Global Engage

AMERICAN SPATIAL BIOLOGY CONGRESS

## SAN DIEGO, USA
Marriott La Jolla
9-10 May 2024
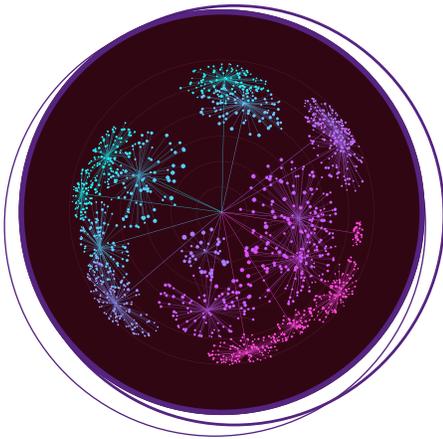
Global Engage is pleased to announce the **American Spatial Biology Congress**, which is confirmed to be held on 9-10 May 2024 at the Marriott La Jolla in San Diego.

Following the success of our International Spatial Biology Congress: Europe for the last 2 years, we are delighted to be hosting a Spatial Biology event in America. In this rapidly developing field, spatial biology provides significant potential for creating novel clinical insights. Recent technological advancements in spatial biology have provided insights into new strategies to prevent and treat disease, particularly the interactions between the tumor and the tumor microenvironment in cancers to target patients to more specific treatments. New spatial research has focused more on the analysis of the transcriptome, epigenome, and metabolomics as well as gene and protein expression to discover how these influence cellular and molecular distributions and interactions.

With a single track over two days, featuring more than 20 presentations, you will discover the latest developments in spatial omics and techniques, bioinformatics, and spatial biology data analysis, as well as the application of spatial biology to disease and drug development. There will also be a dynamic exhibition room filled with providers showcasing their spatial technologies with ample networking opportunities, an interactive panel discussion, roundtables, and a poster competition.

We are also holding our **Digital Pathology & AI Congress: USA** at the same venue on 7th and 8th May 2024. Find out more about the event here: **https://global-engage.com/product/digital-pathology-usa-2024**
Contact **maria@globalengage.co.uk** for a discounted package to attend both meetings.

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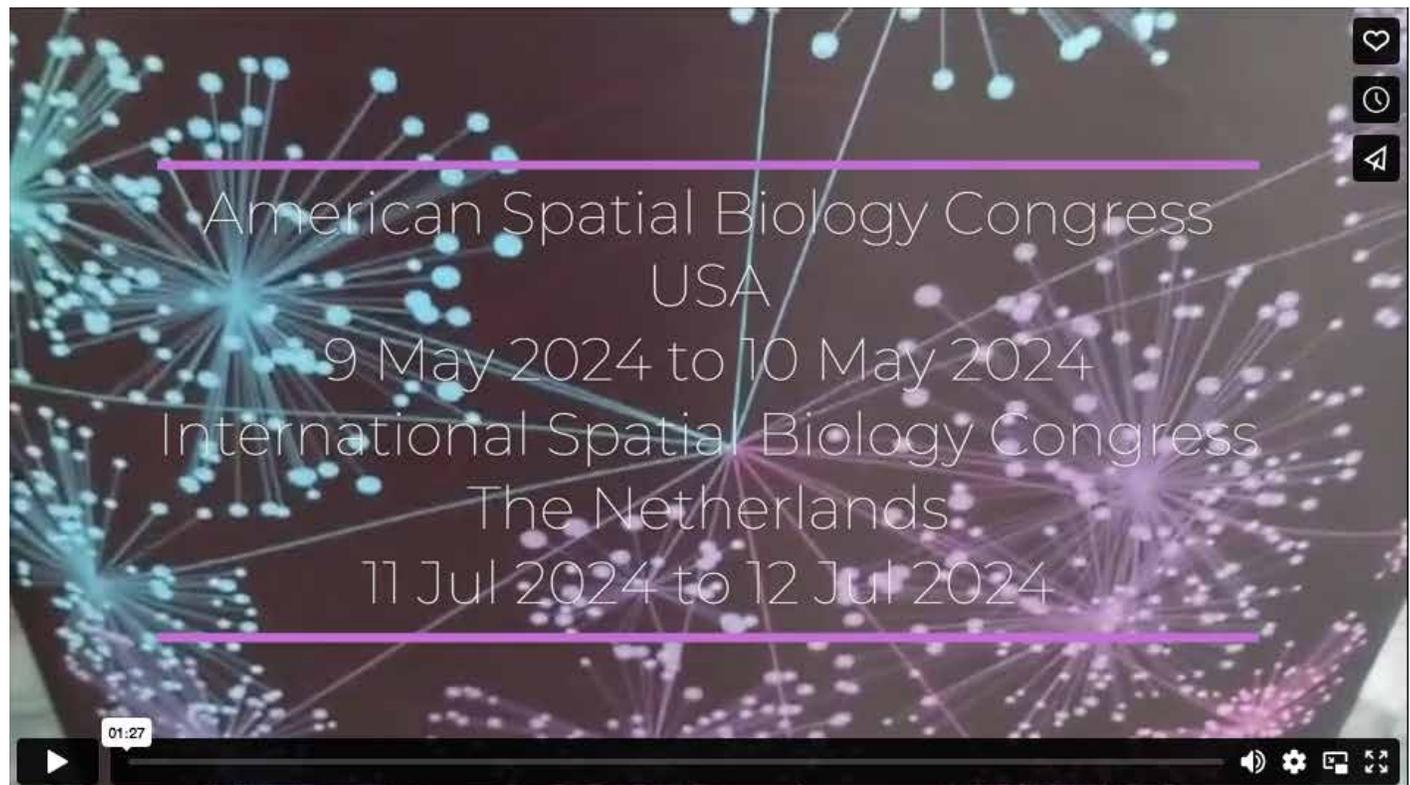
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Spatial multiomics techniques and approaches:
- Spatial genomics and proteomics
- Spatial transcriptomics, metabolomics and epigenomics
- Single cell analysis
- Combining omics data and technologies
- Transitioning from a 2D to a 3D perspective

