WEHI SPATIAL TECHNOLOGY SYMPOSIUM

5th - 6th June 2025

THURSDAY 5TH JUNE

SESSION I

9:00 AM Opening Address

9:10 AM Yutaka Suzuki
Towards Multi-Omics Spatial Analysis to Reveal Cancer Heterogeneity

9:40 AM 10x Genomics / Jeremy Mo (Gold sponsor talk)
Unveiling tumor microenvironment dynamics utilising spatial transcriptomics

10:10 AM Maria Tanzer
Spatial proteomics: Investigating inflammation in situ

10:30 AM Ashraful Haque
Genome-scale Spatial Transcriptomics for studying Immunity to Infection

10:50 AM Dig Vijay Kumar Yarlagadda
Discrete Representation Learning for Modeling Imaging-based Spatial Transcriptomics Data

11:00 AM Morning Tea

SESSION II

11:30 AM Ana Maluenda
Histology in the Spatial Omics Era: how do I make my H&E sample into Spatial Omics?

11:50 AM Ashleigh Solano
SpatialBench: Comparative benchmarking of high-resolution spatial transcriptomics platforms using reference tissues

12:10 PM Leica / Zhou (Vivian) Feng (Silver sponsor talk)
Overcoming the High Multiplexing Barrier: 3D Spatial Omics using STELLARIS SpectraPlex

12:30 PM Andrew Pattison
A spatial atlas of colorectal cancer reveals the influence of stromal niches on tumour differentiation

12:40 PM Somi Kordafshari, Natalie Charitakis, Yang Xu, Denis Bienroth, Jake Robertson

1:00 PM Lunch

SESSION III

2:00 PM Grace Yeo
Mapping molecular and morphological heterogeneity in colorectal cancer

2:30 PM Vizgen / George Emanuel (Gold sponsor talk)
Extending Spatial Transcriptomics to Challenging Tissues: Enabling Discovery with MERFISH 2.0

2:50 PM Helen Fu
Characterising melanoma resistance niches to immune checkpoint inhibitors using spatial transcriptomics and deep learning

3:00 PM Bill Dougall
Spatial mapping of post-treatment specimens to identify therapeutic vulnerabilities and drug mechanism of action in neoadjuvant immunotherapy treated lung cancer patients

3:20 PM Ning Liu
hoodscanR: Profiling single-cell neighborhoods in spatial transcriptomics data

3:30 PM Afternoon Tea

SESSION IV

4:00 PM Ruby Huang
Spatial transcriptomic profiling of ovarian clear cell carcinoma reveals intra-tumor heterogeneity in OXPHOS and epithelial-mesenchymal gradients associated with clinical outcomes

4:20 PM Illumina / Shan Li (Silver sponsor talk)
A high-resolution spatial transcriptomic map of the pregnant mouse brain reveals regionally distinct gene expression regulation related to maternal behavior

4:32 PM Akriti Varshney
Integrating Spatial and Single-Cell Transcriptomics to Resolve Alternative Polyadenylation in the Heart

4:42 PM Marek Cmero
WEHI's Spatial Omics Data Analytics (SODA) Hub: an environment for spatial analysis from data generation to analysis and beyond

4:55 PM Naveed Ishaque
2D, or not 2D? That is the question! (Investigating cell overlaps in spatial transcriptomics data)

5:15 PM Introduction to WEHI Spatial Omics Facility

5:30 PM Network & Poster session

7:00 PM Symposium dinner at University House Melbourne
Registration is required

FRIDAY 6TH JUNE

SESSION V

9:20 AM Alexander Swarbrick
Decoding breast cancer ecosystems with spatially resolved 'omics

9:40 AM Jessica Da Gama Duarte
Using B Cells and Tertiary Lymphoid Structures to Predict Cancer Outcomes

10:00 AM Miltenyi BIotec / Lai Guan Ng (Silver sponsor talk)
Neutrophils: The Power of More Than One

10:20 AM Emma Watson
Advancing High-Plex Spatial Proteomics and Multiomics Using the Lunaphore COMET platform

10:30 AM Morning Tea

SESSION VI

11:00 AM Shamini Ayyadhury
A Panorama of OMICS technologies, A Vision in Space : A pan-Canadian initiative for re-imagining conversations in science

11:20 AM Thierry Jarde
A Spatial Transcriptomic Survey of the Breast Cancer Microenvironment Across Subtypes and Metastases

11:40 AM TrendBio / Element Biosciences / Abbey Cutchin (Silver sponsor talk)
From Sample to Insight: Unlocking High Dimensional Biology with Direct In Sample Sequencing on AVITI24

11:52 AM Joel Moffet
SMINT-3D: An integrative spatial multi-omic workflow for unified analysis and 3-dimensional reconstruction of tumour tissue

12:02 PM Jiadong Mao
Φ-Space ST: a platform-agnostic method to identify cell states in spatial transcriptomics studies

12:12 PM Lisa Waylen
Resolving spatial boundaries in the lateral plate mesoderm

12:30 PM Lunch

SESSION VII

1:30 PM Edwin Hawkins
Multiplexing intravital imaging and spatial transcriptomics to understand bone marrow microenvironments in blood cancer

1:50 PM MGI / Mirana Ramialison (Silver sponsor talk)
2021: A spatial odyssey

2:10 PM Panel Discussion - Tissue Issues: Live, Unfiltered and Slightly Stained!
Davis McCarthy (Host), Shamini Ayyadhury, Edwin Hawkins, Alexander Swarbrick, Ruby Huang

2:55 PM Closing Remarks

SPATIAL TECHNOLOGY SYMPOSIUM 2025

PROGRAM

Day 1 – Thursday 5th June 2025 ***Venue: Davis Auditorium***

Session I

Chair: Pradeep Rajasekhar, Research Officer

9:00	Opening	Tony Papenfuss, Deputy Director – WEHI
9:10	***Keynote***	Yutaka Suzuki – University of Tokyo
9:40	***Gold Sponsor***	Jeremy Mo – Garvan Institute/10x Genomics
10:10	Invited Speaker	Maria Tanzer – WEHI
10:30	Invited Speaker	Ash Haque – Doherty Institute
10:50	Abstract Talk	Dig Vijay Kumar Yarlagadda – Cornell University

Morning Tea
11:00 – 11:30

Session II

Chair: Changqing Wang, PhD Student

11:30	Invited Speaker	Ana Maluenda – WEHI
11:50	Invited Speaker	Ashleigh Solano – WEHI
12:10	***Silver Sponsor***	Roshan Vasani (Vendor Introduction)
	Leica	Zhou Feng (User Talk)
12:30	Abstract Talk	Andrew Pattison – Monash University
12:40	Lightning Talks	Somi Kordafshari – WEHI
		Natalie Charitakis – MCRI
		Yang Xu – WEHI
		Denis Bienroth – MCRI
		Jake Robertson – La Trobe

Lunch
12:50 – 2:00

Session III

Chair: Ilariya Tarasova, Research Officer

2:00	Invited Speaker	Grace Yeo – A*STAR
2:30	***Gold Sponsor***	George Emanuel – Vizgen
2:50	Abstract Talk	Helen Fu – Melanoma Institute Australia
3:00	Invited Speaker	Bill Dougal – QIMR
3:20	Abstract Talk	Ning Liu – SAiGENCI

Afternoon Tea
3:30 – 4:00

Session IV

Chair: Lei Qin, PhD Student

4:00	Invited Speaker	Ruby Huang – National Taiwan University
4:20	***Silver Sponsor***	Shan Li – Illumina
4:40	Abstract Talk	Akriti Vershney – MCRI
4:50	Abstract Talk	Marek Cmero – WEHI
5:00	Invited Speaker	Naveed Ishaque – Charitee Berline
5:20	Facility Talk	Rory Bowden – WEHI Spatial Omics Facility

Networking and Poster Session
5:30 – 6:45

Symposium Dinner
7:00 – 10:00

Day 2 – Friday 6th June 2025 *Venue: Davis Auditorium*

Session V

Chair: Joel Moffet, PhD Student

9:20	Invited Speaker	Alex Swarbrick – Garvan Institute
9:40	Invited Speaker	Jessica Da Gama Duarte – Monash University
10:00	***Silver Sponsor***	Dr Lai Guan Ng – Miltenyi
10:20	Abstract Talk	Emma Watson – WEHI

Morning Tea
10:30 – 11:00

Session VI

Chair: Mengbo Li, Research Officer

11:00	Invited Speaker	Shamini Ayyadhury – University of Toronto
11:20	Invited Speaker	Thierry Jarde – Monash University
11:40	***Silver Sponsor***	Abbey Cutchin – Trendbio/Element
11:52	Abstract Talks	Joel Moffet – WEHI Jiadong Mao – University of Melbourne Lisa Waylen – MCRI

Lunch
12:00 – 1:30

Session VII

Chair: Xueyi Dong, Research Officer

1:30	Invited Speaker	Edwin Hawkins – WEHI
1:50	***Silver Sponsor*** *MGI*	Mr Richard Harrison (Vendor Talk) Prof. Mirana Ramialison (User Talk)
2:10	Panel Discussion	*Panel Guests:* Shamini Ayyadhury, Yutaka Suzuki, Ruby Huang, Alexander Swarbrick *Panel Chair:* Davis McCarthy
2:55	Closing Remarks	Daniela Zalcenstein – WEHI

Speaker Profiles

Prof. Yutaka Suzuki

Head Life Science Data Research Centre
The University of Tokyo

Towards Multi-Omics Spatial Analysis to Reveal Cancer Heterogeneity

In this presentation, I'd like to discuss the latest spatial analytical platforms for understanding micro-heterogeneity of cancers. Particularly, the interaction between tumor cells and their microenvironment is believed to be a decisive factor for tumor development. Herein, we characterize spatial RNA profiles obtained from 30 lung adenocarcinoma patients at various stages, including non-invasive and later invasive stages. These samples were subjected to the spatial transcriptome sequencing analysis in conjunction with higher resolution analysis using in situ RNA profiling. The detailed inspection on each case and the following computational modeling based on the observed diverse profiles revealed that the drastic changes in phenotypic appearances of tumor cells are frequently triggered by their interaction with immune cells. The phenomena coincide with the induction of a series of cellular expression programs, which enable transforming tumor cells and their breaking-through against the immune cell barrier, collectively allowing their further progression. The study provides us with actual features how lung tumor develops through interaction within their microenvironments.

