFLOW

Background: Lymphoid follicles drive humoral immunity across physiologic and disease settings, including autoimmunity and cancer. However, conventional 2D histology lacks true spatial context, limiting structural understanding of lymphoid architecture and hindering precision immunotherapy.

Methods: We developed a scalable, unsupervised 3D reconstruction pipeline using standard H&E serial whole-slide images, formatted as OME-TIFFs for interoperability. This framework pairs pathology foundation models (PFMs) with registration modules for 3D alignment, eliminating labor-intensive manual annotations. Our approach makes volumetric analysis highly accessible to community labs and low-resource settings.

Results: We constructed 3D models from two pediatric tonsils and two non-diseased lymph nodes. Hoptimus1 achieved the highest unsupervised segmentation accuracy (95.15 +- 5%) compared to pathologist review among 18 PFMs. This model successfully delineated distinct lymphoid structures and isolated individual follicles. We identified 313 complete follicles (average volume: 0.062 +- 0.05 mm^3). We next evaluated 2D sectioning for bias and found that secondary follicles are frequently misclassified as primary follicles due to incomplete capture of germinal centers (GC) in 2D. Finally, we performed single-cell segmentation within the 3D model, which revealed detailed microstructures, including the GC light-dark zone interface.

Conclusion: Our pipeline provides a robust framework for 3D tissue reconstruction. This unsupervised approach reduces manual annotation, accelerating analysis and mitigating pathologist burnout. Overcoming 2D limitations, it enables characterization of missed lymphoid architecture and supports multimodal spatial integration for 3D cell profiling. Our approach is broadly applicable to follicular biology in diverse settings, with future applications including tertiary lymphoid structures (TLS) in solid tumors, primary immunodeficiencies, and autoimmune diseases.

11. An Equity Tool: Integrating Medical Trainees into Academic Pathology in Puerto Rico and Caribbean

samir a. nacer, MD — *USF Graduate Medical Education*

DIGITAL PATHOLOGY OPERATIONS · INTEGRATION OF AI · INTEGRATION OF DP

Access to pathology training remains limited for many Caribbean medical students due to gaps in local infrastructure, mentorship, and case exposure. Digital pathology offers an opportunity to address these disparities by expanding access to diagnostic material and collaborative learning environments. This study describes a structured, mentorship-driven model that integrates pre-doctoral students from multiple institutions into real diagnostic pathology projects using whole slide imaging (WSI).Over one academic cycle, eight students participated in four case-based projects spanning neuropathology, hematopathology, breast pathology, and soft tissue pathology. Students independently reviewed the literature, analyzed digital slides, and engaged in mentor-guided discussions focused on morphologic interpretation, differential diagnosis, immunohistochemical correlation, and underlying pathophysiology.All projects resulted in conference-level poster presentations, with one case adapted into a board-style educational format. Participation spanned Puerto Rico, Florida, and other Caribbean settings, demonstrating the feasibility of remote collaboration without reliance on physical infrastructure.This model demonstrates that digital pathology can reduce geographic and institutional barriers while

supporting the development of diagnostic reasoning, research skills, and interdisciplinary collaboration. These findings support digital pathology as a scalable approach to expanding access and strengthening the academic pathology pipeline.

12. ATHENA: Augmented tissue histopathology evaluation and navigation assistant for digital pathology

Chuxuan Li — *University of Pennsylvania*

AI · IMAGE ANALYSIS · INTEGRATION OF AI

Introduction: Modern spatial omics assays are powerful but constrained by cost and capture area, limiting large-scale analysis. Histopathologic review of hematoxylin and eosin (H&E) slides offers a cost-effective, high-resolution alternative for large-scale tissue characterization. We present ATHENA, an integrated computational pipeline that uses routine H&E images to support tissue characterization, expert annotation, and region-of-interest (ROI) selection for downstream molecular analysis.

Methods: ATHENA integrates three components for whole-slide image analysis. A cell-resolution segmentation module is designed to operate efficiently on large images despite memory and GPU constraints, enabling rapid characterization of tissue architecture across diverse cohorts. A human-in-the-loop label propagation module extends sparse expert annotations and directs specialist review toward rare cell types and transitional states. A navigation module identifies representative regions for expert review, reducing the manual burden of pathology annotation.

Results: ATHENA refined coarse manual annotations commonly generated in research workflow and spot-level annotations that are crucial for identifying cell types involved in cell-cell interactions and tumor microenvironment. Within individual samples, ATHENA propagated labels from a small number of expert examples and detected scattered structures such as microvascular proliferation in glioblastoma. These outputs support downstream tasks including pathology scoring and ROI selection by improving consistency of tissue review and helping prioritize regions that capture histologic heterogeneity.

Conclusion: By combining scalable segmentation, expert-guided label refinement, and intelligent navigation, ATHENA links routine morphology with downstream molecular assays. This framework supports more standardized and reproducible tissue review and facilitates morphology-informed experimental design.

13. Automated whole-slide and hotspot Ki-67 quantification in gastrointestinal neuroendocrine neoplasms

Wenfang Liu, MD, PhD — *The Ohio State Univerisity*

ADVANCED IMAGING TECHNOLOGIES · AI · IMAGE ANALYSIS · INTEGRATION OF AI · INTEGRATION OF DP

Background: Ki-67 proliferation index (PI) grading of gastroenteropancreatic neuroendocrine neoplasms (NENs) guides prognosis and therapy. Manual hotspot selection introduces observer variability, and whole-slide and hotspot analyses provide complementary prognostic information, with diffuse G2 tumors behaving worse than focal G2 tumors. We evaluated an automated image analysis application for whole-slide Ki-67 quantification and automated hotspot proposal, comparing results with original pathology reports.

Design: Nine gastrointestinal NENs (pancreas, rectum, appendix, and liver metastases) stained for Ki-67 (MIB-1) were digitally scanned. The application segmented tumor, quantified whole-slide PI, and proposed three candidate hotspots per case. Cases were classified as high-grade (G2/G3, >=3%) or low-grade (G1, <3%). Automated whole-slide and maximum-hotspot calls were compared with reported grades using overall, positive, and negative percent agreement (OPA, PPA, NPA).

Results: Whole-slide analysis evaluated a mean of 399,368 nuclei per case (range 6,845-1,480,514) versus 516 per hotspot. Whole-slide PI ranged 0.4%-75.6%. Compared to manual reports, whole-slide analysis achieved OPA 77.8% (7/9), PPA 80.0% (4/5), and NPA 75.0% (3/4). Maximum-hotspot analysis showed OPA 77.8% (7/9), PPA 100% (5/5), and NPA 50.0% (2/4), identifying focal high-proliferation regions in two G1 cases. The three automated hotspots differed by a mean of 3.2%.

Conclusion: Automated whole-slide and hotspot Ki-67 quantification showed substantial agreement with manual reporting. Maximum-hotspot analysis achieved 100% PPA and detected focal high-proliferation regions. Combining both readouts in a single automated workflow supports reproducible NEN grading.

14. Autonomous multi-magnification AFB scan profile enhances the digital pathology workflow efficiency

Prasanth Perugupalli, MS — *Evident Scientific*

AI · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INTEGRATION OF AI · WORKFLOW

Introduction: Pathology encompasses diverse specimen types with distinct morphological features relevant to clinical diagnosis. Optimizing WSI scanning parameters according to sample-specific characteristics is essential for achieving high image quality. We present an automated, label-associated multi-magnification Acid fast bacilli (AFB) scan optimization profile designed to improve image quality and workflow efficiency. Materials &

Methods: Thirty Ziehl-Neelsen (ZN)-stained slides were volumetrically imaged twice using the Pramana Cubiq scanner: first with default parameters and then with an automated multi-magnification AFB optimization profile. The profile was autonomously triggered following slide label detection, without operator intervention. It involved whole-slide acquisition at 40×, followed by targeted 60× imaging of algorithm-defined regions of interest. High-resolution imaging incorporated dynamic Z-stacking (0.935 µm step size) to improve detection of sparsely distributed bacilli. Default scanning employed a fixed, non-adaptive configuration. Image datasets were evaluated by a pathologist for quality and clinical suitability.

Results: The optimized profile demonstrated higher bacillary yield and superior image quality compared to default scanning across all cases. Multi-magnification WSI enabled 40× whole-slide assessment with targeted 60× high-resolution visualization of regions of interest. Z-stacking supported reliable confirmation of bacilli, enhancing diagnostic confidence. The approach was also more time and storage efficient. Automated profile activation reduced manual intervention and rescans, improving workflow efficiency and turnaround time (TAT).

Conclusion: Automated optimization of scan parameters adapted to sample specific features of interest provides optimal image quality for clinical diagnosis. Additionally, it reduces manual intervention and rescans, thereby improving workflow efficiency in digital pathology laboratories

15. Beyond the black box: demonstrating granular reproducibility of AI-based HER2 IHC scoring

Jake Eden — *Agilent Technologies*

AI · IMAGE ANALYSIS · INTEGRATION OF AI

Intro The adoption of AI-powered image analysis in pathology holds significant promise for supporting and even improving clinical IHC assessment in cases such as HER2 in invasive breast carcinoma. However, advanced technology alone is insufficient, earning the confidence of pathologists requires a robust and transparent evidence base. This study demonstrates reproducibility at a highly granular level, across the full spectrum of HER2 staining intensity, and is a necessary step in building that trust and supporting the responsible transition from traditional to digital pathology practice.Methods 157 FFPE invasive breast carcinoma slides stained with GE001 HER2 IHC were selected to represent the full analytic range (0, 1+, 2+, 3+). Each slide was scanned once daily for three consecutive days on an Agilent S540MD whole-slide scanner. The Visiopharm HER2 APP was applied in identical configuration to all WSIs. Duplicate copies of each WSI were also analysed as an intra-run control. Quantitative outputs included high-level clinical scores and granular metrics including tumor cell counts and membrane staining intensity. Reproducibility was assessed using intraclass correlation coefficient (ICC) and categorical concordance.

Results: The system demonstrated high between-scan reproducibility across all quantitative HER2 outputs. Granular quantitative metrics showed low inter-scan variability, supporting the reliability of the combined scanning and analysis workflow.

Conclusion: These results demonstrate that the Visiopharm HER2 APP, in combination with the Agilent S540MD scanner, produces highly reproducible quantitative HER2 IHC outputs across independent scans. This study establishes a reproducibility framework that serves as a natural foundation for future work, including comparison across scanner models, alternative AI applications, and correlation with pathologist scoring, representing a meaningful and scalable step in bridging traditional and digital pathology practice.

