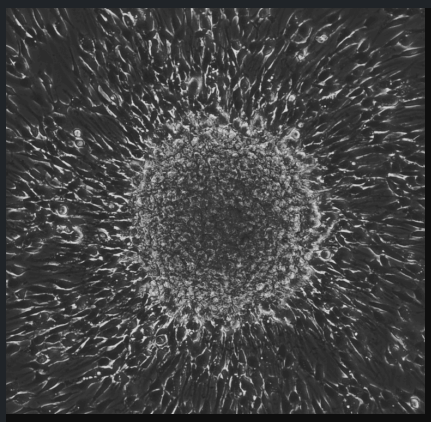
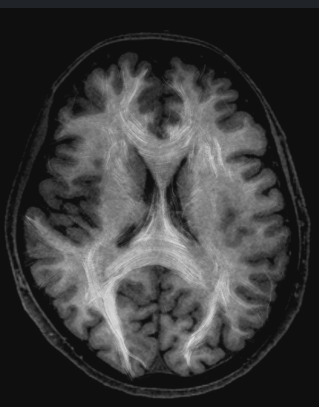
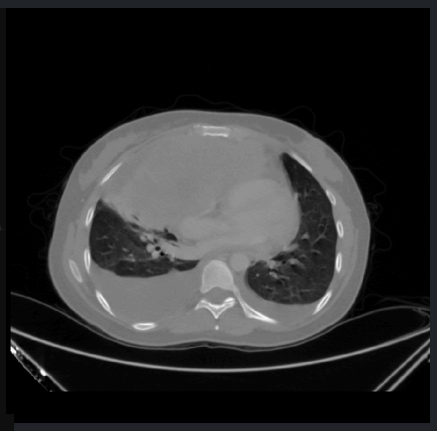
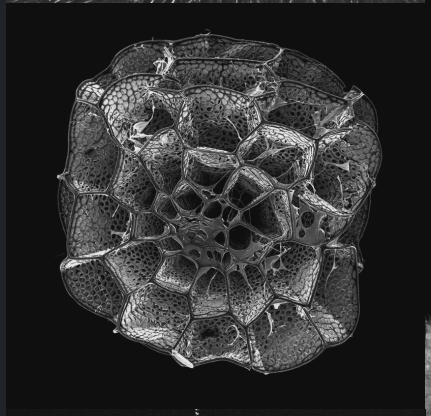
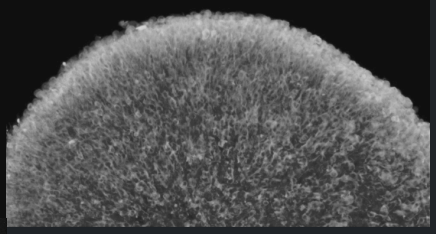
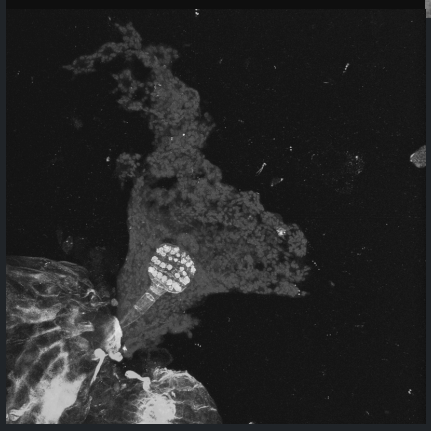

ALL HANDS NODES MEETING 2026

Connecting the Communities

EURO BIOIMAGING

Abstract Book

EVOLVE

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Talks

(listed in chronological order based on the programme)

Tuesday, 15 September

Success Stories in Connecting Communities

A Mouse Proof-of-Concept for Scalable Correlative Multimodal Imaging Toward Multiscale Mapping of the Human Brain's Nested Connectome

Julia Fernandez-Rodriguez, Swedish NMI Node

Understanding the structural organization of the human brain across spatial scales remains a major challenge in neuroscience. The human connectome emerges from densely packed networks of myelinated and unmyelinated axons that form complex micro- and mesoscale circuits within the folded cortex. Diffusion MRI enables non-destructive whole-brain imaging at millimeter to sub-millimeter resolution, but cannot resolve individual fibers or fine microcircuitry. Conversely, light microscopy, X-ray tomography, and electron microscopy (EM) provide micrometer to nanometer resolution, but are usually limited to small tissue volumes and modality-specific preparation workflows, restricting direct multimodal correlation.

