

8TH DIGITAL PATHOLOGY & AI CONGRESS ASIA 2024

10 - 11 September 2024

Lee Kong Chian School of Medicine NTU Singapore (Novena Campus)

The 8th Digital Pathology and AI Congress Asia brings together the pioneers at the point where digital pathology and artificial intelligence converge. This edition will be co-hosted with Bioinformatics Institute (BII), a cornerstone in bioinformatics under the umbrella of the Biomedical Research Council (BMRC) of A*STAR, has consistently championed computational biology and bioinformatics-driven research and innovation.

This edition will be co-hosted with Bioinformatics Institute (BII). Read the open letter, [Embarking on the Era of Digital Pathology and AI: Unveiling the Future of AI Digital Pathology](#), from BII here.

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Computational
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Informatics
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Mattias RANTALAINEN

Associate Professor
& Founder,
Karolinska Institutet
& Stratipath)

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KEYNOTE SPEAKERS

- **Alexander "Sasha" SICULAR**, Executive Lead, Healthcare and Life Sciences (Formerly Head of Digital Pathology), **Google Public Sector**, USA
- **Richard CHEN**, Doctor, **Harvard University**, USA ([NATURE MEDICINE](#))
- **CAO Gang**, Professor, The Brain Cognition and Brain Disease Institute of Shenzhen Institute of Advanced Technology, **Chinese Academy of Sciences**, China ([NATURE BIOMEDICAL ENGINEERING](#))
- **Hoifung POON**, General Manager, **Microsoft Health Futures**, USA ([NATURE](#))

INVITED SPEAKERS

- **LIU Yueping**, Professor & Director of Pathology Department, **The Fourth Hospital of Hebei Medical University**, China
- **ZHANG Jing**, Professor & Vice President of the First Affiliated Hospital (YuHang), **Zhejiang University**, China
- **WANG Hao**, Professor, **National Institutes for Food and Drug Control**, China ([IEEE STANDARD](#))
- **ZHANG Guanglei**, Associate Professor, **Beihang University**, China
- **Aileen WEE**, Emeritus Consultant Pathologist & Emeritus Professor, **National University Hospital & National University of Singapore**, Singapore
- **WANG Liansheng**, Assistant Professor, **Xiamen University**, China
- **David ZHANG**, Professor of Pathology & Oncological Sciences, **State University of New York Downstate Medical Center**, USA
- **Giovanni LUJAN**, Director of Digital and Computational Pathology, **Ohio State University**, USA
- **Gareth TURNER**, Consultant Histopathologist & Honorary Senior Clinical Lecturer, **Oxford University Hospitals NHS Foundation Trust**, UK
- **TAN Char Loo**, Senior Consultant, **National University Health System**, Singapore
- **CHEN Hao**, Assistant Professor, **The Hong Kong University of Science and Technology**, Hong Kong
- **WANG Xiangxue**, Professor, **Nanjing University of Information Science & Technology**, China
- **KHOR Li Yan**, Senior Consultant, **Singapore General Hospital**, Singapore
- **Arvind RAO**, Associate Professor of Computational Medicine and Bioinformatics, **University of Michigan, Ann Arbor**, USA
- **Lewis HASSELL**, Professor of Excellence in Anatomic Pathology, Director of Anatomic Pathology, **The University of Oklahoma**, USA
- **Mohammad Faizal AHMAD FAUZI**, Professor, **Multimedia University**, Malaysia
- **Marwan CHAMI**, Subject Matter Expert Digital Pathology, **Merck Healthcare KGaA, Darmstadt**, Germany
- **Supriya SRIVASTAVA**, Senior Research Fellow, **National University of Singapore**, Singapore
- **Peter SCHUEFFLER**, Professor, **Technical University of Munich**, Germany
- **Lee A.D. COOPER**, Associate Professor of Pathology, Director, Division of Computational Pathology, Director, Center for Computational Imaging and Signal Analytics, **Northwestern University Feinberg School of Medicine**, USA
- **Evan KELLER**, Richard and Susan Rogel Professor of Oncology & Director of the Single Cell Spatial Analysis Program, **University of Michigan**, USA
- **XU Chuan**, Professor, **Jinfeng Laboratory**, China
- **Desiree ABDURRACHIM**, Principal Scientist, **MSD**, Singapore
- **Naoko TSUYAMA**, Project Scientist & Pathologist, **Japanese Foundation for Cancer Research**, Japan
- **Ahmed FADIEL**, Computational Oncology Unit Director & Professor, **University of Chicago**, USA
- **LI Zaibo**, Professor of Pathology and Endowed University Pathology Service Professorship, Director of Cytopathology and Cytopathology Fellowship, Associate Director of Digital and Computational Pathology, **The Ohio State University**, USA
- **Bing REN**, Assistant Professor, **Dartmouth Hitchcock Medical Center and Geisel School of Medicine**, USA
- **Xinmi HUO**, Senior Research Officer, **Agency of Science, Technology and Research**, Singapore



