Genome Institute of Singapore
GIS

Global Engage

2ND SPATIAL BIOLOGY CONGRESS: ASIA

21-22 NOVEMBER 2024

LEE KONG CHIAN SCHOOL OF MEDICINE, NTU SINGAPORE (NOVENA CAMPUS)

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WARM WELCOME

Welcome to Global Engage's 2nd Spatial Biology Congress: Asia

Singapore is once again set to host the 2nd Spatial Biology Congress Asia, a dynamic event at the forefront of cutting-edge research in spatial biology. Following the success of its debut in the same vibrant city, this congress promises an even more impactful experience.

Co-hosted with the Genome Institute of Singapore (GIS), this 2-day event will take place on the 21st and 22nd of November 2024 at Lee Kong Chian, School of Medicine, NTU Singapore (Novena Campus). The conference aims to showcase the diversity of spatial research, covering a broad spectrum of topics such as spatial omics technologies, imaging technologies, AI and data science, development and physiology, disease mechanism, diagnostics and drug discovery, and emerging trends and challenges within the field. Beyond the scientific program, this congress also serves as a platform for collaboration and forging lasting connections. Join us for a program that promises not just scientific insights but also networking opportunities, and the potential to uncover tomorrow's scientific breakthroughs in this rapidly evolving field, both in Asia and beyond.

- 20+ speakers from academia and industry experts
- Case studies from across variety of contexts
- Interactive panel discussions session
- Early career researchers and poster exhibition to promote scientific development
- Networking opportunities

We look forward to welcoming you to Singapore for this insightful event!

SCIENTIFIC COMMITTEE

- **Shyam Prabhakar**, Associate Director and Senior Group Leader, Genome Institute of Singapore (GIS), A*STAR
- **Grace Yeo Hui Ting**, GIS and BII Fellow, Genome Institute of Singapore (GIS) and Bioinformatics Institute (BII), A*STAR
- **Ashraful Haque**, Laboratory Head, The Peter Doherty Institute for Infection & Immunity, University of Melbourne
- **Jonathan Loh Yuin-Han**, Deputy Executive Director, and Research Director, Institute of Molecular and Cell Biology (IMCB), A*STAR
- **Kylie James**, Laboratory Head, Garvan Institute of Medical Research, University of New South Wales

CONFERENCE SYNOPSIS

Spatial multi-omics technologies
- Transcriptome, proteome, genome, epigenome, metabolome
- Imaging vs spatial sequencing
- Panel-based vs whole-transcriptome
- Benchmarking new technologies
- 3D profiling
- Microbiome, host-pathogen interaction

AI and data science
- Foundation models, generative AI
- Spatial data quality and standardization
- Cell segmentation
- Cell types and neighbourhoods
- Cross-modality data integration, batch correction
- Connecting subcellular, cellular and tissue morphology to spatial omics
- Cell-cell interactions
- Scaling to massive datasets

Development and physiology
- Current applications of spatial in basic biology
- Tissue atlasing
- Human development, stem cells
- Aging
- Model organisms, organoids, cell culture
- Perturbative approaches

Disease mechanisms, diagnostics and drug discovery
- Current applications of spatial in biomarker discovery and drug development
- Spatial Biology therapeutic applications in:
  - Oncology
  - Chronic disease
  - Infectious disease, microbiome

Panel discussion
Emerging trends and challenges in spatial omics
- What is the best technology for my question?
- How to design a spatial omics study?
- Practical tips for data analysis
- Does AI change the game?
- New possibilities enabled by new technologies

CONFERENCE FLOOR LAYOUT

Exhibition hall (luncheon & refreshments, poster presentations, and networking drinks reception) - Level 4
CSB auditorium (talk sessions) - Level 4

OPEN LETTER

Date: 13th August 2024

An Open Letter

On behalf of the scientific committee, it is our pleasure to invite you to attend the **2nd Spatial Biology Congress: Asia**, taking place on **November 21-22, 2024**, at **Lee Kong Chian School of Medicine, NTU Singapore (Novena Campus)**. This years' event is co-hosted by the Genome Institute of Singapore (GIS) and Global Engage.

