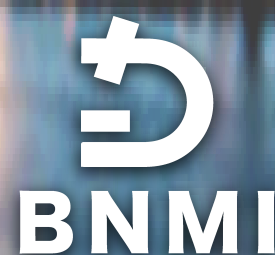# BNMI 2025 SYMPOSIUM

GOTHENBURG, SWEDEN, AUGUST 18-22, 2025

BNMI

Welcome Note

Welcome to the BNMI 2025 Symposium – 4th annual meeting of the **Bridging Nordic Microscopy Infrastructure!**

The **BNMI 2025 Symposium** is hosted by the **Centre for Cellular Imaging** at the **University of Gothenburg**, Sweden, from August 19–22, 2025. This prestigious event will bring together leading scientists from across basic and applied imaging research, Core Facility staff along with key industry representatives, for three days of insightful discussions and collaboration. Held at the Wallenberg Conference Center, the venue is easily accessible, just a short tram or bus ride from Gothenburg's city center.

BNMI 2025 is designed to bring together leading experts from diverse imaging modalities to inspire meaningful dialogue and foster impactful collaborations that drive the field forward. Whether you are an early-career scientist or an established researcher, BNMI 2025 presents a unique opportunity to explore the latest advancements in imaging technologies, acquire new skills, and expand your professional network within a vibrant and supportive community. It will also showcase groundbreaking imaging research from Gothenburg's vibrant scientific community, emphasizing the region's contributions to excellence and innovation in imaging science

A key focus of the symposium is to strengthen interactions between the academic imaging community and industry leaders. Through a dedicated session, company exhibitions, and networking opportunities, participants will engage directly with representatives from the imaging industry—opening doors to new partnerships and technical innovations.

The program will feature a compelling mix of lectures, poster sessions, and selected short talks from poster presenters, covering topics from electron and light microscopy, X-ray imaging, to advanced image analysis. Attendees will have numerous opportunities to engage in both formal discussions and informal gatherings, enriching both scientific dialogue and networking. Sessions will focus on these key areas in imaging research:

- **Smart Microscopy: from Image Analysis to Intelligent Acquisition**
- **Exploring Emerging Frontiers in Artificial Intelligence for Microscopy: An Overview of Trends and Innovations**
- **Imaging Sub-cellular Events at High Resolution using Advanced Light Microscopy**
- **Enabling Imaging Across Scales**

We hope you'll join us in Gothenburg for what promises to be an exciting and educational meeting. On behalf of the entire organizing committee, we look forward to welcoming you during the brightest season of the year. Wishing you a wonderful stay in Gothenburg!

Julia Fernandez-Rodriguez
Chair of BNMI 2025

Pre-Symposium Workshops

Smart Microscopy – Discover how automation is revolutionizing microscopy in our Smart Microscopy workshop. This state-of-the-art approach combines on-the-fly image analysis with fully motorized, computer-controlled microscopes to create adaptive, real-time imaging workflows. By enabling dynamic adjustments to microscope parameters during experiments, Smart Microscopy minimizes human intervention, allowing researchers to efficiently capture rare events, study complex biological systems and acquire statistically meaningful data.

Over one and a half days, participants will delve into the principles and practices of Smart Microscopy, using both commercial and open-source tools. Hands-on sessions will cover target identification, adaptive feedback loops, and integration with external hardware and software for advanced automation. The workshop emphasizes transferable strategies, ensuring participants can develop adaptive workflows tailored to their specific instruments. Join us to explore how Smart Microscopy can enhance your experimental efficiency and data reproducibility.

The workshop will be divided into 4 sessions:
- **CARL ZEISS** – Smart Imaging Workflows for Scalable, Automated Acquisition.
- **Nikon** – Experience Smart Microscopy with BergmanLabora & Nikon
- **Leica** – SpectraPlex for STELLARIS: 3D High-Multiplex Imaging for Spatial Discoveries
- **Webknossos** – Visualize, share, and annotate large 3D images online

Location: Centre for Cellular Imaging, Medicinaregatan 5A-7A, 413 90 Gothenburg

Time: Monday, 18 August (09:00–17:00) – Tuesday, 19 August (09:00–12:00)

Sponsor by:

Optical Tissue Clearing Techniques for 3D Lightsheet – Unlock the potential of deep imaging with this workshop on Optical Tissue Clearing Techniques, designed to complement 3D lightsheet microscopy. Tissue clearing transforms biological specimens into transparent structures, enabling unprecedented imaging depth without physical sectioning. When combined with lightsheet microscopy, tissue clearing allows researchers to visualize intact 3D biological structures—such as neuronal networks and whole organs—with high precision and minimal photobleaching.

This one-and-a-half-day workshop offers hands-on demonstrations in tissue clearing workflows optimized for light sheet microscopy. Participants will be introduced to key concepts through a combination of introductory lectures and live demonstrations. Topics include sample preparation for various tissue types, mounting strategies for systems such as the Zeiss Lightsheet 7 and Miltenyi UltraMicroscope Blaze, as well as basic data management and processing for large datasets.

With an emphasis on adaptability, attendees will learn how to optimize clearing protocols for their specific samples and fluorescence labels—empowering them to apply these techniques to their own research projects.

The workshop is structured into three focused sessions:
- **CARL ZEISS** – 3D imaging of large, cleared samples using the Zeiss Lightsheet 7
- **Miltenyi Biotec** – UltraMicroscope Blaze for 3D imaging at cellular resolution
  Imaging smaller cleared samples with confocal microscopy

Location: Centre for Cellular Imaging, Medicinaregatan 5A-7A, 413 90 Gothenburg

Time: Monday, 18 August (09:00–17:00) – Tuesday, 19 August (09:00–12:00)

Sponsor by:

Bridging Nordic Microscopy Infrastructures

BNMI 2025 Programme

Time	Tuesday 19th of August
12:30 – 13:30	**Registration**
13:30 – 13:40	Welcome to the Core Facility Day: Industry Engagement – *Julia Fernandez-Rodriguez*
13:40 – 14:05	*How investing in Industry Engagement Creates Opportunities for Core Facilities* *Claudia Pfander*, *Industry Board Coordinator, Euro-Bioimaging Bio-Hub, Heidelberg*
14:05 – 15:00	*Christian Garm* – MILTENYI BIOTEC *Rickard Linnskog* – MICROMEDIC_LEICA *Javier Fernandez Collado* – THERMO FISHER *Jesper Kielsgaard* – CARL ZEISS *Oliver Garner* – BERGMANLABORA AB_ NIKON *Norman Rzepka* – WEBKNOSSOS
15:00 – 15:30	Panel Discussion – Moderate by *Claudia Pfander & Julia Fernandez-Rodriguez*
15:30 – 16:00	**Coffee-Break**
16:00 – 16:55	*Tristan Martinez* – OXXIUS *Beatriz Rodrigues* – AGENDO *Yashar Rouzbahani* – ABBELIGHT *Sebastian Beer* – HAMAMATSU *Jan Vavra* – ABBERIOR *Ruediger Bader* – OXFORD INSTRUMENTS GmbH
16:55 – 17:35	Panel Discussion – Moderate by *Claudia Pfander & Julia Fernandez-Rodriguez*
17:35 – 18:35	**Keynote Speaker** *Imaging at the Beach: Development and Application of an Advanced Mobile Laboratory to Enable Cutting Edge Imaging-based Research in the Field* *Rainer Pepperkok*, *Director of Scientific Core Facilities and Services of EMBL* Introduction *Professor Oddmund Bakke*, *Oslo Norway*
18:35 – 20:00	**Welcome Reception**
19:30 – 21:30	Swedish NMI Infrastructure all-hands meeting (only with invitation)

Time	Wednesday 20th of August
8:00 – 9:00	**Registration**
9:00 – 9:15	Welcome *Julia Fernandez-Rodriguez and Oddmund Bakke*
	Smart Microscopy: from Image Analysis to Intelligent Acquisition *Chair: Rafael Camacho, Gothenburg Sweden*
09:15 – 09:45	*Event-triggered microscopy: a decision-making microscope* *Ilaria Testa*, SciLifeLab, Stockholm
09:45 – 10:00	*Real-time feedback control microscopy for automation of optogenetic targeting* *Lucien Hinderling,* University of Bern, Switzerland
10:00 – 10:15	*Smart Microscopy at the Centre for Cellular Imaging: Automation, Data Infrastructure, and Scalable Workflows for Image-Based Quantitative Biology* *Anders Folkesson,* Centre for Cellular Imaging, University of Gothenburg, Sweden
10:15 – 11:00	**Coffee-break & Company Exhibition**
11:00 – 11:30	*Distributed Lab automation Using a Fully Open-Source and Reproducible Software Stack* *Benedict Diederich,* Leibniz Institute of Photonic Technology
11:30 – 11:45	*Euro-BioImaging - another kind of "smart" microscopy* *Claudia Pfander*, Euro-BioImaging ERIC
11:45 – 12:15	*The Science and Fiction of Smart Microscopy in a Facility* *Michael Abanto*, Microscopy Core Facility, University of Basel, Switzerland
12:15 – 13:30	**Lunch & Company Exhibition**
	Exploring Emerging Frontiers in Artificial Intelligence for Microscopy: An Overview of Trends and Innovations *Chair: Giovanni Volpe, Gothenburg Sweden*
13:30 – 13:45	*High-fidelity 3D live-cell nanoscopy through data-driven enhanced super-resolution radial fluctuation* *Hannah Heil,* Department of Clinical Sciences, Lund University, Sweden
13:45 – 15:00	*The microscope on its way to becoming an autonomous intelligent robot!* *Ivo Sbalzarini,* Max Planck Institute MCG, Germany *Generative AI for Inverse Problems in Biomedical Computational Microscopy* *Artur Yakimovich,* CASUS, Helmholtz-Zentrum Dresden-Rossendorf, Germany
15:00 – 15:15	*DeepTrack2: Physics-based Microscopy Simulations for Deep Learning* *Mirja Granfors,* Department of Physics, University of Gothenburg, Sweden
15:15 – 19:00	**Poster Session & Company Exhibition**

Time	Thursday 21st of August
	Imaging sub-cellular events at high resolution using advanced light microscopy *Chair: Hans Blom, Stockholm Sweden*
09:00 – 09:30	***MINFLUX for dynamic structural cell biology*** ***Jonas Ries,*** Max Perutz Labs, University of Vienna, Austria
09:30 – 9:45	***Optical Near-Field Electron Microscopy: a novel non-invasive widefield technique for prolonged super-resolution dynamic imaging*** ***Ilia Zykov,*** University of Vienna, Vienna, Austria
9:45 – 10:15	***Visualizing the native cellular organization by coupling cryo-fixation with expansion microscopy (Cryo-ExM)" Marine Laporte*** ***Marine Laporte,*** Université Claude Bernard Lyon 1, France
10:15 – 11:00	**Coffee-break & Company Exhibition**
11:00 – 12:00	**Keynote Speaker** ***Imaging the Molecular Processes of Cell Division Across Scale*** ***Professor Jan Ellenberg,*** *Director of SciLifeLab, Sweden* Introduction ***Professor Eiríkur Steingrímsson,*** *Reykjavik Iceland*
12:00 – 13:00	**Lunch & Company Exhibition**
	Enabling Imaging Across Scales *Chair: Bjornar Sporsheim, Trondheim Norway*
13:00 – 13:30	***Bridging the scales of biology: one section at a time*** ***Jemima Burden,*** MRC Laboratory for Molecular and Cell Biology, UK
13:30 – 13:45	***End-to-end workflows leveraging high-throughput perturbation microscopy for rare disease druggability*** ***Michael Courtney,*** University of Turku, Finland
13:45 – 14:15	***Cryogenic microscopy of human organoids across scales*** ***Evgenia Zagoriy,*** EMBL, Heidelberg, Germany
14:15– 14:30	***Optical 3D kidney pathology*** ***Hans Blom,*** SciLifeLab, Stockholm, Sweden
15:00	**Social Activity (Boat Tour)**
19:00	**Gala Dinner (Kooperativet Lindholmen)**