08:50	Global Engage Welcome Remarks & Chairpersons' Opening Remarks	
09:00	<p>KEYNOTE ADDRESS Alexander "Sasha" SICULAR, Executive Lead, Healthcare and Life Sciences (Formerly Head of Digital Pathology), Google Public Sector, USA</p> <p>EXPLORING THE ECONOMICS OF DIGITAL PATHOLOGY FOR THE BROADER INDUSTRY AND YOUR OWN IMPLEMENTATION</p> <p>Continued technical advancements in Digital Pathology have not gone unnoticed by decision makers around the world. Yet, has the industry advanced enough to make now the right time for an implementation within your own organization? Each organization will need to reach a decision on the clinical, research and operational merits that digitization can bring to their practice. Assuming you are ready to move forward, how do you start calculating the costs - and benefits? This talk will explore various technical input costs to weigh against the benefits when making these decisions. While every organization will have its own needs, this conversation will offer an economic framework to consider as you explore your options.</p>	
09:30	<p>KEYNOTE ADDRESS CAO Gang, Principal Investigator, The Brain Cognition and Brain Disease Institute of Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences, China</p> <p>SINGLE-CELL SPATIAL MULTI-OMICS AND NEXT GENERATION PATHOLOGY</p> <p>Multicellular organisms elegantly orchestrate the co-transcription of the right genes in a precise spatial-temporal manner. Delineation of the comprehensive spatial-omics will pave the way to understand the molecular function of specific cells in sophisticated organs and is also crucial for next generation pathology. Recently, we developed a high throughput Multi-omics in situ Pair-wise Sequencing (MiP-Seq) strategy to efficiently decipher multiplexed DNA, RNA and Protein in intact tissue at subcellular resolution. This method can differentiate SNP and RNA m6A modification, and was applied to detect tumour gene mutation and allele specific expression of parental genes. MiP-Seq can be combined with in vivo Ca2+ imaging to obtain spatial multi-omics atlas correlated to the neuronal activity. This method contributes to spatial multi-omics and precise diagnosis.</p>	
10:00	<p>Epredia Speaking Session</p> <p>Topic: TBC Abstract: TBC</p> <div style="text-align: right;">  <small>A Member of PHC Group</small> </div>	
10:30	Morning Refreshments/ Poster Presentation/ One-to-One Meetings	
	<p style="text-align: center;">Implementation, Strategy & Technology & Application</p>	<p style="text-align: center;">Computational Pathology & AI</p>
11:30	<p>WANG Hao, Professor, National Institutes for Food and Drug Control, China</p> <p>TREND OF INTERNATIONAL STANDARDIZATION OF AI-ENABLED MEDICAL DEVICE FOR PATHOLOGICAL APPLICATION</p>	<p>Peter SCHUEFFLER, Prof. Computational Pathology, Technical University of Munich, Germany</p> <p>COMPUTER AIDED PATHOLOGY: ON THE CHALLENGES AND CHANCES OF IN A ROUTINE LAB</p>

In this presentation, the progress of current international standardization of AI-enabled medical device is discussed. The topics include general testing and evaluation, specific testing methods. data quality control and terminology. The impact of such standards on AI pathological applications is further analysed, which may help develop specific standards for AI-enabled pathological image processing software.

Transition to a digital workflow in a routine diagnostic lab is challenging due to high costs and extensive change management for both the lab personnel and the medical doctors. However, the transition opens new opportunities and efficiency gains for pathologists: From modern and family-friendly work environments to new AI-assisted diagnostic tools. We present the lessons learned after going fully digital in our pathology lab together with early results of multimodal AI for Glioma subtyping built with the help of digital pathology.

11:55

Lee A.D. COOPER, Associate Professor of Pathology Director, Division of Computational Pathology; Director, Center for Computational Imaging and Signal Analytics, Northwestern University Feinberg School of Medicine, USA

TRANSPARENT PROGNOSTIC MODELING OF INVASIVE BREAST CANCER OUTCOMES

Breast cancer is a heterogeneous disease with variable survival outcomes. Pathologists grade the microscopic appearance of breast tissue using the Nottingham criteria, which are qualitative and do not account for noncancerous elements within the tumor microenvironment. This talk will present the Histomic Prognostic Signature (HiPS), a comprehensive, interpretable scoring of the survival risk incurred by breast tumor microenvironment morphology. HiPS uses deep learning to accurately map cellular and tissue structures to measure epithelial, stromal, immune, and spatial interaction features. It was developed using a population-level cohort from the Cancer Prevention Study-II and validated using data from three independent cohorts, including the Prostate, Lung, Colorectal, and Ovarian Cancer trial, Cancer Prevention Study-3, and The Cancer Genome Atlas. HiPS consistently outperformed pathologists in predicting survival outcomes, independent of tumor-node-metastasis stage and pertinent variables. This was largely driven by stromal and immune features. In conclusion, HiPS is a robustly validated biomarker to support pathologists and improve patient prognosis.

Gareth David Huw TURNER, Consultant and Honorary Senior Lecturer in Haematopathology, Oxford University Hospitals NHS Trust, UK

APPLYING AI TO THE DIAGNOSIS OF MYELOPROLIFERATIVE DISEASES IN HAEMATOPATHOLOGY

Using machine learning on digital pathology images from bone marrow trephines of patients with Myeloproliferative diseases (MPNs), quantitative description of megakaryocyte morphology and reticulin fibrosis identify distinct megakaryocyte phenotypes with clinical utility in distinguishing MPN from reactive samples and associating with underlying driver mutations (1). Automated analysis and continuous indexing of fibrosis (CIF) captures heterogeneity within MPN marrows allowing refined classification and disease monitoring. Combining topological data may help predict patients at increased risk of progression e.g. to assist in the discrimination of ET and pre-fibrotic PMF (pre-PMF) (2). The potential of combining digital imaging for diagnostics and machine learning approaches has applications across histopathology teaching/training, diagnosis/classification, drug trials and basic research, combining single cell transcriptomics for investigation of haematopoietic stem cell biology and its consequences for MPN patients.