Building on the success of the debut, this years' congress promises an even more impactful experience. We have curated a dynamic program featuring keynote presentations, panel discussion, and poster sessions that showcase cutting-edge advancements and innovative approaches within the field of spatial biology.

Key themes of this year's conference include:

- Spatial multi-omics technologies
- AI and data science
- Development and physiology
- Disease mechanisms, diagnostics and drug discovery
- Emerging trends and challenges in spatial omics

Whether you are presenting your own research, engaging with fellow scientists, or simply seeking to stay abreast of the latest developments, we encourage you to mark your calendar and join us in Singapore this November. Your participation plays important role in making this congress an impactful and enriching event for all.

Thank you for your continued dedication to advancing scientific knowledge. We look forward to welcoming you to NTU@One-North.

Warm regards,
Scientific Committee of the 2nd Spatial Biology Congress: Asia

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For more details contact Reuben Raj: Reuben@global-engage.com

CONFIRMED SPEAKERS

RAMANUJ DASGUPTA
Senior Group Leader and Professor, Genome Institute of Singapore (GIS)

UFUK DEGIRMENCI
Head of Spatial Biology, Next Level Genomics Pte Ltd

GE GAO
Professor, Peking University

SHILA GHAZANFAR
Lecturer and ARC DECRA Fellow, University of Sydney

ASHRAFUL HAQUE
Laboratory Head, The Peter Doherty Institute for Infection & Immunity, University of Melbourne

RUBY YUN-JU HUANG
Professor, National Taiwan University

ANAND JEYASEKHARAN
Principal Investigator, Cancer Science Institute of Singapore

NATINI JINAWATH
Associate Professor, Mahidol University

SUMIN LEE
CTO, Meteor Biotech

CHENGYU LI
Senior Investigator, Lingang Laboratory

LIM JACK WEE
Head of CyTOF, Singapore Immunology Network, A*STAR

LAI GUAN NG
Senior Investigator, Shanghai Immune Therapy Institute, Shanghai Jiao Tong University School of Medicine, Renji Hospital

JONATHAN LOH YUIN-HAN
Deputy Executive Director, and Research Director, Institute of Molecular and Cell Biology (IMCB), A*STAR

WOONG-YANG PARK
Director and Professor, Samsung Genome Institute and Sungkyunkwan University

SHYAM PRABHAKAR
Associate Director and Senior Group Leader, Genome Institute of Singapore (GIS), A*STAR

PAUL RASMUSSEN
Regional VP of Sales (APAC), Vizgen

MATTHEW RAWLINGS
Associate Director, Xenium Sales Leader, 10x Genomics

MATTHEW RODRIGUES
Field Application Scientist, RareCyte Inc.

FUCHOU TANG
Professor, Peking University

JULIE TELLIER
Senior Research Officer, Walter and Eliza Hall Institute of Medical Research (WEHI)

SATISH KUMAR TIWARI
Scientist, Singapore Immunology Network (SIgN), A*STAR

BOON-ENG TEH
Sr. Service and Support Manager, Standard BioTools

WU YIXUAN
Scientist, SIgN, A*STAR

GRACE YEO HUI TING
GIS and BII Fellow, Genome Institute of Singapore (GIS) and Bioinformatics Institute, A*STAR

RAYMOND YIP
Senior Research Officer, Walter and Eliza Hall Institute of Medical Research (WEHI)

8:00-9:00 | Exhibition Hall (Level 4) | Registration I Morning Coffee

9:00-9:05 | CSB Auditorium (Level 4) | Welcome Address

Chair:

9:05-9:45

KEYNOTE ADDRESS

FUCHOU TANG

Professor, Peking University

Single Cell Omics Sequencing Technologies: The Third Generation

I will talk about the third-generation sequencing (single molecule sequencing) platform-based single cell omics sequencing technologies, such as single cell genome sequencing (SMOOTH-seq & SMOOTH-seq2, Refresh-seq), single cell epigenome sequencing (scNanoATAC-seq & scNanoATAC-seq2, scNanoHi-C & scNanoHi-C2), single cell transcriptome sequencing (SCAN-seq & SCAN-seq2), single cell Strand-seq (NanoStrand-seq), and single cell multi-omics sequencing (scNanoCOOL-seq) technologies. These technologies will greatly facilitate the understanding of the 'dark matter' in different regulatory layers of our genomes, such as alternative splicing, allele specific chromatin accessibility, DNA methylation, chromatin accessibility & chromatin structure of repetitive elements and blacklist genomic regions.