16. Claudin 18.2 in Gastric Cancer Patients: Correlation Analysis and Artificial Intelligence Research

Yi Zhang — *Jiangsu Cancer Hospital*

AI · IMAGE ANALYSIS

Background: Claudin 18.2 (CLDN18.2) expression in gastric cancer is closely correlated with tumorigenesis, disease progression, invasion, metastasis and patient prognosis. Based on a large cohort of 1,360 gastric cancer cases, this study investigated the associations of CLDN18.2 expression with clinicopathological parameters, other core gastric cancer biomarkers and patient prognosis, and validated the findings in a large-scale database.

Methods: A total of 1,360 surgically treated gastric cancer patients were enrolled in this study. Immunohistochemical (IHC) detection was performed on patient specimens for CLDN18.2 (clone 43-14A), programmed death ligand 1 (PD-L1, 22C3 pharmDx assay), human epidermal growth factor receptor 2 (HER2) expression and microsatellite instability (MSI) status. Meanwhile, artificial intelligence-based digital pathological analysis was conducted on HE-stained sections, and a deep learning-assisted classification model was established for methodological exploration.

Results: Positive CLDN18.2 expression was identified in 34.4% of the enrolled patients. CLDN18.2 positivity was positively associated with non-esophagogastric junction (EGJ) origin, mucinous carcinoma and larger tumor size ($P < 0.05$), and these associations were validated in the large-scale database. Furthermore, artificial intelligence-based digital pathological analysis based on HE-stained sections was performed, and a deep learning-assisted classification model was constructed. The model exhibited favorable predictive performance with an accuracy of 0.75, precision of 0.857, recall of 0.60, F1-score of 0.706 and area under the curve (AUC) of 0.72.

Conclusions: This study comprehensively analyzed the CLDN18.2 expression status of gastric cancer patients in Jiangsu Province, China, as well as its correlations with clinicopathological characteristics, core biomarkers and prognosis.

17. Clinical validation of an AI-assisted tumor annotation workflow in molecular pathology

Mohammad Abbasi, PhD — *Caris Life Sciences*

AI · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INTEGRATION OF AI · WORKFLOW

Introduction/Background: Accurate tumor classification and region-of-interest (ROI) selection are critical in molecular pathology, influencing patient eligibility for molecular tests and assay success. Diagnostic variability, increasing workloads, and limited reproducibility are significant challenges in high-throughput reference laboratories. Artificial Intelligence (AI) can improve consistency and scalability, but adoption requires seamless integration and demonstrated non-inferiority to manual processes while preserving pathologist oversight.

Methods/Design: This Laboratory Developed Test (LDT) validation study evaluated an AI-assisted tumor classification and ROI annotation tool integrated into the dissection workflow of a CAP/CLIA-accredited molecular reference laboratory. The tool was applied to breast cancer FFPE H&E whole slide images, supporting tumor classification, ROI selection for scrape or microdissection, and eligibility determination. A multi-arm study of ~1,300 slides included pathologists and pathology assistants. Endpoints included accuracy, eligibility concordance, inter- and intra-user reproducibility, and pathologist acceptance. The primary objective was to demonstrate non-inferiority versus manual annotation.

Results: The AI-assisted workflow demonstrated non-inferior performance for tumor classification, ROI selection, and molecular eligibility determination. AI reduced inter- and intra-user variability while maintaining pathologist acceptance and consistent eligibility decisions. Integration was achieved without disrupting operations or downstream testing.

Conclusion/Discussion: This study establishes a validated framework for AI-assisted tumor annotation in molecular pathology. By improving reproducibility and efficiency while maintaining workflow integration and pathologist oversight, this approach supports reliable eligibility determination and has potential to improve assay success and patient care in precision oncology.

18. Color management method validation for whole slide imaging scanners

Louise Collins, MInstP — *PathQA*

ADVANCED IMAGING TECHNOLOGIES · IMAGE ANALYSIS · MONITORS/PERIPHERALS (INPUT DEVICES) · QUALITY CONTROL · WORKFLOW

Introduction: In the digital pathology workflow, color variability can be introduced by the deployment of Whole Slide Imaging (WSI) scanners. This variability can be due to different manufacturers, scanner models or variance within the same scanner model. Color management strategies promise standardized color for accurate diagnosis in digital pathology. Also, the requirement for reliable color imaging is likely to be compounded by the development of Artificial Intelligence (AI)

algorithms. A method to relate colors in a WSI to true spectral colors on a tissue slide will show color management can deliver on the promise of standardized color.MethodA commercially available Sierra slide containing histochemically stained biopolymer patches can be used to generate an International Color Consortium (ICC) profile for a WSI device. The Sierra slide image, along with a proprietary algorithm, can be used to generate an ICC profile to standardize the color of a specially adapted WSI scanner. With this WSI device, an image of a tissue slide and the spectral transmission using a spectrophotometer was measured concurrently. Analysis of the color of the image compared to the true spectral color of the tissue sample was compared and quantified.

Results: Tissue slides were scanned for a variety of different histochemical stains. Each of the digital images from the scanner were color corrected using the generated ICC profile. Spectral measurements were taken at multiple locations within the tissue slide. Data demonstrated good correlation between the ICC profile corrected WSI color and the true measured spectral color.

Conclusion: When a Sierra slide is used to generate an ICC profile for a scanner, the color management strategy produces WSI scanner images with true color standardization. Minimizing color variability within the digital pathology workflow using these ICC profiles provides quantitative validation of digital pathology for a human using a light microscope or WSI and for AI.

19. Comparative analysis of prostate biopsy grade-group agreement across digital pathology platforms.

Sansar Tiwari — *Ohio State University*

AI · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INFORMATICS · INTEGRATION OF AI · INTEGRATION OF DP · LOGISTICS WITH WSI

Background: Accurate grading of prostate core biopsies is critical for clinical decision-making, yet variability in grading agreement across digital pathology platforms remains underexplored. As laboratories transition to whole slide imaging, understanding inter-platform concordance is essential for standardizing diagnostic workflows.

Methods: One hundred prostate core biopsy cases were independently graded by two pathology residents (R1, R2) and an artificial intelligence-based review application (AIRA) across three digital pathology platforms. Ground truth (GT) was established from pathology reports signed out by GU pathologists. Grading agreement was assessed using Spearman correlation, mean absolute error (MAE), exact and within-one agreement rates, and quadratic weighted Cohen's kappa.

Results: AIRA demonstrated the highest concordance with GT (Spearman ρ = 0.899, MAE = 0.870, within-one agreement = 84%, weighted kappa = 0.765). R1 performed comparably (ρ = 0.884, kappa = 0.750), while R2 showed the lowest concordance (ρ = 0.866, kappa = 0.645). All raters systematically underscored relative to GT (mean difference: R1 = −0.72, R2 = −0.88, AIRA = −0.69). Inter-resident agreement was substantial (ρ = 0.834, exact match = 69%).

Conclusion: AI-assisted grading achieved performance comparable to or exceeding that of trained residents across digital pathology platforms, though all raters demonstrated a consistent tendency to underestimate GT scores. These findings support further validation of AI tools for prostate biopsy grading standardization in multi-platform laboratory environments.

20. DAB-guided deep learning for robust automated mast cell quantification in gastrointestinal biopsies

XIAO QI — *Fulgent Genetics*

ADVANCED IMAGING TECHNOLOGIES · AI · IMAGE ANALYSIS

Introduction: Mast cells (MCs) are crucial inflammatory markers in various gastrointestinal (GI) pathologies. In eosinophilic esophagitis (EoE), MC density and degranulation are key indicators of tissue remodeling and often correlate better with clinical symptoms than standard eosinophil counts. However, automated MC quantification is hampered by the diffuse nature of tryptase staining (extracellular degranulation). Standard deep learning models struggle to segment these diffuse signals, frequently merging adjacent cells and generating inaccurate counts compared to clean stains like CD117.

Methods: We developed the MAST-AI model to quantify MCs in CD117 and tryptase-stained WSIs, training on 6,148 annotations from 10 WSIs. To resolve the merging effect of diffuse tryptase, we implemented a DAB-guided postprocessing

framework using H-DAB color deconvolution, adaptive thresholding, and watershed splitting. This isolates individual cell nuclei from surrounding extracellular tryptase for precise instance segmentation.

Results: Validation on a held-out GI biopsy cohort showed DAB-guided refinement successfully split merged cell clusters on tryptase slides (Figure 1). Object-level detection metrics demonstrated strong, consistent model accuracy across all individual test cases (Table 1). The unified pipeline handled both CD117 and tryptase without manual parameter adjustment (Figure 2A). Furthermore, the MAST-AI pipeline achieved a strong correlation ($R^2=0.979$, $p<0.0001$) with manual pathologist counts across sampled high-density regions (Figure 2B).

Conclusion: By effectively managing extracellular DAB distributions, our stain-aware approach provides a robust tool for standardized MC quantification across GI tissue. Accurately resolving degranulated MCs is a critical technical prerequisite. This pipeline lays the foundation for future spatial profiling to characterize the mast cell landscape in EoE and other GI diseases, supporting scalable diagnostic workflows.

21. Digital pathology competency in resident training: Equipping physicians for tomorrow's opportunities

Jodi M. Casper, NCMA — *University Hospitals*

DIGITAL PATHOLOGY OPERATIONS

Introduction: As digital pathology (DP) expands within pathology departments, it is imperative to equip pathology residents with the skills and expertise needed to effectively practice pathology in a digital world. University Hospitals (UH) Department of Pathology has a subspecialty model for clinical diagnosis and residency education. However, intraoperative consultations (IOCs) do not have subspecialty coverage. In difficult cases, a second opinion may be sought, but limited by the availability of a specialist, especially after-hours. As 95% of the pathologists at UH are validated to interpret digital slides, an opportunity to facilitate second opinion IOCs using DP was identified. This required training residents to scan slides.

Methods: The 24 residents under went competency-based training in DP, including direct observation of patient identification, slide preparation, loading of slides, reviewing images, and distribution/storage of scanned slides. Training also included instruction on identifying and recording scanning errors, quality control, entering preventative maintenance records, and resolving issues between the scanner, Image Management System (IMS), and Laboratory Information System (LIS). A short quiz was given to ensure competency.

Results: Since the inception of resident competency-based DP training, there has been a significant decrease (>70%) in turnaround time for after-hours second opinion IOCs. Additionally, several subspecialties currently use DP for routine IOCs.