Time	Friday 22nd of August
	Enabling Imaging Across Scales *Chair: Julia Fernandez-Rodriguez, Gothenburg Sweden*
10:00 – 10:40	***Correlative Light and (volume) Electron Microscopy Reveal Rewiring of Organelle Ultrastructure and Interactions in Cancer*** ***Nalan Liv,*** UMC Utrecht, Netherlands
10:40 – 11:15	***3D RNA Imaging of the Whole Brain Using Light Sheet Microscopy*** ***Shigeaki Kanatani***, Karolinska Instituten, Sweden
11:15 – 11:30	***High-content morphological profiling by Cell Painting in 3D spheroids*** ***Christa Ringers,*** Norwegian University of Science and Technology, Norway
11:30 – 11:45	**Closing Remarks**
11:45	**Grab and go Lunch**

Abstracts

SPEAKER ABSTRACTS

Keynotes Speakers

"Imaging at the Beach: Development and Application of an Advanced Mobile Laboratory to Enable Cutting Edge Imaging-based Research in the Field"

Rainer Pepperkok, *Director of Scientific Core Facilities and Services of* European Molecular Biology Laboratory, EMBL, Heidelberg, Germany

The Planetary Biology theme at EMBL aims to recognise and mechanistically understand phenotypic changes that are induced in the natural environment, using the array of tools available for molecular, structural, genomic, cellular, and developmental biology, and the powerful technologies that enable visualisation and perturbation of processes.

In order to achieve these goals and enable exploitation of high-end technology, currently used in cutting-edge laboratories, in the field to study components of ecosystems as close as possible in their natural habitat we developed an Advanced Mobile Laboratory (AML) which enables: (i) cryo-sample preparation for electron microscopy, (ii) advanced fluorescence (feedback) microscopy and (iii) image enabled fluorescence activated sorting for phenotype-genotype characterisation and isolation from field samples.

The AML (https://www.embl.org/groups/mobile-labs/) supported the 1.5 years lasting TREC expedition (https://www.embl.org/about/info/trec/) collecting and analysing sea water, soil and air samples across European coastlines. This enables studying genotype–phenotype relationships and the contributions of environmental factors in influencing phenotypes in their natural context on the molecular and cellular scales and at the ecosystems level. Selected examples of applications addressing the complex relationships between organisms and their environment will be presented.

Jan Ellenberg, Director SciLifeLab, Professor, Karolinska Institutet, Stockholm University & KTH Royal Institute of Technology, Sweden

Invited Speakers

Session 1: Smart Microscopy: from Image Analysis to Intelligent Acquisition – Smart microscopy refers to microscopes that can perform real-time analysis and adjust their imaging parameters on-the-fly based on feedback from the acquired images, without human intervention. These microscopes utilize feedback loops to directly read and process the images, and then feed that information back to optimize the imaging regime

"Event-triggered Microscopy: a Decision-making Microscope"

Ilaria Testa
Science for Life Laboratory, KTH, Stockholm, Sweden

Monitoring the proteins and lipids that mediate all cellular processes requires imaging methods with increased spatial and temporal resolution. STED (stimulated emission depletion) nanoscopy enables fast imaging of nanoscale structures in living cells but is limited by photobleaching. Here, we present event-triggered STED, an automated multiscale method capable of rapidly initiating two-dimensional (2D) and 3D STED imaging after detecting cellular events such as protein recruitment, vesicle trafficking and second messengers' activity using biosensors. STED is applied in the vicinity of detected events to maximize the temporal resolution. We imaged synaptic vesicle dynamics at up to 24Hz, 40ms after local calcium activity; endocytosis and exocytosis events at up to 11Hz, 40ms after local protein recruitment or pH changes; and the interaction between endosomal vesicles at up to 3Hz, 70ms after approaching one another. Event-triggered STED extends the capabilities of live nanoscale imaging, enabling novel biological observations in real time.

"Distributed Lab Automation Using a Fully Open-Source and Reproducible Software" Stack

Benedict Diederich
OpenUC2 GmbH, Germany

We present an open-source operating system for smart imaging and laboratory automation that unifies control of modular microscopes, robotic pipetting systems, and experiment orchestration frameworks. By integrating the openUC2 FRAME microscope, the ImSwitch software (via REST API in a Dockerized environment), and the Opentrons pipetting robot, we aim for a reproducible and scalable workflow for automated microscopy-driven protocols.

At the core of our system is Arkitekt, a graph-based orchestration layer that defines and executes modular experimental workflows. We developed dedicated interfaces to connect imaging hardware and liquid handling devices through standardized APIs, enabling precise temporal and spatial coordination between sample manipulation and image acquisition. The system supports biological use cases by allowing users to define complete protocols—from sample preparation to data acquisition and processing—entirely in software.

Our implementation includes REST-based triggering of microscope functions, scripting of pipetting routines via Opentrons Protocol API, and integration of image processing pipelines through plugins (e.g. ImStitch). Deployment scenarios range from local control to distributed

execution on embedded systems (e.g., Raspberry Pi clusters), enabling scalability from educational setups to high-throughput research environments.

This open-source stack offers a modular, transparent, and extensible solution for smart microscopy and automated experimentation, lowering the barrier to entry for labs seeking flexible and programmable imaging workflows. Further, by relying on the novel OS distribution system „Forklift", we aim for a fully reproducible lab automation workflow, by providing customized, yet fully version-controlled operating system images for different lab components.

"The Science and Fiction of Smart Microscopy in a Facility"

Michael Abanto
Microscopy Core Facility, University of Basel, Switzerland

Session 2: Exploring Emerging Frontiers in Artificial Intelligence for Microscopy: An Overview of Trends and Innovations — In recent years, there has been a growing trend toward adopting AI-based solutions in microscopy. These tools are increasingly being used for optimizing image acquisition (smart microscopy) and improving the overall efficiency and precision of image analysis workflows. The integration of artificial intelligence (AI) is now transforming the microscopy landscape, acting as a "second pair of eyes" to enhance image analysis. AI-powered tools are being trained to perform complex tasks such as object and image classification, segmentation, image restoration, super-resolution imaging, and virtual staining. These advancements are proving invaluable in areas like patient diagnostics and cancer research, enabling scientists to achieve higher resolution and gain faster, more accurate insights.
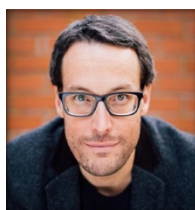
"Discovering Physics from Microscopy Images, and other AI-SciFi"

Ivo F. Sbalzarini
Max Planck Institute of Molecular Cell Biology and Genetics, Germany

Machine learning (ML) and artificial intelligence (AI) are transforming bioimaging. While traditionally, they were confined to image-analysis tasks, modern microscopy setups increasingly use AI and ML in all parts of the workflow. This includes large language models to generate analysis code from human-language input, ML for content-adaptive data processing, directly learning physical models and inferring physical parameters of the observed dynamics, and human-in-the-loop interaction modalities using eye gaze and hand gesture to interact with AI algorithms and with the sample. I will give an overview of current developments and trends and speculate about what can be expected in the short and mid term. In this, I also highlight challenges and risks and propose mitigation strategies to ensure FAIR, open, trustworthy, and energy-efficient use of emerging AI technologies in bioimaging.
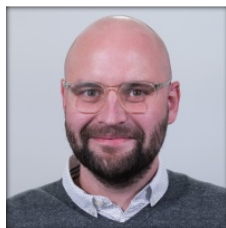
"Generative AI for Inverse Problems in Biomedical Computational Microscopy"

Artur Yakimovich
Center for Advanced Systems Understanding; Helmholtz-Zentrum Dresden-Rossendorf, Germany

Advanced microscopy techniques, including three-dimensional, super-resolution and quantitative phase microscopy, remain at the forefront of biomedical discovery. These methods enable researchers to visualise complex molecular processes and interactions at the level of single molecules or molecular complexes, capturing yet unseen information and pushing the boundaries of our understanding of health and disease. These innovations have been made possible, among others, through rapid progress in biophotonics, as well as computational processing and analysis of image-based data. However, advanced biophotonics comes at the cost of complex equipment, as well as difficult and lengthy data acquisition and necessitates highly trained personnel. We demonstrate in several works that this hurdle can be addressed using generative and discriminative AI algorithms by formulating the conversion from conventional microscopy modalities like widefield, to advanced like super-resolution, as a set of inverse problems. We show that incorporating nuance of the data domain into the algorithm design, as well as leveraging synthetic data pre-training, leads to better performance in these algorithms. Among other examples, we demonstrate how Generative AI algorithms can be utilised for Virtual Staining of virus infection in cultured cells, allowing for quasi-label-free detection of infected cells.

Session 3: Imaging Sub-cellular Events at High Resolution using Advanced Light Microscopy –
Observing sub-cellular structures at the smallest scale is crucial for advancing biomedical research and enhancing our understanding of biological processes. Recent innovations have led to faster acquisition speeds, single-molecule trajectory tracking, high-throughput imaging, and the development of novel probes. These advancements in resolution are driven by specialized sample preparation techniques, optical engineering, and sophisticated image analysis, enabling the detailed exploration of nanoscale structures within cells and tissues. This session will highlight cutting-edge developments in super-resolution imaging such as MINFLUX, MIN-STED, and Expansion Microscopy—an approach that physically enlarges biological samples to achieve nanoscale resolution—demonstrating their transformative impact on visualizing complex cellular structures.
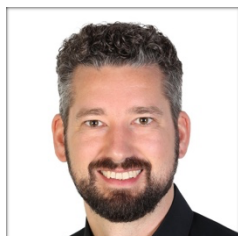
"MINFLUX for Dynamic Structural Cell Biology"

Jonas Ries
Max Perutz Labs at the Vienna BioCenter, University of Vienna, Austria

MINFLUX can localize single fluorophores with unprecedented precision by targeted detection with a scanned, patterned beam. In combination with switchable fluorophores, this allows for super-resolution imaging with single nanometer resolution. As MINFLUX uses the photon budget of a single fluorophore very efficiently, it is also a very promising technique for single-fluorophore tracking, improving speed, precision, and track length by one order of magnitude compared to camera-based tracking.

