SPATIAL BIOLOGY EUROPE:
In-Person

07 - 08 June 2022 | Berlin, Germany

150+
LEADING BIOTECH, PHARMA AND ACADEMIC DELEGATES

40+
PRESENTATIONS, CASE STUDIES AND DISCUSSIONS

3
INNOVATIVE TRACKS COVERING THE LATEST SPATIAL DEVELOPMENTS

Conference Brochure

KEY SPEAKERS INCLUDE

Omer Bayraktar
Wellcome Sanger Institute

Kerstin Hahn
F. Hoffman-La Roche

Katy Borner
Indiana University

Judit Pongracz
University of Pecs

Alvaro Crevenna
European Molecular Biology Laboratory

Nicole Strittmatter
Technical University of Munich

Book Online: www.oxfordglobal.co.uk/spatial-biology-europe/book-now/
Join the Conversation: #OmicsSeries22

OXFORD GLOBAL CONFERENCES

BROCHURE CONTENTS

WELCOME

On behalf of the entire Oxford Global team, I am delighted to welcome you to Spatial Biology Europe: In-Person Congress, this year also supported digitally.

Over the next two days, the event will allow participants, both in-person and online, to engage with content and one another. The Oxford Global team look forward to meeting you over the course of the congress and will be on hand to ensure your time is both productive and enjoyable.

Oxford Global Conferences have been producing cutting edge congresses and summits for the Life Sciences Industry for over 14 years now. We annually bring together thousands of industry leaders and solution providers creating the opportunity to partner, network and knowledge share. I am pleased to let you know that we have now successfully completed a transition from an in-person event organiser to one stop shop platform for all research-critical information pertaining to the 'omics space. We also would like to invite you to visit our Omics Content Portal to find out more about our brand-new membership offering giving you access to the latest technology insights and omics research community we have been building over the last 13 years. You can register for the newsletter to get updates on upcoming activities within this series, stay up to date with industry news and more.

Understanding the organization of cells and tissues and how this organization influences function is fundamental for life sciences research. During our event, you will learn how spatial research & technologies are leading to new discoveries that will prove instrumental in helping scientists gain a better understanding of biological processes and disease. It is also an essential method for predicting response to various therapeutic treatments, as well as a key element in the development of new drugs.

The event programme is designed to deliver a forward-thinking perspective on the opportunities and challenges of spatial biology

impacting on discovery, translational and clinical research. The congress also covers the development and recent advancements of spatial data analysis tools and applications, crucial for data integration as well as tissue & cell analysis.

We are hugely thankful to our speakers, who have given their time to provide interesting, thought-provoking presentations, and to our sponsoring companies, who have worked closely with us to provide you with unique opportunities to access the latest information on solutions and services that can directly impact and improve your research and results. Without their support this event would not be possible, so please do take some time to visit their stands in the exhibition hall and featured sponsor pages in the event app.

New for 2022 is the event delivery format which has been redesigned to ensure that both in-person and online delegates can access presentation recordings immediately on-demand and interact with speakers and one another using our Swapcard platform. Swapcard serves as our content delivery tool and peer to peer networking platform for virtual delegates as well as the event app for those who are joining us in-person. You will gain access to the platform minimum three days prior the event and can enjoy access up to 7 days after the congress to catch up on any talks you have missed.

Lastly as we wanted to create an environment where in-person delegates can converse in smaller groups, all conference rooms will host a series of engaging discussions such as panels and workshops to encourage as much knowledge-sharing as possible.

Once again, welcome to the event — we hope it will prove to be both educational and enjoyable for you.

Peter Franko,
Senior Director Business Development, Events and Membership
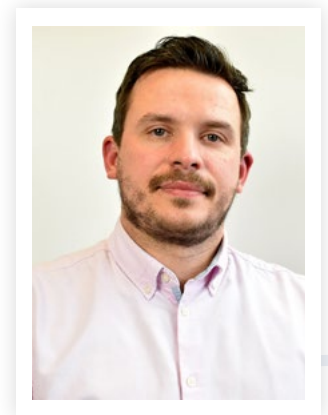
On-site Health & Safety