9:45-10:05

ASHRAFUL HAQUE

Laboratory Head, The Peter Doherty Institute for Infection & Immunity, University of Melbourne

Mapping Immune Cell Interactions in Dense Secondary Lymphoid Organs

We will describe our use of Spatial Transcriptomics at near single-cell resolution to map cellular structure of the mouse spleen at steady state, as well as to search for novel cell-cell interactions during infection with malaria parasites. We will demonstrate how a continuum of T cell states can be mapped to a spatial array, how this approach supported hypothesis testing, and ultimately led to the discovery of a new receptor governing T-cell immunity to experimental malaria. We will also demonstrate how such spatial data can be converted into compelling visual applications for educating and informing others about the structure and function of tissue and organs.

10:05-1035

TECHNOLOGY PARTNER PRESENTATION

WU YIXUAN

Scientist, SIgN, A*STAR

Dissecting the Spatial Localisation of Tissue-Resident Macrophages in the Mammary Gland

Miltenyi Biotec

The mammary glands undergo remarkable structural changes in order to perform their critical lactogenic role during pregnancy, before reverting to a dormant state upon weaning. Rivalled only by the uterus in its magnitude, this remodeling can occur multiple times in an individual's lifetime with remarkable consistency, yet the underlying mechanisms that preserve the tissue's subunit organisation are not well understood. Tissue-resident macrophages as a whole have been shown to be required for aspects of mammary development such as ductal branching. At the same time, recent studies have employed transcriptomic-centric strategies to characterise a lactation-associated subset that is involved in immune surveillance and phagocytosis during pregnancy and involution, respectively, but is largely absent in the inactive state. Nevertheless, the roles of other macrophage subsets in the mammary gland niche remain largely unappreciated. Using 3D light sheet microscopy and the MACSima Imaging System, we identified several distinct mammary macrophage populations that occupy diverse spatial niches during both the inactive and pregnant/lactating states, ranging from adipocyte lobules in the former and alveolar clusters in the latter. Future work will involve the understanding of how these macrophage subsets maintain the overall structural organisation of the tissue despite drastic remodeling of the parenchymal and stromal networks.

10:35-11:25 | Morning Refreshments I Poster Sessions

Spatial Multi-omics Technologies

Chair:

11:25-11:45

CHENGYU LI

Senior Investigator, Lingang Laboratory

Cell Types and Their Functions in the Brain

My research interests include neural mechanism underlying working memory, how different cell types are organized, and how to build better interface to the brain. Recently I led team efforts in mesoscopic brain connectome project for non-human primates. We would like to systematically understand the brain-wide cell-typing and connectivity landscape of macaque brain in single-neuron resolution and in a cell-type specific manner, by combining single-cell RNA-seq, barcode assisted high-throughput retrograde tracing, single-cell resolution Geo-Seq and other cutting-edge methods. We are also actively examining the relationship between neuronal activity and cell types/connectome.

11:45-12:05

GRACE YEO HUI TING

GIS and BII Fellow, Genome Institute of Singapore (GIS) and Bioinformatics Institute, A*STAR

Spatial Characterization of the Colorectal Cancer Tumor Microenvironment

Colorectal cancer (CRC) is a clinically and molecularly heterogeneous disease. Single-cell RNA-sequencing (scRNA-seq) has enabled us to describe the diverse cell types that underlie the CRC tumor microenvironment, but their spatial organization remains poorly understood. To address this, we employ state-of-the-art spatial omics technologies (Cyclic FISH, 10X Genomics Xenium) to generate high-resolution spatial maps of the CRC tumor microenvironment, comprising over 9 million cells from 63 samples and 34 patients.

Our results reveal how the highly stereotypic structure of the normal colon becomes disrupted in the context of cancer. We identify molecular markers related to biological processes such as stem cell renewal and response to hypoxia that exhibit spatial patterning within tumor glands. We also identify tumor-enriched spatial neighborhoods, including a tumor budding neighborhood enriched at the tumor-normal interface of invasive samples. Our study presents the first large-scale spatial resource for understanding the CRC tumor microenvironment.