Conclusion: The future of pathology is digital. Equipping residents with the skills and expertise required to perform in a digital world is imperative. Ensuring resident proficiency in DP decreased turnaround time for second opinion IOCs, reducing potential impacts on patient care. This program has enhanced the residents' exposure to and proficiency with DP, giving them a competitive advantage in the job market and better preparing them to navigate the future of pathology workflow.

22. Do All Tissue Morphologies Have Prognostic Value in Colorectal Cancer? A Proof of Concept

Hikmat Khan, PhD — *The Ohio State University*

AI · IMAGE ANALYSIS · INFORMATICS

Introduction: Pathologists assess many tissue morphologies in colorectal cancer (CRC) specimens, yet the prognostic contribution of each is poorly characterized. Current AI-based models treat whole-slide tissue uniformly, giving limited insight into which morphologies carry prognostic value (PV). As a proof of concept, we explored whether tissue-stratified modeling across 16 CRC morphologies could reveal differential PV, including tumor microenvironment components. By treating each morphology-specific model as a weak classifier, this work motivates future ensemble approaches that aggregate these models into a unified prognostic predictor.

Methods: We analyzed The Cancer Genome Atlas CRC H&E whole slide images from 464 patients (267 alive, 197 deceased; median follow-up 24 months). Slides were classified by MorphDistill, our foundation model, into 16 morphologies (Figure 1, Table 1). For each, we trained a Cox model with 5-fold cross-validation, reporting the concordance (C-index).

Results: C-indices spanned a range (0.500-0.595) across the 16 morphologies. Tumor microenvironment components-loose stroma, smooth muscle, inflammatory infiltrate, and lymphocytes-showed PV comparable to or higher than tumor epithelium (0.556) (Table 1). Pre-malignant and normal epithelial morphologies also ranked numerically above the tumor. High-grade dysplasia and blood vessels carried minimal PV. Given small between-morphology differences in C-index and no pairwise significance testing, rankings are exploratory rather than definitive.

Conclusion: This proof of concept demonstrates the feasibility of isolating morphology-specific survival PV in CRC and suggests that multiple tissue compartments, including tumor microenvironment elements, may carry prognostic information detectable by computational models. We next plan to ensemble these weak classifiers into a unified model with interpretable tissue-level scores for risk stratification, supported by significance testing and external validation.

23. Efficiency of mobile video sharing application (Google Meet®) for real-time telepathology

Celeste M. So — *Zamboanga City Medical Center*

INFORMATICS · WORKFLOW

Telepathology refers to the practice of pathologists from different locations who communicate to arrive at a diagnosis. As of 2016, the estimated pathologist-to-patient ratio is only 1:167,000. The limited number of pathologists available and the bulk of biopsy specimens to be diagnosed is entirely disproportionate thus emphasizing the need for telepathology. However, comprehensive imaging software, high-end communication system, fast and stable internet connection are all expensive. Thus, it is only practical to utilize free voice and video calling application like Google Meet . The objective of this study was to determine the efficiency of a mobile video sharing application (Google Meet) in real-time field image transmission for telepathology specifically identifying how many concordant and discordant diagnoses were done and to determine the acceptance rate of the pathologists in terms of quality of images, quality of voice communication, confidence in diagnosis, and Turn-Around Time (TAT). A total of 171 benign and malignant cases with released histopathology results from January-December 2023 were utilized. The highest concordant diagnoses (100%) were made with malignant GI excision, benign and malignant FGT, benign and malignant male genital tract, malignant lymphoid neoplasm, polyp, papsmear, and ditzels. The lower concordant diagnoses (80%) were from benign breast excision, malignant head and neck excision, and benign lymphoid neoplasm. The shortest Turn-Around Time (TAT) was observed among ditzels with an average of 2 minutes per slide. Longer Turn-Around Time (TAT) was observed among more difficult cases such as malignant cases of the head and neck, soft tissue, and fine-needle aspiration biopsy or smears. More than 90% of the diagnoses made by the pathologists are concordant with the official result. The overall acceptance rate of application of dynamic telepathology is high with a good to average rating in terms of image and audio quality.

24. Ensuring data integrity at the source: advancing digital pathology through structured grossing

Heather Gaburo — *Am Assoc of Pathologists Assistants*

INFORMATICS · INTEGRATION OF DP · QUALITY CONTROL · WORKFLOW

As digital pathology adoption accelerates, standardization of upstream specimen handling remains a critical gap. Specimen gross examination represents the first opportunity to generate structured, interoperable data that influences downstream reporting, imaging, and analytics. The American Association of Pathologists' Assistants Grossing Guidelines, originally developed as an educational resource aligned with College of American Pathologists (CAP) Cancer Protocols and American Joint Committee on Cancer staging requirements, are evolving into a standardized framework to support structured macroscopic data capture. The 4th Edition includes a structured reporting model with standardized terminology and defined required and optional elements. Enhancements include updated submission guidance with visual aids, a detailed breakdown of specimen handling into triage and dissection steps, and the incorporation of considerations for frozen section and ancillary studies. This framework is designed to improve interoperability and consistency across diverse practice settings. A pilot will evaluate feasibility and workflow integration within routine surgical pathology practice. Key assessments will focus on ease of use and clarity of the structured protocols, impact on grossing efficiency and documentation quality, and alignment with current laboratory practices. Evaluation will also assess perceived value for downstream reporting, data quality, and overall standardization within digital pathology workflows. Emerging applications include linking structured macroscopic data with gross and microscopic images, enabling images to be indexed with standardized descriptors and paired with synoptic data as contextual metadata. By improving consistency at the point of data capture, this approach contributes to timely, accurate diagnosis and staging, supports quality assurance and education, and enables integration with broader digital pathology interoperability frameworks.

25. Evaluation of the utility of the Grundium Ocus scanner for cytopathology fluid analysis

Shree Nadkarni, MD — *Icahn School of Medicine at Mount Sinai*

ADVANCED IMAGING TECHNOLOGIES · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INFORMATICS · INTEGRATION OF DP · MONITORS/PERIPHERALS (INPUT DEVICES) · WORKFLOW

Introduction: Digital pathology and whole slide imaging technologies have been increasingly adopted worldwide; however, cytopathology has lagged behind due to challenges posed by three-dimensional cell groups and scan complexity at high magnification. Given a large volume of cytology cases in routine practice, there is a growing need for digital workflows which can support digital review and remote consultation. We designed a pilot study using the Grundium Ocus scanner in an academic setting for review of urine cytology.

Methods: Twenty-six voided urine cytology cases reported between September 1, 2025 and February 28, 2026 were retrospectively collected. The cohort included 23 male and 3 female patients, with an age range of 29 to 94 years across benign, atypical, and malignant final diagnoses. Slides were scanned on the Grundium Ocus M20 using a standardized z-stacking profile of 5 layers with 1 µm layer depth (Figure 1). Digitized images were independently reviewed by 2 cytopathologists and compared with the glass slide diagnoses in a blinded fashion.

Results: A total of 26 voided urine cytology cases were independently reviewed in both glass and digital formats by 2 cytopathologists. When pooled across both reviewers, overall digital-to-glass concordance was 46 of 52 paired interpretations (88.5%). Interobserver agreement between the 2 cytopathologists was 16 of 26 cases (61.5%; kappa = 0.43) for glass slide review and 18 of 26 cases (69.2%; kappa = 0.54) for digital review. Discordant cases were concentrated in the atypical category, reflecting borderline cytomorphologic interpretations rather than frequent diagnostic reclassification.

Discussion/Conclusion: Beyond technical feasibility, this work explores how cytology digital review enables remote collaboration and lower operational barriers in settings without large-scale infrastructure. The findings demonstrate promising utility for digital review of voided urine cytology, with high digital-to-glass concordance.

26. Fast WSI Downsampling for Sustainable Digital Pathology

Wataru Uegami, MD, PhD — *Mayo Clinic*

DIGITAL PATHOLOGY OPERATIONS · LOGISTICS WITH WSI

Introduction/Background: Storage is among the greatest barriers to digital pathology adoption: institutions struggle with growing WSI archives, and some discard WSIs within months of diagnosis. Many pathologists consider 20x acceptable for most cases, and research and AI development operate predominantly at 20x or below; however, higher resolution remains the universal default for diagnostic use, given its superior image quality. Yet WSI resolution has been treated as immutable - fixed at scan time - because changing it seemed impractical.

Methods/Design: We developed an open-source Rust tool supporting DICOM, generic TIFF, and SVS WSI formats, operating directly on the WSI tile-pyramid structure and parallelizing decode, optional resize, and re-encode across CPU cores - purpose-built for WSI internals, not generic image processing. No GPU required. Binaries will be freely available.

Results: Benchmarked on 60 WSIs (54 GB, DICOM, Mayo Clinic), our tool downsampled to 20x tiff formats in 2.95 sec/WSI on a laptop (Apple M4, 10 cores) - fast enough for routine use, ~45x faster than libvips. Output filesize was ~13.7% of original at JPEG Q=87. Pathologist review found no significant visual difference across four resizing algorithms. On a broader TCGA dataset (100 WSIs, multiple institutions and scanner types), our tool succeeded on all files; libvips failed on 38% due to JPEG2000 incompatibility in its default configuration. All outputs confirmed readable by OpenSlide, Bio-Formats, and QuPath.

Conclusion/Discussion: To our knowledge, this is the first publicly available and practical WSI downsampling solution. Beyond reducing file size, this tool opens a new possibility: retaining downsampled WSIs rather than discarding them - making archives more manageable, reducing storage and transfer costs, and ultimately supporting the sustainable and equitable adoption of digital pathology.

27. Feasibility of AI-assisted digital oral cytology for oral cancer screening and risk stratification

Tien-Jen Liu, MD — *AIxMed, Inc.*

AI · IMAGE ANALYSIS · INTEGRATION OF AI

Introduction: Oral cytology is a non-invasive screening method for oral neoplasia, particularly in high-prevalence regions. However, false-negative results and interobserver variability limit its clinical utility. Although AI-assisted digital cytology has shown promise in cervical, urinary, and thyroid applications, its role in oral cytology remains underexplored. This pilot study evaluated whether an AI algorithm could detect and quantify abnormal cells on digital oral cytology slides to support oral cancer screening and risk stratification.

