Microscopy Focus

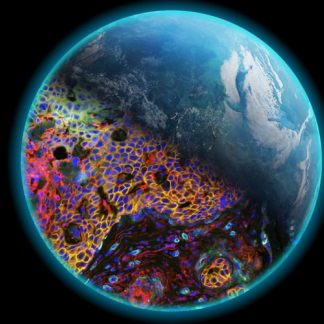*Powered by* **BiteSize Bio**

Leica MICROSYSTEMS

See the Hidden: Spatial Biology
LIVE WORKSHOP

Thursday July 7th, 2022
1-4pm London, 2-5pm Berlin, 4–7pm Dubai

In this next highly anticipated virtual edition of our See the Hidden Workshop Series, we will start to examine some of the emerging microscopy techniques being used to study cells within a spatial 2D and 3D context. We will examine the behavior and identity of cells in diverse tissues, and present proof-of-concept studies to identify local changes in protein content and investigate pathways involved in cardiac tissue injury. New technologies and approaches that leverage fluorescence multiplexing and spatial omics to address spatial cell biology will be discussed, along with the molecular insights they can bring to the treatment of diseases such as heart disease, cancer and immunology.

This online event, featuring live panelists, brings together a series of scientific talks and microscopy showcases. Dr. Ronald N. Germain (NIH) and Dr. Berta Cillero-Pastor (Maastricht University) will talk about how specialized microscopy approaches contribute to their spatial biology research. You will discover streamlined workflows that can enable a better understanding of biological pathways and provide greater knowledge for translational research.

The program centers around four specific areas in microscopy:

• widefield multiplexing
• single-cell/tissue microdissection
• high-resolution confocal microscopy
• Artificial Intelligence (AI)-based analysis.

We will continue to address the theme of advanced microscopy techniques for spatial biology with a follow-up workshop later in the year – so don't miss this opportunity to join us for part 1!

AGENDA

Each presentation will be followed by a live, interactive Q&A session.

WELCOME AND INTRODUCTIONS

13:00 BST | 14:00 CET

Dr. Abdullah Ahmed
Leica Microsystems

SESSION INFORMATION CONTINUED BELOW

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PANEL DISCUSSION ON EMERGING MICROSCOPY TRENDS IN SPATIAL BIOLOGY

13:05 BST | 14:05 CET

Dr. Abdullah Ahmed
Advanced Workflow Specialist

Dr. Ronald Germain
Chief, Laboratory of Immune System Biology and Lymphocyte Biology Section, NIAID (NIH)

Dr. Mauro Luca Baron
Advanced Workflow Specialist

Dr. Berta Cillero-Pastor
Group leader, Department of Cell Biology-Inspired Tissue Engineering MERLN Institute, Maastricht University

Dr. Jens Peter Gabriel
Advanced Workflow Specialist

Dr. Lindsey Marshall
EMEA Customer Success Manager for Aivia AI Image Analysis Software

GAINING INSIGHT INTO TISSUE BIOLOGY USING HIGHLY MULTIPLEX 2D AND 3D TISSUE IMAGING

13:25 BST | 14:25 CET

Ronald received his M.D. and Ph.D. from Harvard University in 1976 and is currently Chief of the Laboratory of Immune System Biology at the National Institute of Allergy and Infectious Diseases, NIH. Over the years, he and his colleagues have made vital contributions to our understanding of Major Histocompatibility Complex class II molecule structure–function relationships, the cell biology of antigen processing, and the molecular basis of T cell recognition. More recently, his laboratory has focused on the relationship between immune tissue organization and control of adaptive immunity studied by utilizing novel dynamic and static in situ microscopic methods that his laboratory helped pioneer. Dr. Germain has published over 400 scholarly research papers and reviews and trained more than 70 postdoctoral fellows. Several of them hold senior academic and administrative positions at leading universities and medical schools worldwide.

Dr. Ronald Germain
Chief, Laboratory of Immune System Biology and Lymphocyte Biology Section, NIAID (NIH)

Individual cells within tissues do not operate in isolation but constantly communicate with neighbors and even distant cells through soluble mediators and the nervous system. To develop a deeper understanding of organismal biology, we need to move up in organizational complexity from cells to tissues, placing the many cell types into spatial context and probing how each cell interacts with and is influenced by neighboring cells.

One technical approach is spatial transcriptomics, many flavors of which have appeared in recent years. There is significant variation in the resolution and depth of mRNA profiling between the different transcriptomic techniques. These methods can use the catalog of transcriptional state information from isolated cell studies to identify corresponding cells in a tissue context. However, used alone, they lack information about cell boundaries and cell state that can only be conveyed by analysis at the protein level.

Nucleic acid-based methods miss details such as the location of membrane contacts, clustering of receptors on membranes, or signaling revealed by post-translational modifications like protein phosphorylation or nuclear localization of active transcription factors. Acquiring these data requires imaging using protein-targeted methods, of which immunofluorescence microscopy is currently the most applicable technology.

This presentation describes recent progress in the development of methods for highly multiplexed analysis of both thin sections and thicker preparations that provide "2D and 3D" information about cell identity and state in diverse mouse and human tissues. These methods are open source and can be widely employed by investigators with access to modern confocal microscopy. Other imaging platforms that are supported will be discussed.