12:05-12:25

NATINI JINAWATH

Associate Professor, Mahidol University

Tumor Microenvironment Study in Breast Cancer with Skin Metastasis Using Spatial Gene Expression Analysis and Patient-Derived Organoid as a Disease Model

Among solid tumors, breast cancer is the most common cause of skin metastasis. To date, the effective treatment for breast cancer skin metastases (BCSM) is still lacking as the knowledge of mechanisms underlying the disease is limited. Spatial transcriptomics has recently emerged as a comprehensive tool to study tumor microenvironment (TME), whose important roles in cancer metastasis are being established. Twenty-eight RNAscope multiplex fluorescent probes were used to detect multiple TME components in the 26 FFPE and 31 fresh frozen breast cancer tissues from

patients with and without BCSM, which revealed CD44+ cancer stem-like cells as the main player involved in BCSM. In addition, IQGAP3+ cancer and immune microenvironment cells, as well as ACTA2+ myofibroblastic CAF (myCAF) were significantly associated with the primary breast cancer cases that developed skin metastasis. Spatial transcriptomics using Visium unveiled pathways that activate endoplasmic reticulum (ER) stress, including hypoxia, glycolysis, and interferon a/g signaling response, as the key pathways behind the involvement of CD44+ cancer stem-like cells in the TME of BCSM. Screening of 133 FDA-approved compounds on organoids derived from primary breast cancer and BCSM tissues demonstrated that HDAC inhibitors and proteasome inhibitors were the most effective drugs against BCSM organoids, likely because these inhibitors can directly inhibit ER stress response and are known to be effective against CD44+ cancer stem-like cells.

12:25-12:40

Contributed Talk

Authors of accepted abstracts will be notified by early October

12:40-13:10

TECHNOLOGY PARTNER PRESENTATION

For sponsorship opportunities, please contact Reuben at **reuben@global-engage.com**

13:10-14:10 Lunch I Poster Sessions

AI and Data Science

Chair:

14:10-14:30

SHYAM PRABHAKAR

Associate Director and Senior Group Leader, Genome Institute of Singapore (GIS), A*STAR

TBD

14:30-14:50

SHILA GHAZANFAR

Lecturer and ARC DECRA Fellow, University of Sydney

Multiscale Approaches for Understanding Single Cell Spatial Omics Data

Technological advances in measuring gene expression in a spatially resolved manner have resulted in several tour-de-force publicly available datasets, often accompanied by sample-matched dissociated single cell RNA-seq or single cell multi-omic measurements. However, methodologies for analyzing such data are in urgent need of development. Currently, many integrative data analysis tasks for spatial genomics are performed using tools designed with dissociated single cell RNA-seq data in mind, effectively ignoring the specific data structures of spatial genomics data. This talk will cover recent methodological developments in harnessing all available information from molecule-resolved spatial omics as well as existing scRNA-seq datasets to address questions in biological and understanding disease.

14:50-15:05

TECHNOLOGY PARTNER PRESENTATION

SUMIN LEE

CTO, Meteor Biotech

Spatially Resolved Laser Activated Cell Sorting (SLACS) for Bridging Spatial and Molecular information for Advanced Cell Sorting

Advancements in imaging and molecular biology have significantly enhanced our understanding of biological phenomena, yet integrating spatial and molecular data remains challenging. Traditional techniques, like H&E and IF staining, alongside next-generation sequencing (NGS), often fail to preserve spatial information during molecular analyses. Spatially Resolved Laser-Activated Cell Sorting (SLACS) addresses this gap by maintaining spatial context while enabling high-precision cell sorting. SLACS isolates cells based on their images, facilitating subsequent molecular assays such as DNA sequencing, RNA sequencing, and proteomics. Demonstrating versatility across various tissues and staining methods, SLACS effectively isolates single entities from complex samples, enhancing the precision and depth of molecular analyses. This innovative approach bridges the gap between imaging and molecular data, advancing research in various fields including cancer research.