Design: Forty-eight oral cytology specimens from 18 patients were collected using paired wash and brush sampling, prepared by ThinPrep, and scanned with the Hamamatsu S360MD. Whole-slide images were analyzed by an AI algorithm for abnormal cell detection and quantification of nuclear-to-cytoplasmic ratio (N/C ratio) and nuclear area (Fig. 1). Histologic diagnoses were classified as normal (normal/mild dysplasia), pre-cancer (moderate/severe dysplasia), or cancer (well- to moderately differentiated squamous cell carcinoma).

Results: Phase 1 evaluated collection methods using 12 slides from 3 patients (6 wash-brush pairs; 5 cancers, 1 normal). The AI detected more abnormal cells in brush than wash specimens (mean, 18.2 vs 2.5), indicating higher cellular yield. Phase 2 assessed 27 brush slides from 11 patients. Mean AI-detected abnormal cell counts increased with histologic severity: 12.9 in normal (n=9), 39.8 in pre-cancer (n=4), and 116.7 in cancer (n=14) (Fig. 1), supporting the potential of AI-based quantification to reflect histologic severity.

Discussion: AI-assisted digital oral cytology detected and quantified abnormal cells, with brush sampling outperforming wash sampling. Abnormal cell counts increased stepwise across histologic categories, supporting the feasibility of AI-assisted oral cytology for cancer screening and risk stratification. Larger studies are warranted for validation.

28. From Diagnostic to Prognostic Risk Scores in GI Cancers: Using AI in H&E WSIs for Clinical Insights

Michael Wan — *Northeastern University*

AI · INTEGRATION OF AI

Background: Using AI to identify and quantify risk scores for diagnoses is a valuable first step toward adding clinical value to this newer whole slide imaging data modality. However, adding prognostic risk scores for GI carcinoma patients is far more impactful for patients and their families. Our group has developed an AI model to recognize normal and abnormal tissue across colorectal GI specimens and is testing our algorithm against progression-free survival (PFS) and rate of disease recurrence based on histology only.

Methods: A total of 505 WSIs spanning colorectal GI specimen pathology cases were selected and digitized at Prima CARE Health, MA, USA from 2020-2025 using Aperio AT2. Each WSI included demographic, diagnostic and 5-year PFS outcome metadata, from which key prognostic biomarkers were extracted via regular expression matching. We developed and applied an algorithmic pipeline combining a vision transformer-based foundation model for local histological feature analysis with a global random forest model for filtering and integrating local outcomes to provide WSI-level understanding and identification of prognostic biomarkers.

Results: Five-fold cross-validation of classification on 371 WSIs representing the two most common colorectal diagnoses in our dataset (tubular adenoma (233), normal colonic mucosa (138)) yielded an accuracy of 85.4 +- 2.6% and a balanced accuracy of 83.9 +- 2.1%. Expanding to minority classes, five-fold cross-validation of classification on 436 WSIs including the next two most common colorectal diagnosis (hyerplastiç polyp (43), sessile serrated lesion (22)) yielded respective micro, weighted, and macro F1 scores of 80.0+-4.4%, 79.2+-5.0% and 62.4+-12.3% .Conclusion. Our findings demonstrate strong model performance on sufficiently supported diagnoses, validating our two-stage approach. The algorithm is now being trained to query PFS data and provide Prognostic Risk Scores for GI cancer patients.First two authors contributed equally.

29. Functional Tissue Unit-based Whole-Slide Representation for Prostate Adenocarcinoma Histopathology

Selim Sevim, MD — *Oregon Health and Science University*

AI · IMAGE ANALYSIS · INTEGRATION OF AI · WORKFLOW

Introduction: We propose a biologically guided approach for learning whole slide image (WSI) representations of prostate tissue from functional tissue units (FTU).

Methods: To build the FTU classification model, we used the Miro-120. The Miro-120 contains 102 needle biopsie and 18 radical prostatectomy WSIs. Each WSI was segmented into 18 FTU categories using the QuPath plugin MiroSCOPE. For training, the dataset was split into training, validation and test sets with ratios of 80-10-10%, respectively with 224x224 tiles at 10x magnification. Using the FTU classification model, we compute the FTU coverage map for each WSIs. To derive representations, we calculate the proportion of each FTU category in the WSIs, resulting in 'FTU Histogram' features. Performance of proposed embeddings for tasks was evaluated with concordance index (C-index).

Results: Biochemical recurrence (BCR) prediction on LEOPARD: Our FTU Histogram approach slightly outperforms Prov-GigaPath (mean C-index+-SD:0.668+-0.047 and 0.661+-0.057, respectively). Gleason 4 (G4) non-cribriform group had the highest mean C-index as individual FTU group with 0.699. Ablation studies revealed the lowest mean C-index obtained after exclusion of G4 non-cribriform group (0.624).BCR prediction on CHIMERA: We compared FTU Histogram, Prov-GigaPath, and only Gleason Grade(GG)-based WSI features. Our approach had the highest value compared to Prov-GigaPath, and GG-based methods (0.757, 0.714, and 0.666, respectively). ISUP grade prediction on PANDA: FTU Histogram (0.515+-0.055) outperformed Prov-GigaPath features (0.394+-0.052). G4 non-cribriform group was found as the individual FTU group with the highest C-index (0.440). Ablation studies showed that the highest C-index was achieved with exclusion of benign glands (0.519).Discussion and

Conclusion: Since the classification is performed at the FTU level, this straightforward aggregation produces interpretable and biologically relevant WSI representations.

30. Harness engineering for submission-ready pathology manuscripts with LLMs and AI tools

Yosep Chong, MD, PhD, MIAC — *The Catholic University of Korea*

AI · INTEGRATION OF AI

Introduction/Background: Large language models (LLMs) and multimodal artificial intelligence (AI) tools are changing how researchers analyze data, generate figures, and draft manuscripts. However, many pathology researchers still use them in fragmented ways, reducing efficiency and consistency. Harness engineering may offer a more reliable workflow linking raw project materials to submission-ready outputs.

Methods/Design: We developed a practical workflow integrating LLMs and complementary AI tools across four steps: (1) review of raw data and source materials, (2) generation and refinement of tables and figures, (3) conversion of outputs into slide- and poster-ready formats, and (4) drafting of manuscript sections with iterative human review. The framework emphasizes prompt design, task decomposition, cross-checking between tools, and researcher oversight. Use cases were based on pathology projects using spreadsheet data, draft figures, slide content, and early manuscript materials.

Results: The workflow supported a coherent transition from raw materials to publication-oriented outputs within a single pipeline. It improved consistency across datasets, visuals, slides, posters, and manuscript text by reducing fragmentation between tasks. It also clarified where AI tools add value, including structuring results, improving visual communication, accelerating Methods and Results drafting, and supporting completion of the Introduction, Discussion, title, abstract, and references. Key checkpoints requiring expert review were also identified.

Conclusion/Discussion: Harness engineering provides a practical framework for using LLMs and AI tools in pathology research communication beyond isolated prompting. By linking data interpretation, visualization, presentation development, and manuscript drafting into one supervised workflow, this approach may improve productivity and support conversion of digital pathology research into submission-ready outputs.

31. Histology deep learning stratifies survival in trastuzumab deruxtecan HER2-negative breast cancer

Thomas Tavolara, Ph.D — *Mayo Clinic*

AI · CLINICAL TRIALS · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INTEGRATION OF AI · WORKFLOW

Trastuzumab deruxtecan (T-DXd) has expanded treatment for HER2-low metastatic breast cancer, yet immunohistochemistry (IHC)-based classification may miss treatment-relevant biology. AI models trained on hematoxylin and eosin (H&E) whole slide images (WSIs) may enable digital biomarkers for stratification. Cox proportional hazards models with 10-fold cross-validation were trained using CONCH features from a single H&E slide per patient selected via large language model (LLM)-assisted pathology report review. Training included 460 progression-free survival (PFS) and 980

overall survival (OS) patients treated with T-DXd or standard therapies (65 T-DXd each). PFS labels were extracted via LLM-assisted electronic health record (EHR) abstraction; OS was derived directly. Inference was restricted to HER2-negative or equivocal T-DXd-treated patients; HER2-low was defined as IHC 1+ or 2+ with negative fluorescence in situ hybridization (FISH). Among T-DXd-treated HER2-negative or equivocal patients (PFS n=63, OS n=56), the model demonstrated no meaningful prognostic stratification for PFS (c-index=0.42) or OS (c-index=0.50). Within HER2 subgroups, no significant separation was observed for PFS (HER2-low n=14, c-index=0.53; HER2 IHC 0 n=31, c-index=0.38) or OS (HER2-low n=10, c-index=0.37; HER2 IHC 0 n=28, c-index=0.56) (Figure 1). In a treatment-biomarker interaction analysis, neither HER2 status (interaction p=0.19) nor model score (interaction p=0.34) significantly modified the T-DXd treatment effect. The digital biomarker demonstrated superior prognostic discrimination versus HER2 status (c-index=0.67 vs 0.56). No significant prognostic stratification or treatment-biomarker interaction was observed among T-DXd-treated HER2-negative or equivocal patients, for either HER2 status or model score. These findings highlight the challenge of identifying predictive biomarkers in small cohorts and support validation in larger prospective T-DXd datasets.

32. IHC membrane enrichment ratio (MER) depends on target localization and stain: analysis of IHCExplore

Megan Fitzpatrick, MD — *PathAI*

AI

Background: Digital immunohistochemistry (IHC) analysis has the potential to yield quantitative, spatially-resolved features to standardize biomarker scoring and discovery. The membrane enrichment ratio (MER) reflects the subcellular localization and degree of internalization of IHC targets and is an emerging basis for developing biomarkers that predict response to antibody-drug conjugates (ADCs). Using IHCExplore*, an AI-powered tool for comprehensive IHC signal characterization, we examined MER across targets and stains with the goals of 1) improved understanding of stain localization patterns and 2) identifying whether target localization patterns can reveal meaningful biology that can be applied to novel targets.

Methods: We deployed IHCExplore on whole slide images (WSIs; N=386) from IHC stains representing cytoplasmic (AE1/AE3, CK20, S100, Synaptophysin, Chromogranin), cytomembranous (CAIX, PDL1, SMMS1, β-Catenin, CK7), and membranous (E-Cadherin, HER2) targets. MER was calculated as the membrane intensity relative to the membrane+cytoplasm intensity in stain-positive cancer cells.

Results: Across stains, MER values were correlated with the pre-specified rank order provided by an expert pathologist (Kendall's τ=0.43, p<1e-5; Fig. 1A). WSIs from two PD-L1 clones (22C3 and SP263) were manually scored by up to 8 pathologists (Fig. 1B). Despite manual scores having similar values between the clones in matched cases (N=23), MER was higher in 22C3-stained slides (Wilcoxon p=0.009), potentially reflecting antibody-specific epitopes (Fig. 1C).