Parameter depth can exceed 60–80 for a single tissue preparation. Ron and his team have developed new deep learning-based methods to enable facile analysis of such complex data sets. They have also created user-friendly software interfaces so investigators unfamiliar with scripting languages can use these.

Together, these staining, imaging, and analytical tools comprise a complete suite of methods for the in-depth study of tissues at cellular and even subcellular resolution.

COFFEE BREAK
14:05 BST | 15:05 CET

OBTAINING SPATIAL CONTEXT WITH CLARITY USING WIDEFIELD MICROSCOPY
14:20 BST | 15:20 CET

Mauro received his degree in Biology from the University of Milan, where he focused on Human Pathology. He then worked for two years in the Institute of Internal Medicine at the University of Milan on innovative techniques for diagnosing Helicobacter pylori and HCV. After his scientific career, he moved to a company involved with diagnostic products, where he spent five years as a Product Specialist in Italy. In 2000, he joined Leica Microsystems Italy as Product Manager Microscopy, covering all aspects of microscopy applications – particularly those related to Laser Microdissection (LMD). In 2009, he became European Field Support Specialist for the Life Science Research Division, primarily responsible for microdissection-related topics in EMEA. Since 2019, Mauro has provided application support for the THUNDER widefield imaging systems in Italy and, more recently, workflows for the Cell DIVE and Mica systems and their applications in multiplexing. He has presented at scientific conferences and hosted workshops all over EMEA, and organized remote training activities for researchers. Mauro enjoys interacting with scientists with different expertise and specimens to find the best applications and imaging workflows.

Dr. Mauro Luca Baron
Advanced Workflow Specialist

SPATIAL OMICS AND BEYOND
14:45 BST | 15:45 CET

Berta Cillero Pastor studied Molecular Biology and Biochemistry at Universidad Autónoma de Madrid. She obtained her PhD at the INIBIC Insitute of La Coruña (Spain) on the effect of pro-inflammatory cytokines in diseased cartilage by using, among other methods, proteomics. She moved then to AMOLF (Amsterdam) to develop new mass spectrometry imaging approaches in the field of orthopaedics. In 2015 she joined Maastricht University as CORE lab leader at the division of Imaging Mass Spectrometry (M4i). Since then, she established her own research line on the application of mass spectrometry imaging and proteomics tools for different biomedical applications.

In 2022 she joined the MERLN insitute as group leader where she employs an interdisciplinary and multimodal approach at the interface of proteomics, mass spectrometry imaging and molecular biology to develop new strategies for regenerative medicine.

Dr. Berta Cillero-Pastor
Group leader, Department of Cell Biology-Inspired Tissue Engineering MERLN Institute, Maastricht University

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Tissue biopsy analyses using matrix-assisted laser desorption/ionization mass spectrometry imaging (MALDI-MSI) provide molecular spatial information crucial to understanding in situ molecular mechanisms associated with a pathology. Recent developments in spatial omics demonstrate that the combination of MALDI-MSI and laser capture microdissection can overcome some challenges in protein identification of MALDI-MSI. Berta's group has previously developed a workflow on single (MSI) conductive slides and demonstrated that the protein content could be analyzed in small amounts of tissue after lipid or metabolite MSI. In this presentation, Berta will present a proof-of-concept study where spatial-omics approaches have been used by combining on-tissue intact protein and lipid analysis coupled to imaging-guided label-free proteomics in different cardiac injury animal models. This state-of-the-art approach allowed the identification of local changes in protein content and the investigation of pathways involved in infarct reperfusion injury, providing a new workflow for developing strategies to minimize myocardial damage after MI.

GET CLOSER TO THE (SPATIAL) TRUTH WITH THE STELLARIS CONFOCAL MICROSCOPE PLATFORM

15:25 BST | 16:25 CET

Jens obtained his Ph.D. in Biology (Neurobiology) from the University of Cologne. He continued to work in this field as a postdoctoral researcher at the Max-Planck Institute for Medical Research (Heidelberg) and the Karolinska Institute (Stockholm). His primary interest was neuronal networks generating behavior, which he studied in zebrafish using methods like electrophysiology, multi-photon calcium imaging, and confocal microscopy. His passion for biological imaging was why Jens joined Leica Microsystems in 2009. As an Advanced Workflow Specialist he is now contributing to scientific progress in different ways: by helping researchers identify which microscope system best fits their requirements and by supporting them through training and application advice.

Dr. Jens Peter Gabriel
Advanced Workflow Specialist

AIVIA – THE FUTURE OF AI MICROSCOPY

15:45 BST | 16:45 CET

Lindsey obtained her Ph.D. in Physiology and Molecular Biology at the National Museum of Natural History (France), followed by post-doctoral research in Regenerative Medicine at the University of Manchester (UK). She began working with state-of-the-art software at a start-up specializing in the application of virtual reality for education and exploration of large microscopy data stacks. Seeing Artificial Intelligence (AI) as the key to significantly speeding up microscopy image analysis, she is delighted to now work with Aivia software. Lindsey enjoys interacting with scientists and especially helping non-programmers to easily apply AI to their analysis workflow, ultimately helping them obtain outstanding results with their images.

Dr. Lindsey Marshall
EMEA Customer Success Manager for Aivia AI Image Analysis Software

CLOSING REMARKS

16:00 BST | 17:00 CET

Dr. Abdullah Ahmed
Leica Microsystems