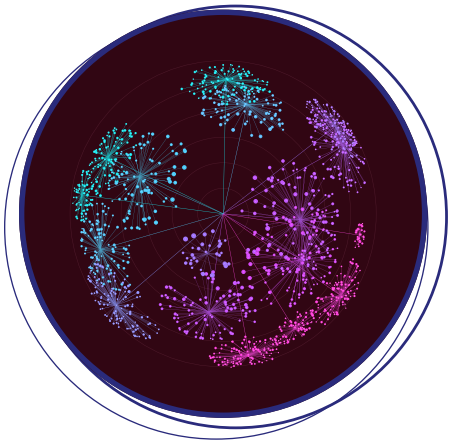
Global Engage

3RD INTERNATIONAL SPATIAL BIOLOGY CONGRESS

THE HAGUE, NETHERLANDS

THE HAGUE CONFERENCE CENTRE

11-12 July 2024



#spatialbiologycongress

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Global Engage

Global Engage is pleased to announce the **3rd International Spatial Biology Congress: Europe**, which is confirmed to be held on 11-12 July 2024 in The Hague, Netherlands.

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 tumour and the tumour 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 30 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 inclusive panel discussion, roundtables, and a poster competition.

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

- Oncology
- Tumour microenvironment
- Personalised medicine
- Biomarker identification and diagnostics

Panel Discussion

- Spatial Biology Data Analysis, Standardisation and Storage
- Applying Spatial Biology to drug development

Roundtables

- 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

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For more details contact Gavin Hambrook: gavin@globalengage.co.uk

CONFIRMED & RESERVED SPEAKERS

FRANCESCA CICCARELLI
Professor of Cancer Genomics, Principal Group Leader, King's College London, The Francis Crick Institute

NIGEL JAMIESON
Professor of Surgery and Consultant HPB Surgeon, Group Leader of Jamieson Spatial Laboratory, Cancer Research UK Clinician Scientist, School of Cancer Sciences, University of Glasgow

ELEANOR O'ROBERTS
Researcher, SciLifeLab

CHRIS HANLEY
Lecturer in Quantitative Cell Biology, University of Southampton

DANA MUSTAFA
Assistant Professor and Leader of the Spatial Biology Laboratory, Erasmus University Medical Center

FANI MEMI (Reserved)
Senior Staff Scientist, Wellcome Sanger Institute

KONSTANTIN MAKSIN
Locum Consultant Cellular Pathologist, Royal Berkshire NHS Foundation Trust

MIAO-PING CHIEN
Associate Professor and Principal Investigator, Erasmus University Medical Centre, Oncode Institute

MENGXIAO HE
Doctoral Researcher, KTH Royal Institute of Technology

STEPHANIE CRAIG
Lecturer in Precision Medicine, Queen's University Belfast

THIERRY VOET
Professor and Director, KU Leuven Institute of Single Cell Omics

VICTOR PEREZ
Postdoctoral Researcher at Schapiro Laboratory, Heidelberg University Hospital

VOLKER BRUNS
Group Manager Medical Image Processing, Fraunhofer IIS

ANDERS ERIKSSON
Lead Field Application Scientist, Canopy Biosciences

BRIAN REICHHOLF
Principal Scientist, Boehringer Ingelheim

DEBAYAN MUKHERJEE
Investigator- Spatial Imaging, Oncology Translational Research, GSK

HENRIK FAILMEZGER
Associate Director, Spatial Data Science, AstraZeneca

LORENZ ROGNONI
Director of Image Data Science, Ultivue

LUCIE CHRASTECKA (Reserved)
Expert Science and Technology, Novartis

MARC CLAESEN
Chief Executive Officer, Aspect Analytics NV

ROBERTO SPADA
Director of Marketing, Standard BioTools

TIANKUI PENG
Senior Application Scientist, SeekGene Biosciences

SENIOR REPRESENTATIVE
Lunaphore

SENIOR REPRESENTATIVE
(Reserved)
Sanofi

SENIOR REPRESENTATIVE
Vizgen

8:50-9:00 **Global Engage Welcome Address**

9:00-9:30

KEYNOTE ADDRESS:
NIGEL JAMIESON
Professor of Surgery and Consultant HPB Surgeon, Group Leader of Jamieson Spatial Laboratory, Cancer Research UK Clinician Scientist, School of Cancer Sciences, University of Glasgow
Insights from molecular mapping of gastrointestinal cancer across space and time
Studying clinical cohorts using spatial transcriptomics technologies offers the potential to impact our understanding of patient's tumours. Our central hypothesis is single-cell spatial characterisation will reveal therapeutic vulnerabilities not apparent when studying immune cell populations without spatial context. We aim to unravel the spatial interplay between cancer cells, and microenvironment as determinants of tumour progression across a variety of GI cancers including pancreatic and colorectal cancers. We have characterised large cohorts of human GI cancers using regional and single-cell transcriptomics strategies in the primary and metastatic setting in effort to better understand the impact of treatment and disease progression.