15:05-15:20

TECHNOLOGY PARTNER PRESENTATION

MATTHEW RODRIGUES

Field Application Scientist, RareCyte Inc.

Next Generation Spatial Biology Imaging – Customer Case Studies

OrionTM is a Spatial Biology imaging powerhouse providing a bridge from translational to biopharma & clinical research, by swiftly delivering data that's reproducible across whole slides at subcellular resolution, without tissue damage. Agile assay development - validation in weeks not months - and fast sample processing - studies in days not weeks - along with same-section bright-field imaging have been used by dozens of customers in biopharma and clinical research.

Customer case studies will be discussed across drug development and clinical research / clinical trial support that utilize the benefits of Orion:

- Uses standard slides & IHC workflows
- Flexible panel design using established antibody clones & kits
- Library of off-the-shelf & easily customized panels across a range of tissues
- Single round stain and scan workflow for agile panel optimization
- Open, whole-slide, data formats for standard interpretation pipelines

15:20-16:05 Afternoon Refreshments I Poster Sessions

Development and Physiology

Chair:

16:05-16:25

RAYMOND YIP
Senior Research Officer, Walter and Eliza Hall Institute of Medical Research (WEHI)
High Resolution Spatial Atlas of Murine and Human Bone Marrow Microenvironment

The bone marrow niche is a complex entity that regulates normal and malignant haematopoiesis, yet its spatial architecture, molecular landscape and cellular composition remain poorly defined. Here, we describe the generation of first-of-its-kind spatially resolved transcriptomic atlas of the murine and human bone marrow at single cell resolution using three independent platforms.

16:25-16:40

Contributed Talk
Authors of accepted abstracts will be notified by early October

16:40-16:55

TECHNOLOGY PARTNER PRESENTATION

BOON-ENG TEH
Sr. Service and Support Manager, Standard BioTools
LIM JACK WEE
Head of CyTOF, Singapore Immunology Network, A*STAR
Rediscovery of T-cell Epitopes as Future Therapeutics

Finding a T cell cancer antigen is like a needle in a haystack. As T.S Eliot wrote “The end is where we start from...”. Here we developed a foundational technology, MHC-I Snap based on de novo MHC- I fragmentation principle to rediscover more T cell epitopes. Our MHC-I Snap technology is central in building a library of tumor-specific antigens for Asian cancers. In an ongoing multi-collaborative effort in Singapore, we have thus established a T cell Monitoring and Vaccination platform (TMoVac) to translate potential T cell epitopes into personalized T cell vaccines for Asia-Pacific prevalent cancers. TMoVac is a diverse platform consisting of Epitope discovery, Epitope validation, Vaccine design and T-cell immuno- monitoring. We will share our ongoing efforts to create values through innovative science and partnership.

16:55-17:40

PANEL DISCUSSION
Emerging Trends and Challenges in Spatial Omics

- What is the best technology for my question?
- How to design a spatial omics study?
- Practical tips for data analysis
- Does AI change the game?
- New possibilities enabled by new technologies

17:40-17:45 Group Photo Session (Speakers and delegates)

17:45 End of Day 1 I Drinks Reception (Open to all attendees)

19:00 Dinner (By invitation only)

8:30-9:00 | Exhibition Hall (Level 4) | Registration I Morning Coffee

Chair:

9:00-9:40

KEYNOTE ADDRESS

GE GAO

Professor, Peking University

Towards a Regulatory Language Model

Human individual cells, as the basic biological units of our bodies, carry out their functions through rigorous regulation of gene expression and exhibit heterogeneity among each other in every human tissue. Recent technological advances in single-cell sequencing have enabled the probing of regulatory maps through multiple omics layers, such as chromatin accessibility, DNA methylation and the transcriptome, offering a unique opportunity to unveil the underlying regulatory bases for the functionalities of diverse cell types. Nevertheless, the disparity between omics-specific feature spaces as well as the ever-increasing data volume pose serious challenge for mining these treasures. Combining massive omics data and leading-edge statistical modeling/machine learning approaches, we'd suggest that a generative model rationally designed with data-oriented, knowledge-based principles will bridge the gap, and further enabling a Regulatory Language Model.