At Oxford Global, the safety and well-being of our clients is our top priority, and we are committed to ensuring that our congresses remain safe and successful.
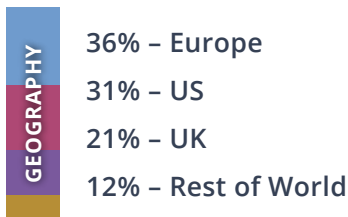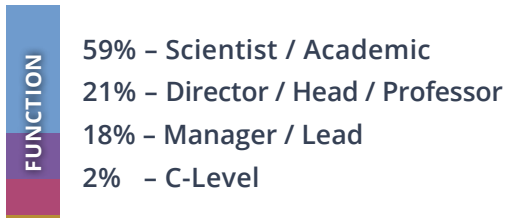
For more information, please see www.oxfordglobal.co.uk/spatial-biology-europe/plan-your-visit/

150+ VPs, Directors & Senior Managers from leading healthcare, biotech, pharma and research institutions in the following fields and more:

- Spatial Capture Technologies
- Spatial Gene Expression
- Digital Spatial Profiling
- Spatial Imaging
- Spatial Data Visualization
- Spatial Phenotyping

- Light microscopy
- Cryosectioning
- Microscopy-based RNA Imaging Techniques
- Spatial Genomics
- Spatial Transcriptomics

- In Situ Hybridization
- Spatial Genomics Technologies
- Spatial Transcriptomics
- Clinical Genomics

2021's Attendee Profile

FUNCTION

59% – Scientist / Academic
21% – Director / Head / Professor
18% – Manager / Lead
2% – C-Level

SECTOR

60% – Academia
25% – Industry
15% – Sponsor / Vendor / Commercial

GEOGRAPHY

36% – Europe
31% – US
21% – UK
12% – Rest of World

These companies & many more:

AstraZeneca

Oncode Institute

SciLifeLab

GRÜNENTHAL

Roche

UPPSALA UNIVERSITET

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wellcome sanger institute

Georgia Tech.

JUSTUS-LIEBIG-UNIVERSITÄT GIESSEN

INDIANA UNIVERSITY

TUM TECHNISCHE UNIVERSITÄT MÜNCHEN

UNIVERSITÉ DE MONTPELLIER

SDU University of Southern Denmark

Formal and informal meeting opportunities offer delegates the chance to discuss key solutions with leading service providers:

- Spatial Biology
- Spatial Genomics
- Spatial Transcriptomics
- Spatial Metabolomics

- Spatial Proteomics
- Biomedical Engineering
- Single Cell
- Clinical Genomics

- Pathology
- Bioinformatics
- Computational Biology
- Translational Research

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Spatial Biology Europe: In-Person features **2 days** of cutting-edge presentations and knowledge-sharing, consisting of **over 40 presentations**, **roundtables, panel discussions and workshops** taking place over both days of the event.

Day One: 07 June 2022

Track 1: Spatial Biology, Spatial Genomics and Multi-Omics Techniques And Approaches

- Multi-stream digital spatial discovery and profiling techniques & approaches
- Transcriptomics & spatial genomics techniques & approaches
- Spatial transcriptomics & spatial genomics techniques/technologies
- Single-cell transcriptome imaging and cell atlas of complex tissues
- Spatial organization of the genome

Track 2: Applications of Spatial Research & Technologies in Biology

- Case studies from the areas of:
  - » Cardiovascular development
  - » Regenerative medicine
  - » Oncology
  - » Neurobiology
  - » Infectious diseases
  - » Immunological diseases
  - » Toxicology studies

Day Two: 08 June 2022

Track 1: Spatial Technologies, Profiling & Bioinformatics

- Spatial atlases / using model systems
- Toward a human reference atlas: anatomical structures, cell types and biomarkers
- Validating spatially varying biomarkers: opportunities and pitfalls
- Spatial technologies and challenges in the adoption of translational drug research
- Utilizing spatial data in new biology
- Overcoming the challenges in spatial data analysis
- Data integration for various omics & standardization
- Machine learning approaches

NICOLE STRITTMATTER
Professor for Analytical Chemistry,
Technical University of Munich

MIAO-PING CHIEN
Principal Investigator & Assistant
Professor,
Erasmus University Medical Center,
Oncode Institute

ANNA KLEMM
Head of Unit, SciLifeLab

ALVARO CREVENNA
Head of Microscopy Facility,
European Molecular Biology
Laboratory