12:20

ZHANG Jing, MD, PhD, President & Vice President of the First Affiliated Hospital (YuHang) of Zhejiang University School of Medicine, China

PARTNERING WITH AI: HOW PATHOLOGISTS CAN THRIVE IN THE DIGITAL AGE

The emergence of digital pathology and artificial intelligence (AI) has introduced uncertainty in the field of pathology. This talk will discuss major advances in digital pathology and AI, and explore their potential impact on the roles of pathologists. While AI excels at automating routine tasks and aiding in analysis, the expertise of pathologists remains crucial. We will examine how AI can augment a pathologist's workflow, improving efficiency and diagnostic accuracy. The discussion will address concerns about job displacement and explore the evolving skillset pathologists will need to thrive in the digital age. This talk aims to provide a balanced perspective on the future of pathology, emphasizing collaboration between humans and AI to deliver exceptional patient care.

LIU Yueping, Professor & Director of Pathology Department, The Fourth Hospital of Hebei Medical University, China

AI-ASSISTED ASSESSMENT AFTER NEOADJUVANT THERAPY FOR BREAST CANCER

Neoadjuvant therapy has become a standard clinical practice for shrinking tumor size, lowering tumor stage, increasing surgical opportunities, and improving breast conservation rates. Postoperative pathological evaluation of residual tumors and lymph node metastasis is closely associated with the prognosis and long-term survival of patients. This paper focuses on the current challenges and complexities associated with evaluating breast cancer after neoadjuvant therapy. We conducted a comparative analysis of the merits and drawbacks associated with conventional assessment methods and AI-assisted assessment, providing comprehensive insights from five key perspectives:

1. AI-assisted assessment of the tumor bed following neoadjuvant therapy for breast cancer.
2. AI-assisted in identifying cases of lymph node metastasis after neoadjuvant treatment for breast cancer.
3. AI-assisted assessment of alterations in tumor infiltrating lymphocytes and immune-related biomarkers following neoadjuvant therapy for breast cancer.
4. AI-assisted prediction of treatment response and prognosis after neoadjuvant therapy for breast cancer.
5. Future prospects for further development.

12:50

Lunch/ Poster Presentation/ One- to- One Meetings

13:50

PANEL DISCUSSION

MAXIMIZING ROI AND WORKFLOW EFFICIENCY THROUGH AI: STRATEGIES FOR EFFECTIVE DIGITAL PATHOLOGY IMPLEMENTATION

This panel will delve into how integrating artificial intelligence (AI) into digital pathology can improve diagnostic accuracy and streamline workflow processes. Experts will share practical strategies for implementing AI tools, maximizing return on investment (ROI), and optimizing workflow efficiency. Gain valuable insights into the transformative power of AI in pathology, and learn how to leverage these technologies to improve patient care and enhance operational outcomes.

CHEN Hao, Assistant Professor, The Hong Kong University of Science and Technology, Hong Kong

TOWARDS MULTIMODAL DATA INTEGRATION FOR ADVANCING PRECISION ONCOLOGY

Artificial intelligence (AI), especially deep learning with large-scale training datasets, has dramatically advanced the recognition performance in many domains including speech recognition, visual computing and natural language processing.

Discussion Points include:

- How can AI integration enhance diagnostic accuracy in digital pathology, and what are the key considerations for successful implementation?
- What strategies can healthcare organizations adopt to maximize ROI when implementing AI tools in digital pathology?
- How does AI impact workflow efficiency in digital pathology labs, and what are the best practices for optimizing workflow processes?
- What are the current challenges and limitations of AI in digital pathology, and how can these be addressed to improve adoption and effectiveness?
- How can healthcare professionals ensure that AI technologies in digital pathology comply with regulatory requirements and ethical standards?

Panelists:

- Lewis HASSELL, Professor of Excellence in Anatomic Pathology, Director of Anatomic Pathology, The University of Oklahoma, USA
- LI Zaibo, MD PhD MBA, Professor of Pathology and Endowed University Pathology Service Professorship, Director of Cytopathology and Cytopathology Fellowship, Associate Director of Digital and Computational Pathology, The Ohio State University, USA
- Ahmed FADIEL, Computational Oncology Unit Director & Professor, University of Chicago, USA
- Bing REN, MD PhD, Assistant Professor, Dartmouth Hitchcock Medical Center and Geisel School of Medicine at Dartmouth, USA

Despite its breakthroughs in above domains, its application to precision oncology remains yet to be explored, where large-scale fully and high-quality annotated datasets are not easily accessible. In this talk, I will share our recent progress on computational pathology with multimodal data integration for precision oncology through the lens of information theory, including cross-modal consistency, multimodal alignment and knowledge decomposition, with versatile applications to disease diagnosis, treatment response prediction, prognosis, etc. Challenges and future directions will also be discussed.

David Y. ZHANG, Adjunct Professor, State University of New York Downstate Medical Center, USA

ARTIFICIAL INTELLIGENCE IN PROSTATE CANCER PATHOLOGY: HYPE OR TODAY'S REALITY

With the wide availability of digital pathology, artificial intelligence (AI) for pathology applications has drawn significant attention and promises great potential in pathology practice. We have developed a robust and flexible image management system (IMS) that allows integrating digital images into pathology practice.