Dr. Yutaka Suzuki, is a professor at Life Science Data Research Center, Graduate School of Frontier Sciences, the University of Tokyo (UTokyo). After he graduated from UTokyo in 1999, he spent one year at Genome Science Center, RIKEN and then moved on to UTokyo where he had researched about fulllength cDNA sequencing analysis. He has become a professor at UTokyo since 2013. His specialty includes full-length cDNA, transcriptome, transcriptional start site, next generation sequencing, Cancer Genomics, and Spatial Biology.

Jeremy Mo

PhD Student
Garvan Institute/10x Genomics

Unveiling tumor microenvironment dynamics utilising spatial transcriptomics

Spatial transcriptomics have allowed for the analysis of cellular state and phenotype at sub-cellular resolution. We have applied this technology to longitudinal samples of breast cancer patients undergoing neoadjuvant chemotherapy, as well as patients undergoing novel therapeutics. We discuss the utility of this technology in identifying signals associated with treatment resistance and response, as well as novel applications with identifying therapeutics within tissue.

Jeremy is a third-year PhD student focusing on spatial analyses within the tumor microenvironment, and is a breast medical oncologist at Westmead Hospital.

Maria Tanzer

Laboratory Head, Inflammation Division
Walter and Eliza Hall Institute of Medical Research

Spatial proteomics: Investigating inflammation in situ

Chronic inflammation results from dysregulated inflammatory signalling and impaired resolution mechanisms. The Tanzer Lab investigates these processes at both fundamental and translational levels — dissecting resolution pathways in vitro, while also examining the drivers and consequences of unresolved inflammation in situ. In this talk, I will present our approach leveraging cutting-edge spatial proteomics to map key cell types and molecular regulators of inflammation and tissue repair. I will illustrate this strategy with a case study on inclusion body myositis and a collaboration on toxic epidermal necrolysis, highlighting how spatial insights can inform our understanding of chronic inflammatory disease.

Maria is a Lab Head and NHMRC Emerging EL2 Fellow at WEHI, where she also completed her PhD studying cell death and cytokine signalling in the context of inflammation. In 2017, she moved to Munich to undertake postdoctoral research in the laboratory of Professor Matthias Mann, a world leader in proteomics, supported by a Marie Skłodowska-Curie Fellowship. Two years ago, Maria established her independent research group, which leverages advanced proteomics to investigate the mechanisms underlying inflammation and its resolution.

Associate Prof. Ashraful Haque

Principal Research Fellow
Doherty Institute

Genome-scale Spatial Transcriptomics for studying Immunity to Infection

Immune responses are initiated in densely-packed, specialised organs including the spleen, with resulting activated immune cells migrating throughout the body to perform functions such as pathogen clearance. Here we will discuss the utility of genome-scale, spatial transcriptomics platforms (e.g CurioSeeker, STOmics & VisiumHD) for discovery science related to the immune system. We will discuss the benefits and analytical challenges of increasing the physical size of tissue samples examined by ST. We will discuss the use of deconvolution algorithms to facilitate spatial examination of progressive changes in T cell-states using a case study in experimental mice. We will discuss novel immune cell behaviour in the lungs during infection with influenza virus, and our recent progress in mapping the healthy adult human spleen.

Associate Professor Ash Haque leads a research team at the Doherty Institute, whose principal interests are to examine cellular immune responses to infection, with a focus on adaptive CD4+ T cells and B cells. The team has recently used a combination of scRNA-seq and ST methods to study T & B-cell differentiation in the spleen during experimental malaria. Ash also serves as current President of the Melbourne Immunotherapy Network, and Deputy Secretary of the Australia & New Zealand Society for Immunology.

Dig Vijay Kumar Yarlagadda

Graduate Student
Cornell University

Discrete Representation Learning for Modeling Imaging-based Spatial Transcriptomics Data

Imaging-based spatial transcriptomics (ST) provides single transcript level spatial resolution for hundreds of genes, unlike sequencing-based ST technologies whose resolution is limited to physical capture regions on slides. Existing methods to identify patterns of interest in imaging-based ST data are built as extensions of single cell analysis methods, mostly ignoring valuable spatial information encoded in the raw imaging data. Here we present a discrete representation learning approach for modeling spatial gene expression patterns in ST datasets. By employing raw coordinates of detected transcripts and positional encoding of cell centroids as inputs, we learn discrete representations using Vector Quantized-Variational Autoencoder to extract multi-scale structures from fluorescence in situ hybridization based ST datasets. We demonstrate the usefulness of discrete representations in terms of the quality of embedding of ST data as well as improved performance on downstream tasks for extracting biologically meaningful cellular neighborhoods and spatially variable genes. We applied the model to dissect the mechanisms of resistance to immunotherapies in metastatic renal cell carcinoma tumors.

Vijay is a computational biology graduate student at Cornell University/ Sloan Kettering Institute in NYC. His research interests lie at the intersection of computer vision and cancer metastasis.

Ana Maluenda

Senior Histologist
The Walter and Eliza Hall Institute of Medical Research

Histology in the Spatial Omics Era: how do I make my H&E sample into Spatial Omics?

As for any experiment, good sample preparation is crucial to produce reliable data; poor preparation often leads to unusable results or "rescue" science. It should be considered with the same importance as experimental design and technology selection. What is often referred to as sample preparation encompasses various steps: harvesting, macroscopic cut-up, processing, embedding and sectioning. This is further complicated by the diversity of tissue types and species, posing challenges to scientists. Examples include differences between archival and freshly prepared samples or frozen vs. FFPE samples. Standardisation across all stages is ideal and should be done. In pre-clinical animal models, a range of resources provide references to standardise tissue histopathology. Though these references may not be Spatial Omics-specific, they offer valuable anatomical and histopathological context/landmarks, useful when searching for regions of interest. However, standardisation is harder in translational or human studies due to variability in sample sources. To increase experimental success and manage high costs, researchers should carefully consider fixatives

and sample preparation methods (frozen vs FFPE), sample storage, tissue preservation and morphology quality control, RNA integrity evaluation and sectioning plans. The use of tissue microarrays or combining multiple blocks on one slide is becoming popular to maximise data output. These approaches have so far been effective but rely on thorough coordination between researchers and core facilities, precise sectioning, clear tissue mapping, and defined inclusion/exclusion criteria. This presentation explores sample preparation in Spatial Omics from a histologist's perspective, providing examples submitted to our Advanced Histotechnology Facility at WEHI. It highlights key challenges, common pitfalls, and practical tips for improving sample quality and experimental outcomes.

Ana currently holds a Senior Histologist position within the Advanced Histotechnology Facility at WEHI. Formally trained as a Veterinary pathologist (USP, Brazil) and Medical Scientist – Laboratory Medicine (RMIT, Australia), she is currently pursuing her Doctor of Veterinary Medicine degree (University of Melbourne) to register for practice. With years of experience in pre-clinical and translational research, biopharmaceutical R&D, CROs and diagnostic laboratories, Ana brings a diverse background to WEHI. She has been involved in a wide range of projects, including haematopoietic, autoimmune, cardiovascular and infectious diseases. Her overseas training and current studies support her contributions in anatomical pathology and in vivo models of disease, with a deep understanding about tissue types, morphology and histopathology. Her years of work as a research assistant and laboratory management offer Ana a great insight into academic research, providing continuous education opportunities and tailoring our facility services to adapt, contribute and progress in the era of spatial omics and complex multiplexing.

Ashleigh Solano

Research Officer

The Walter and Eliza Hall Institute of Medical Research

SpatialBench: Comparative benchmarking of high-resolution spatial transcriptomics platforms using reference tissues

Spatial transcriptomics technologies have revolutionized our ability to map gene expression within intact tissue architecture, providing novel insights into development, disease, and tissue organization. Recognizing the rapid advancements in higher resolution spatial transcriptomics, we developed SpatialBench, a well-designed, in-house, multi-platform benchmarking dataset to systematically evaluate the performance of next-generation spatial technologies using matched biological samples. SpatialBench focuses on a diverse set of high-resolution spatial transcriptomics platforms, including sequencing-based Visium HD and imaging-based in situ technologies such as MERSCOPE and Xenium, which provide subcellular-scale resolution via alternative transcript detection strategies. Notably, these platforms differ in transcriptome coverage, with Visium HD enabling near-comprehensive transcriptome capture, while in situ approaches typically focus on smaller gene panels. SpatialBench leverages malaria-infected mouse spleens, a tissue characterized by complex, highly structured immune cell niches such as germinal centers, providing a biologically rich and defined context to assess specificity, spatial reproducibility, and biological signal recovery at high spatial resolution. Benchmarking analyses demonstrated platform-specific variation in transcript detection sensitivity, background signal levels, reproducibility, and the ability to capture germinal center architecture and biological organization. Expanding upon our previous work (SpatialBenchVisium), SpatialBench broadens benchmarking efforts into the high-resolution spatial transcriptomics domain and provides an open-access resource for the systematic assessment, comparison, and informed selection of emerging technologies within complex immune tissue environments.