NAVEED ISHAQUE
Group Leader, BIH Charite

ANJA MEZGER
Head of Spatial Transcriptomics
Unit, SciLifeLab

INGO EBERSBERGER
Professor, Goethe University

(JOINING ONLINE)
JUDIT PONGRACZ
Professor, University of Pecs

WOLFRAM GRONWALD
Associate Professor, University of
Regensburg

KERSTIN HAHN
Principal Scientist, F. Hoffman-La
Roche

JONATHAN BREWER
Associate Professor & Group
Leader, University of Southern
Denmark

(JOINING ONLINE)
ARUTHA KULASINGHE
Principal Investigator,
University of Queensland

(JOINING ONLINE)
ANDREAS MOOR
Professor,
Swiss Federal Institute of
Technology Zurich

(JOINING ONLINE)
CATHERINE ALIX-PANABIÈRES,
Associate Professor,
University Medical Center of
Montpellier

(JOINING ONLINE)
OMER BAYRAKTAR
Group Leader, Wellcome Sanger
Institute

RAFFAELE CALOGERO
Professor, University of Turin

IOANNIS ALEXOPOULOS
ILH / CIGL Multiscale Imaging
Platform Coordinator, Justus Liebig
University Giessen

KATY BORNER
Victor H. Yngve Distinguished
Professor of Engineering and
Information Science, Indiana
University

ROSALBA GIUGNO
Associate Professor, University of
Verona

(JOINING ONLINE)
MARK BORODOVSKY
Regent's Professor, Georgia
Institute of Technology

ANNA KLEMM
Head of Unit, SciLifeLab

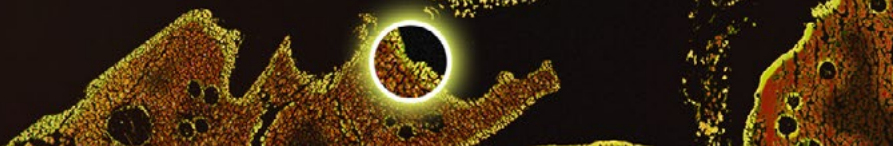**ULF LANDEGREN**
Professor,
Uppsala University

STEWART JONES
Director, Molecular Imaging
AstraZeneca

For more information on our speakers,
please read the biographies available on our **event app**

All Times Shown are CEST (UTC+2)	DAY ONE - 07 JUNE 2022

07:50 — **Oxford Global's Welcome Address & Chairperson's Opening Address**

08:00

Keynote Address: Increasing Our Understanding Of Drug Delivery With Multimodal Imaging

- Deployment of multimodal imaging strategies to study gemcitabine delivery and metabolism and nanomedicine-based drug distribution
- Use of mass spectrometry imaging, immuno mass cytometry, microscopy-based imaging

NICOLE STRITTMATTER, Professor for Analytical Chemistry,
Technical University of Munich

TRACK 1: SPATIAL BIOLOGY, SPATIAL GENOMICS AND MULTI-OMICS TECHNIQUES AND APPROACHES	TRACK 2: APPLICATIONS OF SPATIAL RESEARCH & TECHNOLOGIES IN BIOLOGY
Track Chair: WOLFRAM GRONWALD, Associate Professor, **Universität Regensburg**	**Track Chair:** NICOLE STRITTMATTER, Professor of Analytical Chemistry, **Technical University of Munich**

08:25

Track Keynote Address: From Gene Order To Evolutionary Stable Gene Clusters - A Spatial Approach To Identify Novel Virulence Related Traits In Bacterial Pathogens

- How to exploit the availability of thousands of bacterial genomes from one bacterial genus to shed light on the joint evolutionary fate of neighboring genes
- How to identify evolutionary stable gene clusters
- How these gene clusters help in advancing our understanding of bacterial pathogenicity
- I will use Acinetobacter baumannii as a focal organism in my presentation

INGO EBERSBERGER, Professor,
Goethe University

Track Keynote Address: Functionally And Spatially Annotated Single Cell Sequencing

- High-throughput, microscopy-based single cell sequencing based on desired functional features like spatial locations or cellular migration
- Functionally & spatially annotated single cell sequencing to directly link genotypes to phenotypes of interest and identify otherwise undetectable differentially expressed genes or pathways

MIAO-PING CHIEN, Principal Investigator & Assistant Professor,
Erasmus University Medical Center, Oncode Institute

08:50

Utility Of Multiplexed Immunofluorescence And Spatial Phenomics To Resolve Immune Tumor Heterogeneity