Furthermore, we developed an AI platform to enhance the ability of pathologists to review and diagnosis prostate cancer in biopsy sections. Our study demonstrated that AI can improve accuracy of identifying malignant glands, especially small glands. The objectives are:

1. Review the current development of AI applications in prostate pathology.
2. Present our IMS and AI in prostate biopsy applications.

14:15

14:40

Medmain Speaking Session

Solution Provider Presentation

*For sponsorship opportunities please contact Reuben Raj:
reuben@global-engage.com /+603 2779 0098 ext 1005*

14:55

Early Career Researcher Presentation
TAN Char Loo, Senior Consultant, National University Health System, Singapore

INTEGRATING DIGITAL PATHOLOGY INTO DAILY OPERATIONS: REALITIES AND CHALLENGES

Digital pathology represents a transformative leap forward in the field of diagnostic medicine, revolutionizing the way pathologists examine tissue samples and make critical clinical assessments. By harnessing cutting-edge imaging technology and advanced computational analysis, digital pathology enables the digitization of traditional glass slides, allowing for high-resolution viewing and analysis of tissue samples on computer screens. This innovative approach not only enhances the efficiency and accuracy of pathological evaluations but also facilitates remote collaboration, education, and research in ways previously unattainable with conventional microscopy. As healthcare systems worldwide embrace digitalization, digital pathology emerges as a cornerstone of modern pathology practice, promising to redefine standards of care, accelerate diagnostic workflows, and unlock new frontiers in precision medicine. Hereby, I will be sharing our experiences and the challenges we faced in integrating digital pathology into the department's daily operation.

Early Career Researcher Presentation
Supriya SRIVASTAVA, Senior Research Fellow, National University of Singapore, Singapore

SPATIALLY RESOLVED NICHE AND TUMOR MICROENVIRONMENTAL ALTERATIONS IN GASTRIC CANCER PERITONEAL METASTASES

Peritoneal metastases (PM) in gastric cancer (GC) portend a poor prognosis, yet our understanding of tumor microenvironmental (TME) characteristics associated with GCPM remain limited. In this study, we sought to understand TME features that determine and facilitate peritoneal organotropism from primary GCs. We conducted digital spatial profiling (DSP) on independent tumor and stroma compartments (DSP, GeoMx platform, Nanostring Technologies, Inc) of 55 GC patients with PM. Slides were stained for PanCK (epithelial cells), CD45 (immune cells) and SMA (stroma), and regions of interest (ROIs) were selected based on these markers. A total of 712 ROIs were retrieved after quality control evaluation. Unsupervised clustering of the ROIs revealed a clear distinction between adjacent normal and tumor, and between the tumor and stroma compartments. UMAP analysis demonstrated close clustering and overlap between the PT and PM for tumor ROIs, suggesting transcriptomic similarity.

15:10

Afternoon Break/ Poster Presentation/ One- to- One Meetings

16:10

Desiree ABDURRACHIM, Principal Scientist, MSD, Singapore

MULTI-MODAL AI DIGITAL PATHOLOGY TO ACCELERATE MASH DRUG DISCOVERY

Spatial biology is critical in the study of the liver because of the metabolic zonation in the liver lobules. We leverage AI digital pathology to investigate changes in the liver microenvironment during the progression of Metabolic Associated Steatohepatitis (MASH).

Ahmed FADIEL, Director and Co-Founder of the University of Chicago Medicine, Computational Oncology Unit, University of Chicago, USA

A BIOINFORMATICS APPROACH TO DIGITAL PATHOLOGY

Digital pathology revolutionizes diagnostics with high-resolution whole slide imaging (WSI) but necessitates robust data management solutions. Bioinformatics platforms leverage cloud storage and distributed computing for efficient WSI storage, retrieval, and analysis.

In this talk, I will provide an overview of our multi-modal AI digital pathology toolboxes, which include Second Harmonic Generation (SHG), traditional H&E/Masson's Trichrome/PSR, dual IHC, multiplexed-IF, and integrated spatial omics imaging. I will also highlight how we utilize the technology to understand human disease biology, and through reverse translation, how we guide animal model selection, proof-of-biology, and proof-of-concept, to accelerate our MASH drug discovery pipeline. Beyond discovery efforts, I will also touch upon the industry's effort in leveraging AI digital pathology to aid pathologists in MASH scoring and its potential to improve the efficiency of MASH our clinical trials.

Machine learning algorithms, specifically deep convolutional neural networks (CNNs), automate image analysis tasks like tumor classification and segmentation, achieving superior accuracy and consistency compared to manual analysis. Standardization protocols like DICOM and OME ensure seamless data exchange across disparate platforms, fostering collaboration. Rigorous validation techniques employed by bioinformatics, including statistical analysis and concordance studies, guarantee the reliability and clinical adoption of these algorithms. Secure data encryption and access control mechanisms safeguard patient privacy and HIPAA compliance. By integrating bioinformatics with digital pathology, we unlock its potential to transform patient care, enabling the development of personalized treatment plans and advancing precision medicine initiatives.