9:40-10:00

RUBY YUN-JU HUANG

Professor, National Taiwan University

Identification of the Niche Neighborhood by Single Cell Spatial Transcriptomics

Neighborhoods are important contexts across multiple disciplines. In human behavior, neighborhoods matter in shaping the social processes. In economic development, neighborhoods matter in determining community prosperity. This "neighborhood matters" concept also applies to solid tumors. Clonal heterogeneity in tumor cells and their associated microenvironments could create community effects within tumors and even dictate their treatment responses. Identification of specific niche neighborhoods within tumors thus becomes a crucial task. In this talk, I will show how technologies such as single cell spatial transcriptomics (scST) could be utilized to identify niche neighborhoods encompassing potential founder clones of tumor cells and their associated microenvironments in ovarian clear cell carcinoma, a cancer subtype with high incidence among East Asian women. The presence of this niche neighborhood could be further examined across different spatial profiling platforms to confirm its generalizability.

10:00-10:30

TECHNOLOGY PARTNER PRESENTATION

PAUL RASMUSSEN

Regional VP of Sales (APAC), Vizgen

SATISH KUMAR TIWARI

Scientist, Singapore Immunology Network (SIgN), A*STAR

Mapping the Future of Spatial Genomics with MERSCOPE Ultra™ and MERFISH 2.0

In this presentation, we will introduce the next generation of spatial multi-omics offerings from Vizgen, like our latest platform, the MERSCOPE® Ultra, for in situ spatial genomics, as well as our MERFISH 2.0 Chemistry that facilitates direct RNA profiling of up to 1,000 genes, even in lower-quality tissue samples where RNA fragmentation occurs.

Spatio-temporal Analysis of Microglia Form and Functions in Human Brain Immune Organoids

Microglia, the immune cells present in the brain parenchyma, play various roles in brain development, immunity, and homeostasis. Comprising approximately 10% of all brain cells, these cells actively participate in processes such as synaptic pruning, brain circuitry modelling, and rewiring. The significant role of microglia in brain pathophysiology is evident from their involvement in different neurodevelopmental and neurodegenerative disorders. Existing models for studying early aspects of human brain development and neurodegeneration, such as human brain organoids, often lack microglia. We have developed a novel approach to incorporate microglia into human brain organoids by utilizing hiPSC-derived syngeneic brain-immune organoids. This co-culture model has enabled the exploration of early interactions between microglia and neuronal cells. Additionally, spatial-omics done on the MERSCOPE® Platform have revealed diverse interactions between microglia and neuronal cells and heterogeneous microglial states within microglia-sufficient human brain organoids. The findings on the structure and function of microglia in human brain immune organoids will be presented to illuminate the intricate interactions between microglia and neuronal cells.

10:30-11:20 | Morning Refreshments I Poster Sessions

Development and Physiology

Chair:

11:20-11:40

LAI GUAN NG

Senior Investigator, Shanghai Immune Therapy Institute, Shanghai Jiao Tong University School of Medicine, Renji Hospital

Neutrophils: The Power of More Than One

Neutrophils are specialized cells of the early innate immune response. A long-standing question in the field of neutrophil research is whether a distinct subset of these cells truly exists, or different populations are merely a manifestation of the neutrophil maturation/polarization state. Lineage tracing techniques have been used to distinguish different subsets of myeloid cell types; however, more needs to be done with neutrophils. This talk will discuss how in-depth analysis of physiological and pathological granulopoiesis by multiomics and multiparametric technologies can contribute to better understanding neutrophil populations and discover new functions, with a specific focus on tumor-associated neutrophils.

11:40-12:00

JULIE TELLIER

Senior Research Officer, Walter and Eliza Hall Institute of Medical Research (WEHI)

Unraveling the Diversity and Functions of Tissue-resident Plasma Cells

Antibody-secreting plasma cells (PCs) are generated in secondary lymphoid organs but are reported to reside in an emerging range of anatomical sites. Analysis of the transcriptome of different tissue-resident (Tr)PC populations revealed that they each have their own transcriptional signature indicative of functional adaptation to the host tissue environment. In contrast to expectation, all TrPCs were extremely long-lived, regardless of their organ of residence, with longevity influenced by intrinsic factors. Analysis at single-cell resolution revealed that the bone marrow is unique in housing a compendium of PCs generated all over the body that retain aspects of the transcriptional program indicative of their tissue of origin. This study reveals that extreme longevity is an intrinsic property of TrPCs whose transcriptome is imprinted by signals received both at the site of induction and within the tissue of residence. Terminally differentiated plasma cells reside in multiple tissues to contribute to local immunity.