- The utility of advanced multiplexing techniques to provide the much-needed insight affording a comprehensive study of cellular composition, cellular functions, and cell-cell interactions within the tumor microenvironment (TME)
- How to make use of multi-parameter data within the TME - spatial mapping, dynamic range of expression, and co-localization of markers on individual cells
- The importance of same slide H&E analysis to provide the morphologic context for the multiplexed immunofluorescence (mIF) data
- Demonstration of a streamlined workflow supporting whole slide imaging coupled to advanced quantitative AI-driven image analysis of an 8-plex mIF and H&E fusion on a single tissue slide for a comprehensive tissue immunophenotyping analysis

FLORIAN LEISS, Vice President Digital Health Strategies,
Ultivue

Highly Sensitive, Subcellular Spatial Transcriptomics For Tissue Atlasing, Biomarker Discovery And Beyond

- Using spatial transcriptomics to construct single-cell resolution atlases
- Using Molecular Cartography for highly multiplexed spatial profiling and subcellular phenotyping
- Exploring more case studies for biomarker discovery, pathway analysis, and patient stratification projects

STEPHEN TIRIER, Scientist - Molecular Biology,
Resolve Biosciences

09:20

Neighborhood Analysis On Multiplexed Fluorescence Microscopy Data Of Glioma Tissue

- Multiplexed immunofluorescence: imaging large numbers of cell-specific protein markers on single-cell level in parallel
- Variation in sample handling cause different marker profiles both within and across samples
- The presented workflow uses a machine learning architecture to classify cells and analyzes their spatial relationship in brain tumor tissue samples.

ANNA KLEMM, Head of BioImage Informatics Facility,
**Uppsala University, SciLifeLab**

Automating Spatial Biology Within A Core Facility

- Implementing spatial transcriptomics within a facility setting, how to choose which method
- Initial results from pilot projects
- Automating spatial transcriptomics for a higher throughput platform

ALVARO CREVENNA, Head of Microscopy Facility,
European Molecular Biology Laboratory

09:45 — **Morning Break & Refreshments, Poster Presentation Sessions, 1-2-1 Meetings x4**
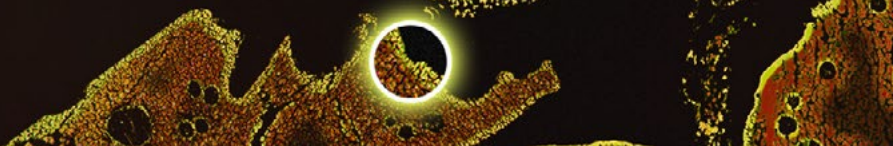
TRACK 1: SPATIAL BIOLOGY, SPATIAL GENOMICS AND MULTI-OMICS TECHNIQUES AND APPROACHES

11:10

Combining Spatial Transcriptomics And Multiplexed Microscopy Reveals Mechanisms Of Immunopathology In Prolonged COVID-19

• Post-acute lung sequelae of COVID-19 are challenging many survivors across the world, yet the mechanisms behind are poorly understood
• We have combined spatial transcriptomics and multiplexed immunofluorescence microscopy to analyze the changes occurring in lung tissue, along disease progression
• Our results delineate an inflammatory cascade of events occurring within fibrovascular niches
• It is initiated by endothelial dysfunction, followed by heme scavenging of CD163+ macrophages and production of CCL18
• This chemokine synergizes with local CCL21 upregulation to influence the stromal composition, favoring endothelial to mesenchymal transition
• The local immune response is further modulated via recruitment of CCR7+ T cells into the expanding fibrovascular niche, featuring an exhausted, T follicular helper–like phenotype
• This process culminates in the formation of tertiary lymphoid structures, which further perpetuate the chronic inflammation
• Our work reveals misdirected immune-stromal interaction mechanisms promoting a self-sustained and non-resolving local immune response that extends beyond active viral infection, and leads to profound tissue repurposing

ANJA ERIKA HAUSER, Head of the Immune Dynamics and Intravital Microscopy Laboratory, **Charité Universitätsmedizin Berlin**

TRACK 1: SPATIAL BIOLOGY, SPATIAL GENOMICS AND MULTI-OMICS TECHNIQUES AND APPROACHES	TRACK 2: APPLICATIONS OF SPATIAL RESEARCH & TECHNOLOGIES IN BIOLOGY

11:40

Simulations Of merFISH / Spatial Transcriptomics Data

• merFISH updates
• Spatial transcriptomics data approaches

JONATHAN BREWER, Associate Professor & Group Leader, **University of Southern Denmark**

Quality Assurance Of Single Molecule Spatially Resolved Transcriptomics Data

Spatially resolved transcriptomics technologies have been rapidly adopted in many areas of life science. However, there is currently a lack of tools that can evaluate the quality of single molecule spatial transcriptomics data. I will present two tools that we have developed for single molecule spatially resolved transcriptomics data: (i) PlanktonPy which systematically address QC against expected ground truths and single cell transcriptomics data, and (ii) SSAM-lite which can visualise and analyse cell-type signals using a light weight web-app that can run on a mobile phone.