Conclusions: While MER reflects biologically expected localization patterns across targets, analytical variables (e.g., antibody clone) may influence this metric, suggesting that assay-dependent factors should be considered in the biomarker discovery process.*For Research Use Only. Not for use in diagnostic procedures.

33. In-line automated image quality control for scalable digital pathology workflows

Kailey Arnone, MS — *Caris Life Sciences*

AI · DIGITAL PATHOLOGY OPERATIONS · INFORMATICS · INTEGRATION OF AI · QUALITY CONTROL · RETURN ON INVESTMENT · WORKFLOW

Background: Manual quality control (QC) of digitized pathology slides is labor-intensive, subjective, and a major bottleneck in high-volume laboratories. Existing QC algorithms (e.g., blur and bubble detection) incompletely address the wide range of imaging artefacts such as missing tissue, stitching errors, and banding. As digital pathology adoption scales, sustainable QC processes are required to reduce technician burden while maintaining diagnostic confidence. AI-driven automated quality control (Auto QC) in-line with image generation provides immediate assessment and automated approval, enabling standardized and scalable workflows.

Methods: Auto QC performance was evaluated in a clinical production setting using seven Pramana SpectralHT clusters. Hematoxylin and eosin (H&E) and immunohistochemistry (IHC) slides were analyzed separately. Quality metrics were tracked longitudinally across six software versions (v5.13.9-v5.20.6). Workflow time savings were measured before and after Auto QC and Digital Slide Queue (DISQ) implementation. Technician time savings were estimated using manual versus automated QC review times and average daily volume.

Results: Iterative laboratory-vendor collaboration drove consistent performance improvement across software versions. Auto QC accuracy exceeded 99.7%, with progressive increases in F1 score and automated approval rates. Average scan-to-distribution time decreased from 39.6 hours to 6.42 hours following Auto QC and DISQ implementation. QC review time was reduced by more than 8 technician hours per day, eliminating the equivalent of one QC-focused shift daily and approximately 48 technician hours per week.

Conclusion: AI-driven Auto QC achieved high accuracy while significantly reducing manual QC workload in a high-throughput clinical setting, supporting scalable deployment of automated QC to improve efficiency, relieve operational burden, and maintain timely patient care through vendor-laboratory optimization.

34. Including Rare Tumor Mimics in AI datasets to improve Diagnostic Efficiency: A Case Report

Bhavi Desai, MBBS — *Baroda Medical College*

INFORMATICS · INTEGRATION OF AI · INTEGRATION OF DP

Introduction: Paragangliomas are rare neuroendocrine tumors that may mimic gynecologic masses when located in the retroperitoneum. Nonfunctional tumors lacking catecholamine-related symptoms pose diagnostic challenges. Underrepresentation of such entities in digital pathology datasets contributes to annotation bias and reduced model generalizability, leading to potential misclassification of rare tumors as common diagnoses.Case: We report a case of a 46-year-old postmenopausal woman presenting with vaginal bleeding and a parametrial mass radiologically diagnosed as a broad ligament fibroid. The patient underwent total abdominal hysterectomy with bilateral adnexa. Histopathological examination and immunohistochemistry (IHC) confirmed paraganglioma. Representative histopathology and IHC images were annotated to highlight diagnostic morphologic and immunophenotypic features and organized into an image-based dataset for analysis.

Results: A retroperitoneal mass showed tumor cells arranged in nests, trabeculae, and sheets with focal Zellballen architecture. Tumor cells showed eosinophilic cytoplasm and vesicular nuclei. IHC showed synaptophysin and chromogranin positivity, with S100 highlighting sustentacular cells, and negativity for epithelial and smooth muscle markers. Ki-67 index was 2-3%. Initial radiologic impression suggested broad ligament fibroid; a definitive diagnosis was established on histopathology and IHC. The annotated dataset aimed to improve representation of rare tumor mimics.

Conclusion: This case highlights a rare diagnostic pitfall in which paraganglioma mimicked a common gynecologic entity, with diagnosis established by histopathology and IHC. Underrepresentation of such rare mimics in training datasets can contribute to misclassification and limit model reliability. Inclusion of well-annotated rare entities is essential to address dataset imbalance, improve model training and enhance diagnostic accuracy in future AI-driven pathology applications.

35. Interpretable Morphology-Driven Classification for Papillary versus Clear Cell Renal Cell Carcinoma

Qiangqiang Gu, PhD — *University of Pittsburgh*

AI · IMAGE ANALYSIS · INFORMATICS · INTEGRATION OF AI

Introduction: Papillary and clear cell renal cell carcinoma (RCC) are biologically distinct subtypes with different clinical outcomes, making accurate classification essential. Artificial intelligence (AI) approaches for whole slide image (WSI) analysis mostly rely on pixel-level representations that may not fully capture pathology-relevant morphology. A patch-level, morphology-driven AI framework based on explicit cellular features was developed to address this limitation.

Methods: The study used the Dartmouth Kidney Cancer Histology Dataset (433 WSIs; 336 clear cell, 97 papillary). A balanced subset of 163 WSIs (82 clear cell, 81 papillary) was split into training (80%) and validation (20%) at the WSI level, with 270 WSIs (254 clear cell, 16 papillary) reserved for independent testing. WSIs were tiled into 256×256 patches; 20 patches per WSI were sampled for model development, and all patches were retained for testing. Cell segmentation was performed using StarDist, followed by extraction of 69 handcrafted features describing nuclear size, shape, and boundary complexity. A supervised classifier was trained using AutoGluon, and feature importance was evaluated using Shapley Additive exPlanations (SHAP).

Results: The selected random forest model ROC-AUC of 0.81 (95% CI: 0.78-0.84) on validation and 0.82 (95% CI: 0.79-0.85) on the independent test set, indicating stable generalization. SHAP analysis (Figure 1) identified nuclear morphology

features as dominant predictors, with variability in solidity, major axis length, elongation, convexity, and boundary roughness showing the strongest contributions and consistent patterns across datasets.

Conclusion: Morphology-driven features capture clinically meaningful signals and enable robust RCC subtype classification. This framework provides improved interpretability and aligns with histopathology assessment.

36. Investigating Polychromatic Polarized Microscopy Signals in Hepatocellular Carcinoma

Sixtus Chidiebere C. Onyima, MD — *vilnius university*

ADVANCED IMAGING TECHNOLOGIES

INTRODUCTION - HCC is responsible for approximately between 85% and 90% of all liver cancers and is the third deadliest cancer in the world today [1]. - Currently, diagnosis is premised on various strategies, mainly histopathology, imaging, and reliance on selected biomarkers [2]. - Nonetheless, it has been shown that conventional methods are inherently limited, particularly in their ability to capture minor structural changes in the tumor microenvironment, particularly those related to collagen disruption and ECM remodeling [3]. - Since tumor progression is consistent with changes in stromal organization, capturing these changes is essential. - PPLM is particularly useful, considering its ability to visualize collagen structure in histopathological samples in a way that illuminates fiber alignment [4]. As such, PPLM can complement routine pathology. METHODS - this study employed a scoping review design - A scoping review has been used due to the novelty of PPLM in HCC. The aim of the research is to map the existing knowledge, identify the approaches used, and recognize any gaps. - Databases for selecting the studies were first identified as follows: PubMed, Scopus, and Google Scholar. - Keywords used (with Boolean connectors): 'Hepatocellular carcinoma,' 'polychromatic polarized light microscopy,' 'polarized microscopy,' 'collagen architecture,' and 'extracellular matrix.' - Studies were only included if they were published between 2014 and 2026, were original research, written in the English language, relevant, and contained sufficient content. - Editorial, irrelevant, and animal-related studies were excluded. - An evidence table was created to summarize the study characteristics and the main findings.

37. Label-Free Missing Tissue Detection via Self-Supervised Learning

Jeremy Minkowitz — *University of Pittsburgh Medical Center*

AI · DIGITAL PATHOLOGY OPERATIONS · INTEGRATION OF AI · INTEGRATION OF DP · LOGISTICS WITH WSI · QUALITY CONTROL

Introduction: Missing tissue from incomplete scanner capture is a major safety concern in digital pathology workflows. Current detection techniques rely on high-magnification images (requiring GPU inference) and/or large labeled training sets (limiting adaptation to new scanner platforms). We present and evaluate a novel approach that identifies missing tissue across any scanner platform without requiring labeled examples.

Methods: Two jointly trained models were used. First, a pretrained segmentation model produces tissue masks from both a low-magnification WSI level and the slide-level macro image. Second, a deformable registration model learns a transform between the two. Joint training uses a self-consistency loss, enabling fine-tuning without labeled data. Given the aligned masks, we flag a slide when tissue present in the macro but absent from the WSI exceeds 5% of total macro tissue area. We trained on >10,000 WSIs and evaluated on an expert-labeled set of 519 WSIs with all major organ systems and specimen types. Performance was assessed using sensitivity, specificity, NPV, and accuracy.

Results: The algorithm achieved 97% specificity, 91% overall accuracy, 58% sensitivity and an NPV of 0.920. Inference runs on a 40X slide in under 3 seconds on CPU. False negatives were concentrated on non-H&E stained slides, likely reflecting lower contrast and variable stain saturation, suggesting that stain-specific segmentation models or transforms could further improve performance.

Conclusion: A low-magnification image self-supervised approach provides an efficient, label-free method for detecting missing tissue at the point of scan. Future work will focus on boosting sensitivity through expanded training data, active learning from deployed slides, additional fine-tuning, and adaptive detection thresholds. The work demonstrates a major safety enhancement tool that can be deployed atop of existing lab IT infrastructure without requiring specialized AI infrastructure or GPUs.

38. Lessons from a large regional transition to enterprise digital pathology

Alexander K. Nobori, MD — *SoCal Permanente Medical Group*

DIGITAL PATHOLOGY OPERATIONS · ENTERPRISE IMAGING · INFORMATICS · INFRASTRUCTURE · INTEGRATION OF DP · LOGISTICS WITH WSI · MONITORS/PERIPHERALS (INPUT DEVICES) · QUALITY CONTROL · WORKFLOW

Background: Large pathology practices transitioning from legacy image management systems (IMS) to enterprise imaging platforms face underdescribed operational challenges. At our institution, eSlide Manager was implemented in 2018, and by 2025 approximately one-third of annual slide volume was scanned in a hybrid digital pathology workflow. Following our institution's regional radiology adoption of Sectra, pathology likewise transitioned from eSlide Manager to Sectra IDS7 and from SVS to DICOM whole slide imaging to advance enterprise imaging and interoperability.