16:25

**Mohammad Faizal AHMAD FAUZI, Professor,
Multimedia University, Malaysia**

REAL-TIME ANALYSIS OF HORMONE RECEPTORS FOR BREAST CANCER TREATMENT RECOMMENDATION

The talk will present a real-time system for the analysis of breast cancer hormone receptors from glass slides, useful in recommending effective treatments for breast cancer patients. The approach is based on automatic detection, segmentation and classification of individual cells in estrogen receptor (ER) immunohistochemistry (IHC) image streams, before Allred scoring is carried out as per standard clinical practice. For real-time implementation, an industrial machine vision camera is mounted to the microscope, streaming the image from the microscope glass slide for digital analysis. The proposed system and setup provide a great platform to incorporate artificial intelligence on conventional glass-based diagnosis and prognosis. This will be especially useful in countries lacking DP facilities and policy.

**Bing REN, MD PhD, Assistant Professor,
Dartmouth Hitchcock Medical Center and Geisel
School of Medicine at Dartmouth, USA**

MACHINE LEARNING IN GASTROINTESTINAL AND LIVER PATHOLOGY

Machine learning (ML) significantly impacts gastrointestinal (GI) pathology. In our institution, ML is applied to both luminal GI and liver pathology. Several deep learning systems have been developed to diagnose celiac disease with an accuracy of 95%, classify four most common colorectal polyps (tubular adenoma, villous adenoma, hyperplastic polyp, and sessile serrated adenoma) with an accuracy of 87%, and differentiate esophageal tissue as either normal, nondysplastic Barrett's, dysplastic Barrett's, or adenocarcinoma with an accuracy of 85%. We also apply ML and co-expression analyses to help identify biomarkers from Digital Spatial Profiler-assayed protein expression patterns inside and away from the tumor, which allows the identification of spatial proteomic signatures of colon tumor metastasis. In addition, we conducted a large-scale validation study of the viability of generative adversarial networks (GANs) for H&E to trichrome conversion, which demonstrates that virtual trichrome technologies may offer a software solution for the diagnosis of liver fibrosis.

<p>16:50</p>	<p>Giovanni M LUJAN, MD, Associate Professor, Director of Digital and Computational Pathology, The Ohio State University, USA</p> <p>EMBRACING THE DIGITAL FRONTIER: THE OHIO STATE UNIVERSITY'S TRANSFORMATION INTO A FULLY DIGITAL ACADEMIC HUB</p> <p>The Ohio State University (OSU, Department of Pathology in the United States stands at the forefront of academic innovation as the first large-scale academic institution in the USA to transition entirely into a Digital Workflow. This pioneering journey reflects a commitment to embracing technology to enhance patient care, educational delivery, research capabilities, and also administrative efficiency. The digital transformation at OSU is redefining the health care and educational landscape, offering seamless access to cutting edge tools to assist in our role as diagnosticians as well as collaborative research and learning platforms. This presentation outlines the key strategies, challenges, and triumphs of OSU's digital journey, highlighting our current status and a look into the foreseeable future.</p>	<p>Marwan CHAMI, Subject Matter Expert Digital Pathology, Merck Healthcare KGaA, Darmstadt, Germany</p> <p>A DEEP LEARNING IMAGE ANALYSIS WORKFLOW FOR ANTIBODY DRUG CONJUGATE (ADC) TARGETS</p> <p>Tumor cell (TC) membrane markers are frequently used as predictive biomarkers in selection of cancer patients for drugs directed at membrane bound targets, like antibody-drug conjugates (ADCs). However, scoring of TC membrane biomarkers can be challenging, leading to inconsistency, and limiting the value as predictive biomarker. Hence, the need for a more robust, reliable, and quantitative membrane detection approach. Here, we report on our deep learning approaches with the goal to provide advanced quantification of TC membrane-based immunohistochemistry (IHC) biomarkers.</p>
<p>17:15</p>	<p>Evan KELLER, Richard and Susan Rogel Professor of Oncology & Director of the Single Cell Spatial Analysis Program, University of Michigan, USA</p> <p>SINGLE CELL AND SPATIAL ANALYSIS OF UROLOGIC CANCERS</p> <p>The recent explosion of high plex methods to evaluate biomolecules at the single cell level in situ has opened the door to identifying novel interactions between tumor cells and their microenvironment, spatial relationships between cell types and signaling processes, and potential biomarkers for prognosis and predictiveness. Using these methods, we have (1) identified spatiotemporal changes in tissue structure, cell composition and signaling associated with androgen deprivation in a murine model; (2) determined putative biomarkers in prostate cancer biopsies that may improve accuracy of tumor grading; and (3) delineated a mechanism through which renal clear cell carcinoma progresses to a renal sarcomatoid cancer subtype. These studies demonstrate how single cell and spatial analytic methods can inform both mechanistic and translational studies.</p>	
<p>17:40</p>	<p>End of Day 1/Networking Drinks Reception</p>	