12:00-12:15

Contributed Talk

Authors of accepted abstracts will be notified by early October

12:15-12:35

RAMANUJ DASGUPTA
Senior Group Leader and Professor, Genome Institute of Singapore (GIS)
Spatio-temporal Analysis of Nasopharyngeal Cancer Identifies Therapy-induced Remodeling of the Tumor-immune Microenvironment

12:35-12:50

TECHNOLOGY PARTNER PRESENTATION

MATTHEW RAWLINGS
Associate Director, Xenium Sales Leader, 10x Genomics
Combine the Power of Single Cell & Spatial to Make the Impossible, Possible. That's Xenium Potential.

Reveal new insights into cellular structure and function by enabling the mapping of 100s–1,000s of RNA targets in fresh frozen and FFPE samples with true tissue context. Built on years of innovation in single cell and spatial technologies, Xenium is a complete platform that streamlines going from tissue section to data, with a state-of-the-art analyzer and a wide selection of curated panels and/or customization options. Xenium's Onboard Analysis automatically processes data during a run allowing immediate interactive visualization with the powerful and intuitive Xenium Explorer.

Xenium offers best-in-class sensitivity, specificity, and highly confident transcript-to-cell assignments using multimodal cell segmentation. Upcoming platform developments included an increased breadth of RNA target investigation with 5,000-plex gene panels for mouse and human tissue, and in-line multiplex protein detection for even greater biological insights.

12:50-13:05

TECHNOLOGY PARTNER PRESENTATION

UFUK DEGIRMENCI
Head of Spatial Biology, Next Level Genomics Pte Ltd
Ensuring Quality in Spatial Genomics: Robust QC Frameworks for Experimental Success Using NanoString Spatial Toolbox

Ensuring data accuracy and reproducibility is crucial in spatial genomics. This presentation will explore the importance of quality control (QC) in this field, focusing on the NanoString Spatial Toolbox. We will discuss essential QC frameworks, from sample preparation to data analysis, and strategies for minimizing variability and validating spatially resolved molecular data. By leveraging the advanced capabilities of the NanoString Spatial Toolbox, researchers can achieve high-fidelity data acquisition and interpretation. Attendees will gain practical insights into implementing these QC frameworks to enhance the quality and reproducibility of their spatial genomics research.

13:05-14:05 Lunch I Poster Sessions

Disease Mechanisms, Diagnostics, and Drug Discovery

Chair:

14:05-14:25

WOONG-YANG PARK
Director and Professor, Samsung Genome Institute and Sungkyunkwan University
Spatial Transcriptome Analysis Reveals the Impact of the Cancer Microenvironment on Treatment Resistance in Colorectal Cancer

The cancer microenvironment, composed of various cell types within the tumor tissue, plays a crucial role in cancer progression, treatment response, recurrence, and metastasis. Variations in immune cell composition within the cancer microenvironment among patients may be attributed to the intrinsic characteristics of cancer cells. In this study, we utilized biopsy tissues from a clinical trial of colorectal cancer treated with targeted anticancer drugs to analyze cell-to-cell interactions influencing treatment response via spatial transcriptome analysis. Our findings demonstrate that the surrounding microenvironment differs according to colorectal cancer cell type, which may account for variations in treatment resistance. These insights suggest the potential for developing novel therapeutic strategies aimed at modulating the cancer microenvironment to overcome treatment resistance.