Analysis and interpretation of spatial data, bioinformatics, and computational tools:
- Data standardization
- Computational platforms
- Bioinformatics
- Tissue imaging and analysis using AI

Application of Spatial Biology in translational and clinical medicine:
Spatial Biology therapeutic applications in:
- Oncology
- Tumor microenvironment
- Personalised medicine
- Biomarker identification and diagnostics

Panel Discussion:
Proposed options:
- Spatial Biology Data Analysis, Standardisation and Storage
- Applying Spatial Biology to drug development

Roundtables:
Proposed options:
- Challenges with spatial biology data standardisation and analysis
- Spatial Biology beyond cancer- how spatial biology is applied to other disease areas
- Role of AI in Spatial Biology

	Track 1
Day 1	Spatial multiomics techniques and approaches Analysis and interpretation of spatial data, bioinformatics, and computational tools
Day 2	Application of spatial biology in translational and clinical medicine

CONFIRMED & RESERVED SPEAKERS

ANKA EHRHARDT
Director, Analytical Research and Development, Cell-based sciences, Merck & Co

LINGYAN SHI
Assistant Professor, Bioengineering University of California, San Diego

NICHOLAS BANOVICH
Associate Professor and Director, TGen's Center for Single Cell and Spatial Multiomics

STEPHEN WONG
Scientist and Chair Professor, Houston Methodist Hospital and Professor of Weill Cornell Medicine

AHMET COSKUN
Principal Investigator, Georgia Institute of Technology

AKIL MERCHANT
Associate Professor of Medicine, Director, Spatial Molecular Profiling Core, Co-Director Lymphoma Program, Co-Director Heme/Onc Fellowship, Division of Hematology and Cellular Therapy, Cedars-Sinai Medical Center

ARVIND RAO
Associate Professor of Computational Medicine and Bioinformatics, University of Michigan

ELIZABETH NEUMANN
Assistant Professor, University of California Davis

FLORICA CONSTANTINE
Doctoral Student, Department of Statistics, University of California, Berkeley

KYOUNG JAE WON
Associate Professor, Department of Computational Biomedicine, Cedars-Sinai Medical Center