08:50	Global Engage Welcome Remarks & Chairpersons' Opening Remarks	
09:00	<p>KEYNOTE ADDRESS Richard CHEN, Doctor, Harvard University, USA</p> <p>A GENERAL-PURPOSE SELF-SUPERVISED MODEL FOR COMPUTATIONAL PATHOLOGY Quantitative evaluation of tissue images is crucial for computational pathology (CPath) tasks, requiring the objective characterization of histopathological entities from whole-slide images (WSIs). The high resolution of WSIs and the variability of morphological features present significant challenges, complicating the large-scale annotation of data for high-performance applications. To address this challenge, current efforts have proposed the use of pretrained image encoders through transfer learning from natural image datasets or self-supervised learning on publicly available histopathology datasets, but have not been extensively developed and evaluated across diverse tissue types at scale. We introduce UNI, a general-purpose self-supervised model for pathology, pretrained using more than 100 million images from over 100,000 diagnostic H&E-stained WSIs (>77 TB of data) across 20 major tissue types. The model was evaluated on 34 representative CPath tasks of varying diagnostic difficulty. In addition to outperforming previous state-of-the-art models, we demonstrate new modeling capabilities in CPath such as resolution-agnostic tissue classification, slide classification using few-shot class prototypes, and disease subtyping generalization in classifying up to 108 cancer types in the OncoTree classification system. UNI advances unsupervised representation learning at scale in CPath in terms of both pretraining data and downstream evaluation, enabling data-efficient artificial intelligence models that can generalize and transfer to a wide range of diagnostically challenging tasks and clinical workflows in anatomic pathology.</p>	
09:30	<p>KEYNOTE ADDRESS Hoifung POON, General Manager, Microsoft Health Futures, USA</p> <p>MULTIMODAL GENERATIVE AI FOR PRECISION HEALTH The dream of precision health is to develop a data-driven, continuous learning system where new health information is instantly incorporated to optimize care delivery and accelerate biomedical discovery. The confluence of technological advances and social policies has led to rapid digitization of multimodal, longitudinal patient journeys, such as electronic medical records (EMRs), imaging, and multiomics. In this talk, I'll present our research progress on multimodal generative AI for precision health, where we leverage real-world data to pretrain powerful multimodal patient embedding, which can serve as digital twins for patients. This enables us to assimilate multimodal, longitudinal information for millions of cancer patients, and apply the population-scale real-world evidence to advancing precision oncology in deep partnerships with real-world stakeholders.</p>	
10:00	<p>Leica Speaking Session</p> <p>Topic: TBC Abstract: TBC</p>	
10:30	Morning Refreshments/ Poster Presentation/ One-to-One Meetings /Group Photo Session	
	Implementation, Strategy & Technology & Application	AI for Imaging and Digital Image Analysis

11:30

Arvind RAO, Associate Professor of Computational Medicine and Bioinformatics, University of Michigan Ann Arbor, USA

MACHINE LEARNING APPROACHES TO THE INTERPRETATION OF THE TUMOR MICROENVIRONMENT USING SPATIAL IMMUNO-PROFILING & SPATIAL TRANSCRIPTOMICS, FOR PERSONALIZED MEDICINE

Spatial profiling technologies like hyper-plex immunostaining in tissue, spatial transcriptomics etc have the potential to enable a multi-factorial, multi-modal characterization of the tissue microenvironment. Scalable, quantitative methods to analyze and interpret spatial patterns of protein staining and gene expression are required to understand cell-cell relationships in the context of local variations in tissue structure. Objective scoring methods inspired by recent advances in statistics and machine learning can serve to aid the interpretation of these datasets, as well as their integration with other, companion data like genomics. In this talk, we will discuss elements of spatial profiling from multiple studies as well as paradigms from statistics and machine learning in the context of these problems. This talk will also discuss the use of AI/ML and spatial analytics of the tumor microenvironment to derive spatial biomarkers of immunotherapy.

11:55

WANG Xiangxue, Professor, Nanjing University of Information Science and Technology, China

IMAGE BASED BIOMARKER FOR CANCER PROGNOSIS AND TREATMENT RESPONSE PREDICTION

The spatial arrangement of cells within tissues and tumors can provide valuable information for predicting cancer prognosis and treatment response. The diagnosis and prognosis prediction of cancer typically rely on pathological analysis and biochemical examinations of the diseased tissue. However, these methods overlook the heterogeneity of cancer cells within tumors and the complex interactions between different cell types. Spatial arrangement and structural analysis, such as spatial transcriptomics and imaging techniques, offer new tools for

ROUNDTABLE DISCUSSION TOPICS

Table 1

DATA QUALITY AND AVAILABILITY IN DIGITAL PATHOLOGY: STRATEGIES FOR ENSURING ACCURACY AND ACCESSIBILITY

Discuss the strategies for ensuring the accuracy and accessibility of data in digital pathology, including quality control measures, data management practices, and collaborative initiatives to improve data sharing and availability.

Moderator: Lee A.D. COOPER, Associate Professor of Pathology, Director, Division of Computational Pathology, Director, Center for Computational Imaging and Signal Analytics, Northwestern University Feinberg School of Medicine, USA

Table 2

EXPLORING THE POTENTIAL OF LLM AND GENERATIVE AI IN PATHOLOGY

Discuss the potential of large language models (LLMs) and regenerative artificial intelligence (AI) in pathology, including their applications in image analysis, diagnosis support, and data interpretation. Explore how these technologies can enhance pathology practice by improving accuracy, efficiency, and decision-making processes.

Moderator: Bing REN, MD PhD, Assistant Professor, Dartmouth Hitchcock Medical Center and Geisel School of Medicine at Dartmouth, USA

Table 3

CANCER CARE: THE ROLE OF DIGITAL PATHOLOGY, AI, AND WSI IN ADVANCING RESEARCH, TREATMENT, AND DIAGNOSTIC PRECISION

Examine how digital pathology, artificial intelligence (AI), and whole slide imaging (WSI) are revolutionizing cancer care. Discuss their impact on research, treatment, and diagnostic precision, highlighting advances in image analysis, molecular profiling, and personalized medicine.