14:25-14:45

JONATHAN LOH YUIN-HAN
Deputy Executive Director, and Research Director, Institute of Molecular and Cell Biology (IMCB), A*STAR
Spatial Cartography of Developing Human Immune Organs Enables the Geopositioning of Rare Accessory Cells

The thymus is the major site for thymopoiesis. We applied Stereo-seq transcriptomics technology to establish high-resolution spatial atlas of the human and mouse thymuses. Our study identified thymus architecture consisting of sub-structures including the outer cortex, inner medulla and septa. Further, we discovered cortical and medullary niches with different constituent cell types whereby thymic epithelial cells, thymocytes, and immune cells such as macrophages and dendritic cells co-localize and interact. We further investigated the signalling pathways and master regulators enriched in the different niches. Using computational approach, we uncovered the spatial localization of Thymic mimetic cells which express Transcription Factors, of peripheral tissues, such as MYOG, SOX2, SOX11, SPIB and ASCL1. Overall, we have elucidated a high-resolution spatial cartography of the human developing thymus enabling the geopositioning of known thymic cell types and the illumination of the rare mimetic TECs.

14:45-14:50 Poster Winner Award Ceremony

14:50-15:05

Contributed Talk
Authors of accepted abstracts will be notified by early October

15:05-15:25

ANAND JEYASEKHARAN
Principal Investigator, Cancer Science Institute of Singapore
Prognostic Significance of Spatial Distribution in Diffuse Large B-cell Lymphoma

Point process analyses, commonly used in ecology and geography to map spatial distribution, have seen limited application in tumour heterogeneity studies. We explored spatial point process analyses in diffuse large B-cell lymphoma (DLBCL), the most common haematological malignancies, using multiplexed immunohistochemistry and cellular phenotyping, followed by multi-omic and clinicopathological analyses. Building on prior work showing that MYC and BCL2 co-expression without BCL6 (M+2+6-) in DLBCL confers poor prognosis, we modelled the spatial organisation of these M+2+6- cells across four independent cohorts. Geyer point process models stratified patients into "clustered" and "dispersed" groups, with the latter showing significantly shorter overall survival. Multi-omics revealed that "dispersed" M+2+6- cases had an immunologically cold microenvironment, enriched in Tregs and exhausted CD4+/CD8+ T cells, with malignant B-cells expressing immune checkpoints such as LAG3. This study highlights the clinical and biological significance of malignant cell spatial distribution in lymphoma.

15:25 Closing Remarks

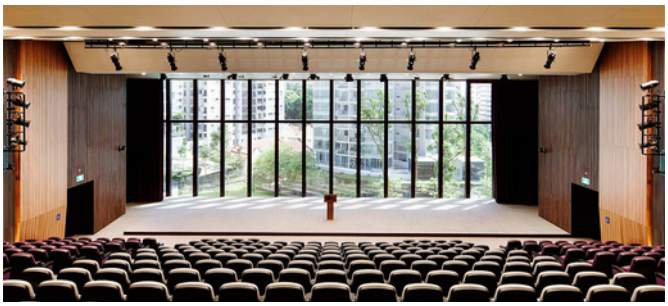
15:30 End of Day 2

VENUE INFORMATION

LEE KONG CHIAN SCHOOL OF MEDICINE, NTU SINGAPORE (NOVENA CAMPUS)

11 Mandalay Road Singapore 308232

Conveniently located within walking distance from Novena MRT.



CALL FOR **ABSTRACT**

Abstract submission for the 2nd Spatial Biology Congress Asia is now closed.

We would like to thank everyone who submitted their work. Authors of selected abstracts will be contacted, and the announcements will be made during the week of 7th October 2024.

POSTER PRESENTATIONS

MAKING A POSTER PRESENTATION – CLOSING DATE 25TH OCTOBER 2024

Poster presentations will take place during breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters.

In order to present a poster at the forum you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first come first served basis (subject to checks and successful registration). Representatives from solution provider organizations are not eligible to enter the competition but are welcome to present posters at the meeting.

NEW FOR 2024 – BEST POSTER AWARD

The 'Best Poster Award' is given to the best poster at the conference. Judges will select ONE best poster among the conference participants. Poster winner will receive a certificate and monetary award worth **SGD 250**

SUBMISSION INSTRUCTIONS

Download poster presentations form: **HERE**
For any inquiries, please contact Haley at haley@global-engage.com

We will require the form (downloadable from the event website) to be submitted by **25th October 2024**. This is the formal deadline however space is another limiting factor so early application is recommended.