Here, I will introduce the principle of MINFLUX and its opportunities and limitations for dynamic cellular imaging. I will then discuss our recent result in which we used MINFLUX to track the stepping motion of the motor protein kinesin-1 as it walks on microtubules in living cells and present first results on using dual-color MINFLUX to monitor conformational changes of proteins during their action in living cells.

"Visualizing the Native Cellular Organization by Coupling Cryo-fixation with Expansion Microscopy (Cryo-ExM)"

Marine Laporte
Université Claude Bernard Lyon 1, France

Super-resolution fluorescent microscopy (SRM), encompassing expansion microscopy (ExM) since few years now, allows to locate proteins with nanometer resolution in a cellular context. However, SRM often requires cell fixation with aldehyde-based chemical crosslinkers, such as paraformaldehyde, or protein precipitation with cold methanol which potentially alter the native cellular state and the following interpretations. Cryo-fixation has proven to be the gold standard for efficient preservation of the native cell ultrastructure compared to chemical fixation; However, it is not widely used in fluorescence microscopy owing to implementation. We recently developed a method combining cryo-fixation to ExM (Cryo-ExM), which allow nanoscale observation of a wide cellular compartment in their native state. We could demonstrate that Cryo-ExM allows the native preservation of membrane-based organelles such as mitochondria, endoplasmic reticulum, Golgi and lysosomes together with the cytoskeleton component actin and microtubules and preserve all the structure in the same way, contrary to chemical fixations. Moreover, direct comparison with the gold-standard chemical fixation PFA-GA for the preservation of cellular structure, demonstrate that cryo-fixation bypassed drawbacks associated with this chemical fixation such as antigen accessibility due to strong protein-protein crosslinking.

In summary, we introduce a new method to perform super-resolution expansion microscopy by coupling cryo-fixation of a biological specimen with ExM, providing a universal framework to visualize subcellular compartments without chemical fixation artefacts. Importantly, this method also demonstrates that the classical cryo-substitution protocols developed for electron microscopy are compatible with expansion microscopy by replacing the EM resin with hydrogel monomer solutions. Therefore, this approach may also be applicable on tissues cryo-fixed by high-pressure freezing as well as in hydrogel-based tissue clearing. Finally, as expansion microscopy is also compatible with SIM, STED or dSTORM [18–20], our method now allows all these microscopy modalities to image cells in their native state, paving the way for further studies of complex and rapid dynamic cellular processes.

Session 4: Enabling Imaging Across Scales – The rapid advancement of imaging technologies over the past two decades has propelled significant biological and medical discoveries. Integrating complementary imaging modalities enables a comprehensive, multi-scale view of a sample, capturing both structural and functional parameters from the same specimen. Breakthroughs in electron and light microscopy now provide unprecedented visualization of molecular structures. As imaging modalities increasingly overlap across microscopic, mesoscopic, and macroscopic scales, they offer deeper insights into complex biological processes, including development, immune function, and disease progression. The future of multi-scale imaging will not only depend on advances in hardware and probes but also on computational innovations in data analysis and integration, further enhancing our understanding of health and disease.

"Bridging theSscales of Biology: one section at a time"

Jemima Burden
Laboratory for Molecular Cell Biology, University College London, UK

Biological processes occur at multiple scales, from the molecular level where protein interactions can elicit complex signalling cascades to cellular interactions that span mm to cm in length scales. Understanding how these processes work during healthy homeostasis as well as during disease and treatment states is the challenge facing numerous researchers across the fields of cell and developmental biology, drug discovery, as well as diseases relating to cancer, metabolic disorders and neurodegeneration. To tackle these challenges many use multimodal approaches to bridge these length scales. In this talk, I will share several example applications where using correlative light and volume electron microscopy has been instrumental in bridging these complex scales and enabled scientific advances.

"Cryogenic Microscopy of Human Organoids Across Scale"

Evgenia Zagoriy[1], Edoardo D'Imprima[1, 2], Julia Mahamid[1, 3]
[1]Structural and Computational Biology Unit, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany; [2]Correlative Light Electron Microscopy Core coordinator, Istituto Clinico Humanitas IRCCS - Humanitas Research Hospital; [3]Cell Biology and Biophysics Unit, European Molecular Biology Laboratory, Heidelberg, Germany.

Advances in cryo-focused ion beam-scanning electron microscopy (cryo-FIB/SEM) and cryo-electron tomography (cryo-ET) have enabled the transformative study of macromolecular complexes in their native cellular environments at near-atomic resolution. Concurrently, fluorescence imaging techniques have progressed significantly, facilitating the study of cellular processes in both space and time across a range of models. The integration of multiple modalities for the imaging of the same specimen aims to address challenges of in situ cryo-tomography, while harnessing its unique potential to deliver high-resolution macromolecule structures.

Cryo-ET is often constrained by low contrast in tomograms, making it difficult to identify macromolecules or events of interest, especially in crowded environments and in the absence of prior structural information. Additionally, the small field of view offered by cryo-ET complicates the study of rare events and impedes screening efforts. Here, fluorescence microscopy offers significant advantages, including high contrast and relatively large field of view. However, the resolution of fluorescence microscopy is typically several orders of magnitude lower than that of cryo-ET. This discrepancy creates a challenge in precisely and reliably registering images from these modalities. Cryo-FIB/SEM volume imaging represents another key technique that can bridge the resolution gap between diffraction-limited fluorescence microscopy and cryo-electron tomography.

To allow seamless combination of all the above modalities for the imaging of challenging frozen-hydrated multicellular specimen, we have developed an instrumental setup that integrates confocal cryo-fluorescence microscopy, cryo-FIB-SEM volume imaging, and the extraction of vitrified sample blocks for cryo-FIB lamella preparation, enabling detailed cryo-ET analysis. We demonstrate the application of this workflow in cryo-correlative light and electron microscopy (CLEM) to investigate high-pressure frozen human organoids at multiple scales,

while maintaining the native architecture and function of macromolecular complexes in their cellular environment.

Correlative Light and (volume) Electron Microscopy Reveals Rewiring of Organelle Ultrastructure and Interactions in Cancer

Nalan Liv
Center for Molecular Medicine, University Medical Center Utrecht, Netherlands

Alterations in the biogenesis, function, and interactions of intracellular organelles are hallmarks of diverse pathologies, including cancer. Visualizing these organelles and their crosstalk with high spatio-temporal resolution is essential for understanding their functional regulation. We have developed advanced Correlative Light and Electron Microscopy (CLEM) workflows that integrate the molecular specificity and live-cell capabilities of fluorescence microscopy (FM) with the nanometer-resolution ultrastructure provided by electron microscopy (EM). Our approaches include both 2D on-section CLEM for morpho-functional characterization and 3D live-cell volume CLEM—combining dynamic imaging with large-volume EM (including FAST-EM)—to capture rare and transient inter-organelle interactions in their full 3D ultrastructural context.

Applying these methods to the endo-lysosomal system, we correlate molecular markers, functional readouts (e.g., enzyme activity, pH, calcium content), and single-organelle dynamics with ultrastructural features in a single dataset. In an inducible HER2-positive breast cancer model, our integrated FM–(v)EM approach revealed profound organelle remodeling upon HER2 induction: lysosomes became denser and redistributed toward the cell periphery, mitochondria elongated with altered cristae organization, and the endoplasmic reticulum transitioned from sheet-like to tubular forms. Lipid droplets emerged uniquely in HER2-positive cells, suggesting enhanced lipid biosynthesis. Notably, we observed a marked increase in contact sites between lysosomes and the ER or mitochondria—key hubs for calcium exchange, metabolite transfer, and metabolic adaptation—validated by proximity ligation assays. These findings demonstrate that HER2-driven cancer cells rewire organelle ultrastructure and inter-organelle communication to support aggressive metabolic phenotypes. Our CLEM and FAST-EM workflows offer unprecedented opportunities to dissect the spatial, temporal, and functional regulation of organelle networks in health and disease, opening new avenues for therapeutic target discovery.
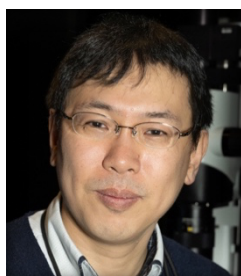
"3D RNA Imaging of the Whole Brain Using LightSheet Microscopy"

Shigeaki Kanatani
Karolinska Institutet, Stockholm, Sweden

Tissue clearing combined with light sheet microscopy has enabled high-resolution imaging of entire brains. However, these approaches have predominantly targeted proteins, as spatial RNA imaging remains technically challenging due to difficulties associated with detecting RNA within intact tissue volumes.

Here, we introduce TRISCO (Tris buffer–mediated retention of in situ hybridization chain reaction signal in cleared organs), a tissue-clearing method specifically developed for

comprehensive 3D spatial RNA imaging in intact brains. TRISCO overcomes major barriers such as RNA degradation, insufficient tissue transparency, and non-uniform labeling across large volumes, while effectively preserving RNA signals.

Using TRISCO, we successfully visualized diverse RNA species—including cell identity markers, noncoding RNAs, and neuronal activity-dependent transcripts— throughout whole mouse brains, as well as those from rats and guinea pigs. This method enables detailed, three-dimensional transcriptional analysis at single-cell resolution using light sheet microscopy.

Contribution Talks

Session 1: Smart Microscopy: from Image Analysis to Intelligent Acquisition

"Real-time Feedback Control Microscopy for Automation of Optogenetic Targeting"

Hinderling, Lucien, *Landolt, Alex E.; Grädel, Benjamin; Dubied, Laurent; Frismantiene, Agne; Dobrzynski, Maciej; Pertz, Olivier*
Institute of Cell Biology, University of Bern, Baltzerstrasse 4, 3012 Bern, Switzerland

Optogenetics have revolutionized our ability to study cellular signaling by enabling precise control of cellular functions with light. Most classical implementations rely on fixed or manually updated illumination patterns, limiting their ability to accommodate for living systems that move, change shape or rapidly adapt their signaling states. Here, we present a real-time feedback control microscopy (RTM) platform that combines automated image segmentation, feature extraction, and adaptive hardware control to dynamically adjust optogenetic stimulation based on live cell behavior. By continuously analyzing biosensor signals, the RTM platform updates illumination patterns in real-time, maintaining region-specific stimulation, inducing traveling activity waves, or selectively activating single cells within a tissue. This fully automated, Python-based framework is built on open standards for microscope control and data handling, supporting large-scale experiments and long-term time-lapse studies. It eliminates the need for human intervention to reposition light patterns or select target cells, thereby enabling reproducible, systematic and high-throughput interrogation of spatiotemporal signaling. Automated and adaptive optogenetic perturbations provide a powerful tool to study how local signaling events shape cellular behavior, from subcellular structures, through single-cell migration, to emergent tissue-level processes.