Moderator: Lewis HASSELL, Professor of Excellence in Anatomic Pathology, Director of Anatomic Pathology, The University of Oklahoma, USA

researchers to analyze the spatial locations of cells within tissues or tumors, thereby deepening our understanding of the tumor microenvironment and the interactions between cancer cells and neighboring cells. With advancements in computational algorithms and artificial intelligence, mining the spatial relationships of cells within tumors from biomedical data and establishing their associations with cancer patient prognosis can offer new approaches and means for precise treatment of cancer patients. The speaker has been engaged in the analysis of pathological images and the fusion of multimodal medical information, and has made preliminary explorations in the prognosis and treatment prediction of malignant tumors such as lung cancer.

Table 4

NAVIGATING DIGITAL PATHOLOGY REGULATIONS AND COMPLIANCE FOR QUALITY ASSURANCE

Discuss the regulatory landscape of digital pathology, including key regulations and standards that govern its implementation. Explore strategies for ensuring compliance, including quality assurance measures, documentation requirements, and staff training.

12:20

EARLY CAREER RESEARCHER

Xinmi HUO, Senior Research Officer, Computational Digital Pathology Lab (CDPL), Bioinformatics Institute (BII), Agency of Science, Technology and Research, Singapore

A COMPREHENSIVE AI MODEL DEVELOPMENT FRAMEWORK FOR DIGITAL PATHOLOGY: USING GLEASON GRADING IN PROSTATE CANCER AS AN EXAMPLE

This presentation introduces a generalized framework designed for the development of AI-based digital pathology solutions, with prostate cancer (PCa) Gleason grading serving as a specific application showcase. The framework addresses prevalent challenges such as inconsistent image quality, ongoing data integration, and scanner variability. It integrates A!MagQC for image quality control, A!HistoClouds for cloud-based annotations, and employs a Pathologist-AI Interaction (PAI) for continual model enhancement. Initially trained on Akoya-scanned images using advanced generalization techniques, this model demonstrates strong generalization across various scanners. Comprehensive testing on whole slide images from five different scanners showed significant improvements: the detection of Gleason patterns achieved an increase in F1 scores from 0.73 to 0.88, and the model reduced Gleason scoring time by 43%. The adaptability of this framework not only enhances diagnostic accuracy and efficiency in prostate cancer grading but is also applicable to other areas of pathology.

EARLY CAREER RESEARCHER

LAU Mai Chan, Assistant PI; Head of Computational Immunology Platform; Adjunct Assistant Professor, Bioinformatics Institute (BII), A*STAR; Singapore Immunology Network (SigN), A*STAR; Lee Kong Chian School of Medicine, NTU, Singapore

GENERATIVE AI FOR ROBUST SPATIAL BIOMARKER DEVELOPMENT

Our research addresses key challenges such as the lack of effective biomarkers and the limited understanding of the tumor microenvironment. In this talk, I will discuss how advanced spatial omics techniques have enhanced our understanding of this complex environment. Our preliminary analysis demonstrates the potential of multi-omics biomarkers compared to conventional approaches. I will also share our recently published work on using virtual staining to make spatial omics data more accessible from clinically available histology H&E slides. Finally, I will showcase our web-based visualization tool, which enhances both our virtual staining methods and multi-omics analysis of the tumor microenvironment.

12:35

Poster Competition Winner Presentation

Poster competition abstract submission deadline is 19th August 2024.

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12:50	Lunch/ Poster Presentation/ One- to- One Meetings	
13:50	<p>KHOR Li Yan, Senior Consultant, Singapore General Hospital, Singapore</p> <p>JOINING THE AI FRAY – CHALLENGES AND REWARDS FROM A HISTOPATHOLOGIST’S PERSPECTIVE</p> <p>Having collaborated with AI scientists from government agencies, research institutes and commercial vendors to develop and validating AI algorithms for histopathology, this talk will discuss the:</p> <ul style="list-style-type: none"> • outline the unexpected challenges and rewards • provide insights from my varied experience <p>For pathologists who are interested in getting their feet wet in algorithm development, this talk will include lessons learnt on providing high quality DP image data for algorithm development, the process of transferring mutual domain knowledge (between pathologist and AI scientist) relevant to the project, encountering limitations on DP image formats and SDKs, providing high quality annotations in an internet-separated environment, time-boxing of project goals for efficient results and considerations for the re-training of an algorithm with new data.</p>	<p>WANG Liansheng , Professor, Xiamen University, China</p> <p>PATHOLOGICAL IMAGE ANALYSIS: FROM MICROSCOPIC TO ULTRA-MICROSCOPIC</p> <p>This presentation explores the frontier of pathological image analysis. We delve into the advancements in deep learning that have revolutionized the analysis of pathological images, enabling not only the identification of diseases at earlier stages but also the prediction of disease progression and response to treatment. Our approach harnesses the power of computational analysis to interpret complex patterns within pathology images and multiplex data sets. We highlight several applications where these techniques have been successfully applied, including tumor classification, grading, and the mapping of genetic aberrations. Furthermore, the presentation will address the challenges of integrating pathology data with other multiplex data sources, such as genomic and proteomic data, to achieve a comprehensive understanding of disease mechanisms. Through case studies and recent research findings, we aim to demonstrate how the synergy between deep learning and ultra-microscopic image analysis is paving the way for a new era in precision medicine and diagnostic pathology.</p>
14:05	<p>XU Chuan, Professor, Jinfeng Laboratory, China</p> <p>THE PRACTICAL IMPLEMENTATION OF ARTIFICIAL INTELLIGENCE ASSISTED DIGITAL PATHOLOGY IN CLINICAL AND TRANSLATIONAL RESEARCHES</p> <p>The detection of progression and recurrence at early stage from molecular pathology perspective is essential for companion diagnostics in anticancer therapy. Artificial intelligence (AI) assisted digital pathology with ultrasensitive detecting capacities which can identify biomarkers presented in low abundance may serve as potential instruments.</p>	<p>ZHANG Guanglei, Associate Professor, Beihang University, China</p> <p>EXPLICITLY BRIDGE PATHOLOGICAL AND NATURAL IMAGE WITH PUZZLES</p> <p>Pathological image analysis is a crucial field in computer vision. Due to the annotation scarcity in the pathological field, most of recent works have leveraged self-supervised learning (SSL) trained on unlabeled pathological images, hoping to mine the representation effectively. However, there are two core defects in current SSL-based pathological pre-training: (1) they do not explicitly explore the essential focuses of the pathological field, and (2) they do not effectively bridge with and thus take advantage of the knowledge from natural images.</p>