9:30-9:55

KEYNOTE ADDRESS:
FRANCESCA CICCARELLI
Professor of Cancer Genomics, Principal Group Leader, King's College London, The Francis Crick Institute
Topic TBC

9:55-10:25

LORENZ ROGNONI
Director of Image Data Science, Ultivue

10:25-11:35 Morning Refreshments / One-to-One Meetings / Poster Presentations

SPATIAL MULTI-OMICS TECHNIQUES & APPROACHES

11:35-11:55

THIERRY VOET
Professor and Director, KU Leuven Institute of Single Cell Omics
Methods and applications for spatial multi-omics
- Methods for spatial transcriptomics and other modalities
- Integration of Multiple Spatial Omics Modalities
- Spatial biology in health and disease

11:55-12:15

MIAO-PING CHIEN
Associate Professor and Principal Investigator, Erasmus University Medical Centre, Oncode Institute
Microscopy-based functional & spatial single cell sequencing
Our lab has developed microscopy-based functional single-cell sequencing (FUNseq) and analysis technologies, which can be applied to subtype heterogeneous populations of cells and link tumorigenic phenotypes to causative genotypes. FUNseq can be combined with single-cell genome, transcriptome and proteome profiling, providing a comprehensive understanding of cellular dynamics. In this talk, I will delve into the application of FUNseq technology in profiling subpopulations of cancer cells displaying different dynamic phenotypes of interest, particularly aberrant cell mitosis associated with chromosomal instability. We have also expanded the technology to enable spatial profiling of tumor cells with deep scRNAseq and single cell resolution. I will elaborate on how we applied this method to profile cells situated in different spatial locations in cell monolayers as well as tissue slices.

12:15-12:30

MARC CLAESEN
Chief Executive Officer, Aspect Analytics NV
Dedicated Software to Support High Throughput Spatial Multi Omics Applications
Spatial omics technologies enable detailed molecular analyses from tissue sections. In parallel, multi-omics approaches combining different omics levels to obtain a holistic view are increasingly in demand. However, spatial multi-omics studies can generate hundreds of gigabytes of complex data, creating a daunting bioinformatics task. Dedicated software for the management, integration, and QC of spatial multi-omics is required. Aspect Analytics provides software enabling spatial multi-omics research across a range of techniques and user bases. Our platform supports a variety of spatial applications, e.g. different spatial transcriptomics platforms, multiplexed antibody detection, and classical histopathology. Our software can extract maximal knowledge from data, scale up for high-throughput applications, provide integrated data management, reporting capabilities and more, bridging the gap between bioinformatics research and development, and enterprise-grade platforms.

12:30-12:45

ANDERS ERIKSSON
Lead Field Application Scientist, Canopy Biosciences
Precise spatial multiplexing with ChipCytometry: An open-source solution to high-throughput spatial biology
- Spatial biology is an interdisciplinary field examining the spatial organization of biological entities in ecosystems, merging genomics, imaging, and computational biology.
- Recent advancements in spatial biology leverage innovative technologies, enabling precise visualization and analysis of biological processes.
- ChipCytometry, a novel highly multiplexed technology, preserves both spatial context and multiplexing, allowing deep profiling of immune cell diversity at single-cell resolution, aiding in understanding the immune system's role in cancer progression.

12:45-13:05

BRIAN REICHHOLF
Principal Scientist, Boehringer Ingelheim
Comparing spatial data and imaging mass cytometry data

13:05-14:05 Lunch

14:05-14:20

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 21st June 2024.

14:20-14:40

ELEANOR O'ROBERTS
Researcher, SciLifeLab
Unlocking Cellular Complexity Through Multiplexed Immunofluorescence - the Spatial Proteomics Unit at SciLifeLab
Spatially resolved omics technologies have emerged in recent years and have undoubtedly changed the way we understand the spatial organization of complex multicellular biological systems. The aim of the Spatial Proteomics unit is to do full-service multiplexed immunofluorescence projects covering discovery, translational and diagnostic research questions. In the unit we offer two main technologies: the Phenocycler-Fusion from Akoya Biosciences uses conjugated antibodies detected in cycles by addition of fluorescent reporters; and the COMET from Lunaphore uses off-the-shelf antibodies in sequential rounds of immunofluorescence. Both these methodologies allow us to run targeted spatial proteomics analysis of up to 40 markers at single cell level in tissue sections. Furthermore, the unit also works on method development and implementation of new services such as isPLA and multiomics analysis.