Dr. Solano is a Postdoctoral Scientist at the Walter and Eliza Hall Institute of Medical Research in Melbourne. She joined Professor Matthew Ritchie's lab in April 2024, where she applies her expertise in imaging and data analysis to advance spatial transcriptomics. During her PhD in Biophysics from the University of Melbourne's School of Physics, Dr. Solano conducted research under the supervision of Associate Professor Elizabeth Hinde. Her doctoral work bridged physics and cell biology, developing and applying advanced imaging techniques, including fluorescence lifetime imaging microscopy and fluorescence fluctuation spectroscopy, to study chromatin organization and protein dynamics in living cells. She also created software tools to enable quantitative, high-resolution live-cell imaging. At WEHI, Dr. Solano's focus is on systematically benchmarking high-resolution spatial transcriptomics platforms and developing robust data analysis pipelines to ensure accurate, reproducible spatial omics results.

Roshan Vasani

Applications Specialist
Leica Microsystems

Zhou Feng

Honours Student
Jinan University/The Walter and Eliza Hall Institute of Medical Research

Overcoming the High Multiplexing Barrier: 3D Spatial Omics using STELLARIS SpectraPlex

SpectraPlex for STELLARIS is a comprehensive solution for 3D high-multiplex imaging in spatial biology. It provides a streamlined workflow to simplify panel creation, automate acquisition settings, and acquire data through advanced unmixing algorithms. With SpectraPlex you can ensure data quality and reliability across scales. SpectraPlex facilitates new insights into cellular organization, interactions, and spatial phenotyping. Get the power to see more and the productivity to do more, whether in cancer research, immunology, or neuroscience.

Roshan is an Applications Specialist at Leica Microsystems, holding a Doctorate in Biomaterials, specializing in iotechnology applications and a Master's degree in Nanotechnology

(Vivian) Zhuo Feng has just graduated from a Bachelor of Science degree at Jinan University in Guangzhou, China, majoring in the biotechnology. She focused on the lung cancer and learned cellular and molecular techniques for 3 years there. Zhou joined the InSPIRE program and worked on gamma-delta T cells' new marker in Dale Godfrey's lab at the Peter Doherty Institute, getting the training in immunology and flow cytometry where she discovered her passion for neuroscience and immunology. Zhou has recently completed a visiting honours program at WEHI in the Rogers Lab and Tonkin Lab, where she aimed to set up a 10-plex confocal imaging panel using stellaris to observe the interesting interactions between the neural cells and toxoplasma-injected neurons.

Andrew Pattison

Computational Biologist
Monash University

A spatial atlas of colorectal cancer reveals the influence of stromal niches on tumour differentiation

Colorectal cancer (CRC) is the third most common cancer worldwide and the second leading cause of cancer-related mortality. Tumour architecture is spatially heterogeneous, ranging from the necrotic core to the invasive front, accompanied by diverse stromal and immune responses that influence tumour progression and treatment outcomes. To explore the spatial organisation of the tumour-immune microenvironment, we profiled the expression of ~1,000 genes in 846,469 cells from 23 tumour and normal tissue samples using the CosMx Spatial Molecular Imager (SMI).

Andew Pattison is currently working as a father to a 2 year old toddler and 10 month old baby with a secondary role as a computational biologist studying colorectal cancer in the Abud lab at Monash University. He obtained his PhD in biochemistry/computational biology from Monash University in 2018 but is still completing his studies on what kids will eat for dinner. His background is staying awake past 10pm, RNA biology, cancer genomics and scRNA-Seq analyses with a focus on immunotherapy. Currently he is working on Play-Doh ponies, identifying farm animals from pictures and supporting the Abud lab members with their computational analyses.

Somi Kordafshari

Postdoctoral Scientist
The Walter and Eliza Hall Institute of Medical Research

Uncovering the cellular and molecular architecture of rare breast cancer subtypes through single-cell and spatial transcriptomics

ABSTRACT:

Rare breast cancer subtypes are associated with markedly poorer clinical outcomes compared to common forms, largely due to their heterogeneous behaviour and the lack of defined molecular targets. This clinical gap highlights the pressing need to unravel the biological mechanisms underlying tumour progression and metastatic potential in these rare subtypes. To address this, we applied the single-cell Fixed RNA Profiling assay to FFPE archival samples from aggressive, under-characterised breast cancer subtypes. Profiling ~600,000 individual cells, this high-resolution dataset enabled the construction of a detailed single-cell transcriptomic atlas, offering new insights into cellular diversity and transcriptional programs that were previously masked by bulk RNA-seq approaches. Building on this, we are employing the Xenium spatial transcriptomics platform to examine the in situ cellular architecture and communication networks within tumour tissue. Integrating spatial data with single-cell profiles is providing insights into patterns of cell-type localisation and ligand-receptor interactions across these rare breast cancer subtypes. Together, this study presents a powerful framework combining single-cell and spatial transcriptomics to dissect the molecular complexity of rare breast cancer subtypes.

Dr Somi Kordafshari is a postdoctoral scientist in the Breast Cancer Lab at WEHI. She completed her PhD in microbial genetics at the University of Melbourne, where she led several genomics-based studies on vaccine adaptation and attenuation using advanced molecular techniques. Driven by a passion for translational research, she transitioned into cancer biology and now investigates rare breast cancer subtypes using high-resolution single-cell and spatial transcriptomics. She brings broad expertise across RNA sequencing platforms and a wide range of molecular assays, contributing extensively to the lab's research projects. She currently leads a major study focused on rare breast cancers, integrating snRNA and spatial transcriptomics. Somi successfully optimised the FFPE snRNA-seq pipeline within the lab and has processed over 250 samples from fresh, frozen, and FFPE tissues for single-cell RNA and ATAC assays, consistently generating high-quality data with robust cell recovery. Her work has produced one of the largest single-cell FFPE datasets in breast cancer to date, revealing novel insights into tumour–immune interactions and spatially organised cellular niches

Natalie Charitakis

Murdoch Childrens Research Institute
The Walter and Eliza Hall Institute of Medical Research

Using spatial transcriptomics to understand the molecular mechanisms underlying cardiac rhabdomyomas

Cardiac rhabdomyomas are benign tumours that while extremely rare in the general population, are the most common form of primary cardiac paediatric tumour. The cause of cardiomyocyte proliferation leading to these masses is unknown and currently, their presence can lead to severe health complications depending on their anatomical presentation. Although the rhabdomyomas have been shown to spontaneously regress. Here we use spatial transcriptomics data generated through the 10X Genomics Visium platform to profile the transcriptome of cardiac rhabdomyomas from 3 separate patients and mine the data within the VR-Omics framework, developed for the analysis and visualisation of spatial transcriptomics data. Here we observe transcriptional perturbations that are consistent across the patients and may be key to the rise of abnormal cardiomyocyte populations present within cardiac rhabdomyomas that are orthogonally validated using a traditional bioinformatics workflow.

Natalie is a bioinformatician at the Murdoch Children's Research Institute within the heart regeneration and disease team. She recently submitted her PhD co-supervised by her current lab and the Transcriptomics and Bioinformatics labs focusing on the application of spatial transcriptomics to investigate heart development and paediatric heart disease and is now focusing on the application of 3D spatial transcriptomics datasets

Yang Xu

PhD Student
The Walter and Eliza Hall Institute of Medical Research

stPipe: A flexible and streamlined R/Bioconductor pipeline for preprocessing sequencing-based spatial transcriptomics data

Spatially resolved transcriptomic analysis methods are rapidly maturing, with both academic and commercially available technology solutions able to generate high quality data at varying resolutions. Different platforms (e.g. 10X Visium, Slide-seq and Stereo-seq) have their own protocols and customised analysis pipelines, which presents challenges when the goal is to obtain uniformly pre-processed data for benchmarking or for further downstream analysis using established tools. The current lack of open-source solutions that can deal with sequencing-based spatial transcriptomics (sST) data from different platforms motivated our development of the stPipe R package. stPipe provides a comprehensive and modular analysis pipeline that handles the following aspects of analysis: (i) data preprocessing from raw fastq files to obtain a spatially resolved feature count matrix; (ii) collection of appropriate quality control metrics during pre-processing to ensure unwanted artefacts can be removed; and (iii) adoption of standardised data storage containers to allow results to be easily passed on to downstream analysis packages for different goals (including clustering, cell-cell communication, etc). stPipe builds upon functionality in the scPipe package to allow in-depth exploration of the strengths and weaknesses of different sST technologies, guide analytical method selection and lead to the development of new and improved data processing pipelines. stPipe is available as an R package from GitHub and has be submitted to Bioconductor for the next release.