Herein, we demonstrated the application of AI-driven assay in discovering novel targets and pathological features of cancer patients related to clinical outcomes and their underlying mechanisms in immune escape and treatment tolerance with examples from recent finding from our lab.

To explicitly address them, we propose our PuzzleTuning framework. Firstly, we identify three task focuses that can effectively bridge knowledge of pathological and natural domain. Secondly, we devise a novel multiple puzzle restoring task, explicitly pre-training the model. Thirdly, we introduce an explicit prompt-tuning process to incrementally integrate the domain-specific knowledge, aligning the domain gap between natural and pathological images. Experimental results verified our PuzzleTuning framework.

14:30

Aileen WEE, Emeritus Consultant Pathologist & Emeritus Professor, National University Hospital & National University of Singapore, Singapore

YOUR PATH WITH AI: CAN AI-ASSISTIVE TOOLS LEAD THE WAY FORWARD IN HISTOLOGICAL ASSESSMENT OF LIVER FIBROSIS IN MASH?

Artificial intelligence (AI) and digitised whole-slide images (WSI) have enabled the use of AI-assistive tools in Pathology to improve histopathological interpretation. Evaluation of liver fibrosis in metabolic dysfunction-associated steatohepatitis (MASH) is important in both clinical practice and interventional trials. AI-assistive tools such as qFibrosis have been shown to improve pathologist agreement for fibrosis scores in MASH patients. There is also potential for digital pathology with AI (DP/AI) analyses in overcoming current limitations of conventional static ordinal scoring systems, such as assessing treatment-induced changes like fibrosis regression. DP/AI tools which provide a quantitative, continuous evaluation of fibrosis have the capability to capture subtle changes in fibrosis that are more reflective of the dynamic nature of fibrosis. The potential and shortcomings of AI-assistive tools for liver fibrosis assessment in MASH are discussed.

Naoko TSUYAMA, Project Scientist & Pathologist, Division of Pathology, Cancer Institute, Japanese Foundation for Cancer Research, Japan

INTEGRATING GROSS SPECIMEN PHOTOS AND WSI FOR ENHANCED DIGITAL MAPPING OF HISTOLOGICAL REGIONS

Integrating pathology data is essential in addressing complex diagnostics, the increasing number of specimens, and the pathologist shortage. The advent of digital pathology platforms has heightened the focus on the integrated analysis of whole-slide images (WSIs) alongside data from varied modalities, such as gross photo images paired with WSIs. Pathologists initially perform a visual inspection of specimens to decide which areas require sectioning for histological examination. These sections are then processed into glass slides and converted into WSIs. Traditionally, pathologists assess these images separately. However, recognizing that both image sets are derived from identical specimen sections but exhibit different modalities is critical. Correlating macroscopic and microscopic images is vital for digitally mapping histological regions to their corresponding specimen surfaces. This presentation will explore our department's daily diagnostic routine for this procedure and highlight the benefits of this integrated approach for enhancing diagnostic accuracy and data management efficiency.

14:55

End of Day 2/ Conference Ends



POSTER PRESENTATION



This conference definitely provides an ideal platform to showcase your works with a captive audience. Whether looking for funding, job opportunities or simply wanting to share your work with a like-minded and focused group, poster presentations are an excellent way to join the heart of the congress.

Poster presentation abstract submission deadline is 19th August 2024.



POSTER COMPETITION



We are pleased to announce that we will be hosting a competition as part of this conference.

Poster Competition Requirements:

- **Submission of poster form**
- **Submission of poster in pdf form**
- **Submission deadline: 19th August 2024**

Two exceptional entries will be selected to receive the following rewards:

- **\$1000 Travel Grant**
- **15-Minute Speaking Position on the Conference Program**
- **Certificate of Participation**
- **Certificate of Achievement – Poster Competition**

Representatives from solution provider organisations or experts already speaking on the program are not eligible to enter the competition but are welcome to present posters at the meeting as normal.

**Download poster presentation/competition abstract form [HERE](#).
Contact: haley@global-engage.com for any inquiries**