LEAH SCHAFFER
Postdoctoral Scholar, University of California, San Diego

MARYAM AFKARIAN
Richard A. and Nora Eccles Harrison Endowed Chair in Diabetes Research, Depner Endowed Professor of Medicine, Division of Nephrology, Department of Medicine, University of California, Davis

WILLIAM HWANG
Assistant Professor, Physician-Scientist/ Principal Investigator, Associate Director, Radiation Biology & Research Program, Associate Member, Harvard Medical School, Massachusetts General Hospital, MGH Cancer Center, Broad Institute of Harvard and MIT

YANXIANG DENG
Assistant Professor of Pathology and Laboratory Medicine, University of Pennsylvania, Perelman School of Medicine

ALEXANDER KLIMOWICZ
Senior Principal Scientist, Boehringer Ingelheim

AMOS LEE
Chief Executive Officer, Meteor Biotech, Co. Ltd

ANDREAS WIESNER
Head of Product Management, Lunaphore Technologies

ANIA MIKUCKA
Senior Tissue Analysis Scientist, Ultivue

ANJALI RAO
Research Scientist, Research Data Science, Gilead Sciences

EDDIE MOLAR
Principal, Former Vice President Data Science, MeRealm LLC, Juvena Therapeutics

LAURA DILLON
Vice President, Translational Medicine & Bioinformatics, Incendia Therapeutics

PRIYANK PATEL
Senior Scientist, Boehringer Ingelheim

SANDRA DIAZ GARCIA
Scientist, Johnson & Johnson

SRIPAD RAM
Digital pathology and image analysis group lead, Pfizer

TRAVIS CLIFTON
Head of Clinical Sciences, Incendia Therapeutics

SENIOR REPRESENTATIVE
Miltenyi Biotec

8:50-9:00 — Global Engage Welcome Address & Morning Chair's Opening Remarks

9:00-9:30
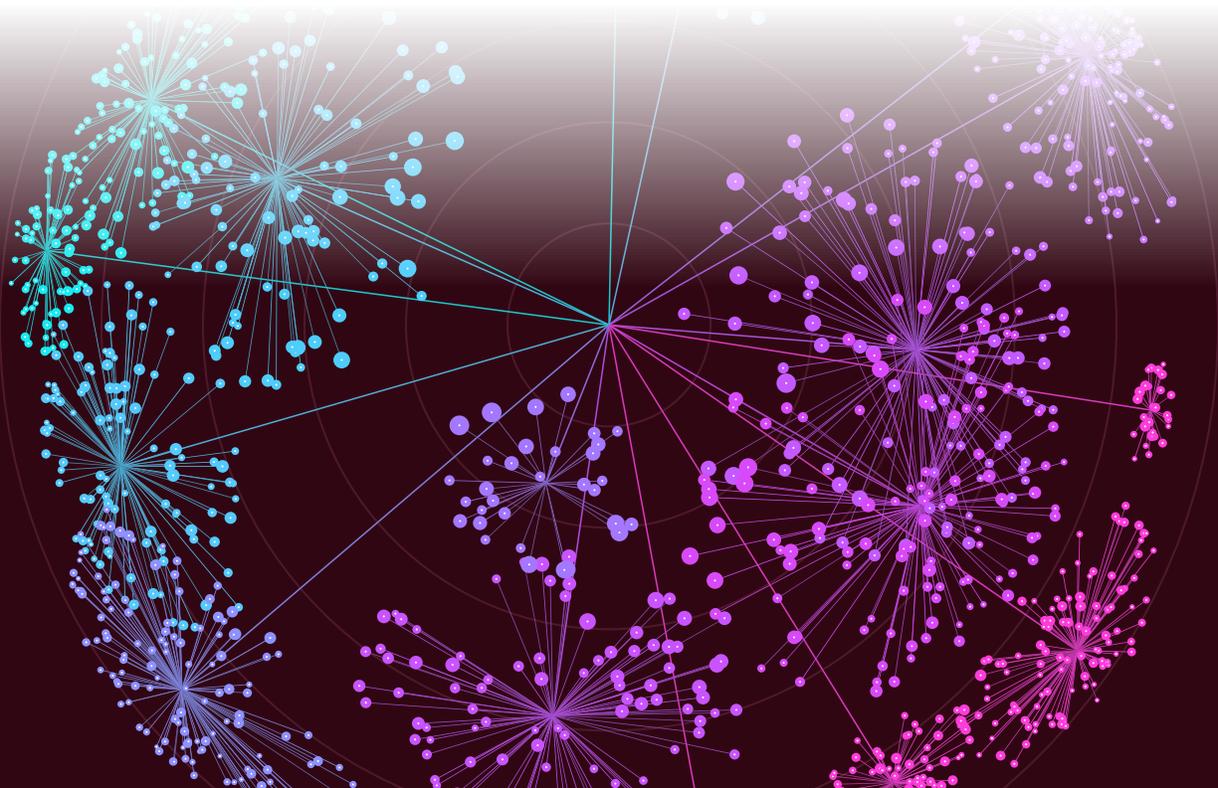
KEYNOTE ADDRESS:
LINGYAN SHI
Assistant Professor, Shu Chien-Gene Lay Department of Bioengineering, University of California, San Diego
Optical Imaging of Spatiotemporal Metabolic Heterogeneity in Aging and Diseases
Metabolism is a complex biochemical process in living organisms that involves different biomolecules and consists of various reaction steps. To understand the multi-step biochemical reactions involving various components, it's essential to elucidate in-situ dynamics and the correlations between different types of biomolecules at subcellular resolution. In this context, we integrated deuterium-probed pico-second stimulated Raman Scattering (DO-SRS), multiphoton fluorescence (MPF), and second harmonic generation (SHG) into a single microscopy system to study metabolic activities in cells, tissues, and animals during aging and diseases. Our current multimodal microscopy becomes a super-resolution (59nm) multiplex imaging platform by developing A-PoD and PRM deconvolution algorithms. Combining with deuterated molecules (glucose, amino acids, fatty acids, etc.) as probes, the metabolic heterogeneity of brain, adipose, liver, muscle, retina, kidney, lung, and ovaries, etc. (from Human, Mouse, and Drosophila) are quantitatively imaged.