14:40-14:55

ROBERTO SPADA
Director of Marketing, Standard BioTools
High-plex whole slide spatial biology assays powered by the Hyperion XTi
Introducing Hyperion XTi, a revolutionary Imaging Mass Cytometry System. 5x faster detection, unparalleled sensitivity for dim markers, walk-away flow cytometry, and new imaging modes. Ultra-fast whole slide imaging and intelligent ROI selection redefine high-throughput cytometry.

14:55-15:10

SENIOR REPRESENTATIVE
Lunaphore

ANALYSIS AND INTERPRETATION OF SPATIAL DATA, BIOINFORMATICS, AND COMPUTATIONAL TOOLS

15:10-15:30

VOLKER BRUNS
Head of Medical Image Analysis group, Fraunhofer IIS
Do it yourself - Programming-free Spatial Proteomics Image Analysis for Biologists
The analysis of multiplexed immunofluorescence scans does not have to be difficult and does not have to involve programming. In his talk, Volker will walk through a typical cell typing and spatial analysis of a proteomics scan step by step and explain challenges as well as different options. A focus will lie on the MIKAIA software, developed by the Medical Image Analysis (MIA) research group of Fraunhofer IIS. This cross-vendor analysis solution seeks to enable biologists to carry out these quantitative analyses themselves, without having to rely on a bioinformatician.

15:30-16:20 Afternoon Refreshments / One-to-One Meetings / Poster Presentations

16:20-16:40

EARLY CAREER RESEARCH PRESENTATION:
MENGXIAO HE
Doctoral Researcher, KTH Royal Institute of Technology
Single-tissue section Omics profiling
- An approach combining spatially resolved transcriptomics and single nuclei RNA sequencing from a single tissue section, enhancing molecular insights into tissue architecture.
- Validation and Application: Demonstrated effectiveness using mouse brain tissue sections and application on human breast cancer specimens, showcasing the method's versatility and potential in medical research.
- Technological Advancement in Archival Tissue Analysis: it offers a pioneering approach for in-depth analysis of archival FFPE tissue sections, addressing current challenges in spatial transcriptomics, cell type identification, and tumour clone analysis.

16:40-17:10

SENIOR REPRESENTATIVE
Vizgen

17:10-17:30

EARLY CAREER RESEARCH PRESENTATION:
VICTOR PEREZ
Postdoctoral Researcher at Schapiro Laboratory, Heidelberg University Hospital
Building an analysis pipeline for antibody-based multiplexed images
- Reproducibility and scalability in analysis pipelines.
- Orchestrating the variety of algorithms applied in multiplexed images.
- Integration of new modules/algorithms into pipelines with nf-core

17:30-17:50

STEPHANIE CRAIG
Lecturer in Precision Medicine, Queen's University Belfast
Help, my image is haunted: how to reduce image artefacts in your multiplex immunofluorescent research
- How to validate your MIF protocol to avoid unwanted guests
- Good housekeeping - the importance of continued QA/QC following assay validation
- Minimise Impact - Computational methods to overcome inherent MIF-dependent image bias

17:50-18:10

HENRIK FAILMEZGER
Associate Director, Spatial Data Science
Spatial heterogeneity of cancer associated protein expression in immunohistochemically stained images as an improved prognostic biomarker
In oncology it is crucial to determine the expression of biomarkers that can help to stratify patients into potential responders vs. non-responders. The status of these biomarkers is typically scored visually by a pathologist, mostly without considering the spatial heterogeneity of the protein's expression in the tissue. We present two novel image analysis-based approaches for quantitative scoring of spatial marker expression heterogeneity. The first approach is based on a co-occurrence analysis of the marker expression in neighboring cells. The second approach accounts for the local variability of the protein's expression by tiling the tissue and assigning local heterogeneity phenotypes per tile. We apply our scores to quantify the spatial expression of HER2, CMET, CD44, and EGFR in immunohistochemically stained tissue sections of colorectal cancer.