Yang is a second-year PhD Candidate in Ritchie Lab at the Walter and Eliza Hall Institute of Medical Research (WEHI). He completed his Bachelor of Science at the University of Sydney, followed by a Master of Science Degree at Nanyang Technological University in Singapore. His research focuses on method development and benchmarking in spatial transcriptomics

Denis Bienroth

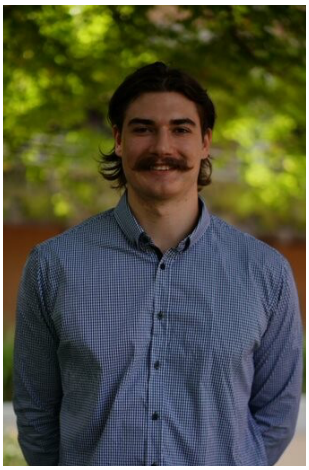
Software Engineer
Murdoch Childrens Research Institute

Automated Integration of Multi-Slice Spatial Transcriptomics Data in 2D and 3D using VR-Omics

We are in an era defined by data abundance, yet much of the biological insight within remains inaccessible due to the complexity of analysis pipelines and the lack of intuitive tools. This bottleneck not only delays discovery but slows translational outcomes across biomedical research. At the same time, spatial transcriptomics (ST) is transforming our ability to study gene expression in situ, preserving the spatial context crucial for understanding tissue architecture, cellular neighbourhoods, and multicellular interactions. While adoption of ST technologies has surged in recent years, the analytical potential remains under-realised due to fragmented, non-interoperable tools. To address this gap, we present VR-Omics, a platform-agnostic, end-to-end software suite for the automated integration, analysis, and 3D visualisation of multi-slice spatial transcriptomics data. Supporting a range of commercial ST providers, VR-Omics enables both 2D and 3D exploration of spatial data, making complex spatial relationships accessible to both computational and non-computational researchers. In a recent application, VR-Omics revealed dysregulated metabolic networks in rare cardiac

rhabdomyomas through co-planar slice analysis, discoveries that remained hidden using conventional tools, while reducing analysis times by over fourfold.By bringing together automation, interoperability, and novel visualisation, VR-Omics empowers researchers to move beyond static snapshots towards holistic, spatially-informed insights, paving the way for the next generation of spatial biology.

Denis Bienroth earned his Master of Science in Electrical Engineering/SoftwareDevelopment in Communication Technology from the Technical University in Kaiserslautern, Germany. He began his career as a software developer at the German Research Institute for Artificial Intelligence (DFKI) in 2018 and the Fraunhofer Institute, working on developing applications for medical training. Denis later moved into the field of industry, joining Empolis to develop cloud-based knowledge management solutions. In June 2021, he relocated to Melbourne, Australia, to work with Associate Professor Mirana Ramialison as software developer in bioinformatics at the Murdoch Children's Research Institute. Currently, Denis focuses on developing software in the field of biology and bioinformatics, mainly focusing in the automated analysis and visual exploration of omics and other data.



Jake Robertson

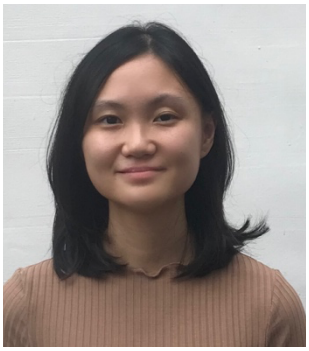
PhD Student

La Trobe University

Vascular smooth muscle cell de-differentiation in coronary artery disease promotes plaque instability

Myocardial infarction (MI) is the leading cause of death globally, primarily due to coronary artery disease (CAD). CAD is characterized by plaque development from lipid accumulation, immune cell infiltration and vascular smooth muscle cell (VSMC) phenotype changes within the vessel wall. Up to 70% of MI's occur due to fibrous cap instability, a process for which the underlying mechanisms remain poorly understood. Our aim was to identify key cell types involved in fibrous cap formation and degradation in human coronary arteries. We hypothesized that synthetic VSMCs promote fibrous cap formation in CAD, and that plaque instability results from their de-differentiation into macrophage-like phenotypes. Eight cryopreserved human left anterior descending coronary artery samples with varying degrees of CAD progression were analysed. Single-cell RNA sequencing (scRNAseq) and spatial transcriptomics were performed on fixed samples using probe-based transcript targeting and subsequent sequencing, followed by analysis with the Seurat package in R Studio. ScRNAseq of 32,481 cells identified nine major cell clusters, including endothelial cells, VSMCs, fibroblasts, macrophages, B cells, T cells, leukocytes, adipocytes, and neuronal cells. Gene ontology enrichment analysis revealed distinct biological VSMC subtypes associated with disease and spatial analysis showed varying prevalence of these VSMC subtypes in different stages of plaque progression. Synthetic VSMCs were highly, expressed in the fibrous cap of early disease, but not in the later stages. Conversely, late-stage disease samples were characterised by enriched Macrophage-like VSMC gene signatures within the fibrous cap of advanced plaques. This study provides new insights into mechanisms of VSMC heterogeneity in human CAD and highlights the phenotypic transition from synthetic to macrophage-like VSMCs may drive plaque instability. Future studies should explore therapeutic targeting of these transitions to prevent MI.

Jake is a final year PhD student at La Trobe University from the Centre for Cardiovascular Biology and Disease Research (CCBDR). His research focuses on multiomics approaches to investigate cardiovascular disease, including using single cell RNA sequencing, spatial transcriptomics and imaging mass cytometry. Jake's current research was conducted in conjunction with the not-for-profit organisation, CAD frontiers and the Sydney Heart Biobank.



Grace Yeo

GIS/BII Fellow
Genome Institute of Singapore/Bioinformatics Institute

Mapping molecular and morphological heterogeneity in colorectal cancer

Colorectal cancer (CRC) exhibits extensive molecular and morphological heterogeneity. While single-cell RNA-sequencing (scRNA-seq) has revealed the diverse cell types within the tumor microenvironment, the complex interplay between heterogeneous epithelial cell states and their spatial niches remains poorly understood. In this talk, I will present a large-scale effort to generate a cellular-resolution spatial atlas of primary colorectal cancer comprising over 9 million cells from more than 60 patients. By integrating across normal and diseased tissues, we identify molecular signatures such as stemness and hypoxia response that exhibit distinct spatial patterning within tumor glands. We also identify an invasive epithelial state at the tumor-normal interface, associated with tumor budding.

I will also discuss ongoing work aimed at bridging molecular profiling and computational histopathology. Recent advances in self-supervised foundation models have shown great promise for predicting clinical phenotypes from hematoxylin and eosin (H&E)-stained images. We demonstrate that models can be fine-tuned to predict spatial transcriptomic profiles directly from H&E, with robust generalization to external cohorts. Moreover, fine-tuned models enable interpretable de novo domain segmentation without requiring labor-intensive manual annotations. Together, these studies highlight how spatial omics is a powerful tool for understanding molecular and morphological heterogeneity in cancer.

Grace Yeo is a GIS/BII Fellow in the Single Cell and Spatial Omics Domain at GIS. She received her PhD from MIT in the Computational and Systems Biology program under the supervision of Dr. David Gifford. During her PhD, she developed computational analysis pipelines for novel scRNA-based perturbation assays, as well as deep learning methods for modeling biological processes such as cellular differentiation. At GIS, she works closely with the Shyam Prabhakar Lab to develop imaging and downstream analysis pipelines for spatial DNA and RNA assays applied to colorectal cancer. Her research interests revolve around the integration of modern machine learning methods with state-of-the-art –omic technologies for studying complex biological systems.

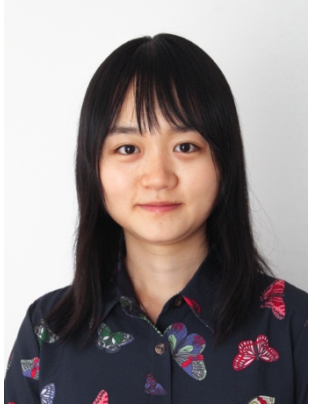
George Emanuel

Co-Founder & VP, Instruments
Vizgen Inc.

Extending Spatial Transcriptomics to Challenging Tissues: Enabling Discovery with MERFISH 2.0

High-plex spatial transcriptomics at single-cell resolution has transformed biological research, offering unprecedented insights into complex systems. However, archived tissues preserved using formalin fixation and paraffin embedding (FFPE), common in clinical and archival repositories, pose a challenge due to degraded or crosslinked RNA, limiting transcriptomic analysis. MERFISH 2.0™ addresses this critical barrier through an optimized chemistry and sample preparation workflow that significantly enhances transcript detection efficiency in degraded tissues.

George is a scientific cofounder and VP Instrumentation at Vizgen. Trained as a biophysicist at Harvard University in the lab of Prof. Xiaowei Zhuang, he has spent more than a decade developing highly-multiplexed RNA fluorescence in situ hybridization based technologies. This includes inventing a high-throughput, image-based screening technology and demonstrating the capacity of MERFISH technology to profile 10,000 genes in a single intact sample. Within Vizgen, George is responsible for the MERSCOPE instrumentation, enabling researchers to apply MERFISH technology to their own research.