"Smart Microscopy at the Centre for Cellular Imaging: Automation, Data Infrastructure, and Scalable Workflows for Image-Based Quantitative Biology"

Anders Folkesson
Centre for Cellular Imaging, University of Gothenburg, Sweden

The Centre for Cellular Imaging (CCI), a national core facility within the University of Gothenburg, integrates state-of-the-art light and electron microscopy with advanced computational workflows to enable image-based quantitative biology. Leveraging automation, adaptive imaging, and robust data infrastructure, the CCI has developed scalable tools for data acquisition, processing, and FAIR-compliant management. This includes OMERO-based systems for secure data workflows, web-enabled microscope integration, and software pipelines for large-scale image reconstruction. Key applications include automated segmentation of complex neuronal structures and large image tile stitching. Collaborations with academia, industry, and global infrastructure networks ensure alignment with community needs, while ongoing development focuses on interoperability, usability, and expanded training. These efforts position Smart Microscopy as an operational, adaptable, and sustainable capability, poised to become a standard service for diverse biomedical imaging projects.

"Euro-BioImaging – Another Kind of "Smart" Microscopy"

Claudia Pfander
Euro-BioImaging ERIC

Euro-BioImaging – as a European Research Infrastructure - offers all scientists open access to a large portfolio of imaging instruments, expertise, training opportunities, and image data services. The more than 120 technologies offered by Euro-BioImaging can be accessed at Euro-BioImaging Nodes, which comprise almost 240 internationally renowned imaging facilities distributed across Europe.

To the technical experts at imaging core facilities, Euro-BioImaging provides access to the largest cross-European network of imaging scientists, and a platform for exchange of experience and new collaborations on technology development. Euro-Bioimaging connects facilities with similar technologies and research questions, and builds bridges to leading companies in the imaging sector through its Industry Board, to drive innovation and co-develop new instrumentation, tools and workflows that meet the needs of imaging facilities.

We will outline models of collaboration from sharing workflow solutions between facilities and industry in our Smart Microscopy Working Group to new technology validation for service provision in the IMAGINE project.

Session 2: Exploring Emerging Frontiers in Artificial Intelligence for Microscopy: An Overview of Trends and Innovations

"High-fidelity 3D live-cell nanoscopy through data-driven enhanced super-resolution radial fluctuation

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Image reconstruction based on fluctuations proves exceptionally powerful for long-term live-cell imaging, surpassing resolution limitations by extracting super-resolution details from brief image sequences captured at low light levels [1]. The latest iteration, eSRRF (enhanced-SRRF)

[2], not only enhances reconstruction accuracy but also integrates automated parameter optimization based on image fidelity and resolution. Based on this quantitative image quality metrics a reconstruction parameter combination yielding the best compromise between both measures is automatically suggested to the user. This feature helps to maximize image resolution, while circumventing reconstruction artifacts [3] and minimizing user bias. As an image processing approach eSRRF can be applied to a wide range of microscopy approaches for 2D superresolution imaging. To go beyond this, achieving high-fidelity 3D live-cell nanoscopy, we have also extended the eSRRF reconstruction algorithm to 3D. Realizing 3D eSRRF requires the simultaneous detection of fluorescence fluctuations across multiple focal planes, facilitated by a multifocus microscope (MFM) [4]. This innovative approach has enabled volumetric super-resolution imaging in live cells, boasting acquisition speeds of approximately 1 volume per second. Notably, it has enabled the super-resolution visualization of the dynamic rearrangement of the mitochondrial network in U2OS cells in 3D, capturing changes over several minutes.

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"DeepTrack2: Physics-based Microscopy Simulations for Deep Learning"

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DeepTrack2 is a flexible and scalable Python library designed to generate physics-based synthetic microscopy datasets for training deep learning models. It supports a wide range of imaging modalities, including brightfield, fluorescence, darkfield, and holography, enabling the creation of synthetic samples that accurately replicate real experimental conditions. Its modular architecture empowers users to customize optical systems, incorporate optical aberrations and noise, simulate diverse objects across various imaging scenarios, and apply image augmentations. DeepTrack2 is accompanied by a dedicated GitHub page, providing extensive documentation, examples, and an active community for support and collaboration: https://github.com/DeepTrackAI/DeepTrack2.

Session 3: Imaging Sub-cellular Events at High Resolution using Advanced Light Microscopy

"Optical Near-Field Electron Microscopy: a novel non-invasive widefield technique for prolonged super-resolution dynamic imaging"

_Zykov I. 1__, Jafarian H. 1, Stam W.G. 2, Neu P. 2, Moradi A. 2, Tromp R.M. 3, Amaro M. 4, van der Molen S.J. 2, Ju mann T. 1_

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Electron microscopy enables atomic-scale resolution in both dry and liquid environments. However, it has limitations due to the high energies the electrons transfer to the sample, which can induce structural damage. In contrast, light microscopy o ers a non-destructive imaging tool but is limited in temporal or spatial resolution.

Optical Near-field Electron Microscopy (ONEM) [1] is a novel imaging technique that combines non-invasive visible light probing with a nanoscale resolution electron microscopy readout. In ONEM light interacts with the sample placed in the near-field proximity to the flat photocathode. The emitted electrons' flux corresponds to the local electric field intensities at the photocathode plane. These photoelectrons are subsequently imaged using an aberrationcorrected Low Energy Electron Microscope. We present the first implementation of ONEM and benchmark its resolution capabilities on the sub-second scale. We then demonstrate proof-ofprinciple experiments in vacuum and environmental chamber. Measurements of nanophotonics samples show spatial resolution better than 30 nm. Electrochemistry measurements and live-cell imaging show ONEM's ability to image sample dynamics in a native environment over hours without damaging the system of interest. Being able to non-destructively image samples in situ, our new method can be applied to studying sensitive systems, e.g. protein dynamics in a lipid bilayer.

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Session 4: Enabling Imaging Across Scales

"End-to-end workflows leveraging high-throughput perturbation microscopy for rare disease druggability"

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Rare diseases include >7000 distinct pathological conditions affecting up to 10% of the population. Any one rare disease is diverse, depending for example which protein functions are perturbed by a given missense mutation. Clinical categorisation of most missense mutations as variants of uncertain significance, VUS, leaves patients without clear diagnosis and curtails investment in therapeutic development. This multilevel diversity and uncertainty among rare diseases are obstacles to traditional research approaches.

High-throughput perturbation microscopy, HTPM, is arguably the readout best suited to revealing phenotypic impacts of VUS while facilitating reverse screens for compounds ameliorating phenotypes. By engaging with a patient-advocacy group for the rare disease SynGAP-NSID and embedding within a HTPM-focused screening infrastructure platform affiliated with EU-OPENSCREEN, our team aims to develop workflows to address this challenge, with a focus on end-to-end automation of sample preparation, perturbation imaging and data management including image processing and data analysis.

Specifically, we use advanced cell systems, including mixed primary cultures and human iPSC-derived systems in 384 well plates, to model rare diseases. Gene delivery systems ensure uniform long-term multiplexing of optical actuators and reporters. These offer dynamic

response readouts of either subcellular protein mobilisation or single cell signalling across cell circuits. The non-invasive nature of imaging allows longitudinal monitoring over weeks, followed by end-point immunofluorescence analysis. Deep learning-enabled image processing is followed by machine learning-assisted data analysis. Unsupervised approaches reveal the diversity of cellular and molecular responses, whereas supervised learning identifies, from disease models, specific phenotypic signatures for downstream compound screening.

This workflow has, to date, identified the effects and side-effects of drugs distributed to distinct subpopulations of cells and the dynamic switching of individual cells between behavioural clusters, classified diverse SynGAP missense variants into separate phenotypic classes to simplify subsequent compound screening, and established contact-free perturbation assays for screening cellular and molecular phenotypes.

"Optical 3D kidney pathology"

*Unnersjö-Jess David[1,2,3]; Ebbestad Robin[1]; Fatehi Arash[3]; Brismar Hjalmar[1,2]; **Blom Hans[1]***
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Morphological alterations to the kidney filter are seen in most types of renal diseases. Due to the nanoscale dimensions of the filter, visualization of alterations presently uses electron microscopy in clinical settings (image inset top right below). We have instead developed optical 3D kidney pathology, which has the potential of advance diagnostic support in renal medicine. Our easier and faster method allows imaging whole biopsy selected material with nanoscale resolution (center image below). Our data-rich optical nanoscale pathology workflow can further detect disease alterations earlier and better.
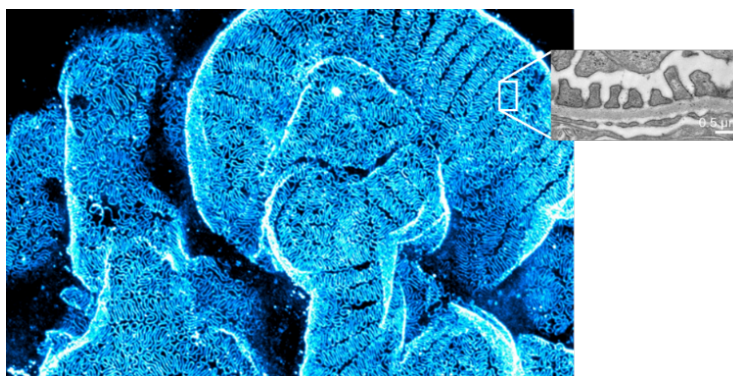
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"High-content morphological profiling by Cell Painting in 3D spheroids"

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Cell Painting is a widely used assay for morphological profiling of 2D cell cultures and proves valuable in a broad range of applications with its detailed visualization of subcellular architectures. 3D cell cultures more closely resemble physiological conditions, making them meaningful models for studying drug perturbations. However, despite their physiological relevance, 3D models are challenging to image. Limited light penetration through their dense cell layers complicates accurate characterization.

To overcome this limitation, we introduce a scalable method that integrates Cell Painting with tissue-clearing – a technique that enhances optical transparency – making deep multi-channel imaging of 3D spheroids possible. Our end-to-end analysis pipeline then combines automated spheroid detection, cell segmentation, morphological feature extraction, and between- and within-spheroid normalization to reduce plate and depth variations in the resulting morphological profiles.

We demonstrate this method using colorectal cancer cell spheroids generated in ultra-low attachment (ULA) microplates. We identify distinct phenotypic changes upon compound treatments using morphological profiles either from maximum intensity projections or from single cells, show that the latter profiles are more robust, and find that drugs group by biological pathway. Finally, we contrast 2D and 3D Cell Painting and discover different responses to DNA-damaging drugs in spheroids versus adherent cells.

We believe that this work lays the foundation for multi-channel image-based screening in 3D spheroids.

Posters

1: *Simplifying particle tracking: An accessible guide for experimental researchers*

Domenzain, Aarón; Lech, Alex 1; *Volpe, Giovanni 1; Manzo, Carlo 2; Rey, Marcel 3*
1 University of Gothenburg; 2 University of Vic; 3 University of Münster

Particle tracking is a fundamental technique across multiple scientific domains, including colloidal and soft matter physics, cell biology, nanotechnology, and medical diagnosis. Challenges arise from the intrinsic diversity of imaging techniques and samples.

This tutorial provides a structured approach to particle tracking using both simulated and experimental data of different colloidal particles imaged with fluorescence and brightfield microscopy techniques. Acknowledging that there is no one-size-fits-all solution, we present both standard and deep learning algorithms to tackle multiple scenarios.