9:30-9:55

KEYNOTE ADDRESS:
NICHOLAS BANOVICH
Associate Professor and Director, TGen's Center for Single Cell and Spatial Multiomics
Characterizing disease driven alveolar remodeling in situ using spatial transcriptomics
- Image based spatial transcriptomics to profile gene expression in over 1 million cells from 19 individuals.
- Novel transcript based niche analyses to identify pathologic and sub-pathologic tissue remodelling.
- Granular annotation of alveolar dysregulation using airspace segmentation.

9:55-10:25

ANIA MIKUCKA
Senior Tissue Analysis Scientist, Ultivue
Topic TBC

10:25-11:15 — Morning Refreshments / One-to-One Meetings / Poster Presentations

SPATIAL MULTIOMICS TECHNIQUES AND APPROACHES

11:15-11:35

YANXIANG DENG
Assistant Professor of Pathology and Laboratory Medicine, University of Pennsylvania, Perelman School of Medicine
Spatial multi-omics profiling of mammalian tissues
In this talk, I will begin with discussing the emergence of a whole new field – spatial omics – and then present a new technology platform called DBiT-seq – microfluidic Deterministic Barcoding in Tissue for spatial multi-omics sequencing. It demonstrated co-mapping of whole transcriptome and a large panel of proteins with high spatial resolution. I will also show the latest progress of DBiT as a platform technology to enable, for the first time, spatial profiling of epigenome (histone modifications and chromatin accessibility) at cellular level. Integration with single-cell data allows for accurate cell type annotation in relation to spatial location in tissue. The rise of NGS-based spatial omics is poised to fuel the next wave of biomedical innovation.

11:35-11:55

ELIZABETH NEUMANN
Assistant Professor, University of California Davis
Diversity Matters: Multiomic Spatial Exploration of complex biological systems
Organ systems are composed of unique cell types that actively coordinate to enable higher order functions. Even slight deviances in the molecular or cellular states of these systems can result in debilitating disorders whose severity, treatment course, and overall treatment outcome vary widely from patient to patient. This level of complexity likely contributes to promising therapeutics failing within clinical trials and, thus, require further exploration. Thus, the Neumann lab focuses on developing and applying multimodal imaging and profiling techniques to study complex human diseases, such as renal cell carcinoma, Alzheimer's Disease, and spina bifida.