NAVEED ISHAQUE, Group Leader, **BIH Charite**

12:05

Making Your Research Visible - Spatial Omics At The National Genomics Infrastructure, Sweden

ANJA MEZGER, Head of Spatial Transcriptomics Unit, **SciLifeLab**

Tumor Heterogeneity Explored By Single Circulating Tumor Cells (CTCs): Liquid Biopsy For Precision Medicine In Cancer Patients

(Joining Online) CATHERINE ALIX-PANABIÈRES, Associate Professor, **University Medical Center of Montpellier**

12:30

Panel Discussion: Spatial Resolved Transcriptomics Evolution

• High resolution (few targets) vs high-throughput (whole transcriptome), why one or the other?
• Spatial transcriptomics on FFPE tissue arrays – feasible?
• Is spatial transcriptomics suitable to be integrated with other modalities?

Panellists:
RAFFAELE CALOGERO, Professor, **University of Turin**
ALVARO CREVENNA, Head of Microscopy Facility, **EMBL**
ANNA KLEMM, Head of BioImage Informatics Facility, **Uppsala University, SciLifeLab**
ANJA MEZGER, Head of Spatial Transcriptomics Unit, **SciLifeLab**
DAVID CHAMBERS, Systems Biology Head, **Grünenthal**

Panel Discussion: Will Spatial Technologies Replace Single Cell Technologies In The Future?

• Applications of both technologies – what scenarios people use single cell or spatial sequencing?
• Pros and cons of these technologies
• Challenges ahead

Moderator: MIAO-PING CHIEN, Principal Investigator & Assistant Professor, **Erasmus University Medical Center, Oncode Institute**

Panellists:
NAVEED ISHAQUE, Group Leader, **BIH Charite**
OZGUN GOKCE, Independent Research Group Leader, **Institute for Stroke and Dementia, LMU**

12:55

Precise Single-Cell, Spatial Phenotyping With CellScape

• How to quantify the expression of dozens of protein biomarkers in in-tact tissue sections with single-cell resolution
• How ChipCytometry™ technology can be used to uncover the spatial distribution of immune cell subsets

(Joining Online) SPENCER SCHWARZ, Product Manager **Bruker**

Scaling Up Deep Spatial Phenotyping of the Tissue Microenvironment

• Breakthrough spatial biology applications such as spatial phenotyping span the discovery-to-clinical continuum. To minimize time and maximize value along the continuum, it is imperative to make discoveries happen faster and at scale
• See the latest data using the PhenoCycler™-Fusion system, the fastest single-cell spatial biology solution
• Hear how deep spatial phenotyping with a 100-plex panel can reveal insights into distinct cellular neighborhoods and their role in regulating immune and metabolic functions of certain cancers

BJÖRN WENDIK, Senior Field Application Scientist, **Akoya Biosciences**

13:25 — **Lunch Break & Networking Sessions x3**

TRACK 1: SPATIAL BIOLOGY, SPATIAL GENOMICS AND MULTI-OMICS TECHNIQUES AND APPROACHES	TRACK 2: APPLICATIONS OF SPATIAL RESEARCH & TECHNOLOGIES IN BIOLOGY

14:30

Spatial Transcriptomics Correlated Electron Microscopy

- Spatial transcriptomics methods identify cell types and states in a spatial context but lack morphological information which electron microscopy, provides at nanometer resolution
- We developed Spatial Transcriptomics-correlated Electron Microscopy to address this limitation by correlating MERFISH from Vizgen's MERSCOPE with electron microscopy
- We applied our technology to characterize the damage-associated microglial identities in mouse white matter, linking the morphology of foamy microglia and interferon-response microglia with transcriptional signatures

OZGUN GOKCE, Independent Research Group Leader,
Institute for Stroke and Dementia, LMU