The first part of the tutorial is particle detection, which includes two classic methods: thresholding and Crocker & Grier, followed by the deep learning algorithms U-Net (supervised learning) and LodeSTAR (self-supervised learning). The second part is trajectory linking, where we use a classical algorithm using TrackPy, the Hungarian algorithm combined with LapTrack and deep learning: graph neural network-based trajectory linking with MAGIK.

Each method of this tutorial is self-contained and modular, and any detection algorithm we present can be combined with any trajectory linking algorithm to suit the needs of the user.

2: *"The CCTeta subunit of the molecular chaperone CCT forms dynamic foci in mammalian when expressed as a monomeric GFP fusion cells"*

Eberhard, Anna-Caterina; *Grantham, Julie*
Department of Chemistry and Molecular Biology, the University of Gothenburg

The eukaryotic chaperonin CCT (Chaperonin-containing TCP1) is an essential folding oligomer that maintains proteostasis by facilitating the proper folding of proteins such as actin and tubulin. Emerging evidence suggests that individual monomeric CCT subunits may possess distinct, non-canonical functions. Notably, tumor database analyses have shown enhanced expression of several CCT subunits in cancer, underscoring the importance of understanding their roles in disease contexts. This study aims to explore the functions of the monomeric CCTη subunit by investigating the unique intracellular foci formation occurring upon transfection of GFP-tagged CCTη in mammalian cells, a feature not observed with other CCT subunits. Live-cell imaging further revealed that these foci exhibit dynamic behavior, progressively merging into larger assemblies, while structured illumination microscopy (SIM) demonstrated that they do not associate with or move along microtubules. Therefore, the subunit-specific formation of intracellular foci by GFP-CCTη, indicates either a specific monomeric function that enables it to independently form foci, or distinct processing of the CCTη subunit leading to accumulation via interactions with other cellular components. These results suggest that CCTη may play

additional roles beyond its canonical chaperone function, which could have important implications for understanding its contribution to cancer and other disease states.

3: *"BioImage Informatics, SciLifeLab, Sweden"*

*Maximilian Senftleben, Suganya Sivagurunathan, Kristína Lidayová, Jonas Windhager, Christophe Avenel, Gisele Miranda, Carolina Wählby, **Anna Klemm***
BioImage Informatics Unit (BIIF), SciLifeLab, Sweden

The BioImage Informatics unit (BIIF) develops new computational technologies and provides access to expertise and state-of-the art software for processing and quantitative analysis of all kinds of microscopy image data, primarily for applications in the life sciences. BIIF is a SciLifelab unit, and part of the National Bioinformatics Infrastructure Sweden NBIS. We are active within the GloBIAS and EuroBioImaging networks.

Services
- Advice on best-practice and guidance on overall experimental design for research involving microscopy imaging and quantitative data analysis.
- Guidance on image analysis assay development, including image processing algorithm development and software engineering to address challenging project goals.
- Advice on best-practice and guidance on high throughput/large-scale image processing using computing clusters, including data transfer and storage during the activity of the project.
- Guidance on large-scale data analysis and visualization.
- Dissemination of bioimage analysis knowledge in courses and workshops.

4: *"Glycosylation Regulates Nanoscale Clustering of Na,K-ATPase as Revealed by Super-Resolution Microscopy"*

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The Na,K-ATPase (NKA) is a critical transmembrane protein complex responsible for maintaining cellular electrochemical gradients. NKA is a heterotrimeric complex composed of alpha (α), beta (β), and gamma (γ) subunits. Glycosylation of the β subunit is necessary for its trafficking from the endoplasmic reticulum to the plasma membrane. While the functional role of the β subunit glycosylation is well-established, its impact on NKA organization at the cell surface remains unclear.

Here, we investigate the role of glycosylation on membrane protein organization and dynamics by comparing the wild type (WT) β subunit to a glycosylation-deficient mutant. We used super-resolution microscopy to investigate the role of glycosylation for NKA membrane dynamics and nanoscale distribution. Fluorescence Recovery After Photobleaching (FRAP) revealed a reduced mobile fraction of glycosylation-deficient mutants. Single Molecule Localisation Microscopy (SMLM) showed differential clustering patterns between the mutants and the WT. Our experimental imaging data are supported by findings from molecular assembly simulations using GlycoSHIELD-MD that indicate a shielding effect of NKA β N-glycans. Taken together,

these findings suggest that glycosylation not only has a role for trafficking but can also regulate the nanoscale organization of NKA in the plasma membrane. Further research direction is focused on single- and dual-color MINFLUX imaging of the alpha and beta NKA subunits to elucidate the overall clustering pattern of the pump in different cell states.

5: *Comparative stimulated Raman scattering imaging and spectral analysis of human skin, artificial and melanoma skin models*

Gilia C. M. Ruiz and *Jonathan R. Brewer*
Department of Biochemistry and Molecular Biology, Danish Molecular Biomedical Imaging Center (DaMBIC), University of Southern Denmark (SDU), Denmark

Stimulated Raman Scattering (SRS) microscopy is a powerful label-free technique for imaging biomolecular composition in biological tissues. In this study, we applied SRS imaging and spectral analysis to compare structural and biochemical differences among three skin models: ex vivo human skin, in vitro artificial skin, and in vitro melanoma model. High-resolution SRS images and Raman spectra were acquired from distinct skin layers, including the Stratum Corneum, viable epidermis (live cells), dermis (collagen-rich region), and water-rich regions. Each layer exhibited unique spectral fingerprints, particularly in CH2 and CH3 stretching regions ($\sim$2845–2940 cm^{-1}), Amide I ($\sim$1650 cm^{-1}), Amide III ($\sim$1260 cm^{-1}), and OH-stretch ($\sim$3400 cm^{-1}). Comparative analysis revealed that human skin samples showed stronger CH_2 bands and sharper Amide I peaks, indicative of higher lipid order and well-organized protein structures. Artificial skin displayed attenuated lipid signals and altered protein/lipid ratios, suggesting incomplete barrier maturation. Melanoma models showed stronger protein signals and regional chemical variations, revealed by spectral decomposition of Raman data. SRS imaging visually confirmed these findings, showing differences in lipid-rich layer thickness, collagen density, and cellular architecture across models. This study demonstrates the potential of SRS microscopy to assess structural and biochemical integrity across skin models and highlights its applicability in dermatological research and skin-on-chip platforms for disease modeling and drug testing.

6: *"Advanced Light Microscopy (ALM) support"*

Agostinho Ana; Edwards Steven; Wennmalm Stefan; Blom Hans; Brismar Hjalmar
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Abstract: ALM services projects demanding fluorescence microscopy support to resolve the cellular nanoscale (e.g., ExM, SIM, STED, SMLM, MINFLUX). We also support single molecule dynamics investigation with several sensitive techniques (e.g., FCS, FCCS, FRET-FCS, STED-FCS, MINFLUX tracking). Single-cell ultra-fast volumetric imaging of biological processes at high-resolution is provided by lattice light-sheet microscopy (LLSM). Volumetric light-sheet fluorescence microscopy (LSFM) allows imaging live and/or optically cleared larger samples. To get more information on how to get advanced imaging support visit our home-page: https://www.scilifelab.se/units/integrated-microscopy-technologies/

7: *"Live-Imaging of Mitochondrial Dynamics"*

Påvénius, Linnéa *(1); Erlandsson, Anna (2); Lindskog, Maria (3); Brismar, Hjalmar (1,4)*
1 Science for Life Laboratory, Department of Women's and Children's Health, Karolinska Institutet, Stockholm, Sweden; 2 Department of Public Health and Caring Sciences, Molecular Geriatrics, Rudbeck Laboratory, Uppsala University, Sweden; 3 Department of Medical Cell Biology, Uppsala University, Sweden; 4 Science for Life Laboratory, Department of Applied Physics, Royal Institute of Technology, Stockholm, Sweden

Organelle structure and dynamics have proven much more important and diverse than previously thought. Mitochondria are highly motile organelles that have the ability to quickly change morphology and location within the cell in order to adapt to metabolic flux and conditions. The underlying mechanisms that rule mitochondrial structure and localisation thought the cell remain a subject for investigation. However, mitochondrial dysfunction has been identified as a hallmark for many diseases and syndromes. Most prominently neurodegenerative diseases such as Alzheimer's and Parkinson's disease have been associated with mitochondrial fraction and dysfunction. While the processes in neurons have been meticulously studied, the changes to astrocytes have been less investigated but proven of increasing importance for the pathological development. Each synapse is modulated by an astrocytic process that is in the size range of 20-200nm. It has been repeatedly shown that about 40-50% of these processes have mitochondria, an unexpected find since mitochondria range in the sizes up in the micron range. Several factors such as neurotransmitter release, neuronal activity and high energy demand have been proposed to, and shown, to attract and position mitochondria in proximity to these events. Both microtubule-based and actin-based transport and positioning have been shown to play an important role in the dynamics. However, they do not entirely account fully for these processes. We are applying live super-resolution imaging with Airyscan confocal and live-SIM to iPSC derived astrocytes under different metabolic conditions in a polarised system to investigate the impact on mitochondrial dynamics and positioning.

8: *"3D Spatial Transcriptomics: A MERFISH Platform for High-Resolution Transcriptomics Profiling"*

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Spatial transcriptomics (SP) is an advancing technology in genomics that reveals the complex molecular landscape of cells and tissues. Imaging-based SP techniques enable visualization and quantification of numerous RNA species within individual cells, even at subcellular resolution.

We have developed an automatic, imaging-based platform that uses computational algorithms to localize individual transcripts in 3D. This platform is based on the MERFISH (Multiplexed Error-Robust Fluorescence In Situ Hybridization) technology, which combines fluorescence in situ hybridization (FISH) with multiplexed barcoding. Our platform supports a wide range of samples, including cell cultures and tissues, and allows at present detection of up to 140 genes pr. library. To improve signal-to-noise and spot detection, we have incorporated tissue clearing in our protocol, reducing background autofluorescence.

For data analysis, we use the MERlin pipeline, applying pixel-based decoding to identify and locate RNA molecules in 3D. The spatial distribution of these genes is visualized using TissUUmaps, offering an interactive view of gene expression.

By combining error-robust encoding and high-resolution microscopy, MERFISH enhances the accuracy and sensitivity of RNA molecule detection compared to traditional FISH. Its versatility makes MERFISH a valuable tool for exploring the complex molecular landscape of cells and tissues, with applications in developmental biology, cellular organization, and disease research.

9: *Advances in multiphoton microscopy – acousto-optical scanners enable ultra-high temporal resolution, voltage imaging, virtual imaging plane rotation, true 3D random scanning, and real-time 3D motion correction*

Nikita Mikhailov, Denes Palfi, Tamas Tompa, Balazs Chiovini, Viktoria Kiss, Zsolt Mezriczky, Anna Mihaly, Katalin Ocsai, Gergely Katona, Balazs J. Rozsa

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Multiphoton imaging is a vital tool for in vivo studies. Being able to penetrate as deep as 1 mm from the cortex surface, multiphoton imaging provided great insight into the neurobiology of a living brain with a high spatial resolution.

However, until the recent past, the temporal resolution of multiphoton microscopy could not reach the level of classical electrophysiology – the technique providing direct information on the cell's membrane potential.