Xiaohang (Helen) Fu

Postdoctoral Computation Biologist
Melanoma Institute Australia

Characterising melanoma resistance niches to immune checkpoint inhibitors using spatial transcriptomics and deep learning

Melanoma is the deadliest form of skin cancer. Despite the significant clinical efficacy of immune checkpoint inhibitor (ICI) therapy in metastatic melanoma, a large proportion of patients still do not respond to ICIs. A critical gap remains in defining the underlying factors of resistance and spatial heterogeneity within the tumour microenvironment (TME). To address this, we used single-cell spatial transcriptomics to map the architecture of tumour biopsies from two cohorts comprising 91 stage IV and 58 stage III melanoma patients. We developed an interpretable deep learning method that encodes biology within spatial neighbourhood niches to predict resistance to ICIs and uncover underlying factors. Our method achieved AUCs of 0.81 for the stage IV cohort and 0.77 for the stage III cohort in external validation. Our method revealed signatures of spatial niches, gene markers, localisation, and potential drug targets that are associated with ICI resistance. These results demonstrate the potential of our approach in enhancing the understanding of individual patient biology and predicting resistance to support tailored treatments.

Xiaohang (Helen) Fu is a postdoctoral computational biologist at Melanoma Institute Australia. Prior to her current role, she was a postdoctoral researcher at the School of Mathematics and Statistics at the University of Sydney. She received her PhD in Computer Science from the University of Sydney in 2023, and her Bachelor of Biomedical Engineering (Honours) with First Class Honours in 2018 from the University of Auckland. Her research interests are at the interface of deep learning, biomedical imaging, and spatial transcriptomics.

Bill Dougal

Group Leader
QIMR Berghofer

Spatial mapping of post-treatment specimens to identify therapeutic vulnerabilities and drug mechanism of action in ne***oa***djuvant immunotherapy treated lung cancer patients.

Non-small cell lung cancer (NSCLC) remains the leading cause of cancer-related death world-wide, despite major advances in immunotherapy, chemotherapy, and radiotherapy. Neoadjuvant immune checkpoint inhibitor (NeoICI) therapy improves clinical outcomes for patients with early-stage, resectable NSCLC and has now been incorporated into standard-of-care. However, not all patients respond to NeoICI, highlighting the importance of exploring novel combination immunotherapy regimens, driven by the potential for synergistic effects that could enhance anti-tumor immune response.

High-dimensional analysis of tissue samples from neoadjuvant “window of opportunity” studies offers a powerful approach for dissecting drug mechanisms and response to therapy in humans. We have integrated analysis of scRNAseq and high-content spectral flow cytometry on disaggregated tumour samples along with spatial transcriptomic (Bruker CosMx 6k SMI platform) and proteomic profiles (Akoya/CODEX) assessed on FFPE sections of tumour and tumour-draining lymph nodes (tdLN) obtained at surgery. The tumour undergoes profound treatment-associated remodeling and we characterised spatially-organized immune/tumour cell neighbourhoods which correlated with degree of pathologic response. Analysis of spatially-constrained cell-cell (CCI) and ligand-receptor (L-R) interactions in poor-responding patients reveal key cytokine pathways which may drive resistance to NeoICI. In order to inform mechanisms of drug response and rationalise novel NeoICI combinations, our analysis also focused on alterations in spatially-constrained CCI/L-R interactions within the tdLN that corresponded to therapy response and correspond with compartments which express novel drug targets. Our advanced molecular framework precisely maps how crucial immune and stromal cell types are organized into distinct spatially-defined groups and how treatment reshapes these groups, correlating with therapy response and drug mechanisms. This research highlights the vital role of tdLNs in immunotherapy by uncovering key immune interactions and pathways that drive treatment success. These insights can enhance precision oncology for NeoICI in NSCLC and other early-stage cancers

Dr Bill Dougall leads the Translational Oncology Discovery Laboratory at QIMR Berghofer and is the manager of the National Centre for Spatial Tissue and AI Research (NCSTAR) at QIMR Berghofer. Prior to his academic appointment in 2021, Dr Dougall worked in industry as a Staff Scientist in the Molecular Biology Department at Immunex Corporation and as Scientific Director at Amgen, Inc. He led multiple drug development programs in oncology and autoimmune disease through IND and Phase I-III testing, including world-wide registration of Prolia and Xgeva, agents widely used in metabolic bone disease and oncology patients. Dr Dougall has extensive experience with pharmacodynamic and patient stratification biomarker development (including IHC and transcriptomics) and has contributed to the translational design of over 20 oncology clinical trials (PI-III). He has authored more than 80 peer-reviewed publications (>17,000 citations) and holds seven patents.

Ning Liu

Postdoctoral Researcher

SAiGENCI, University of Adelaide

hoodscanR: Profiling single-cell neighborhoods in spatial transcriptomics data

Spatial transcriptomics reveals the complex spatial architecture of tissues, but current analytical tools often fall short of fully utilizing this rich information. Understanding cellular neighborhoods is important for investigating biological processes and disease mechanisms, yet existing methods struggle to detect mixed cellular neighborhoods and provide detailed single cell-level neighborhood profiles. To address these limitations, we developed hoodscanR, a Bioconductor R package for comprehensive neighborhood analysis in spatial transcriptomics data. hoodscanR identifies cellular neighborhoods using an efficient k-nearest neighbor search, generates cell-level neighborhood annotations, and quantifies neighborhood complexity using entropy and perplexity metrics. Applying hoodscanR to breast cancer and lung cancer datasets from different technology platforms, we demonstrate its ability to detect complex mixed neighborhoods and identify nuanced spatial patterns. Furthermore, hoodscanR enables neighborhood-based differential expression analysis, revealing transcriptional changes driven by the spatial composition of the tumor microenvironment. In conclusion, hoodscanR is a powerful software package to explore cellular neighborhoods within spatial transcriptomics datasets. By allowing researchers to investigate complex tissue biology with greater precision, hoodscanR has the potential to accelerate discoveries in cancer research, immunology, and other biomedical fields.

Dr Ning Liu is a senior bioinformatician at the Adelaide Centre for Epigenetics (ACE) and the South Australian Immunogenomics Cancer Institute (SAiGENCI). He specialises in developing computational algorithms and tools for spatial transcriptomics and proteomics, single-cell multi-omics, and epigenetics, with a focus on cancer and developmental biology. Dr Liu completed his PhD in Bioinformatics at the University of Adelaide in 2021, followed by a postdoctoral position at the Bioinformatics Division of WEHI until 2024. He has published in high-impact journals such as Nucleic Acids Research, Genome Biology and Nature. He is the developer of multiple Bioconductor packages including hoodscanR, standR, and scider, and is actively involved in mentoring, teaching, and bioinformatics training both locally and internationally.

Ruby Huang

Head Life Science Data Research Centre
The University of Tokyo

Spatial transcriptomic profiling of ovarian clear cell carcinoma reveals intra-tumor heterogeneity in OXPHOS and epithelial-mesenchymal gradients associated with clinical outcomes

Intratumoral heterogeneity is intrinsically comprised of molecular alterations of tumor cells and extrinsically from interconnections with microenvironments. This study explores the spatial heterogeneity of ovarian clear cell carcinoma (OCCC), a rare cancer with significance to East Asian women. We profiled 21 tumor whole slide sections (2 patients) from matched ovarian and metastatic sites in a discovery and a validation cohort (7 patients, 11 tumor sections) with spatial transcriptomic (ST) platforms including GeoMx and Visium CytAssist. Three subclusters of OCCC tumor cells enriched in oxidative phosphorylation (OXPHOS), inflammation, and DNA repair pathways were identified with preferential geospatial localizations in tumor centers and invasive margins/tumor-stromal interfaces following epithelial-mesenchymal gradients. Functional studies revealed that OCCC cells undergoing partial EMT had metabolic shifts and lost the expression of LCN2, an iron metabolism-related gene, possibly via the concomittent down-regulation of SOX9. These ST subcluster was confirmed to associate with the known progsnotic features of OCCC in large public datasets such as CSIOVDB. OXPHOS ST subcluster was enriched in the EpiCC molecular subtype while LCN2 expression showed a negative correlation with EMT scores and was also enriched in the OXPHOS ST subcluster and EpiCC, suggesting its role in the epithelial state. Single-cell ST in CosMx further identified 9 geospatially distinct cancer cell populations including the LCN2-high cancer subclone with a high epithelial score. Our findings provide an in-dpeth exploration of the ST landscape in OCCC and highlight the interconnetedness between OXPHOS and epithelial-mesenchymal gradients within spatial complexities.

Professor Ruby Huang obtained her MD degree from National Taiwan University (NTU) in 1999 and is a board certified Obs & Gyn Specialist. She obtained her PhD degree in Anatomy and Cell Biology from NTU in 2008 and subsequently moved to Singapore and worked in A*STAR, NUH and NUS. She was recruited back to NTU in 2019 under the global talent recruitment program Yushan Scholar Program supported by Ministry of Education in Taiwan. She is currently Professor of the School of Medicine of NTU.