11:55-12:25

AMOS LEE
Chief Executive Officer, Meteor Biotech, Co. Ltd
SLACS: Revolutionizing Molecular Analysis in Genomics, Transcriptomics, and Proteomics
Spatially-Resolved Laser Activated Cell Sorting (SLACS) is a transformative technology reshaping molecular biology. Specializing in isolating specific cell populations, SLACS enhances DNA and RNA sequencing by providing high-purity genetic material from targeted cellular niches. This precision is crucial for understanding complex genetic variations in diseases like cancer. In RNA sequencing, SLACS captures unique transcriptomic profiles, offering insights into gene regulation and expression patterns at a fine spatial resolution. Extending its utility to proteomics, SLACS integrates with mass spectrometry, enabling detailed protein analysis in specific microenvironments. As a versatile tool, SLACS not only deepens our understanding of molecular dynamics but also drives forward diagnostic and therapeutic innovations.

12:25-12:45

SANDRA DIAZ GARCIA
Scientist, Johnson & Johnson
Innovation in Preclinical & Translational Safety: Spatial Target Expression Profiling
Target Expression Profiling (TEP) is essential for assessing target risk in drug development. Analyzing human tissues reveals crucial target expression patterns for evaluating therapeutic efficacy and safety. The DSP GeoMx instrument facilitates spatial transcriptome analysis, enabling simultaneous detection of multiple RNA targets. This proof-of-concept (POC) study demonstrates DSP's value by providing comprehensive, anatomically resolved gene expression data across key tissues relevant to safety. The generated dataset supports longitudinal querying, aiding in biomarker discovery, enhancing understanding of tissue gene expression profiles. These insights are invaluable for optimizing drug development, ensuring both efficacy and safety are thoroughly assessed, thereby advancing precision medicine initiatives.

12:45-13:45 — Lunch

13:45-14:00

POSTER COMPETITION WINNER TALK:
if interested in submitting a poster and/or applying to present a poster on the programme, please **CLICK HERE** and apply before the deadline 19th April 2024.

14:00-14:20

WILLIAM HWANG
Assistant Professor, Physician-Scientist/Principal Investigator, Associate Director, Radiation Biology & Research Program, Associate Member, Harvard Medical School, Massachusetts General Hospital, MGH Cancer Center, Broad Institute of Harvard and MIT
Integrative multi-modal spatial approaches to study human oncology
- Role of spatial multi-omics in the study of cancer biology
- Spatial methods with single-cell resolution and diverse readouts including transcriptomics, proteomics, and morphomics
- Experimental and computational approaches to integrate multi-modal spatial data and glean unique biological insights

14:20-14:35

ANDREAS WIESNER
Head of Product Management, Lunaphore Technologies

Lunaphore

True spatial multiomics: when RNA meets protein on the same section
- Spatial profiling of both RNA and protein markers on the same tissue at the single-cell level is required for the discovery and validation of spatial biomarkers.
- Here, we show a novel multiomics approach that integrates RNAscope™ and sequential immunofluorescence (seqIF™) to simultaneously identify RNA and protein targets on the same tissue section in a fully automated workflow.
- This unique approach will enable researchers to generate highly reproducible data to characterize novel molecular signatures and support the development of targeted therapies.

14:35-14:50

15-Minute Solution Provider Presentation
For sponsorship opportunities contact Gavin Hambrook
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ANALYSIS AND INTERPRETATION OF SPATIAL DATA, BIOINFORMATICS, AND COMPUTATIONAL TOOLS

14:50-15:10

KYOUNG JAE WON
Associate Professor, Department of Computational Biomedicine, Cedars-Sinai Medical Center
Studying cell-cell interaction and data integration using high resolution spatial transcriptomics data
- Neighbouring cell (or cell contact) dependent gene expression change
- Investigating tumor microenvironment.
- Data integration for large amount of spatial data