Methods: Sectra IDS7 was implemented across 13 pathology departments spanning 16 hospitals in a practice of 120 pathologists. The hybrid workflow used prospective on-demand scanning triggered by a WSI order in the laboratory information system, with selected specimen types scanned automatically by protocol. Implementation included pathology-specific worklist redesign, user acceptance testing, structured issue tracking and triage, training, and go-live support.

Results: After December 2025 go-live, 59,102 cases and 207,341 slides were scanned over the first 4 months of implementation. Mean pathologist-level scanned case proportion was 34% of assigned cases. Median time from slide scan to WSI availability in Sectra improved from 9 to 3 minutes after system upgrades. Sectra was used in 1,928 molecular workflow cases and 268 cases presented at tumor boards. Among 27 survey respondents, 74% were satisfied or very satisfied with Sectra, 78% rated implementation effectiveness as good or excellent, and 81% preferred Sectra to eSlide Manager.

Conclusion: Regional transition from eSlide Manager to Sectra IDS7 was feasible at scale, advancing enterprise digital pathology. Successful deployment required local optimization of pathologist-facing workflow and adapted training and support. Remaining opportunities include broader digital case availability, more reliable WSI order execution, and continued workflow optimization.

39. More than Concordance: Lessons from Digital Pathology Scanner Validation

Harjot Mann, DO — *Westchester Medical Center*

DIGITAL PATHOLOGY OPERATIONS · INFORMATICS · INFRASTRUCTURE · INTEGRATION OF DP · LOGISTICS WITH WSI · MONITORS/PERIPHERALS (INPUT DEVICES) · QUALITY CONTROL · WORKFLOW

Background: Whole slide imaging validation is required before digital sign-out, but concordance alone may not capture barriers to safe implementation. We evaluated scanner validation in a surgical pathology workflow, focusing on glass versus digital diagnostic concordance and operational readiness for clinical deployment.

Design: A quality improvement initiative was performed during validation and pilot implementation of Leica Aperio GT450 scanners. Two pathologists performed glass versus digital review in the intended clinical environment, with concordance classified as exact match, wording discrepancy but concordant, or discordant. Workflow and technical issues encountered during pilot rollout were documented, including incomplete tissue capture, scan failures, downtime, throughput limits, viewer organization, workstation performance, and staffing needs. (Table 1)

Results: Glass versus digital concordance was high across both observers. For pathologist 1, glass and digital review were concordant in 107 of 107 eligible cases (100%). For pathologist 2, glass and digital review were concordant in 57 of 58 eligible cases (98.3%). Quality assessment showed acceptable glass slide clarity, staining, and tissue integrity, with digital review showing acceptable focus, color balance, stitching, and completeness. Despite strong concordance, important implementation barriers were identified, including incomplete capture of tissue extending beyond the coverslip, skipped slides, server connection loss, throughput limitations, case organization issues, and workstation-related lag.

Discussion: High glass versus digital concordance supported feasibility of digital pathology for primary diagnosis in this validation cohort. However, digital pathology validation extends beyond interpretive concordance to include reliable image capture, quality control, workflow integration, and operational resilience. Safe clinical deployment requires phased rollout and clear glass fallback criteria.

40. Multi-hop patch graphs capture whole-slide architecture for lung cancer subtyping

Franca FN. Nik, PhD — *SUNY Upstate Medical University*

AI · IMAGE ANALYSIS

Introduction. Lung adenocarcinoma (LUAD) subtyping from hematoxylin and eosin (H&E) whole-slide images (WSIs) depends on how tissue regions are arranged across the slide, not on any single high-power field. The five recognized patterns (lepidic, acinar, papillary, micropapillary, solid) are defined at whole-slide scale, which is where the diagnostic call is made. Patch-based deep learning methods that aggregate only local neighborhoods miss this long-range morphology. Graph-based aggregators capture short-range relations but have trouble representing multi-region organization.Method. Each WSI is represented as a patch-level graph where nodes are deep learning patch embeddings and edges are feature-similarity weights. To model global architecture, we propagated information through multiple graph steps so that each patch could interact with distant regions through indirect paths. The resulting representation lies on a constrained manifold; a geometry-aware loss preserves this structure during training. Evaluation used BMIRDS (137 LUAD WSIs, five-class subtyping) and WSSS4LUAD (10,091 patches, multi-label histopathology classification).Results. On WSSS4LUAD, the multi-hop diffusion representation improved accuracy by 7.5% over the strongest local-aggregation baseline. On BMIRDS, overall accuracy matched the best baseline (+0.1%), but the two methods disagreed on which slides they got right: the diffusion model recovered slides with mixed architectural patterns that baselines misclassified under the dominant local subtype. Ablating the geometry-aware loss removed the WSSS4LUAD gain.Conclusion. Long-range patch relations give a WSI representation closer to how pathologists read architecture in LUAD. The method matters most on cases where architecture, not cytology, drives the diagnosis.

41. Perturbation fidelity for scanner-robust lung adenocarcinoma subtyping

Meghdad Sabouri Rad, PhD — *SUNY Upstate Medical University*

AI · INTEGRATION OF AI

Introduction. Lung adenocarcinoma (LUAD) subtyping from hematoxylin and eosin (H&E) whole slide images (WSIs) guides prognosis and chemotherapy choice. A subtyper trained at one laboratory can silently flip its answer at another (different staining, a different scanner) while still reporting high confidence on the wrong call. Pathologists see nothing to flag.Methods. We added a feature-space term called Perturbation Fidelity (PF) to the usual cross-entropy and supervised contrastive losses. In standard training, neural collapse pulls the logit margin (the usual confidence score) away from the true distance to the decision boundary; PF pushes them back together under gradient-aligned perturbations. Pathology-Aware Margin-Adaptive PF (PA-MAPF) builds on PF with four low-rank artifact bases (stain, deformation, blur, scanner) learned during training and initialized by principal component analysis on synthetic corruptions. Nine backbones (ResNet-50/101, ConvNeXtV2, EfficientNetV2, ViT-L, with and without attention-based multiple instance learning [ABMIL]) were tested on BMIRDS-LUAD (143 WSIs, 203,226 patches, 5-fold cross-validation) and WSSS4LUAD (87 WSIs, three-class).Results. PA-MAPF reached 96.4 +- 5.1% accuracy on BMIRDS-LUAD with ResNet-101+Attn. Blur-induced accuracy loss fell by roughly 30% and clean accuracy held. The improvement over cross-entropy carried across all nine backbones and onto WSSS4LUAD. Training cost 1.45× the cross-entropy baseline and added 2% parameters. Full per-backbone numbers, statistical testing, and corruption-drop curves are on the poster.Conclusion/Discussion. Pathologist-in-the-loop triage becomes possible once a model's uncertainty reflects actual failure. Standard subtypers cannot support this workflow: their confidence remains high on exactly the slides that fail under stain or scanner change. PA-MAPF is therefore less a new subtyper than a precondition for safe multi-site WSI deployment.

42. Planning scanner capacity and staffing in digital pathology: A trace-driven simulation framework

Matthew G. Bayes, MD, MPH — *Baylor COM / Texas Children's Hospital*

DIGITAL PATHOLOGY OPERATIONS · INFRASTRUCTURE · LOGISTICS WITH WSI · RETURN ON INVESTMENT · WORKFLOW

Introduction: The transition to digital pathology introduces complex operational challenges in slide scanning, staffing, and turnaround time. While whole slide imaging (WSI) adoption is accelerating, few quantitative tools exist to model workflow performance or prospectively identify bottlenecks. We developed a trace-driven discrete event simulation (DES) framework to model real-world slide digitization workflows and predict system performance under real-world operational constraints.

Methods: A DES model was implemented in Matlab Simulink to simulate slide flow from glass slide preparation through scanning, post-processing, and availability in the electronic medical record. Model inputs were derived from empirical workflow data, including hourly slide arrival rates, slides per case, and scanner performance characteristics. System constraints included technician availability windows and scanning throughput. The framework enables parameterization of staffing levels, scanner counts, and workload patterns for scenario-based analysis.

Results: Simulation outputs included turnaround time, scanner utilization, and queue dynamics across operational scenarios. The model identified bottlenecks in post-scan processing and late-day slide arrivals, with delays disproportionately affecting same-day availability targets. Scenario testing demonstrated that incremental changes in staffing and scanner allocation produced nonlinear gains in throughput and reductions in turnaround time.

Conclusion: This trace-driven DES framework provides a quantitative approach to modeling digital pathology workflows and predicting system performance. By enabling rigorous evaluation of operational tradeoffs, it supports data-informed WSI infrastructure planning and workflow decision-making.

43. Predictive diagnostic safety using agentic artificial intelligence and failure mode analysis

n/a Poombal, MBBS — *UMass Chan Medical School-Baystate*

AI · INTEGRATION OF AI · QUALITY CONTROL · WORKFLOW

Introduction: Diagnostic errors impact patient safety and operational efficiency. While traditional quality management looks backward, failure mode and effects analysis (FMEA) offers a proactive approach. Agentic artificial intelligence (AI) autonomous systems capable of multi-step reasoning enable a shift from reactive to predictive quality management. This study explores an integrated agentic AI-FMEA framework to develop a scalable, closed-loop safety ecosystem.

Design: A survey of 43 pathologists (Nov 2023-Feb 2024) identified vulnerabilities in workflows. A structured FMEA assessed failure modes based on severity, occurrence, and detectability to determine risk priority numbers (RPN). Failures with high RPN were linked to specialized agentic AI strategies, including computer vision for artifact detection and natural language processing (NLP) for report validation. A conceptual framework for autonomous multi-agent coordination was developed.

Results: A total of 266 errors were identified: pre-analytical (69%), analytical (22%), and post-analytical (9%). Specimen mislabeling was the highest-risk failure (RPN 480). The framework features four specialized agents, i.e., Specimen Integrity, Analytical Quality, Diagnostic Consistency, and Reporting Validation agents, that automate quality control. These agents use autonomous planning to provide real-time decision support, reducing diagnostic discrepancies and operational delays.