Here we present the advances in multiphoton microscopy that became possible with the usage of a new type of deflectors based on acousto-optical crystals. Being free from any physically moving parts they boosted the temporal resolution of scanning beyond 10 µs, and allowed combining 3D anatomical structure with voltage imaging with a frequency high enough to mimic the temporal resolution of electrophysiology.

The same absence of moving parts brought the ultimate flexibility of the imaging patterns with an unprecedented example of "arbitrary plane scanning" – quasi-virtually rotated plane, that permits imaging of coronal, axial, sagittal, and any other tilted sections of the brain without actual rotation of the objective or animal.

The most recent advance of the high-frequency high-flexibility scanners – is a three-dimensional online motion correction that eliminates relative focus point–sample displacement.

10: *"Satellite glial cell subtypes mapped to reveal distinct spatial organization and neuronal associations"*

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Satellite glial cells (SGCs) envelop the neuron cell bodies (somata), axon hillocks, and initial axon segments of sensory neurons in the dorsal root ganglia (DRG). SGCs are crucial in supporting the functions and maintaining the microenvironment of sensory neurons. However, when activated, SGCs exhibit abnormal behaviors linked to the development of chronic pain in conditions such as nerve injuries, diabetes, exposure to neurotoxic agents (e.g., certain chemotherapeutics), viral infections, and inflammation. Despite their importance, knowledge of SGC diversity is limited to transcriptional profiling, leaving their functional roles unexplored. This study provides a detailed in situ characterization of SGC subtypes in the DRG. We combined single-cell RNA sequencing with imaging techniques supported by deep learning to identify, validate, and spatially map distinct SGC subtypes within their anatomical environment.

We identified and described several SGC subtypes: (1) Classical SGCs: The predominant type surrounding neuron somata, expressing the markers FABP7, KIR4.1, GS, and CX43 in both murine and human DRG. (2) OCT6+ SGCs: In mouse DRG, found around the initial segments of axons and occasionally incorporated into classical SGC sheaths to form mosaic structures. (3) SCN7A+ SGCs: In mouse DRG, characterized by low expression of traditional SGC markers and forming unique sheaths around non-peptidergic neurons, possibly linked to itch-related (pruritic) conditions and in human forming a distinct outer layer surrounding the inner SGC layer. (4) Interferon-responsive SGCs: In mouse DRG, expressing interferon response genes, indicating a role in antiviral defense. (5) Non-classical SGCs: Lacking conventional SGC markers and surrounding certain small-diameter neurons in mouse DRG, suggesting potential new specialized subtypes to be further studied.

This work provides a foundational exploration of SGC heterogeneity, revealing their spatial organization and potential functions. Furthermore, these findings set the stage for advancing research on SGCs roles within the peripheral somatosensory nervous system and its associated disorders.

11: *"Comprehensive Characterization of Rainbow Trout Hepatic 3D Spheroids Using Microscopy and a Multimode Detection Platform"*

Chand, Prem *1; Song 2, You 2; Campsteijn 1, Coen 1; Jha 3, Awadhesh 3; Gomes 2, Tania 2; Ballina 1, Laura Rodriguez de la 1; Hultman 2, Maria T. 2*

(1) University of Oslo, Norway; (2) Norwegian Institute for Water Research (NIVA), Norway ; (2) Norwegian institute for water research; (3) University of Plymouth, United Kingdom

The demand for alternative ecotoxicology methods is increasing, especially with a focus on New Approach Methodologies (NAMs) to provide reliable in vitro models for chemical hazard assessments. Many existing cell-based assays rely on primary or continuous cell cultures

effective for acute toxicity but often lack the necessary complexity for long-term exposure studies. However, few alternative models support comprehensive, long-term toxicity evaluations, essential for understanding chronic impacts.

A novel 3D spheroid model derived from rainbow trout (Oncorhynchus mykiss) primary hepatocyte (RT-HEP-SP) has emerged as a promising NAM, preserving key morphological, physiological, and biochemical properties for weeks, making it suitable for chronic toxicity studies. However, broader application of the RT-HEP-SP system requires thorough characterization and validation. In this study, high-resolution confocal microscopy, 2 photon excitation microscopy and fluorescent microscopy was employed to assess various markers, such as spheroid morphology (cytoskeleton, DNA and nuclear integrity, bile canaliculi formation), viability (metabolic activity, hypoxia within the spheroid core), and physiological response (reactive oxygen species [ROS] induction, mitochondrial membrane potential) during chemical exposure.

A Biomarker Toolbox was developed with sensitive and reproducible markers for oxidative stress, biotransformation (e.g., aryl hydrocarbon receptor, EROD,), and viability (e.g., lactate dehydrogenase). These biomarkers were validated through short-term (24 96 hours) exposures to model chemicals with distinct toxic modes of action (MOAs), including copper, 17 β-ethinyl estradiol (EE2), benzo[a]pyrene, and carbonyl cyanide m-chlorophenyl hydrazone (CCCP), confirming the model s responsiveness and reproducibility.

Initial findings indicate that RT-HEP-SP are a reliable model for assessing cytotoxicity, membrane integrity, and oxidative stress, with no core hypoxia detected. RNA-seq analyses reveal their molecular complexity and suitability for the assessment of chemicals with different MOAs. This model shows strong potential as an ecotoxicity screening tool for various chemicals.

12: "*Imaging at the Center for Advanced Bioimaging (CAB)*"

Kjeldgaard-Nintemann, SJ; *Christensen, NM*
Center for Advanced Bioimaging Denmark, Faculty of Science, University of Copenhagen, Denmark

The Center for Advanced Bioimaging (CAB) Denmark at the University of Copenhagen offers expert training and access to a comprehensive bioimaging instrument park to users from a broad spectrum of research areas. Available modalities range from routine widefield microscopy to electron microscopy and high-end confocal and multiphoton microscopy for imaging label-free and in-depth.

13: "*descSPIM-Hubble, a high-resolution, low-cost and easy-to-build light-sheet microscope*"

Edwards, S.J.; *Senftleben, M.L.; Otomo, K.; Susaki, E.A.; Brismar, H.*

Science for Life Laboratory, Department of Applied Physics, KTH Royal Institute of Technology, Stockholm, Sweden; Science for Life Laboratory, Department of Applied Physics, KTH Royal Institute of Technology, Stockholm, Sweden; Department of Biochemistry and Systems Biomedicine, Juntendo University Graduate School of Medicine; Department of Biochemistry and Systems Biomedicine, Juntendo University Graduate School of Medicine, Nakatani Biomedical Spatialomics Hub, Juntendo University Graduate School of Medicine; Science for Life Laboratory, Department of Applied Physics, KTH Royal Institute of Technology, Stockholm, Sweden

descSPIM (desktop-equipped SPIM for cleared specimens) is an affordable and easy to-build light-sheet microscope designed for rapid imaging of optically cleared samples. Since its release, descSPIM has been installed in research groups worldwide, highlighting its ability to address a growing demand for cleared tissue imaging. However, the relatively low resolution of descSPIM may not be sufficient for all imaging applications. We have further developed the descSPIM platform by designing and building descSPIM-Hubble, allowing (1) high resolution (1.09 mm laterally and 4.06-6.40 mm axially) volumetric imaging of optically cleared specimens, (2) stripe artifact reduction using a galvanometric mirror (3) open-source with parts-list and build instructions, (4) simplified microscope control using ImSwitch and (5) low-cost (€25,000 - €50,000 depending on laser configuration). descSPIM-Hubble makes high resolution imaging of optically cleared samples more accessible and inclusive.

14: *"Core Facility for Integrated Microscopy"*

Braunstein, Thomas Hartig
The Core Facility for Integrated Microscopy, University of Copenhagen

The Core Facility for Integrated Microscopy (CFIM) was officially inaugurated in September 2010. It is located at the Faculty of Health and Medical Sciences, University of Copenhagen.

CFIM offers a wide range of state-of-the-art light and electron microscopes. Scientists and students coming to CFIM find not only light and electron microscopes ready to use for their research, but also the necessary technical assistance and support. At the present time we have approximately 650 registered users.

In the past, light and electron microscopy have always been physically separated with little interaction. As our name indicates, our vision is to integrate different microscopy techniques, increasing the inter-disciplinary microscopical approach to scientific imaging questions.

15: *"Extracting structural information from 3D MINFLUX imaging"*

Mebus, Viktor; *Ebbesen, Morten; Brewer, Jonathan*
University of Southern Denmark

Nanoscale 3D MINFLUX imaging provides unprecedented resolution for visualizing labeled cellular structures, enabling insights at the molecular level. Despite its potential, the lack of standardized tools for processing and quantifying 3D point cloud data remains a major barrier to broader adoption. To address this, we present an intuitive, R-based Shiny application designed for the quantitative analysis of 3D MINFLUX datasets.

Our platform allows users to perform essential preprocessing steps including interactive data filtering and DBSCAN clustering. It further supports advanced spatial analysis, such as calculating nearest-neighbor distances, local curvature, and surface area estimation. The app facilitates intuitive data exploration and visualization, enabling users to extract quantitative biological insights from complex nanoscale structures without requiring deep programming expertise. This tool aims to standardize 3D MINFLUX data analysis and make it more accessible to the broader biomedical imaging community.

16: *"Single cell spatial genomics at the nanoscale: Connecting genomic structure and gene regulation"*

Grini, Jonas, V.; Beckwith, Kai
Department of Biomedical Laboratory Science, Norwegian University of Science and Technology

The spatial organization of the genome is critical for gene regulation. This is perhaps made most evident in genes regulated by distal enhancers that by some means must be brought into contact with the promoter regions with which they interact. The Cohesin complex structures the genome by creating DNA loops and has been found to be vital for the transcription of several genes. Furthermore, nuclear positioning, for example by translocations of genes to nuclear speckles has also been demonstrated to enhance transcription. The molecular mechanisms coupling global and local structural alterations to transcription remains poorly understood.

We employ highly multiplexed DNA-FISH, combined with RNA-FISH and protein labeling, to visualize genomic structures and link them to transcriptional activity in single cells. By focusing on super-enhancer-regulated genes with known associations to nuclear speckles, we aim to uncover the structural components underlying gene regulation. Our findings will provide mechanistic insights into how genomic architecture governs gene expression.

17: Danish Bioimaging Infrastructure Image Analysis Core Facility (DBI-INFRA IACF)

Tricia Loo Yi Jun, *Julia Mertesdorf*
University of Copenhagen, Denmark

The Danish Bioimaging Infrastructure Image Analysis Core Facility (DBI-INFRA IACF) runs an open service in image analysis to help life scientists visualize, analyze, and extract quantitative information from their bioimaging datasets. Our experts handle image analysis tasks with sound scientific foundations, for imaging modalities ranging from light and electron microscopy to (pre-)clinical imaging.

Our team works with you to discuss and define your image analysis needs, guide and train you in the most suitable software solutions and, when needed, develop image analysis workflows customized to your research project. All services, including project meetings, training, booking and access to our image analysis workstations, software and storage can be provided either on-premise or remotely.