Powerful, Open And Fully Automated: Ultra-High Content Imaging With The MACSima™ Imaging Platform

- Miltenyi Biotec will be presenting the MACSima ultra-high content imaging platform
- Learn about MICS technology and how it enables hundreds of protein markers to be visualized from fixed tissue
- Milteyi Biotec offer thousands of validated antibodies and predefined panels but the platform is also open to 3rd party antibodies

OLIVER PETTERS, Sales Specialist Imaging,
Miltenyi Biotec

15:00

Panel Discussion: Spatial Bioinformatics – Overcoming The Challenges

- Spatial transcriptomics and single cell RNA-seq data integration
- Spatial information integration in clustering algorithm
- Depicting novel tissue regions by mean of spatial transcriptomics

Moderator: RAFFAELE CALOGERO, Professor, **University of Turin**

Panellists:

OZGUN GOKCE, Independent Research Group Leader, **Institute for Stroke and Dementia, LMU**

FLORIAN LEISS, Vice President Digital Health Strategies, **Ultivue**

Spatial Biology In The Therapeutic Decision-Making Process Of Non-Small Cell Lung Cancer

Non-small cell lung cancer (NSCLC) is frequently diagnosed at an advanced disease stage resulting in limited treatment options, poor prognosis, and unacceptably high mortality. Despite modern treatment modalities, palliative chemotherapy is recommended to patients from disease stages IIIA or above. Although regularly improved international guidelines exist, the individual decision is important and is based on the patient's overall health status, tumor parameters and the potential risk/benefit of the selected therapy. The individual therapy response, however, remains hard to predict.

Meticulous collection of clinical data and tumor information accumulated by spatial biology techniques as well as 3D tissue cultures started to reveal a more accurate picture identifying markers for personalized clinical decision making.

(Joining Online) JUDIT PONGRACZ, Professor,
University of Pecs

15:25

Visualization Of Diverse RNA Biomarkers For Translational And Clinical Research: mRNA, Splice Variants And MicroRNAs

- Overview of the RNAscope technology, including HiPlex, BaseScope, miRNAscope and Co-Detection assays
- Demonstration of single cell and sub-cellular resolution for spatial gene expression
- Examples of RNAscope applications in key research areas including Neuroscience, Oncology, Cell and Gene therapy, and more
- Utility of RNAscope technology for diagnostic assays, including HPV

Senior Representative,
Bio-Techne

Trailblazing The Future Of Spatial Biology

- Map the whole transcriptome of entire H&E or immunofluorescence stained fresh frozen and FFPE tissue sections with morphological context
- Streamline Visium histology workflows with facilitated transfer of analytes from tissues sectioned on standard glass slides to Visium slides with CytAssist
- Get the most recent product updates on Visium Gene+Protein expression, Visium HD and Xenium In Situ Analyzer

JOHANNA STERGIADOU, Science & Technology Advisor,
10x Genomics

15:55 | **Afternoon Break, Refreshments, Poster Presentation Sessions & 1-2-1 Meetings x3** |

17:00

Roundtable Discussion: Adopting Spatial Technologies & Overcoming The Challenges

- What are the main barriers to spatial biology adoption?
- How do we encourage the adoption of spatial biology?
- What are the key messages regarding spatial biology we need to convey?
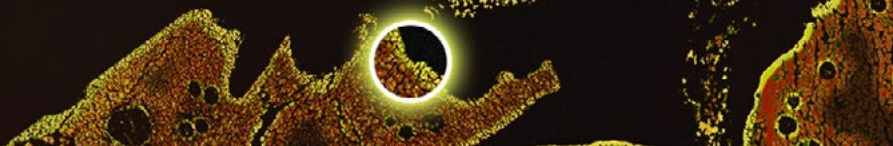
Moderator: DAVID CHAMBERS, Systems Biology Head, **Grünenthal**

Spatial Biology In Intestinal Homeostasis And Cancer

(Joining Online) ANDREAS MOOR, Professor,
Swiss Federal Institute of Technology Zurich

TRACK 1: SPATIAL BIOLOGY, SPATIAL GENOMICS AND MULTI-OMICS TECHNIQUES AND APPROACHES	TRACK 2: APPLICATIONS OF SPATIAL RESEARCH & TECHNOLOGIES IN BIOLOGY

17:25

Spatial Transcriptomics To Probe Colorectal Cancer Heterogeneity

• Characterization of CRC consensus molecular subtypes (CMS) and the tumor microenvironment using spatial transcriptomics
• A deconvolution-based approach reveals CMS-related tumor heterogeneity and delineates receptor ligand interactions