Shan Li

Sr. Staff Product Manager, Global Product Management
Illumina

A high-resolution spatial transcriptomic map of the pregnant mouse brain reveals regionally distinct gene expression regulation related to maternal behavior

Pregnancy in mammals triggers the remodeling of brain connectivity with associated changes in gene expression, all in preparation for motherhood. These changes include rewiring of neural circuitry distributed over several distinct brain regions, altered neuropeptide signaling, increased white matter integrity and increased neuropeptide content and volume of cerebrospinal fluid. These changes are associated with the regulation of maternal behavior as well as physiological changes during pregnancy. Due to technological limitations, it has been challenging to generate a high-resolution view of the coordinated gene expression changes that occur in various brain regions during pregnancy.
To provide a more comprehensive understanding of these processes, we used a novel Illumina high-resolution spatial transcriptomics (ST) platform to elucidate whole transcriptome gene expression in fresh frozen brain sections from virgin and pregnant (E18.5) mice. This ST solution is fully compatible with H&E staining and utilizes a large capture area, allowing for parallelized histological and high-sensitivity molecular analysis of 4-8 intact brain sections, without requiring precise mounting in small defined target zones. The large single-well design also reduces experiment complexity and simplifies library preparation while minimizing section-to-section processing variability. After sequencing the spatial libraries, we generated single-cell-resolution gene expression maps from multiple coronal sections of both virgin and pregnant mouse brains. Spatial gene expression, as well as cell typing by using existing brain scRNA-seq data as a reference, demonstrated that our data closely matches the expected gene expression profiles and cell type distributions of various brain regions. Through differential gene expression analysis, we identified >2000 regulated genes in multiple cell types across the pregnant brain. The most dramatic gene expression changes were observed in glutamatergic neurons of the habenular nucleus, a region involved in mood and stress regulation. In the habenula and surrounding regions, we observed gene regulation consistent with altered cell-to-cell communication, mediated by signaling pathways involved in neuron protection, survival and regeneration. In choroid plexus cells of the pregnant brain we observed elevated expression of genes involved in prolactin signaling as well as in downstream signaling pathways. This finding suggests prolactin may be involved in fluid balance control or control of nutrient and metabolite transport during pregnancy. In white matter of the pregnant brain we identified two genes, Sgk1 and IL33, undergoing opposite regulation specifically in oligodendrocytes, suggesting potential roles in myelination, neuroplasticity or cell survival. Finally, we found that the neuropeptide galanin is co-expressed with oxytocin and vasopressin at a higher level in the paraventricular nucleus of the pregnant brain. This finding highlights the synergistic roles of these neuropeptides in regulating maternal behaviors. Overall, this study demonstrates the power of Illumina's high- resolution spatial transcriptomic solution and provides a comprehensive spatial atlas of pregnancy-related gene expression regulation in distinct mouse brain regions

Shan has MSc. in Biomedical Sciences from King's College London and PhD in Breast Cancer Research from the City of Hope National Cancer Center. Before Joining Illumina, she was a Post-Doc at UCSD Pharmacology focusing on transcriptional regulation research of cancer metastasis and development. As a product manager at Illumina, she has managed a variety of new product introductions and launch events across Illumina assay portfolio. Her most recent focus and excitement is the development of Illumina spatial technology.

Akriti Varshney

Research Officer

Murdoch Childrens Research Institute

Uncovering Alternative Polyadenylation in Single-Cell and Spatial Transcriptomics Using PolyApiper

This work analyses cardiac gene expression from the Human Heart Cell Atlas using PolyApiper, a novel tool for detecting alternative polyadenylation (APA) from single-cell and spatial RNA-seq data. Integrating both data types allows exploration of APA variation across cell types and spatial regions in the healthy heart. As a key post-transcriptional mechanism, APA influences mRNA stability, localisation, and translation, offering potential insight into gene regulation underlying heart development and disease.

Akriti completed her PhD in an RNA Systems Biology lab at Monash University in December 2024. She now supports research as a Research Officer in the Transcriptomics and Bioinformatics group at the Murdoch Children's Research Institute, where she analyses single-cell and spatial RNA sequencing data to uncover molecular mechanisms underlying muscle development, ageing, and disease.

Marek Cmero

Senior Research Officer

The Walter and Eliza Hall Institute of Medical Research

WEHI's Spatial Omics Data Analytics (SODA) Hub: an environment for spatial analysis from data generation to analysis and beyond

Spatial omics has the potential to enable precision diagnostics due to the wealth of information obtained from combining bioimaging, transcriptomic and proteomic technologies. Management and analysis of spatial data has remained a challenge, with large data volumes, numerous technologies and lack of standardised processing pipelines adding to the complexity. The WEHI Spatial Omics Data Analytics (SODA) Hub has been established to provide streamlined environment for users of spatial technology at the institute, from data and metadata management to analysis pipelines.
In this presentation, we will outline how the SODA-Hub will support spatial research at the institute by handling data ingestion and metadata collection, streamlining the movement of large data sets and organising data in a way that is FAIR (findable, accessible, interoperable, and reusable). The OME Remote Objects System (OMERO) image management system serves as the foundational platform of the environment and will provide spatial researchers with the ability to view, analyse and organise their spatial data. To streamline analysis, SODA-Hub will provide a suite of pipelines, including cell segmentation and downstream tools for the MERSCOPE, Xenium and COMET platforms, implemented in performant Nextflow pipelines and accessible via a user-friendly web-interface provided by Seqera Platform. This streamlining of spatial research at the institute will lead to better research outcomes, and ultimately better health outcomes for patients.

Marek is a Senior Research Officer with a joint appointment in the Bioinformatics and Advanced Technology & Biology divisions at WEHI. With a background in computer science and bioinformatics, he completed his PhD in cancer genomics at the University of Melbourne. Currently, he leads pipeline development for the Spatial Omics Data Analytics (SODA) hub at WEHI. Additionally, Marek dedicates one day per week to maintaining pipelines and workflows for sequencing bioinformatics in the Advanced Genomics Facility. Marek is passionate about developing robust and scalable computational solutions to drive biological discoveries.

Naveed Ishaque

Group Leader
Berlin Institute of Health at Charité

2D, or not 2D? That is the question! (Investigating cell overlaps in spatial transcriptomics data)

Spatially resolved transcriptomics (SRT) technologies can measure gene expression in cells in tissue. A common step in contextualising the data generated by these SRT methods is to assign observed gene expression to cells. In order to do this, the precise borders of cells need to be identified - this process is called cell segmentation.

In my presentation I will provide cartoon examples of how gene expression is measured by SRT methods, describe some exisiting cell segmentation strategies, show some scenarios that demonstrate why cell segmentation isn't easy, introduce the concept of cell-segmentation-free analysis of SRT data, describe some of the cell-segmentation-free analysis tools developed in my group (SSAM, Sainsc) and conclude on how cell-segmentation-free analysis can fit into a traditional SRT data analysis workflow

Naveed studied Computing at Imperial College and slowly made his way into bioinformatics where his PhD research was on using computational methods to better understand the genomics basis of molecular plant-pathogen interactions. Since then he moved to the field of cancer research and is now leading the Computational Oncology research group at the Berlin Institute of Health at Charite

Alex Swarbrick

Program Director and Lab Head
Garvan Institute of Medical Research

Decoding breast cancer ecosystems with spatially resolved 'omics

The tumor microenvironment (TME) is a critical regulator of cancer initiation, progression, and therapeutic response. A detailed understanding of the regulatory logic of the TME will enable the development of novel therapeutic strategies to remodel the TME and improve the sensitivity of tumours to therapeutic agents. In this presentation, I will describe my lab’s latest work using single-cell and spatially-resolved ‘omics to define cellular and molecular determinants of stromal & immune remodeling in solid cancers.

Alex is a Senior Principal Research Fellow and Director of the Cancer Ecosystems Program in the Garvan Institute of Medical Research; a Professor at UNSW Sydney and an NHMRC Senior Leadership Fellow. Alex completed his PhD at UNSW Sydney, followed by a postdoctoral fellowship with J. Michael Bishop at UCSF. His lab combines cellular and spatial ‘omics analysis of human cancers with disease models to gain systems-level insights into disease aetiology and the development of novel treatment strategies.

Jessica Da Gama Duarte

Laboratory Head and Senior Research Fellow
Monash University

Using B Cells and Tertiary Lymphoid Structures to Predict Cancer Outcomes.

Prostate cancer remains one of the most prevalent cancers detected in males, but adequate prognostic biomarkers that can distinguish between indolent and aggressive disease are currently lacking. An inflamed tumour microenvironment can lead to the development of tertiary lymphoid structures (TLS), which can mount adaptive effector and memory immune responses than can inform patient outcomes. In functional TLS, B cells can undergo dynamic tumour antigen-driven development into antibody-secreting cells (ASCs).
In this study, we aimed to develop in-house Opal™-TSA multiplex immunohistochemistry panels to adequately identify B cells, ASCs, and TLS, as well as characterise TLS based on their maturity. We then used these panels to investigate their prognostic value in a prostate cancer cohort of 64 low- and high-grade individuals, using treatment naïve prostatectomy tissue sections.
We successfully developed two in-house mIHC panels, including a B cell and TLS panel. ASCs were more commonly seen surrounding tumour areas (chi-square p-value=0.0024). Interestingly, a third of specimens lacked tumour-infiltrating ASCs (31%, n=20/64). ASCs were more abundant in patients with high-grade disease when located in both intratumoural (chi-square p-value=0.0188) and peritumoural regions (chi-square p-value=0.0001). It was evident that most relapse patients contained abundant intratumoural ASCs (chi-square p-value=0.0248). When investigating TLS, these were detected in most patient samples (73%, n=47/64), in both proximal and distal tumour areas. TLS were mostly mature (92%, n=43/47), and often surrounded by ASCs. Mature TLS were more abundantly seen in relapse patients (chi-square p-value=0.0012).
In conclusion, B cells and TLS in the tumour microenvironment of prostate cancer patients can be used to distinguish between low- and high-grade disease and to predict the likelihood of disease relapse.