15:10-15:30

AHMET COSKUN
Principal Investigator, Georgia Institute of Technology
Topic TBC

15:30-16:40 | Afternoon Refreshments / One-to-One Meetings / Poster Presentations

16:40-17:00

EARLY CAREER RESEARCHER PRESENTATION:
FLORICA CONSTANTINE
Doctoral Student, Department of Statistics, University of California, Berkeley
Analyzing Spatial Transcriptomics Data from Kidney Transplant Biopsies
- Describe a multi-tissue, multi-disease spatial transcriptomics dataset of kidney transplant biopsies
- Overview of cell type inference and annotation of the dataset
- Present results from a statistical analysis characterizing the differences in spatial organization and gene expression between diseases

17:00-17:30

SENIOR REPRESENTATIVE
Miltenyi Biotec
Topic TBC

17:30-17:50

EARLY CAREER RESEARCHER PRESENTATION:
LEAH SCHAFFER
Postdoctoral Scholar, University of California, San Diego
A multi scale map of proteome organization from integration of protein interactions and images
Cells regulate growth and function through a hierarchical structure of subcellular protein assemblies. Much of this structure remains uncharted, resulting in recent efforts to map subcellular organization at different physical scales. Here, we report a global architectural map of human cell protein assemblies, based on integration of near-proteome-wide affinity purification mass spectrometry-based protein interactions and immunofluorescent imaging in U-2 OS cells. The resulting whole cell U-2 OS multi-scale hierarchical map contains protein assemblies across biological scales, spanning from small protein complexes to large organelles. The U-2 OS multi-scale integrated cell map places >5000 proteins into 270 distinct subcellular protein assemblies. The global proteome architecture map provides a resource for cellular biology discovery and the systematic determination of protein functions and structures.

17:50-18:10

SENIOR REPRESENTATIVE
Invitation Out
Topic TBC

18:10 | End of Day 1

8:50-9:00 | **Global Engage Welcome Address & Morning Chair's Opening Remarks**

9:00-9:30

KEYNOTE ADDRESS:
STEPHEN WONG
Scientist and Chair Professor, Houston Methodist Hospital and Professor of Weill Cornell Medicine
A modelling and analytic pipeline of spatial imageomics data for revealing novel cell-cell communication pathways in tumor immune microenvironments with use cases in virus-infected brain metastasis and cancer-Alzheimer's disease comorbidity
- Present a spatial biology modeling and analytics pipeline that integrates spatial omics and multiplex imaging data to identify novel cell-cell communication and crosstalk targets in tumor microenvironments.
- Showcase the application of the spatial biology pipeline in revealing that human cytomegalovirus (HCMV) infection contributes to breast cancer brain metastasis through the creation of an immune-suppressive tumor microenvironment.
- Showcase the application of the pipeline in investigating molecular pathways of cancer that offer protection against the development and progression of Alzheimer's disease.

9:30-9:55

KEYNOTE ADDRESS:
ANKA EHRHARDT
Director, Analytical Research and Development, Cell-based sciences, Merck & Co
Spatial biology utility for industry applications

9:55-10:25

30-Minute Solution Provider Presentation
For sponsorship opportunities contact Gavin Hambrook
gavin@globalengage.co.uk

10:25-11:15 | Morning Refreshments / One-to-One Meetings / Poster Presentations

11:15-12:05

PANEL DISCUSSION:
Spatial Biology: Advancing Disease Research & Drug Discovery

STEPHEN WONG (Moderator)
Scientist and Chair Professor, Houston Methodist Hospital and Professor of Weill Cornell Medicine

NICHOLAS BANOVICH
Associate Professor and Director, TGen's Center for Single Cell and Spatial Multiomics

ELIZABETH NEUMANN
Assistant Professor, University of California Davis

Challenges in Spatial Biology (SB):
- Overcoming technical barriers in acquiring and analyzing spatial data within tissue samples.
- Harmonizing spatial datasets with established omics and advanced imaging modalities.
- Navigating the computational complexities of processing expansive and intricate spatial data.

Technological Innovations:
- Strategies for the standardization and management of spatial data.
- Breakthroughs in spatial transcriptomics and proteomics techniques.
- Creation and enhancement of computational tools and algorithms for analysis in 3D and 4D (time) spaces.