Conclusion: Integrating agentic AI-FMEA creates a proactive safety framework focused on purposeful innovation. Automating process steps shifts the pathologist's role toward high-level oversight, reducing workforce pressures and improving safety. Successful implementation relies on strong data governance and interoperability to prevent avoidable diagnostic errors in digital pathology.

44. Quality control issues affecting digital pathology workflows

Jetton jf. Freeman — *University Hospitals*

QUALITY CONTROL

Introduction: In a perfect world, each slide scanned would be pristine, but in reality, many slides contain preanalytical or scanning defects. Technicians are trained to find defects and imperfections before the slide is scanned, as these details can affect the outcome of scan quality. Pre-scan quality control (QC) enhances pathologist satisfaction and reduces delays in diagnosis. In contrast, lack of pre-scan QC has a domino effect, necessitating additional time spent locating and re-scanning slides, and addressing preanalytical defects. The result is a breakdown of digital pathology (DP) workflow, creating delays for the problem case and other cases awaiting scanning.

Methods: We examined the impact of QC in a clinical laboratory that uses DP for primary diagnosis. The technicians review all slides before scanning, visually checking for imperfections including smudges, overhanging labels, misaligned and multiply coverslips, and air bubbles. After the scan is complete, the technician check the image quality to ensure that there is no missing tissue, that the tissue is in focus, and that there are no other artefacts or defects. These scanning defects are reported on a (QC) log for further review.

Results: The DP lab scanned a total of 385,721 clinical slides for primary diagnosis in 2025. After reviewing scans, technicians recognized 6,035 defects (1.56%). Following QC review and error correction, the scanned slides were sent to the pathologist. Pathologists requested rescans only 302 times (0.078%).

Conclusion: This three-tier system provides accurate results. Technicians review each slide before and after scanning to ensure image quality and diagnostic utility. This proactive systematic approach ensures technical reliability, maintains

consistency, and builds operational effeciency. This reduces error potential and provides more reliable patient outcomes. These measures meet safely and compliance guidelines for continous improvement to enhance patient care.

45. Standardizing digital pathology for AI development: an infrastructure for global clinical trials

Ravyn M. Duncan, PhD — *Molecular Pathology Laboratory Network*

AI · CLINICAL TRIALS · DIGITAL PATHOLOGY OPERATIONS · INFRASTRUCTURE · LOGISTICS WITH WSI · QUALITY CONTROL · REGULATORY ISSUES · WORKFLOW

Centralized pathology review in clinical trials currently focuses on isolated digital pathology components without integration or infrastructure support across sites. This fragmentation introduces variability, delays, and quality risks, and amplifies inconsistencies in AI-driven pathology. We developed a model that produces standardized image sets, yielding site reproducibility and enabling global deployment under regulatory-aligned frameworks.A digital pathology infrastructure was established using pre-configured compact scanners deployed directly to clinical trial sites capable of 40x magnification and z-stacking. Scanner acquisition profiles are locked, require minimal bench space, and enable rapid activation at resource-limited sites. The workflow requires ~5 minutes hands-on time, after which images are automatically and securely transferred to a centralized image management platform for immediate availability. Real-time centralized QC allows for remote correction prior to downstream analysis. This model reduces operational complexity at the site level and aligns with CAP/CLIA, ISO 15189, and GDPR regulations, enabling global participation in clinical trials.Pre-deployment validation confirmed end-to-end integration including centralized pathology review. Early data demonstrate reduced turnaround times, decreased QC failure rates, and concordance with glass slide review. Standardization of scanner type and acquisition parameters enable consistent image generation across sites, while real-time QC allows immediate resolution of quality issues, reducing variability and re-reads.This novel infrastructure-driven approach transforms digital pathology in clinical trials. By combining low-burden site operations with image standardization and real-time QC reviews, this model facilitates scalable participation across diverse geographic regions, including developing research economies, while generating harmonized datasets required for reproducible AI applications.

46. Subgroup-aware calibration for WSI survival models across institutions

Meghdad Sabouri Rad, PhD — *SUNY Upstate Medical University*

AI · INTEGRATION OF AI

Introduction. Whole slide image (WSI) survival models can inform oncology treatment decisions only when predicted probabilities are accurate on the deployed population, not just correctly ranked. Multiple instance learning (MIL) models routinely miscalibrate for specific patient groups (sex, Eastern Cooperative Oncology Group [ECOG] performance status) and drift further at a new institution. Post-hoc recalibration needs target-site outcome data, which clinics rarely have.Methods. MASurv is a discrete-time hazard MIL model with a training-time calibration term tied to clinical nuisance variables (sex, ECOG) within matched risk groups, plus a secondary term enforcing agreement across slides from the same patient. Patch features came from Virchow2. MASurv was trained on 662 SUNY Upstate lung cancer patients (5-fold cross-validation) and applied without retraining to 509 patients from The Cancer Genome Atlas Lung Adenocarcinoma (TCGA-LUAD) cohort. ABMIL, TransMIL, DTFD-MIL, and DeepAttnMISL served as baselines.Results. On SUNY dataset, MASurv cut worst-subgroup integrated calibration index (ICI) by 25% over the standard baseline (0.188 vs 0.249) and single-slide ICI by 36% (0.157 vs 0.246). Discrimination was unchanged (concordance index [C-index] 0.710). On TCGA-LUAD, MASurv alone kept discrimination (C-index 0.680) and distributional calibration (D-calibration p=0.143, ICI 0.079, 4.6× lower than the best baseline); all baselines failed D-calibration externally (p0.36). Internal C-index ranking did not predict external ranking (Spearman ρ = −0.70); DeepAttnMISL was tied for best on SUNY dataset and fell to last on TCGA-LUAD.Conclusion. Training-time subgroup calibration produces WSI survival models that are more equitable within an institution and stay calibrated at a new one without local outcome data. Internal C-index does not predict deployment calibration; external-cohort testing should precede clinical use.

47. The end of the beginning: a pragmatic roadmap to AI development and implementation for clinical use

George M. Yousef, MD PhD FRCPC MSc — *University Health Network*

AI · IMAGE ANALYSIS · INFRASTRUCTURE · INTEGRATION OF AI · INTEGRATION OF DP · REGULATORY ISSUES · WORKFLOW

Introduction: The scope of AI applications in clinical pathology practice is rapidly evolving. As technologies continue to revolutionize the everyday life of pathologists, a pragmatic roadmap was developed in order to safely and effectively implement AI into clinical practice.

Design: University Health Network (UHN) is a multicenter academic institution in Canada serving over 34 satellite sites through its recently-implemented fully digital pathology workflow. We also established the UHN AI hub to provide integrated AI-assisted pathology service. Here we discuss the basic foundations of the development and implementation of AI for clinical use.

Results: The spectrum of AI applications for pathology practice can be categorized into overlapping groups; including image analysis, development of image-analysis, diagnostic, decision support, and integrated diagnostics algorithms. The emerging concept of agentic AI can also play a critical role in improving workflow (through case prioritization, QC, ordering IHC).

Discussion: There are several key requirements for the development of AI models in pathology, including access to large, well-curated datasets, avoiding the risk of bias, and monitoring independent algorithm validation. It is also important to consider secure data sharing and privacy preservation. The regulation of AI algorithms varies among different countries, ranging from the need for FDA approval, to lab-developed tests, or usage for research purposes only. The evaluation of the clinical value of an AI algorithm is a complex topic that goes beyond technical performance assessment. It includes assessment of workflow efficiency and improving turnaround time, clinical utility, decision impact, and cost effectiveness. Precautions that should be considered when implementing clinical AI algorithms include the potential for model aging, overreliance on AI, understanding the algorithm performance level (which depends on your needs), and legal/ethical considerations.

48. The Zero-Keyboard Era in Pathology: From Report Standardization to Actionable Data Architecture

zaineb ayoubi, MD — *CHU Mohammed VI de Tanger*

AI · INTEGRATION OF AI · INTEGRATION OF DP · WORKFLOW

Background: The pathology diagnostic process, from gross examination to final reporting, faces significant operational hurdles. Reporting alone can account for up to 34.6% of a pathologist's workload (Jonhan HO/2014), yet reports frequently have missing elements. This results in miscommunication between pathologists and clinicians, and hinders the efficiency of the pathologists' workMethodsTo mitigate these challenges, we developed 'Pathodraft,' an innovative application leveraging advancements in digital pathology and Artificial Intelligence (AI). It provides a nominative access to each resident and professor, to ensure traceability, and uses precreated forms to generate reports. Presentation of the patho draft appThe system is structured around six principal modules: a Dashboard for real-time metrics and creative analytics; a Reports manager with advanced filtering; a Template editor supporting versioning and tags; a Knowledge Graph linking histopathological entities to assist future diagnoses; a centralized Patient database; and a color-coded Tagging system for organ-based classification.Characteristics and visionPathodraft implements a 'Zero Keyboard' philosophy, utilizing structured forms, AI transcription and automatisation. For example, automatically calculating SBR scores or TNM staging based on form selections, eliminating manual computation and typing.It offers two automated formats:Synoptic Reports: Providing a visual standard that boosts clinician-pathologist communication.Descriptive Reports: Offering detailed histological portrayals and highlighting diagnostic reasoning for complex or atypical cases.It also stores data in a spreadsheet based on the encoded variables used in the forms facilitating data analysis.

Conclusion: Pathodraft optimizes data entry enhancing workflow and reducing administrative burdens. It also supports institutional research, epidemiological surveillance, and the continuous optimization of laboratory performance.

49. Training-Free Tumor Region Identification in Breast Cancer Whole Slide Images

Saghir Alfasly, PhD — *Mayo Clinic*

AI · IMAGE ANALYSIS · QUALITY CONTROL

Background: Automated tumor region detection in whole slide images (WSIs) typically requires large annotated training datasets. Quality control (QC) models, routinely deployed to filter artefact tiles before downstream analysis, learn rich tissue representations that may encode diagnostically relevant morphological features. We hypothesized that these representations could support tumor localization without any task-specific retraining.

Methods: We present a dual-purpose framework that repurposes a QC vision transformer (ViT, 2.7 million parameters, 192-dimensional embeddings) pre-trained via DINO self-supervised distillation on 4.95 million tiles from 52 tissue types (TCGA and Mayo Clinic), and then fine-tuned as a binary QC classifier (99.79% validation accuracy). Tiles were extracted at 5x equivalent magnification (64x64 pixels). From a small support set (approximately 25 slides, 10% of the cohort), tumor and normal tissue prototypes were constructed via k-means clustering (k=20 per class) in the frozen embedding space. Test tiles were then scored using a nearest-prototype distance margin.