Doctor Jessica Da Gama Duarte is a Victorian Cancer Agency Mid-Career Research Fellow (2024-2027) and expert in B cell tumour immunology and tertiary lymphoid structures. During her Doctoral studies at the University of Cape Town (South Africa) she developed a cancer-specific custom protein array platform and the accompanying bioinformatic software that will be used in this study. The underlying technology of this array was recognized as being of high quality, leading to it being patented by the University. Following the submission of her Doctoral thesis in 2015, she was recruited to the ONJCRI, Australia as a Postdoctoral Research Fellow. Here, she became an expert in multispectral immunohistochemistry, developing several in-house panels for the characterisation of immune infiltrates in solid tumours. She recently relocated to Monash University as a Lab Head and Senior Research Fellow. Here, she leads a small research team (3 PhD students, 1 Honours student, and 2 research assistants), and is closely mentored by senior scientists and clinicians. Since 2018, she has secured AU$4M in philanthropic, government, and industry funding as sole or lead CI. She is currently working on research projects that are aiming towards early detection of cancer onset and recurrence, prediction of immunotherapy benefit and/or toxicity, and understanding the role of B cells, antibody production, and Tertiary Lymphoid Structures in anti-tumour immunity.

Ng Lai Guan

Head Life Science Data Research Centre
The University of Tokyo

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.

Dr Ng conducted his PhD study at the Garvan Institute of Medical Research in Sydney, Australia. Following his postdoctoral training at Centenary Institute, Dr Ng joined Singapore Immunology Network (SIgN) to establish his own laboratory in 2009. Over the next 13 years, Dr Ng established himself as a leader in the field of myeloid cell biology. His research primarily focuses on unraveling the complexities of myeloid cell ontogeny, cellular behavior, and tissue adaptation. In 2023, Dr. Ng accepted a new position as a Senior Investigator at the Shanghai Immune Therapy Institute, where he also serves as the Director of the Center for Systems Immunology and a Professor at Shanghai Jiao Tong University in China. Dr Ng's contributions to the field of immunology research is exemplified by his multiple publications in leading journals such as Science, Nature, Science Immunology, Immunity, Journal of Experimental Medicine and Nature Protocols. He has also been listed as one of the Highly Cited Researchers by Clarivate for 5 consecutive years (2020-2024)

Emma Watson

Senior Research Officer

The Walter and Eliza Hall Institute of Medical Research

Advancing High-Plex Spatial Proteomics and Multiomics Using the Lunaphore COMET platform

Understanding the spatial organisation of cellular phenotypes within intact tissue architecture is critical for uncovering mechanisms of disease progression and tissue homeostasis. The Lunaphore COMET platform enables high-throughput, multiplexed immunofluorescence imaging of up to 40 protein markers at subcellular resolution in a single tissue section. Leveraging microfluidic technology for rapid and homogeneous reagent delivery, COMET achieves reproducible, iterative staining without the need for tissue stripping or antigen retrieval between cycles. Recent advancements now also allow for the simultaneous detection of up to 12 RNA targets in parallel with protein markers, enabling integrated spatial multiomic analyses within the same sample.

At WEHI, we have recently implemented the COMET platform as part of our growing suite of spatial omics capabilities. We have generated initial proof-of-concept data from human tissue samples, which is now being expanded to larger patient cohorts. This work highlights the technical capabilities of the COMET system and potential applications in translational research.

Dr Emma Watson is Senior Research Officer in WEHI's Centre for Dynamic imaging, where she leads spatial proteomics imaging initiatives. Her research focuses on the development and application of multiplexed imaging technologies and lightsheet microscopy to spatially resolve molecular and cellular dynamics in complex biological systems. Emma completed her PhD in 2017 and recently returned from a postdoctoral fellowship at the Max Planck Institute for Molecular Biomedicine in Germany. Her current work integrates spatial omics with high-resolution microscopy to advance our understanding of tissue organisation and infectious disease progression.

Shamini Ayyadhury

Director

Panoramics – A Vision

A Panorama of OMICS technologies, A Vision in Space : A pan-Canadian initiative for re-imagining conversations in science

No one is an island. And yet, individual creativity and growth are essential drivers of collective evolution and community advancement. How can we strike a balance between promoting individual development and cultivating a sense of unity—rooted in empathy and community engagement—that leads to meaningful knowledge acquisition in spatial and single-cell scientific exploration? Panoramics – A Vision was founded on these very principles: to

enlighten, challenge, and inspire both the individual and the collective. Our goal is to foster education, creativity, and entrepreneurship within the field of spatial and single-cell sciences.

Shamini Ayyadhury is the Founding Director of Panoramics – A Vision. Under her guidance, Panoramics has emerged as a vibrant hub for collaboration, knowledge exchange, and innovation in the spatial biology space. She is also a Machine Learning Computational Postdoctoral Fellow at the Acceleration Consortium (University of Toronto, Canada). She holds a PhD in Neuroscience from McGill University (Montreal), a Master's in Integrative Neuroscience from Imperial College London, and a Bachelor of Science from the National University of Singapore. She is also the co-founder and Chief Technology Officer of Astraea Bio, a Spatial Consultancy and Analysis start-up, where she strives to position AB as a trailblazer in the field, where scientific excellence meets visionary impact. Her scientific journey spans globally recognized institutions, including Nanyang Technological University, the National Neuroscience Institute, the Singapore Institute for Clinical Sciences (ASTAR), and the Singapore Immunology Network (ASTAR). With a versatile background that bridges computational method development, experimental design, and high-dimensional imaging analysis, Dr. Ayyadhury brings a rare blend of technical depth and creative scientific leadership. Dr. Ayyadhury is a recognized expert in spatial biology analysis, a trusted consultant, and an emerging thought leader in the field.

Thierry Jarde

Laboratory Head
Monash University

A Spatial Transcriptomic Survey of the Breast Cancer Microenvironment Across Subtypes and Metastases

Breast cancer is a heterogeneous disease influenced not only by tumour-intrinsic features but also by the surrounding microenvironment, including cancer-associated fibroblasts (CAFs), which play key roles in modulating tumour progression, immune responses, and therapeutic outcomes. To investigate spatial and cellular diversity across disease states, we are applying CosMx Spatial Molecular Imaging with the Human 6K Discovery Panel to a cohort of 28 breast cancer patients, representing all major subtypes—luminal A, luminal B, luminal A/B, HER2-enriched, triple-positive and triple-negative—along with matched lymph node metastases, adjacent normal tissues and healthy samples.

This unique dataset comprising of more than 3 million cells, enables both inter- and intra-patient comparisons, allowing us to examine how CAF phenotypes and spatial positioning vary not only between subtypes, but also across tissue compartments within the same patient. Our analysis aims to characterise spatially distinct CAF populations and their potential interactions with immune and malignant cells across different tumour contexts.

Dr Thierry Jarde is Head of the Stem Cell Niche Signalling and Cancer Laboratory in the Department of Anatomy and Developmental Biology at Monash University and Director of the Organoid Program at the Monash Biomedicine Discovery Institute. He is also a Victorian Cancer Agency Mid-Career Research Fellow. He is a cancer biologist who has worked for the last 15 years with organoids and mouse models to study stem cell function in health and disease.
He completed his doctoral studies at the School of Pharmacy (Clermont-Ferrand) in France before conducting postdoctoral training under the supervision of Professor Trevor Dale at the School of Biosciences (Cardiff University, UK) and Professor Helen Abud at the Biomedicine Discovery Institute (Monash University), where he studied the role of WNT and NRG1 signalling in cancer stem cell biology. Thierry has expertise in the field of stem cells (e.g. Cell Stem Cell, EMBO, PNAS), cancer biology (e.g. Gastroenterology, EMBO Mol Med) and organoid technology (e.g. Nature Communications, Gut, Oncogene). He has published 38 papers and successfully managed >3M in research funding (e.g. NHMRC, Victorian Cancer Agency, National Breast Cancer Foundation, Cabrini Foundation and CASS Foundation grants).

Abbey Cutchin

Director of Product Management
Element Biosciences

From Sample to Insight: Unlocking High Dimensional Biology with Direct In Sample Sequencing on AVITI24

Deciphering cellular complexity and elucidating biological mechanisms demand tools that go beyond single-modality measurements. AVITI24 is a first-of-its-kind integrated sequencing and multiomics platform that delivers simultaneous in situ transcriptomics, proteomic, and morphological profiling at single cell resolution. By eliminating the need for traditional library preparation, AVITI24 simplifies workflows while preserving spatial and phenotypic context and delivering comprehensive biological insights within a single day. Powered by Element's ABC sequencing, AVITI24 provides highly accurate multimodal data and enables a broad range of applications – from drug response pathway deconvolution and genetic perturbation screens to immune profiling and dynamic cell state analysis. AVITI24 empowers researchers to explore cell identity, signaling, and function with greater precision and scale, advancing high dimensional biology across a diverse biological systems and experimental contexts.

Abbey Cutchin is the Director of Product Management at Element Biosciences, where focuses on the development of the AVITI24 platform. In her role, she works closely with the R&D and commercial teams to define, develop, and launch new multiomics assays and applications on AVITI24. She was previously at 10x Genomics, where she focused on developing applications for single cell and spatial multiomics in cancer research.