You can contact us through the IACF webpage (www.dbi-infra.eu/iacf) to take part in a free *Call4Help* consultation or to submit an image analysis project. Projects involving software or methodological development must be submitted online and are bound to fees estimated during a free quotation prior to project start. Software training and support are provided on demand on our workstations and at a fixed hourly cost. We are additionally involved in teaching bioimage analysis during workshops and training schools, and we actively promote community standards for sharing and preserving scientific image and associated software. Since opening for service in 2023, the IACF has worked on 25 user projects by providing custom workflows or training solutions, and have reached out to many more through our free consultation services and training courses.

The facility received funding from a national infrastructure grant (DBI-INFRA 2022-2027, Danish Ministry of Higher Education and Science) and aims to actively promoting open science and enforcing high sharing and reproducibility standards through good practices, dedicated data and software repositories. To this end, we will systematically try to reach agreements with the researchers to define a timeline for sharing the assets developed in the facility, especially for those with high re-usability potential. The facility also aims to establish a new open service model embracing professional project management practices, fair service billing, and an optimal utilization of existing local resources and expertise.

18: *"DeepTrack2: High-Quality Microscopy Simulations for Deep Learning"*

Lech, Alex 1; *Granfors, Mirja 1; Midtvedt, Benjamin 1; Pineda, Jesús 1; Bachimanchi, Harshith 1; Volpe, Giovanni 1; Manzo, Carlo 2,*
1 University of Gothenburg; 2 University of Vic

DeepTrack2 is a flexible and scalable Python library designed for simulating microscopy data to generate high-quality synthetic datasets for training deep learning models [1]. It supports a wide range of imaging modalities, including brightfield, fluorescence, darkfield, and holography, allowing users to simule real experimental conditions with ease. Its modular architecture enables users to customize experimental setups, simulate a variety of objects, and incorporate optical aberrations, realistic experimental noise, and other user-defined effects, making it suitable for various research applications. DeepTrack2 is designed to be a powerful yet accessible tool for researchers in fields that utilize image analysis and deep learning, as it eliminates the need for labor-intensive manual annotation. This helps accelerate the development of AI-driven methods by providing largescale, high-quality data that is often required by deep learning models. DeepTrack2 has already been used for a number of applications in cell tracking, classifications tasks, segmentations and holographic reconstruction. Its flexible and scalable nature enables researchers to simulate a wide array of experimental conditions and scenarios with full control of the features. DeepTrack2 is available on GitHub, with extensive documentation, tutorials, and an active comminity for support and collaboration [2].

References
[1] B. Midtvedt, S. Helgadottir, A. Argun, J. Pineda, D. Midtvedt, G. Volpe (2021). Quantitative Digital Microscopy with Deep Learning. Applied Physics Reviews, volume 8, article number 011310.
[2] https://github.com/DeepTrackAI/DeepTrack2
*Corresponding

19: *"Smart Microscopy Working Group: highlights and future Plans"*

Rafael Camacho[1], Benedict Diederich[2,3], Anders Folkesson[1], Manuel Gunkel[4], Aliaksandr Halavatyi[4], Hannah S. Heil[5], Lucien Hinderling[6,7], Nils Norlin[8], Christopher Rhodes[4], Philipp Seidel[9], Claudia Pfander[10]
[1] Centre for Cellular Imaging, Core Facilities, University of Gothenburg, Sweden; [2] Leibniz Institute for Photonic Technologies Jena, Germany; [3] openUC2 GmbH, Jena, Germany; [4] European Molecular Biology Laboratory, EMBL Heidelberg, Germany; [5] Department of Clinical Sciences, Faculty of Medicine, Lund University, Lund, Sweden [6] Institute of Cell Biology, University of Bern, Switzerland; [7] Graduate School for Cellular and Biomedical Sciences, University of Bern, Switzerland; [8] Lund University Bioimaging Centre, Lund University, Lund, Sweden; [9] Zeiss Microscopy GmbH, Jena, Germany; [10] Euro-BioImaging, Heidelberg, Germany

Adaptive microscopes that autonomously fine-tune their acquisition parameters, respond to biological events, and seek experimental outcomes, are highly demanded by scientists. Achieving this vision requires coordination and intense collaboration among microscopy

specialists, engineers, software developers, AI scientists, and many other stakeholders working in a highly interdisciplinary environment.

Facilitating this coordination and interaction has been the goal of the Smart Microscopy Working Group which was founded in 2022 with support from the EuroBioimaging Industry board. The group has continued to grow and branch out in 2024 and 2025. In this period, we welcomed new members to connect European research infrastructures like Netherlands BioImaging. We collected references and reviewed research trends on automation-driven microscopy methods, actively working toward the publication of a white paper to provide useful guidance for potential users and contributors. Similarly, we have started to develop common training material to be used in future courses where researchers who are not microscopy specialists learn how to integrate microscopy automation and feedback strategies into their work. A significant cohort of the group collaborated on a proposal to fund smart microscopy development across a broad consortium of research institutions, infrastructures, and companies, momentum that we hope to sustain on new initiatives.

Since its inception, we have experimented with the format of our meetings, including conventional research talks, hackathons and challenges, and team coordination on specific papers and proposals. The working group is unique in that stakeholders from industry and academia come together to create synergies by bringing together the needs of technically experienced biologists and the technical solutions developed by the companies to advance the field of smart microscopy either with commercial products or academic open-source solutions. What sets the group apart is the freedom to connect the details of contributors' innovations with broader themes like technical interoperability, teaching, and technology access. Given the diverse audience we will continue this valuable forum to promote a unified concept of smart microscopy to researchers.

20: *"Euro-BioImaging Finland receives "lighthouse" status and record funding"*

Irina Belaia, Tiina Saanijoki, Pasi Kankaanpää
Turku BioImaging, University of Turku and Åbo Akademi University, Finland tbi-office@bioimaging.fi

Euro-BioImaging Finland (www.eurobioimaging.fi) consists of two Nodes, Finnish Advanced Microscopy Node and Finnish Biomedical Imaging Node. Euro-BioImaging Finland has just been selected to the Finnish national roadmap of research infrastructures 2025-2028, with a record funding of 28 M€ from the Research Council of Finland. Euro-BioImaging Finland has also been selected as a "lighthouse", an exceptional forerunner infrastructure.

Lighthouse infrastructures need to: 1) be at the forefront of providing services for science and innovation, 2) have no overlaps with other infrastructures, 3) have broad and demonstratable impact on society, 4) have wide utilization from many sectors, 5) have a proven track record in international networks, 6) have professional staff and management, 7) have a diverse and stable financial base, and 8) take into account the green transition. There are only six lighthouse infrastructures in Finland, so being selected as one is significant. In addition, Euro-BioImaging Finland has just received European Regional Development Funding and national regional development funding to develop open access image analysis services for digital agriculture, marine biology, and environmental protection. This type of development is increasingly important for the broad impact of imaging, and relevant for instance in Finland for obtaining the lighthouse status. These developments highlight Euro-BioImaging Finland's pivotal role in advancing imaging technologies for science, industry, and society nationally and internationally.

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Local Organizing Committee

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Anders Folkesson
Karl Zhang
Simon Leclerc
Massimo Micaroni
Jens Berndtsson
Julia Fernandez-Rodriguez, Conference Chair

Exhibition

Rafael Camacho
Karl Zhang
Simon Leclerc

Karl Zhang   **Rafael Camacho**   **Anders Folkesson**   **Simon Leclerc**   **Massimo Micaroni**   **Jens Berndtsson**

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Venue
Conference Centre Wallenberg
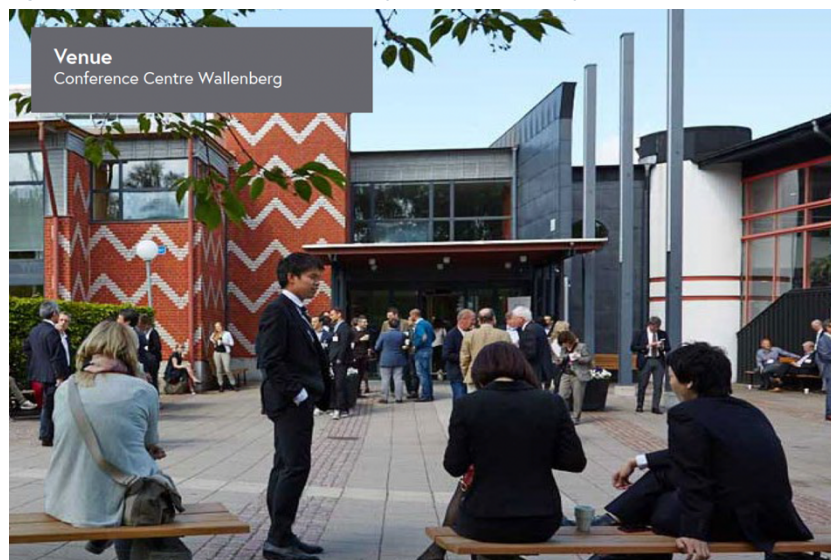
About BNMI

The **Bridging Nordic Microscopy Infrastructure (BNMI, https://bnmi.eu/)** consortium unites microscopy infrastructures across the Nordic countries to enhance regional competitiveness and foster collaboration. Through workshops, symposia, staff exchanges, and mobility grants, **BNMI** promotes the use of advanced microscopy, drives innovation, and strengthens expertise, ensuring that the Nordic region remains at the forefront of scientific discovery.

The **BNMI** has already played a pivotal role in strengthening and expanding these national infrastructures by facilitating trans-national access across the Nordic region. This collaborative effort has empowered researchers to leverage state-of-the-art microscopy technologies regardless of their location, enabling transformative discoveries in biology, medicine, and beyond. Through **BNMI**, scientists from smaller or less-equipped institutions have gained access to advanced tools and workflows, bridging gaps in expertise and infrastructures that previously limited their research potential. By working together, open-access microscopy infrastructures across the region have already enhanced knowledge exchange and fostered productive collaborations.

Description of the Imaging Nordic consortium

- *In Denmark*, the _Danish BioImaging Infrastructure_ *(DBI-INFRA)* was launched in April 2022 as a national distributed bioimaging infrastructure that brings together open-access bioimaging platforms supporting imaging technologies across scales. The DBI-INFRA consortium comprises seven partner institutions - Aalborg University, Aarhus University, the University of Southern Denmark, Roskilde University, the Danish Cancer Institute, the Technical University of Denmark, and the University of Copenhagen - hosting ten open-access imaging core facilities.

- *In Finland*, the _Finnish Advanced Microscopy Node_ *(FiAM)* is a national roadmap infrastructure offering open access to state-of-the-art biological imaging technologies, training, and image data analysis services. FiAM comprises nine imaging facilities hosted by the University of Helsinki, the University of Turku, Åbo Akademi University, and the University of Oulu, with the University of Eastern Finland and Tampere University as associate partners.

- *In Iceland*, the _Biomedical Center, University of Iceland_ *(BMC-UI)* is an official collaboration between research groups working in biomedical molecular life sciences in Iceland across institutions. The primary goal of BMC-UI is to establish core facilities that bring together researchers in Iceland under a unified framework, maximizing the use of available infrastructures and fostering cross-disciplinary collaborations.