Results: On an internal cohort of 259 breast cancer H&E WSIs (neoadjuvant setting), evaluated across three independent folds (207 test WSIs per fold), the method achieved a mean tile-level AUROC of 0.862 +-0.008, AUPRC of 0.822 +-0.004, and F1-score of 0.817 +-0.003, without any model retraining.

Conclusions: QC model embeddings encode tissue morphology sufficient for prototype-based tumor localization without task-specific training. Repurposing existing QC infrastructure simultaneously as an artefact filter and a morphology feature extractor provides a practical, annotation-efficient pathway for the region of interest detection, particularly in settings where large labelled cohorts are unavailable.

50. Transfer learning and feature aggregation for renal cell carcinoma subtype classification

Yu Fan Lin, MD — *National Yang Ming Chiao Tung University*

AI · IMAGE ANALYSIS

Introduction/Background: Renal cell carcinoma (RCC) includes multiple subtypes with distinct prognostic and therapeutic implications. Clear cell RCC (ccRCC) is the most common, while chromophobe RCC is less frequent but clinically important. Although typically distinguishable, overlapping features may occur in limited biopsies or suboptimal samples. Digital pathology enables computational analysis, but many deep learning approaches require large annotated datasets.

Methods/Design: We developed a computational pipeline integrating deep feature extraction and slide-level aggregation to differentiate ccRCC from chromophobe RCC using hematoxylin and eosin whole-slide images. Eighteen slides (9 ccRCC, 9 chromophobe RCC) were analyzed using a patch-based approach. Image patches were processed with a pre-trained ResNet50 model to extract 2048-dimensional feature vectors. Features were aggregated using mean, standard deviation, 95th percentile, and maximum pooling. Principal component analysis was applied for dimensionality reduction, followed by logistic regression with class balancing. Performance was evaluated using leave-one-out cross-validation.

Results: Approximately 89,000 patch-level features were extracted. The model achieved an area under the receiver operating characteristic curve (AUC) of 0.889 and balanced accuracy of 0.83. Confusion matrix analysis showed 8 chromophobe RCC correctly classified (1 false positive) and 7 ccRCC correctly classified (2 false negatives). The model demonstrated clear separation between subtypes.

Conclusion/Discussion: Pre-trained deep feature extraction combined with classical machine learning can effectively distinguish RCC subtypes, even with limited data. This approach provides a practical framework for computational pathology and may support diagnostic workflows. Future work will include larger datasets and advanced models such as attention-based multiple instance learning.

51. UniScan-Ki67: Domain Normalization for Multi-Scanner Ki-67 Immunohistochemistry Using CycleGAN

Daehong Lee, Dr., Ph.D. — *AIVIS Inc.*

AI · IMAGE ANALYSIS

Introduction/Background: Although scanner variability has been widely studied in H&E images, it has been less investigated in IHC. Optical differences across scanners can introduce domain shift, reducing the reliability of AI models trained on a single scanner domain. We propose UniScan-Ki67, a framework to normalize Ki-67 IHC images across scanners by aligning heterogeneous data to a unified reference domain.

Methods/Design: We developed a CycleGAN-based generative model to transform images from non-reference scanner domains (Domains B and C) into a reference scanner domain (Domain A). A dataset of 60,000 Ki-67 IHC image patches (512 × 512 at 20× magnification) was used for training. Performance was evaluated using structural similarity index (SSIM), Fréchet inception distance (FID), and feature-space cluster distance (δ). For downstream validation, a YOLO26 cell detection

model trained on Domain A data was tested on raw images from all domains and normalized images from non-reference domains (n = 1,470).

Results: UniScan-Ki67 achieved high structural fidelity, with a mean SSIM of 0.9563 and FID of 3.9629. Cluster distance analysis showed that normalized Domain B images were significantly closer to the reference domain ($\delta B = 0.1175$, $p < 0.001$). In downstream evaluation, the baseline YOLO26 model showed substantial performance degradation on images from non-reference scanners, with Domain B mAP dropping to 0.0789. After UniScan-Ki67 normalization, detection performance improved substantially, with Domain B mAP increasing to 0.7885 and Domain C mAP increasing to 0.7892.

Conclusion/Discussion: The UniScan-Ki67 framework effectively mitigates domain shift in multi-scanner Ki-67 IHC images. This approach improves detection performance across heterogeneous scanners and supports scalable, reliable deployment of Ki-67 cell detection across imaging platforms.

52. Virtual Slide Still Images Versus Traditional Photomicrography: An Assessment of Perceived Quality

Yoko Fujita, MD, PhD — *Houston Methodist*

ADVANCED IMAGING TECHNOLOGIES · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INFRASTRUCTURE · INTEGRATION OF DP · LOGISTICS WITH WSI · QUALITY CONTROL · WORKFLOW

Background: WSI (whole slide imaging) allows creation of still photos through screen capture or still image export functionalities. However, the quality of still images captured from virtual slides has not been formally compared with those obtained using traditional photomicrography using physical light microscopes. Herein, we assessed perceived image quality for such images in a cohort of pathologists.

Design: H&E, special stains, and immunohistochemically stained slides were imaged. An Olympus BX41 microscope and Leica DMC6200 camera were used at 2x-40x objective magnification versus virtual slides obtained using a Roche Ventana DP200 scanner at 20x. Snapshot function in QuPath software was used to create still images. Microscopic fields of view and acquisition settings were identical for each subset of images for WSI or the physical light microscope. TIFF image files were converted to JPEG, 900x900 pixels at 300 dpi. Ten paired still images were displayed in an online survey (Figure 1). Participants were blinded to the photographic method used, and images were rated on a 1-5 Likert scale. A paired student's t-test was used to compare average image ratings.

Results: Results are shown in Table 1. A total of 37 survey participants were 20 practicing pathologists, 15 pathology residents/fellows, and 2 medical students. Photos taken with a physical microscope obtained higher average ratings versus using virtual slides. The difference in average image rating was statistically significant ($p<0.05$) overall and when stratified for various participant characteristics, with the exception of medical students and using a laptop to view the images in the survey.

Conclusion: WSI-derived still images were rated lower than conventional photomicrographs, suggesting opportunities for future optimization. Strategies may include screen/display or software settings, specialized post-processing workflows, or platform-specific image export strategies.

53. Virtual Staining from H&E WSIs for Rapid NSCLC Subtyping and Improved Diagnostic Workflow Efficiency

Rafay Azhar, Dr. — *ViewsML Technologies*

AI · DIGITAL PATHOLOGY OPERATIONS · IMAGE ANALYSIS · INFORMATICS · MULTIPLEX TECHNOLOGIES · WORKFLOW

Background: Accurate subtyping of non-small cell lung carcinoma (NSCLC) into adenocarcinoma and squamous cell carcinoma is essential for molecular testing and therapy selection. Conventional workflows rely on multiple immunohistochemical (IHC) stains, increasing turnaround time (TAT) and consuming limited tissue. We evaluated a virtual staining approach that reconstructs lineage-specific markers directly from digitized hematoxylin and eosin (H&E) whole-slide images (WSIs) to enable rapid, tissue-preserving subtyping and early stratification.

Methods: Forty NSCLC cases (20 adenocarcinoma, 20 squamous cell carcinoma) were analyzed. H&E and corresponding IHC slides were digitized as WSIs and spatially registered. Napsin-A and TTF-1 highlighted adenocarcinoma, while p40 and CK5/6 highlighted squamous cell carcinoma. All markers were applied across cases to ensure subtype discrimination. Supervised

machine learning models generated cell-level biomarker predictions from H&E alone. Concordance with IHC and preservation of lineage-specific expression were evaluated.

Results: Virtual staining recapitulated subtype-specific patterns, with adenocarcinoma showing Napsin-A and TTF-1 localization and squamous cell carcinoma showing p40 and CK5/6 enrichment. Cross-lineage suppression supported subtype discrimination. Performance was assessed using ROC analysis and area under the curve (AUC). The platform enabled cell-level classification and spatial mapping of tumor identity from H&E, supporting early subtype assignment.

Conclusions: Virtual staining from WSIs enables rapid NSCLC subtyping from a single H&E slide, reducing reliance on IHC and preserving tissue for molecular assays. Early subtype determination supports patient stratification for testing (e.g., EGFR, ALK, KRAS), improving efficiency and reducing TAT. This approach supports scalable integration into digital pathology workflows.

54. Whole slide quality assurance via tile-level deep learning artifact detection in renal biopsies.

Odia Molen — *Arkana*

AI · QUALITY CONTROL · WORKFLOW

Background: We previously performed a manual survey of 826 WSIs from 413 renal biopsies and quantified seven artifact types across 1.1 million tiles, providing a reference cohort for model calibration. Artifacts were present in 1.7% of tiles, with tissue folds, dust, and air bubbles predominating.

Methods: A ConvNeXt classifier was trained on nine classes: eight artifact types (Air, Dust, Focus, Glitch, Marker, Nonrenal, Staining Agents, Tissue) and one Artifact-free class. ConvNeXt extends convolutional networks by combining CNN spatial extraction with transformer representational capacity. Class imbalance was mitigated by oversampling with augmentation. The model was calibrated against the 826-WSI cohort to match the empirical 1.7% artifact rate.SQS = 1 − Σ(wk × pk(t)) / Ntissue where k ∈ artifact classes, w_k = severity weight, $p_k(t)$ = tile probabilitySeverity weights (w_k) range from 0.30 (Marker, low clinical impact) to 0.90 (Focus, non-interpretable). Slides were stratified into four tiers: High Quality (>= 0.75), Acceptable (0.55-0.74), Flagged (0.35-0.54), and Reject/Re-scan (< 0.35). Tier cutoffs were derived empirically by mapping SQS against artifact burden across the cohort.

Results: Tile-level precision was 0.88 and recall 0.80 on a hold-out test set. SQS stratification identified 95.4% of slides as High Quality, 4.0% Acceptable, 0.5% Flagged, and 0.1% Reject/Re-scan (Figure 1). Trichrome slides showed higher artifact burden than PAS (2.19% vs 1.17%), driven by dust (0.88% vs 0.21%).

Conclusions: A deep learning model calibrated to an 826-WSI renal biopsy cohort achieves artifact detection matching the manual survey. The SQS, 1 minus artifact probability, provides an interpretable slide-level quality metric enabling automated pre-sign-out triage and exclusion of artifact-compromised slides from AI training pipelines. The identification of higher dust burden in Trichrome slides provides a potential target for future process improvement.