KERSTIN HAHN, Principal Scientist,
F. Hoffman-La Roche

Spatial Genomics In The Era Of Immunotherapy (& COVID-19)

• The development of spatial tissue signatures of response to immunotherapy
• Why Spatial: From discovery to biomarker development
• New insights into COVID-19 biology

(Joining Online) ARUTHA KULASINGHE, Principal Investigator,
The University of Queensland

17:50

Prediction Of Gliomas From Full MRS Data

WOLFRAM GRONWALD, Associate Professor,
Universität Regensburg

Mapping Human Tissue Architecture And Pathology Using Spatial Transcriptomics

Spatial transcriptomic technologies promise to resolve cellular wiring diagrams of tissues in health and disease, but comprehensive mapping of cell types in situ remains a challenge. First, I will present cell2location, a principled Bayesian model that can resolve fine-grained cell types in spatial transcriptomic data and create comprehensive cellular maps of diverse tissues. We comprehensively assess cell2location in three different tissues and demonstrate its versatility for mapping complex tissue architecture. Second, I will introduce our work on dissecting tissue pathology in severe COVID-19 and demonstrate how integrated single cell and spatial transcriptomics can map the cellular landscape of alveolar damage in the human lung.

(Joining Online) OMER BAYRAKTAR, Group Leader,
Wellcome Sanger Institute

18:15

Networking Drinks | Sponsored by 10x Genomics

19:00

Networking Dinner, Bon Dia Restaurant, Hotel Palace Berlin
A complimentary 3-course meal
Please speak to a member of staff if you are yet to RSVP

DAY TWO - 08 JUNE 2022

TRACK 1: SPATIAL TECHNOLOGIES, PROFILING & BIOINFORMATICS

Morning Track Chair: ROSALBA GIUGNO, Associate Professor, **University of Verona**

08:00

Track Keynote Address: Sparsely Connected Autoencoders: A Multi-Purpose Tool For Single Cell OMICs Analysis

• We have recently developed a new class of autoencoders, called Sparsely Connected Autoencoders (SCA), which have the advantage of providing a controlled association among the input layer and the decoder module
• SCA can be used to depict new biologically interesting features from single cell omics data
• SCA represents the bioinformatics version of a "Swiss Army knife" for the extraction of hidden knowledgeable features from single cell OMICs data

RAFFAELE CALOGERO, Professor,
University of Turin

08:35

Clustering Spatial Transcriptomics Data

• Analysis of computational methods for clustering ST data
• How space, expression and histological imaging influence the clustering results
• Metrics to evaluate ST clustering

ROSALBA GIUGNO, Associate Professor,
University of Verona

09:00

Spatial Biology Made Easy: Streamline Your Hyperplex Assays

• Learn how sequential immunofluorescence (seqIF™) overcomes current challenges in multiplex assay optimization and low reproducibility
• Discover COMET™, the only true high-throughput solution for hyperplex seqIF™ with high reproducibility
• See how you can easily develop customized panels to streamline your research from immune oncology to infectious diseases.

DIEGO DUPOUY, Co-Founder & Chief Technology Officer,
Lunaphore Technologies

TRACK 1: SPATIAL TECHNOLOGIES, PROFILING & BIOINFORMATICS

09:30

Multi-Scale Light Microscopy Approaches In Lung Research

- The Multiscale Imaging Platform of the Institute of Lung Health provides support in all major steps of light microscopy workflows: sample preparation, image acquisition, data handling and analysis
- The field of lung research is challenging with a wide range of sample sizes and the need to image structures varying from a few nm up to cm. Furthermore, large scale acquisitions require specific data handling approaches, automation in image analysis and implementation of machine learning or artificial intelligence algorithms
- Characteristic applications as examples, represent the big challenges of light microscopy in lung research and provide an insight of the applied approaches

IOANNIS ALEXOPOULOS, ILH / CIGL Multiscale Imaging Platform Coordinator,
Justus Liebig University Giessen

09:55

Morning Refreshment, Networking Sessions, Poster Presentation Sessions x3

11:00

Highly Multiplexed Immunohistochemistry

- Visualize 40+ markers at subcellular resolution simultaneously with unprecedented speed with the Hyperion+ Imaging System