Joel Moffet

PhD Student
The Walter and Eliza Hall Institute of Medical Research

SMINT-3D: An integrative spatial multi-omic workflow for unified analysis and 3-dimensional reconstruction of tumour tissue

Gliomas are cancers of the brain with a five-year survival rate of 22%, with current standard of care unable to prevent disease progression. The leading edge of the tumor is a key architecture involved in both recurrence and progression, but spatially resolved characterisation of this region is lacking. Increasing the dimensionality at which we interrogate glioma – into space and across omics platforms – will improve our understanding of the underlying mechanisms causing biological dysfunction. We have developed a spatial multi-omic integration pipeline, SMINT, to integrate transcriptomics and metabolomics at the

leading edge across serial sections of IDH-mutant glioma. We found that nuclei-only segmentation, while containing only 40% of segmented cell transcripts, enables accurate cell type annotation across different tissues and platforms, but cannot account for multinucleated cells. By combining spatial transcriptomics and metabolomics, our integrative analysis demonstrated tissue regions that are transcriptionally distinct with an associated unique metabolic landscape, identifying increased OPC-like tumor cells that may drive invasion. By interpolating between sections via Kriging, we can extend our pipeline to develop a 3D model of disease architecture (SMINT-3D). Validated with mouse brain and human glioma using MERFISH, Xenium and CosMx, Kriging displays promising accuracy (60-70%) in predicting the spatial changes to cellular neighborhoods across serial sections spaced over 200 microns apart, offering a cost-effective approach to reconstructing 3D tissue. There is significant need to improve our understanding of the leading edge in glioma, which will be enhanced by innovative spatial multi-omic strategies. Investigating glioma by combining our SMINT pipeline with Kriging interpolation will improve our ability to identify spatial drivers of tumorigenesis and develop effective treatments for patients.

Joel is a 3rd year PhD student in the Brain Cancer Research Laboratory at WEHI. He completed undergraduate studies in 2020 at the University of Western Australia, majoring in Genetics and Statistics, before receiving First Class Honours in Medical Research at the Harry Perkins Institute in 2021. His current research aims to characterise the complex intricacy of brain cancers in three dimensions, using emerging spatial -omic platforms and genetically engineered mouse models

Jiadong Mao

Postdoctoral Research Fellow

The University of Melbourne

Φ-Space for biological discovery in Stereo-seq data with cancer lineage tracing

Φ-Space is a computational tool that maps cells and spatial units to continuous phenotypic states. Φ-Space achieves this by leveraging reference datasets with multiple phenotype layers (e.g. cell type, disease condition and pseudo-time) from bulk or single-cell RNA-seq experiments. When applied to spatial RNA-seq data, Φ-Space proves to be a platform-agnostic method which discovers cell states in complex tissue microenvironments. In this talk, I will focus on some case studies involving Stereo-seq data from cancerous tissues with cancer clone lineage tracing using SPLINTR cellular barcoding. We will showcase how Φ-Space has revealed cell state diversity of acute myeloid leukaemia (AML) clones, providing the basis for explaining how AML clones evolve through transcriptional plasticity in situ. We will then introduce how the Φ-Space-based pipeline has yielded promising results for deciphering molecular mechanisms behind the formation of desmoplastic and replacement growth patterns in liver metastases.

Dr Jiadong Mao is a postdoctoral research fellow at the Lê Cao Lab in Melbourne Integrative Genomics (MIG) and holds a PhD in statistics from the University of Melbourne. His research focuses on creating innovative computational tools to address analytical challenges in biomedical studies involving high-throughput sequencing data. Passionate about advancing biomedical research, particularly in stem cell and cancer biology, he has developed Φ-Space and Φ-Space ST, reference-based tools designed to unravel developmental and disease-altered cell states in single-cell and spatial omics datasets. Jiadong's work aims to bridge computational biology with biomedical discovery, providing new insights into complex cellular processes. He initiates and maintains collaborations with biomedical and statistical researchers from both Australian and international institutions such as Peter MacCallum Cancer Centre, MD Anderson Cancer Center, University of North Carolina Chapel Hill, KU Leuven, Florey Institute and Ludwig Maximilian University of Munich. He is currently supervising three PhD students and three master students. He is actively teaching and mentoring junior colleagues to enhance their statistical and computational skills.

Lisa Waylen

Research Officer

Murdoch Childrens Research Institute

Formation of Boundaries in the Lateral Plate Mesoderm

Spatial patterning, the process by which cells organize into distinct spatial domains, is crucial for establishing morphogenic boundaries and functionally relevant structural demarcations. The lateral plate mesoderm (LPM) is a bilateral tissue which arises from the embryonic mesoderm during gastrulation and contributes to lineages as diverse as the cardiovascular, haematopoietic, musculoskeletal, and renal systems. This development programme relies on the robust expression of spatially restricted genes, where variation in expression may lead to catastrophic developmental defects and disease. The regulatory mechanisms which delineate the boundaries of these spatial domains remain largely cryptic, with few of the regulatory gene components identified. To address the challenge of identifying all genetic components actively expressed at the LPM boundaries, we used 19 established marker genes to describe the molecular signature of the LPM and predicted 247 novel determinants of the LPM boundaries through unbiased, computational modelling of spatially resolved transcriptomic data. Hierarchical clustering was used to model these gene targets to identify novel, spatially restricted expression regions within the LPM, and mined, bioinformatic gene annotations were used to infer the position of progenitor domains. This work contributes new insights into the complex development of embryonic boundaries critical for spatial tissue organisation, and a wealth of novel, unannotated candidates for further characterisation and study.

Lisa Waylen is a postdoctoral researcher in the Transcriptomics & Bioinformatics Group at the Murdoch Children's Research Institute. She completed her PhD in 2023 under the supervision of Professor Mirana Ramialison, where she explored the formation of spatial boundaries in the lateral plate mesoderm. Lisa's research focuses on understanding how spatial tissue patterns emerge during development, with a particular emphasis on early cardiac formation. She uses spatial transcriptomics and computational modelling to uncover the molecular mechanisms that drive these complex biological processes.

Edwin Hawkins

Head, Colonial Foundation DiagnosticsCentre, Inflammation Division Laboratory Head
The Walter and Eliza Hall Institute of Medical Research

A/Prof. Edwin Hawkins is an immunologist and cancer biologist. His laboratory uses in vitro and in vivo live cell microscopy to understand development of immune disorders and hematological malignancies. He conducted his PhD in the Immunology division at the Walter and Eliza Hall Institute (Melbourne, Australia) then relocated to the Peter MacCallum Cancer Centre (Melbourne, Australia) where he studied mechanisms that regulate lymphocyte fate and development of leukemia. In 2012, Edwin moved to Imperial College London (U.K., London) with Cristina Lo Celso to establish 2-photon microscopy techniques that allow long-term tracking of immune cells and leukemia development in vivo. Edwin returned to the Walter and Eliza Hall Institute as a laboratory head in October 2015 to establish his own research program focusing on developing new imaging techniques to understand hematopoiesis, inflammation and cancer. Edwin is also the Head and Chief Scientific Officer of the Colonial Foundation Diagnostics Centre, a joint initiative of WEHI and RMH, which uses cutting-edge spatial biology technologies, supported by state-of-the-art analytical approaches, including AI and ML, to deliver enhanced diagnosis and, in turn, personalised care for patients, with a focus on immune and inflammatory diseases.

Richard Harrison

Business Director
MGI

MGI - The Multi-Omics Company

2025 is the 10th anniversary of DNBseq entering the market and 9 years since the creation of MGI. In that short period MGI has created the industries largest portfolio of sequencing platforms including both long and short read, the largest range of lab automation products, and has firmly taken the lead as 'The Multi-Omics Company' with a complete range of single cell and spatial technologies including STOmics, which provides the highest resolution and greatest field of view.

With decades of experience in the life sciences, Richard has held key roles at leading global biotech companies ABI, Life Technologies, Bio-Rad, Thermo FIsher and MGI. After managing DNA sequencing at ABI during the first Human Genome Project, Richard pioneered forensic DNA technology across Asia-Pacific. At Bio-Rad Richard introduced digital PCR, accelerating the Asia Pac region's adoption of non-invasive liquid biopsy. Now at MGI, Richard brings his deep expertise to advance cutting-edge genomics across Australia and New Zealand—driven by a passion for innovation and belief in MGI's mission.

Mirana Ramialison

Group Leader

Murdoch Childrens Research Institute

2021: A spatial odyssey

We are witnessing a paradigm shift in translating genomic data into action, driven by the rise of “spatial-omics” technologies. For the first time, we can profile every cell’s genome while maintaining spatial information. This is crucial, because existing methods only allow sequencing of cells either in bulk or isolation, lacking the possibility to investigate cell-to-cell interactions. Providing the missing link of cellular interactions in native 3D environments has already led to precise discoveries on genetic causes of diseases, improved diagnosis, better treatment strategies, and enhanced patient outcomes. Here I will discuss recent advances and challenges in spatial transcriptomics and present our proposed solutions in spatial data analysis, to overcome major roadblocks in the widespread adoption of spatial-omics technologies.

Associate Professor Mirana Ramialison is Group Leader of the Bioinformatics and Transcriptomics Laboratory at the Murdoch Children’s Research Institute in Melbourne, and heads the reNEW Bioinformatics Hub of the Novo Nordisk Foundation for Stem Cell Medicine. A/Prof Ramialison received her Engineering degree from the University of Luminy, after which she worked as a programmer at the ERATO differentiation project in Kyoto. She obtained her PhD from the European Molecular Biology Laboratory in Heidelberg in 2007, and joined the Victor Chang Cardiac Research Institute in Sydney as an EMBO and HFSP Post-Doctoral Fellow in 2010. As an NHMRC/Heart Foundation Career Development Fellow, she established her first laboratory at the Australian Regenerative Medicine Institute (Monash University) in 2014. She is currently a Heart Foundation Future Leader Fellow, winner of the 2023 Shirley E Freeman Innovation Award.