To address these scale and modality gaps, we developed a proof-of-concept Correlative Multimodal Imaging (CMI) pipeline for serial acquisition of complementary imaging modalities on the same mouse brain tissue sample. Within the European BUILD (Big mUltimodal hIgh-resolution atLas Data Management) consortium, standardized workflows were established for tissue preparation, multimodal imaging, cross-correlation, and distributed data management across specialized facilities. The pipeline integrates 3D Polarized Light Imaging (3D-PLI), X-ray tomography (micro-CT), and volume EM, including single-beam SEM, MultiSEM, and FIB-SEM.

In a representative workflow, a mouse brain section was first imaged by polarized light microscopy to assess large-scale fiber orientation. The same section was then processed for micro-CT and scanning electron microscopy. Micro-CT defined volumes of interest and provided a three-dimensional reference dataset for cross-modality registration. Selected regions were subsequently imaged at ultrastructural resolution using MultiSEM and FIB-SEM, enabling visualization of myelinated axons, synaptic architecture, and subcellular features. Large-scale EM datasets were aligned in WEBKNOSSOS using Voxelytics (Scalable Minds, Potsdam, Germany) through feature-based matching, hierarchical affine alignment, and tile-wise intensity normalization. This scalable CMI framework establishes a methodological foundation for multiscale brain mapping from the millimeter to the nanometer domain within the same specimen. By integrating complementary imaging modalities and harmonizing cross-site workflows, it enables high-resolution structural atlas generation across species and provides a translational platform to investigate pathological alterations in myelination and connectivity, including multiple sclerosis. The resulting cross-aligned connectomic datasets will be spatially anchored and integrated into the publicly accessible Human Brain Atlas within EBRAINS, contributing to open, multiscale connectomics.

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Malaria: A Case Study for Cross-Domain Collaboration and European Imaging Expertise

Junel Solis, Finnish Advanced Microscopy Node

Malaria remains a global health challenge, with the latest WHO report estimating 282 million cases and 610 000 deaths worldwide. In this presentation, we use research on *Plasmodium falciparum* – the most prevalent and deadly malaria parasite – as a case study for how cross-domain collaboration across European imaging infrastructures can accelerate discovery.

Through Euro-BioImaging and the ISIDORe project, teams spanning infectious disease biology, volume electron microscopy, and computational image analysis worked together to investigate the ookinete stage of the parasite – the form that traverses the mosquito midgut, a critical and poorly understood step in transmission.

This collaboration has led to better understanding of the ookinete ultrastructure. We discuss how teamwork has enabled our results, and demonstrate the value of coordinated European imaging expertise.

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Strategic Marketing for Imaging Core Facilities and Nodes

Baubak Bajoghli, Austrian BioImaging

The strategic importance of marketing and communication for imaging core facilities and research infrastructures has received limited attention. However, implementing a coherent marketing strategy is essential for attracting new users, strengthening stakeholder relationships and communicating institutional impact effectively.

To elucidate the factors influencing user acquisition and to examine the extent to which imaging core facilities operate in a market-oriented manner, an empirical study involving qualitative, semi-structured interviews with heads of imaging core facilities or Nodes was conducted to gain in-depth insights into their strategic, organizational, and communication practices. In total, 16 experts from nine European countries participated in the study. The interview data were analyzed systematically to identify recurring patterns and relationships between organizational structures, strategic orientation and communication-related activities.

The findings reveal that user acquisition is shaped by three central factors: (1) visibility and awareness; (2) pricing strategies; and (3) access to external funding models. Internal visibility, achieved through teaching activities, onboarding programs and close integration into institutional structures, enhances usage within the home institution. In contrast, external visibility relies heavily on institutional communication support, strategic networking and participation in national and European research infrastructures.

Building on these insights, the study adapts the Market Orientation (MARKOR) framework from nonprofit marketing to the specific context of imaging core facilities. The adapted model integrates the key dimensions of information generation, information dissemination, and organizational responsiveness, thereby providing a structured approach to strategic marketing in research-oriented service units.

The study concludes that imaging core facilities require a systematic and strategically anchored marketing and communication approach to expand their user base, enhance their institutional relevance, and ensure long-term financial and scientific sustainability within an increasingly competitive research environment.