18:10 End of Day

8:50-9:00 **Global Engage Welcome Address**

9:00-9:30

KEYNOTE ADDRESS:
SENIOR REPRESENTATIVE
Invitation Out
Topic TBC

9:30-9:55

DEBAYAN MUKHERJEE
Investigator- Spatial Imaging, Oncology Translational Research, GSK
Application of Spatial Multiplex Imaging in Oncology and Biomarker research
- Application of Spatial Imaging in Pre-clinical and Translational Oncology Research
- Multi-modal approach in Oncology research
- Improving Robustness and Reproducibility for Multiplex Imaging and Spatial analysis

9:55-10:25

TIANKUI PENG
Senior Application Scientist, SeekGene Biosciences
Commercialized Spatial Transcriptomics at Physical Single-Cell Level: Mapping Expression to Location
SeekSpace, a spatial single-cell technology developed by SeekGene Biosciences, offers a novel approach to spatial transcriptomics. By utilizing spatial labels and position probes, single cells are accurately marked and dissociated into individual states before being processed through the SeekOne® DD system for cell labeling. This process results in the creation of separate single-cell transcriptome libraries and spatial libraries, facilitating the integration of single-cell transcriptomes with spatial positional information. SeekSpace achieves physical single-cell resolution, providing precise characterization of cell types and states while mitigating RNA cross-contamination. Moreover, it enables simultaneous detection of gene expression and spatial positioning on the same tissue slice. Notably, SeekSpace streamlines experimental procedures by eliminating the need for determining tissue permeabilization conditions, offering a user-friendly approach to spatial omics research.

10:25-11:35 Morning Refreshments / One-to-One Meetings / Poster Presentations

11:35-12:25

PANEL DISCUSSION:
Applying Spatial Biology to drug development

DANA MUSTAFA (Moderator)
Assistant Professor and Leader of the Spatial Biology Laboratory, Erasmus University Medical Center

DEBAYAN MUKHERJEE
Investigator- Spatial Imaging, Oncology Translational Research, GSK

11:35-12:25

ROUNDTABLE DISCUSSION:

Proposed Roundtable Topics:
- Spatial Biology beyond cancer- how spatial biology is applied to other disease areas
- Role of AI in Spatial Biology
- Application of Spatial Biology to drug development

12:25-12:55

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

12:55-13:55 Lunch

APPLICATION OF SPATIAL BIOLOGY IN TRANSLATIONAL AND CLINICAL MEDICINE

13:55-14:10

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 21st June 2024.

14:10-14:30

CHRIS HANLEY
Lecturer in Quantitative Cell Biology, University of Southampton
Fibroblast heterogeneity drives disease progression and therapy resistance in multiple solid cancers
- This presentation will cover recent work in lung and oral cancers integrating single-cell, spatial and bulk tissue transcriptomics
- Spatial co-localisation was found between distinct fibroblast subpopulations and different states of epithelial differentiation in lung cancer.
- Novel fibroblast subpopulations were identified in oral cancers associated with discrete immunological niches from immune hot and cold tumours

14:30-14:50

KONSTANTIN MAKSIN
Locum Consultant Cellular Pathologist, Royal Berkshire NHS Foundation Trust
Endothelial S100 protein as a novel assessment tool of doubtful cases "dysplasia vs invasive cancer" in cervical pathology
Anti-S100 antibody is not currently applicable in routine histopathology practice as an immunohistochemistry (IHC) marker of tumour vascularity. However, there is evidence of its high potential as a helpful tool in tumour growth evaluation and differentiation between in-situ and invasive lesions with S100-protein positive endothelial cells identification. Two types of malignant lesions, squamous cell carcinoma (SCC) and adenocarcinoma (AC), of the cervix were stained by manti-S100 antibody. The morphological appearance of SCC was covered up by intensive inflammatory processes, on the other hand, the AC morphological appearance was difficult to differentiate between adenocarcinoma in- situ and early invasive stage. The expression of S100 protein in the endothelial cells of tumour vessels revealed significant differences in non- neoplastic, in-situ and invasive forms. The highest expression of S100 protein was observed in the invasive forms which allowed to distinguish it from in-situ changes and to define the direction of tumour spreading. Anti-S100 antibody has high potential in tumour vascularity and invasiveness evaluation, particularly in doubtful cases. However, this IHC method requires clarification due to overlapping with other S100- positive cells, probably through the co-staining with using additional endothelial markers, such as CD31 or CD34.

14:50-15:10

FANI MEMI (Reserved)
Senior Staff Scientist, Wellcome Sanger Institute
Topic TBC

15:10-15:30 **SENIOR REPRESENTATIVE**
Sanofi
Topic TBC

15:30 End of Conference

POSTER PRESENTATIONS

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 to be submitted by the 21st June 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 21st June 2024

1. Submit your entry prior to the closing deadline (1 entry per person)
2. Two entries for the 3rd International Spatial Biology Congress: Europe 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.

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.