- *In Norway*, the _Norwegian Advanced Light Microscopy Imaging Infrastructure Network_ *(NALMIN)* was established in 2014. NALMIN has until now secured two major infrastructure grants from the Norwegian Research Council, in addition to major support from its host institutions. Today, NALMIN is a well-established network of imaging platforms with facilities located in all major life science research organizations in Norway.

- *In Sweden*, the _Swedish National Microscopy Infrastructure_ *(NMI)* Since 2016, the National Microscopy Infrastructure has operated as a distributed research platform with specialized nodes at Stockholm University, University of Gothenburg, Umeå University, and the Royal Institute of Technology (KTH), which serves as the host institution. Additionally, since 2024, Karolinska Institute and Lund University have joined as associate partners. NMI's mission is to provide researchers in academia and industry open- access to cutting-edge microscopy technologies and expertise.

Partners

University of Gothenburg

NordForsk is an organisation under the Nordic Council of Ministers that provides funding for and facilitates Nordic cooperation on research and research infrastructure,
https://www.nordforsk.org/

SciLifeLab is an institution for the advancement of molecular biosciences in Sweden, funded as a national research infrastructure by the Swedish government
https://www.scilifelab.se/

Media Partners

Microscopy and Analysis

Microscopy and Analysis (M&A) is renowned for its authoritative scientific content, tailored for both users and developers of microscopy. We provide hands-on information about novel techniques and applications in Light Microscopy, Electron Microscopy, Scanning Probe Microscopy, Image Processing, and X-Ray Analysis. In addition to the latest news and updates from various societies, M&A also keeps you informed about upcoming meetings, conferences, and cutting-edge products for scientific research.

Conference | Microscopy | Electron and Ion Microscopy | X-Ray Analysis | Image Processing   20 January 2025

4th annual meeting of the Bridging Nordic Microscopy Infrastructure
BNMI 2025 Symposium

Media

📅 August 18 - 21, 2025 📍 Gothenburg , Sweden   +👤 Register now

About

The 4th annual meeting of the Bridging Nordic Microscopy Infrastructure (The BNMI 2025 Symposium) will be hosted by the Centre for Cellular Imaging at the University of Gothenburg, Sweden, from August 19–22, 2025. This event will bring together leading scientists from across basic and applied imaging research, along with key industry representatives, for three days of insightful discussions and collaboration. Held at the Wallenberg Conference Center, the venue is easily accessible, just a short tram or bus ride from Gothenburg's city center.

Whether early in your career or as an experienced researcher, BNMI 2025 offers a unique opportunity to stay updated on cutting-edge imaging technologies, learn new techniques, and build valuable connections within the imaging community. The symposium will also showcase imaging research conducted by Gothenburg's scientific community.

The program will feature a compelling mix of lectures, poster sessions, and selected short talks from poster presenters, covering topics from electron and light microscopy, to X-ray imaging, to advanced image analysis. Attendees will have numerous opportunities to engage in both formal discussions and informal gatherings, enriching both scientific dialogue and networking. Sessions will focus on these key areas in imaging research:

- Correlative Multimodal Imaging: Imaging across multiple scales
- Super-resolution and Nanoscale Imaging: Innovations at the nanoscale
- Mesoscopy: Capturing dynamic interactions within cells, organoids, tissues, and whol organisms
- Smart Microscopy: From advanced image analysis to intelligent acquisition
- New Frontiers: Exploring cutting-edge imaging applications

Keywords

Symposium | Microscopy | Nordic Microscopy Infrastructure | BNMI 2025

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We would like to extend our sincere gratitude to all our **Sponsors** for their generous support and commitment to advancing the field of imaging and microscopy. Your involvement is instrumental in making the **BNMI 2025 Symposium** a vibrant platform for knowledge exchange, innovation, and collaboration.

Your presence not only enriches the scientific program but also offers invaluable opportunities for attendees to engage directly with the latest technologies shaping the future of imaging.

Thank you once again for partnering with us to make this event a success!

Event Information

Registration & Information Desk
Wallenberg Conference Centre
Opening hours: Tue 19th or August 12.30-19.00
Wed-Fri 8.00-9.00

Conference centre opening hours:
Wallenberg Conference Centre
Tue-Wed general open hours from 8.00-20.00
Thu 8.00-15.00, Fri 8.00-12.00

Wallenberg Conference Centre

Wifi
Eduroam
GUguest (ask information desk)

Break & Lunches
Coffee-breaks will be served at the **foyer of the Wallenberg Center** during designate times (see program)

Lunches will be served at the **Lyktan Restaurant**, Wallenberg Center (see program)

Poster presentation
All posters should be appended during registration on Tuesday 19th August afternoon, or Wednesday, August 20th at 9.00 am, and disassemble Friday August 22nd before 11:00 am. The Organising Committee will not be responsible for posters that are not removed!

Presenters are requested to attend their poster during the "Poster Session" on Wednesday 20th of August and 15.15 pm

Exhibition
Opening hours:
Monday 18th of August: only for equipment in the rooms: 15.00 – 18.00
Tue 19th of August 8.00 (installation) - 20.00
Wed 8.00 - 19.00
Thu 8.00 -15.00
Fri 8.00 -10.30 (disassemble)

Public transport

To Wallenberg Conference Centre: Please use the:
Västtrafik Travel planner (https://www.vasttrafik.se/#!/en/) to find a suitable connection. Best is to add "Medicinaregatan 20A Göteborg" as the destination in the Travel Planner.

Bus: stops at Medicinaregatan
Trams: 6, 7, 8, stops at Medicinaregatan
From the tram & bus stop there is only a few minutes' walk to the conference centre. All trams have ticket machines (Single ticket 37 SEK and is valid during 90 min). Payment method: Bank card.
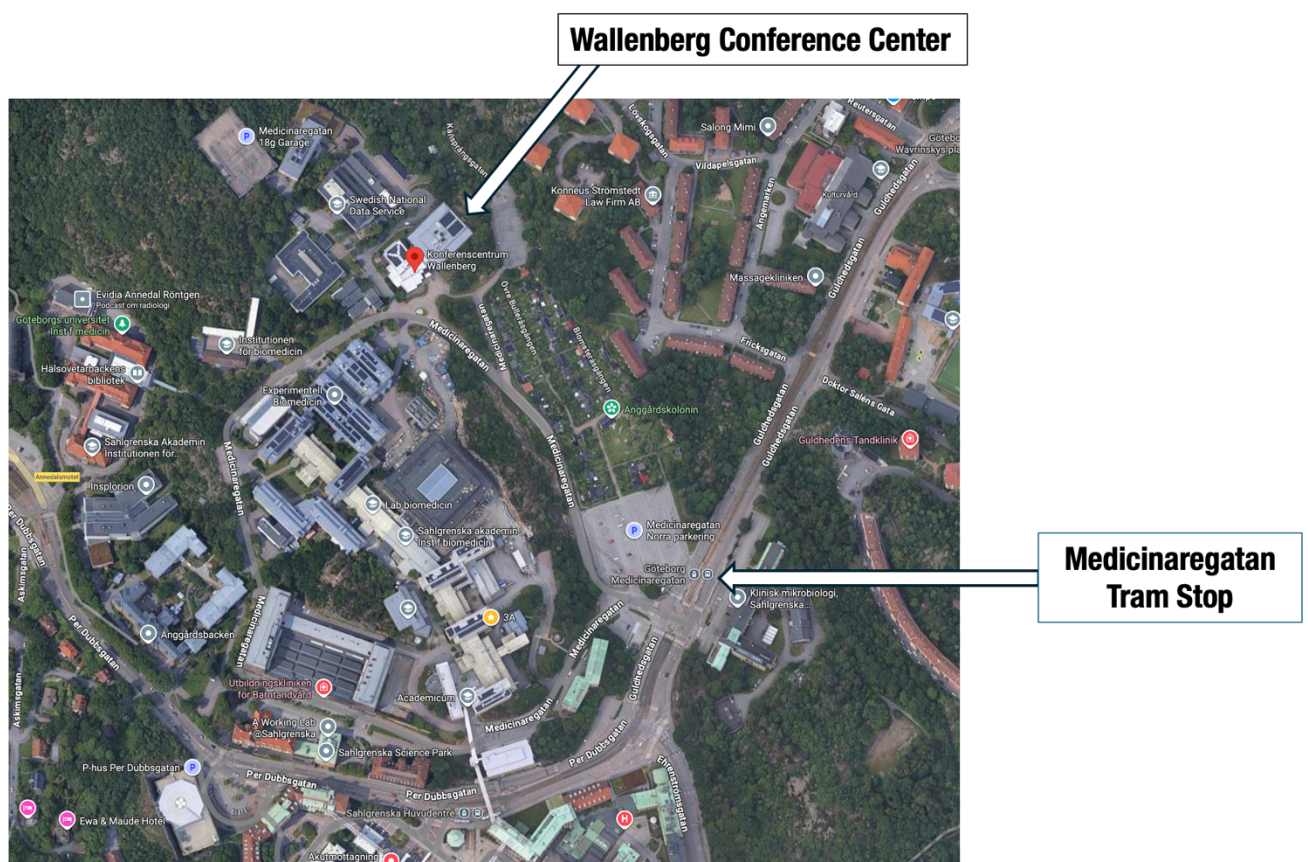
Social Events

Boat Tour, Thursday 21st of August

Place: Departing with buses from Wallenberg Conference Centre

Time: 15.30 Stenpiren (leave) – 17.30 Lindholmspiren (arrive)

You are welcome onboard the beautiful boat M/S S:t Erik is a classic archipelago boat built around the turn of the last century, that will take you on a guided cruise in the archipelago of Gothenburg! The boat is departing from Stenpiren and the cruise takes approx. 2,5-3 hr. The tour includes refreshments.

Conference Dinner, Thursday 21st of August

Place: Kooperativet Lindholmen

Address: Lindholmen, Anders Carlssons gata 2, Information: info@kooperativet.se

Time: 19.00

HISTORY – From Shipbuilding Giants to Culinary Greatness – Welcome to Kooperativet!

Step into a venue where Gothenburg's industrial past meets its vibrant present. Located on the historic Norra Älvstranden in Hisingen, the site of **Kooperativet Lindholmen** once echoed with the sounds of hammering steel and ocean-bound ambition. This was the home of Götaverken, one of Sweden's most iconic shipyards, founded in 1841 and a pillar of Gothenburg's maritime legacy for more than a century.

In its heyday, Götaverken launched vessels that sailed the world. The shipyard expanded with the opening of Arendalsvarvet in 1963, and its original site became known as Göteborgsvarvet. Although Arendalsvarvet closed in 1989, and the last operational division — the Cityvarvet repair yard — finally ceased in 2015, the legacy of innovation and industry remained anchored here.

Then came the transformation! On April 21, 2016, the historic Magasin MI4 and MI5 reopened their doors with a bold new purpose: **Kooperativet Lindholmen**, Gothenburg's vibrant new hub for food, festivities, and unforgettable events. Where ships once took shape, people now gather to celebrate life, flavor, and community.

Welcome aboard!