Impact on Disease Research:
- Examining spatial heterogeneity within tumors to inform cancer therapies.
- Deciphering the dynamics of cell interactions within tissue environments and their disease implications.
- Aiding the discovery and characterization of biomarkers and potential therapeutic targets.

Advancements in Drug Discovery:
- Utilizing spatial biology to identify and confirm new drug targets.
- Supporting drug development through in situ assessments of treatment effectiveness and action mechanisms.
- Tailoring personalized medicine approaches by considering the spatial distribution of drug targets.

ROUND DISCUSSIONS:

Roundtable 1: **Applying Spatial Biology to Clinical Medicine: Challenges and Opportunities**
TRAVIS CLIFTON
Head of Clinical Sciences, Incendia Therapeutics
A more thorough evaluation and understanding of tumors has the potential to improve the precision of pathologic evaluation, understand biology, guide treatment decisions, and improve outcomes. However, applying novel methods comes with unique challenges in implementation, reimbursement, and regulatory approval. This session will discuss near-term opportunities to improve clinical medicine utilizing emerging spatial technologies and strategies ways to get them to patients as quickly as possible.

Roundtable 2: **Topic TBC**
PRIYANK PATEL
Senior Scientist, Boehringer Ingelheim

Roundtable 3: **Emerging Frontiers in Discovery: How can AI/ML address critical spatial multiomic challenges?**
EDDIE MOLAR
Principal, Former Vice President Data Science, MeRealm LLC, Juvena Therapeutics
Explore and share how AI/ML tools and platforms are beginning to accelerate discovery and how they could address outstanding challenges.
- Critical Needs in Spatial Multiomics: We will first Identify key challenges in spatial + multiomics data acquisition, integration, analysis, and interpretation. e.g. data preprocessing, object recognition/segmentation, classification & phenotyping, spatial pattern identification, complex data integration such as clinical, single-cell RNASeq, tissue atlases, disease ontologies, pathways, and generating insights and hypotheses.
- Emerging Applications of AI/ML Bridging the Gap Between Data and Discovery: Next, we will share examples of how AI/ML tools are used today in research and spatial multiomics-related analyses.
- Future Directions and Challenges: Finally, we will address the future directions and challenges in this field. This might involve discussing the need for open-source AI tools specifically designed for spatial multiomics, fostering collaboration between data scientists and biologists, and ensuring ethical considerations in AI-driven discovery.

12:05-12:35

30-Minute Solution Provider Presentation
For sponsorship opportunities contact Gavin Hambrook
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AMERICAN SPATIAL BIOLOGY CONGRESS 2024

APPLICATION OF SPATIAL BIOLOGY IN TRANSLATIONAL AND CLINICAL MEDICINE

12:35-12:55

SRIPAD RAM
Digital pathology and image analysis group lead, Pfizer
A quantitative metric to characterize immune-cell infiltration in human and murine tumor specimens
- Introduce a novel metric called the biodistribution (BioD) score that provides a quantitative characterization of the spatial distribution of immune cells in a histological section.
- Demonstrate how BioD score can be used to study the spatial localization patterns of different immune cell subsets in preclinical and clinical tumor specimens and provide mechanistic insights into immune-cell infiltration.

12:55-13:55 | Lunch

13:55-14:10

POSTER WINNER PRESENTATION:
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please **CLICK HERE** and apply before the deadline 19th April 2024.

14:10-14:30

AKIL MERCHANT
Associate Professor of Medicine, Director, Spatial Molecular Profiling Core, Co-Director Lymphoma Program, Co-Director Heme/Onc Fellowship, Division of Hematology and Cellular Therapy, Cedars-Sinai Medical Center
Single Cell Spatial Biomarkers in Lymphoma
- Spatial Profiling of lymphoma reveals tumor microenvironment features which correlate with genetic sub-groups of lymphoma.
- Spatial Biomarkers can predict relapse after autologous stem cell transplant.
- Metabolic profiling can be incorporated with spatial profiling.