Co-funded by the European Union

Imaging 4 All: Supporting Scientists from Underserved Regions to Access Global Imaging Resources

Deniz Saltukoglu, Global BioImaging

Global BioImaging, with funding from the Wellcome Trust, established a global mobility funding programme to support researchers from low- and middle-income countries (LMICs) affiliated with not-for-profit institutions in accessing imaging instruments, expertise, and training opportunities worldwide.

This programme aims to lower barriers to imaging infrastructure and capacity development in low-resource settings. It enables researchers to conduct experiments using advanced imaging technologies, gain hands-on experience in sample preparation and imaging modalities at leading core facilities and laboratories, and participate in specialised training courses. At the same time, it supports the broader dissemination of imaging approaches and fosters community building within the global bioimaging field.

The initiative began accepting applications in September 2024, with funded activities continuing until the end of October 2026 within the scope of the grant period. Over this two-year period, three open calls have been implemented, resulting in 342 applications from 44 countries, with more than 150 expected to be funded. Host institutions span over 20 countries, with Euro-BioImaging nodes representing a large share of hosts, highlighting its key role in enabling imaging access, training, and knowledge exchange.

This talk will present the programme structure, implementation, and uptake. It will highlight selected examples of funded scientific projects across the different tracks, provide statistical insights into applicants, host institutions, and preferred imaging technologies, and offer an initial assessment of the programme's emerging impact.

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National Coordination of Imaging RIs

Constructing the New Euro-BioImaging Finland "Lighthouse" Research Infrastructure

Irina Belaia & Pasi Kankaanpää, Euro-BioImaging Finland

The national organization of imaging in Finland has been substantially developed over the last decade. In 2025, this was taken to the next level, when a new Euro-BioImaging Finland consortium was formed for the national roadmap. This consortium comprises the best imaging units from 7 universities and 3 university hospitals. It includes two Euro-BioImaging Nodes: Finnish Advanced Microscopy Node and Finnish Biomedical Imaging Node.

Thanks to extensive dialogue between the Research Council of Finland and the research infrastructure community, getting selected to the new roadmap included direct funding. This meant that, for the first time, the biological and biomedical imaging communities in Finland now have joint funding. In addition, Euro-BioImaging Finland was selected as one of the six national Lighthouses – frontrunner infrastructures with the largest impact.

One challenge in building up Euro-BioImaging Finland was high-quality imaging units already part of national operations, but not yet part of Euro-BioImaging Nodes. These were included in the infrastructure with the aim to develop them to become Euro-BioImaging Node members in the coming years.

Euro-BioImaging Finland (www.eurobioimaging.fi) is now one of the largest and most significant of all Finnish research infrastructures. This has made it more visible both in terms of academic and industrial collaborations, as well as public decision-making.

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From Passive Membership to Strategic Engagement: A Model for Maximizing Participation in International Research Infrastructure Organizations

Rachel Hamri, Israel BioImaging

For small countries with limited research resources, membership in international scientific organization forums is a strategic necessity. Such membership provides access to world-class research infrastructures unavailable domestically, critical mass intellectual integration into international scientific communities, participation in global decision-making processes in scientific development, and the opportunity to forge collaborations that would otherwise remain out of reach. With that goal in mind, Israel has invested significantly in membership in more than 20 European research infrastructure organizations, including Euro-BioImaging, of which Israel is a founding member. However, membership alone does not guarantee active participation on part of the scientists of a country. For example, as evident in Euro-BioImaging's early annual reports, Israeli scientific participation was marginal — reflecting a gap between formal membership potential and effective engagement. This gap appears to be a common occurrence over multiple forums. To address this need, the capabilities of the Israel Research Core Facilities (IRCF) were brought to bear. IRCF represents a national umbrella organization established in 2022, connecting 32 academic institutions, 168 core facilities, and over 600 research technology professionals through a coordinated national ecosystem of discipline-based networks, training programs, and an open-access infrastructure database. In a pilot initiative, IRCF was appointed as the national coordinator for four European research infrastructure organizations, including Euro-BioImaging. Rather than limiting itself to serving as an administrative contact point, IRCF developed a coordinated engagement framework that specifically targets the scientific population of interest, thereby funneling opportunities for systematic dissemination more efficiently. Furthermore, the local nodes were restructured by broadening academic participation based on IRCF databases. Navigation of administrative forms was simplified, and a hands-on support system was established for researchers preparing applications. As a result of these measures, a positive impact has become evident through the substantial increase in both applications submitted by Israeli researchers to Euro-BioImaging calls and by their successful outcomes. This process encompasses a general and transferable governance model demonstrating how national umbrella organizations can transform international memberships from passive representation into active scientific capacity-building. Active dissemination of Euro-BioImaging’s potential will help maximize the return of any country's investment and enrich the Euro-BioImaging forum by transforming it into the vibrant community hub it was created to be.