ROBERTO SPADA, Director of Marketing,
Fluidigm

11:30

Human Reference Atlas: Construction And Usage

KATY BORNER, Victor H. Yngve Distinguished Professor of Engineering and Information Science,
Indiana University

11:55

How To Perform Bioinformatics Analysis Of Spatially Resolved Transcriptomics Data Using A Point-And-Click Interface

Using Partek® Flow® bioinformatics software we will demonstrate how to analyze a spatial RNA-Seq experiment from start to finish including:
- Analyze multiple samples per study
- Remove batch effects with multiple options
- Identify cell types based on gene expression profiles
- Automatically classify cell types
- Interactively explore clusters in their spatial context
- Perform differential gene expression analysis and integrate expression data with tissue data
- Discover biomarkers that define a tissue or cluster
- Perform trajectory analysis
- Perform biological interpretation with pathway enrichment

(Joining Online) ALEX RUTKOVSKY, Field Application Scientist,
Partek

12:25

Lunch Break & Networking Sessions x3

Afternoon Track Chair: DAVID CHAMBERS, Systems Biology Head, **Grünenthal**

13:30

SiLC-MS (Single Live Cell Mass Spectrometry) Analysis In The Context Of Drug Discovery

- The ability to visualise unlabelled compounds inside the cell at physiological dosages can offer valuable insight into the compound behaviour both on and off-target
- SiLC-MS is a semi-automated methodology that allows the collection of intracellular contents using the prototype of SS2000 an automated sampling system developed by Yokowaga
- We demonstrate that dosed compound can be identified in a single cell after sampling using the prototype of SS2000, endogenous metabolites can also be identified that can further the understanding of the drug's mechanism. Low sample requirement of the system makes it applicable to studying rare cell types

CARLA NEWMAN, Scientific Leader, Cellular Imaging and Dynamics,
GlaxoSmithKline

14:00

Roundtable Discussion 1: Addressing Antibody Specificity

- Validating antibodies
- Challenges

Moderator: ULF LANDEGREN, Professor, **Uppsala University**

Roundtable Discussion 2: Challenges Of Light Microscopy Workflows In Spatial Research

- Choosing the right microscopy technique for spatial research
- Challenges in image analysis of large microscopy data

Moderator: IOANNIS ALEXOPOULOS, ILH / CIGL Multiscale Imaging Platform Coordinator, **Justus Liebig University Giessen**

14:25

Afternoon Break, Refreshments, Poster Presentation Sessions & 1-2-1 Meetings x1
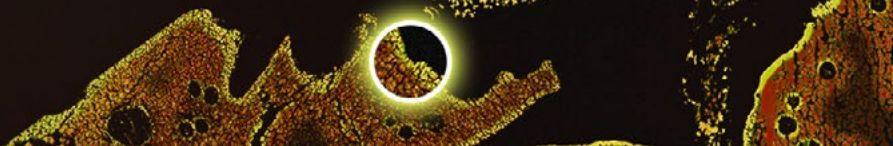
TRACK 1: SPATIAL TECHNOLOGIES, PROFILING & BIOINFORMATICS

15:00	**Spatial Image Data Analysis** ANNA KLEMM, Head of BioImage Informatics Facility, **Uppsala University, SciLifeLab**
15:25	**Spatial Biology For Drug Development** STEWART JONES, Director, Molecular Imaging **AstraZeneca**
15:50	**Tools For In Situ Detection Of Nucleic Acids & Proteins** • In situ proximity ligation assays • Multiplex protein detections ULF LANDEGREN, Professor, **Uppsala University**
16:15	**Overcoming Hidden Challenges in Spatial Biology: Getting Accurate Annotation Of A Reference Transcriptome** *(Joining Online)* MARK BORODOVSKY, Regent's Professor, **Georgia Institute of Technology**
16:40	**End Of Conference**

SPATIAL BIOLOGY NETWORKING DRINKS

Tuesday 7th June, 6:15pm

in the Exhibition Hall

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followed by

NETWORKING DINNER

A complimentary, sit down 3-course dinner

Tuesday 7th June, 7:00pm

in the Bon Dia Restaurant,
Hotel Palace Berlin

Please speak to a member of staff if you are yet to RSVP

We hope to
see you there,

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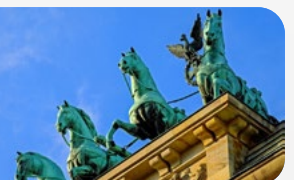
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