14:30-14:50

LAURA DILLON
Vice President, Translational Medicine & Bioinformatics, Incendia Therapeutics
Decoding immune exclusion in cancer for patient stratification
- Implementing spatial biology methods to assess immune exclusion in cancer
- Quantifying stromal features to gain insights into response to immunotherapy
- Decoding tumor immune phenotypes for patient stratification and precision medicine

14:50-15:10

ARVIND RAO
Associate Professor of Computational Medicine and Bioinformatics, University of Michigan
Machine learning approaches to the interpretation of spatial imaging & transcriptomics for personalized medicine
- Discussion of spatial immune profiling platforms and data science challenges
- Use of ML/AI for analysis and interpretation of high throughput spatial profiling data for immunotherapy
- Bioinformatics for spatial transcriptomics

15:10-15:30

ALEXANDER KLIMOWICZ
Senior Principal Scientist, Boehringer Ingelheim
Analysing fibroblast heterogeneity in fibrosis disease, using single cell sequencing heterogeneity data

15:30-15:50

MARYAM AFKARIAN
Richard A. and Nora Eccles Harrison Endowed Chair in Diabetes Research, Depner Endowed Professor of Medicine, Division of Nephrology, Department of Medicine, University of California, Davis
Spatial proteomics of kidneys from diabetes to DKD class III
- Diabetic kidney disease (DKD) is the leading cause of chronic and end-stage kidney disease in the US and worldwide. We need to understand molecular complexity of disease in human tissues before diagnosis and treatment would benefit from translation of what we have learned from animal models.
- Introducing our Spatial TissuE Proteomics pipeline (STEP) at UC Davis- what do we find when we use this pipeline to examine human DKD
- Pitfalls and areas of unmet need in application of spatial proteomics to human disease

15:50-16:10

ANJALI RAO
Research Scientist, Research Data Science, Gilead Sciences
Leveraging single cell and spatial transcriptomic profiling of FFPE tissue to drive novel early target identification in Crohn's Disease
Spatial transcriptomics provides a unique opportunity to integrate histological and transcriptomic information to increase our understanding of disease biology and drive new target discovery. Here, we take advantage of the technological innovation that allows matched single cell and spatial transcriptomics from FFPE tissue and apply this to a curated patient cohort. Using advanced bioinformatics analysis and histologically guided features, we report a novel framework to guide target discovery in inflammatory diseases.

16:10 | Conference Close

MAKING A POSTER PRESENTATION

Poster presentation sessions will take place in 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. We also issue a poster eBook to all attendees with your full abstract in and can share your poster as a PDF after the meeting if you desire (optional). Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this Congress. 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).

MAKING A POSTER PRESENTATION

We will require the form (downloadable below) to be submitted by the 19th April 2024. This is the formal deadline however space is another limiting factor so early application is recommended. Therefore, please contact us with any questions you have as soon as possible.

POSTER COMPETITION – CLOSING DATE 19th April 2024

1. Submit your entry prior to the closing deadline (1 entry per person)
2. Two entries for the American Spatial Biology Congress will be selected by the judges
3. The 2 winners of the poster presentation will be each be given a 15-minute speaking position on the conference agenda and will be notified in advance of the meeting
4. The judge(s) will make the decision based on the abstract(s) submitted
5. The winner will also receive a certificate from the organisers
6. Representatives from solution provider organisations or experts already speaking on the program are not eligible to enter the competition but are welcome to present posters at the meeting as normal

SUSTAINABILITY

Venues with Sustainability Goals

We are committed to selecting venues with more sustainable practices. These will cover energy supply, food & waste, water use, recycling and plastics. The Marriot La Jolla is **Tripadvisor GreenLeaders Certified**. The hotel website shows a carbon footprint of 11.6 kgs per room night. The hotel footprint calculator **Greenview** reveals that the US average is 17.6 kgs per night (higher for 4 & 5* hotels.)

Catering

You will have some great food choices while you are with us. We have worked with the caterer to increase the proportion of plant-based items. We have also built a plan with the venue to avoid waste through how they serve meals and how any leftovers are processed. Our aim is that you have some great meals, whilst with us, but with less environmental impact by the time you leave.

Travel

An international meeting does involve travel but where it is practical, please consider more sustainable alternatives to flying. The app will also have a discussion space to arrange ride shares.