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Training & Community Building at the Portuguese Platform of BioImaging (PPBI)

Gabriel Martins & Luisa Cortes, Portuguese Platform of BioImaging

The PPBI (www.ppbi.pt) is a national research infrastructure dedicated to the advancement and democratization of bioimaging technologies. Its primary mission is to foster synergy between researchers, academic institutions, and industry by providing centralized, open access to state-of-the-art bioimaging resources and expert technical support, thereby strengthening both basic and applied life sciences research in Portugal and beyond. The infrastructure functions as a comprehensive support ecosystem, offering more than just equipment and access. It provides a full spectrum of services including experimental design, sample preparation, high-end image acquisition, advanced data processing, and analysis. As a national node of the Euro-BioImaging ERIC, PPBI facilitates international collaboration and integrates Portugal into the global bioimaging roadmap.

Technical Scope and Expertise: The resources at PPBI cover a wide range of imaging modalities, spanning scales from the subcellular to the organismal level, and different technologies which include:

- Advanced Light Microscopy: Confocal (point-scanning/spinning disk), two-photon, light-sheet, super-resolution (SIM, SMLM), and live-cell imaging.
- Electron Microscopy: Transmission (TEM) and scanning (SEM) capabilities.
- Bioimage analysis Support: Dedicated workstations for high-throughput image analysis and processing.

Access to PPBI resources is governed by an Open Access policy based on scientific merit and technical feasibility, ensuring that the best research receives the support it needs. By maintaining a highly qualified staff, the platform ensures that researchers—from beginners to experts—receive essential training, consulting, and project planning assistance. This collaborative model not only maximizes the impact of R&D projects but also empowers the next generation of scientists through regular workshops, specialized training courses, and hands-on mentorship. The PPBI functions through four specialized Working Groups dedicated to optimizing national bioimaging services:

- Training WG: Delivers advanced technical education and workshops for staff and users.
- Quality Control WG: Standardizes protocols to ensure data reliability and reproducibility.
- Image Analysis WG: Provides expertise for processing and quantifying bioimage datasets.
- Communication WG: Oversees outreach and ensures community awareness of available infrastructure and services.

Here we showcase our latest efforts for community-wide training on instrumentation QC, on advanced techniques for staff, on bioimage analysis for researchers, public activities and network-building.

Co-funded by the European Union

Wednesday, 16 September

Beyond Science Fiction: Emerging Technologies and Multimodal Imaging

Language in the Brain: from Descriptions of Functions to Modelling of Representations and Mechanisms

Riitta Salmelin, Finnish Biomedical Imaging Node

Over the past few decades, real-time tracking of cortical current flow (magneto/electroencephalography, MEG/EEG) and accurate localisation of blood oxygenation changes (functional magnetic resonance imaging, fMRI) have offered windows to the functional architecture of the human brain. The neuroimaging domain has reached its first level of maturity: we now know how to measure and quantify different types of signals and, phenomenologically, we know what type of group-level functional effects to expect in a large variety of experimental conditions. Specific brain areas, networks and electrophysiological dynamics have been proposed to be linked with various perceptual, motor and cognitive functions and their disorders. To reach the next phase in human neuroscience, we need to advance from group-level descriptions to quantitative model-based individual-level predictions. These developments will be illustrated with focus on language function for which descriptive models, largely based on observations of patients with language disorders, are being supplemented by computationally explicit models of mechanisms and representations. Machine learning approaches are essential tools in this endeavour.

Co-funded by the European Union

Molecular-Scale Kinesin Dynamics and Microtubule Architecture Revealed by MINFLUX Nanoscopy

Takahiro Deguchi[1], Tobias Engelhardt[2], Nikolay Sergeev[3], Varsha Mahapatra[4], Roman Schmidt[2], Nestor Castillo[3], Sebastian Schnorrenberg[1], Lukas C. Kapitein[4], Timo Zimmermann[1], Jonas Ries[3]
[1]EMBL Imaging Centre, [2]Abberior Instruments GmbH., [3]University of Vienna, Max Perutz Labs.
[4]Department of Biology, Faculty of Science, Utrecht University.

Intracellular transport relies on the coordinated action of motor proteins and the cytoskeletal architecture on which they operate. While kinesins are central to this process, directly observing their conformational dynamics and interactions with microtubules has remained challenging in living cells due to nanometer-scale motions and rapid timescales.

Minimal photon flux (MINFLUX) is a super-resolution microscopy technique that enables direct interrogation of motor protein dynamics and microtubule organization with unprecedented spatiotemporal resolution. By maximizing photon efficiency, MINFLUX achieves nanometer localization precision at sub-millisecond temporal resolution [1], enabling tracking of single kinesin dynamics in their native cellular environment.

For this project, we used a MINFLUX microscope at the EMBL Imaging Centre. Using truncated kinesin constructs, we resolved conformational and discrete stepping dynamics in living cells, demonstrating that fundamental aspects of motor function can be captured under physiological cellular conditions [2]. Extending this approach to neuronal axons revealed processive kinesin stepping within the crowded and polarized microtubule network.

In addition, tracking of full-length kinesin in living cells uncovered complex motion patterns, including backslipping and side-stepping, suggestive of contributions from multiple motors. Beyond motor dynamics, MINFLUX tracking of kinesin bound to microtubules provides a means to probe cytoskeletal organization itself, enabling nanoscale mapping of microtubule polarity and architecture in biologically relevant contexts.

Together, these results establish MINFLUX as a versatile tool to investigate molecular-scale dynamics and the nanoscale organization of the cytoskeleton within the cellular context, opening new avenues for studying intracellular transport within the structural and physiological complexity of cells.

1. Balzarotti, Eilers, Gwosch, et al., "Nanometer resolution imaging and tracking of fluorescent molecules with minimal photon fluxes," Science (2017).
2. Deguchi, et al., "Direct observation of motor protein stepping in living cells using MINFLUX," Science, (2023).

Co-funded by the European Union

The Maastricht Node – at the Forefront of Multimodal Imaging

Marc van Zandvoort, AMMI Maastricht

The Advanced Maastricht Molecular Imaging Node (AMMI) is a mixed Node within Euro-BioImaging, enthusiastically supporting the goals of openness to users. We consist of several core research labs, covering a broad range of imaging techniques. We offer Electron Microscopy, Correlative EM-OM, Advanced Optical Microscopy, Mass Spectroscopy Imaging, and pre-clinical imaging. Using the available techniques, we investigate a broad set of topics within the biomedical and biological fields. This ranges from cells and viruses, via organoids and animal models, to plant and in-field crop imaging.

In this presentation, I will give an overview of the techniques available to external users and the recent updates of our Nodes, garnished with examples on how these techniques can be applied. I will also discuss options to visit us and give examples on visitors and interactions we have and had. Additionally, I will discuss our role in building networks via expert groups and European projects.

Co-funded by the European Union

Unraveling the Neurovascular Nexus: Multimodal Approaches to Vascular Factors and Neurodegeneration

Amanda Kiliaan, Dutch PRIME Node

Background: Managing midlife cardiovascular risk factors has reduced the age-specific incidence of neurodegenerative diseases like Alzheimer's. However, the precise mechanisms linking vascular and neurodegenerative factors remain poorly understood. Uncovering their exact causal pathways and chronological sequence is critical for developing effective treatments.

Methods & Models: At our Preclinical Imaging Center (PRIME), we utilize multimodal, translational, longitudinal approaches to bridge this gap. We integrate advanced neuroimaging with high-resolution microscopy, longitudinal blood and tissue profiling, and cognitive testing. To map disease progression, we combine *in vivo* vascular mouse models—tracking real-time chronological changes, functional decline, and early biomarkers—with post-mortem human brain tissue to validate findings against end-stage human pathology.

Conclusion: This cross-species, multi-scale framework offers a powerful strategy to disentangle the complex interplay between vascular dysfunction and neurodegeneration. Identifying these precise temporal sequences will reveal novel therapeutic targets. In this talk, examples of these multimodal research approaches will be presented.

Co-funded by the European Union

Novel Applications of Imaging Technologies

Evaluation of Tissue-Clearing Protocols for Preserving Fluorescence in Intact Bone

Cristina Clemente Toribio, Smart Optical Microscopy (SOM) Node, Spain

We are implementing whole-tissue clearing methodologies in our unit, with a specific focus on bone, which has some peculiarities that make it an interesting tissue for clarification. First of all, bone is a tissue that has high autofluorescence due to the presence of a high concentration of erythrocytes, which contain hemoglobin making the tissue highly autofluorescent. Second, it is a very dense and mineralized tissue, mostly in the periphery (the compact bone), becoming a difficult structure for light to penetrate, making it difficult to visualize the bone marrow structure, which is the part where most biological processes occur. Third, it is a difficult tissue to make histological cuts while maintaining the structure of the bone marrow because of the large differences in density within the tissue.

For all this reasons, our objective is to achieve optimal clearing of intact mouse bones while preserving endogenous fluorescence and the structure of the bone marrow, enabling high-resolution three-dimensional visualization of tumor architecture by laser confocal microscopy.

Our experimental model consists of mouse tibias with GFP-positive tumors and tibias from mice with GFP-positive tumors treated to prevent tumor formation, allowing us to assess protocol robustness across biologically distinct samples and correlate the data obtained with flow cytometry performed on the humerus of the same mouse.

To this end, we compare three of the most commonly used clearing protocols—CUBIC, iDISCO, and SOLID—evaluating their efficiency both with and without the incorporation of a reagent to reduce heme autofluorescence, tetrakis.

The inclusion of tetrakis is particularly relevant for samples containing endogenous fluorescence, such as GFP in our case, where residual heme groups can significantly impair light penetration and increase noise relative to the real signal. By testing each protocol under both conditions, we aim to determine how heme-clearing efficiency influences transparency, structural preservation, and fluorescence maintenance.

Following clearing, all specimens are imaged using confocal microscopy to quantify clearing efficiency, penetration depth, signal-to-noise ratio, and preservation of fine structural details. These imaging metrics provide a comprehensive evaluation of how each protocol performs in mineralized tissues and how tetrakis contributes to improving optical clarity.

Preliminary observations show differences among protocols in terms of fluorescence retention, highlighting the importance of selecting appropriate clearing strategies for bone imaging. By integrating protocol comparison with fluorescence preservation analysis, our work aims to identify the most effective approach for whole-bone clearing and autofluorescence reduction.

Co-funded by the European Union

Biogri – Transferable Imaging Intelligence for Agricultural and Environmental Innovation

Chris Bühling, Finnish Advanced Microscopy Node

Advanced image analysis has become one of the most important methodologies in modern biomedical research, driven by rapid developments in artificial intelligence, multimodal imaging, and scalable data analysis. Increasingly, these same analytical approaches are proving transferable beyond traditional health sciences into broader environmental and societal applications.

The Biogri project explores how advanced imaging expertise developed within biomedical research can be translated into agricultural and environmental innovation. Co-funded by the European Union, and coordinated by Turku BioImaging, the project combines cross-disciplinary expertise in image analysis, drone imaging, artificial intelligence, and data management to develop scalable image-data-driven solutions for agriculture and environmental monitoring in Southwest Finland.

A central focus of the project is the integration of drone, satellite, and multispectral imaging with custom developed analysis pipelines capable of identifying biologically and environmentally relevant patterns from large-scale image datasets. The project investigates applications such as crop health monitoring, invasive species detection, stress and disease identification, and optimization of agricultural practices through imaging-based decision support. Biogri is built around the concept of transferable imaging intelligence: analytical methods originally developed for biomedical image analysis are adapted to agricultural and environmental datasets, enabling new forms of precision monitoring and scalable data interpretation. The project also emphasizes interoperable data workflows, remote accessibility of image analysis services, and practical collaboration with farms, companies, public organizations, and international partners.

The multidisciplinary structure of the project highlights the growing role of imaging as a unifying research methodology across scientific domains. By bridging biomedical imaging, environmental monitoring, and digital agriculture, Biogri demonstrates how advanced image analysis can contribute not only to scientific innovation, but also to sustainability, climate adaptation, and regional development.

Co-funded by the European Union

X-ray Virtual Histology: Illustrative Case Studies from the Trieste Phase Contrast Flagship Node

Elena Longo, Phase Contrast Imaging (PCI) Flagship Node Trieste

X-ray virtual histology is a powerful 3D diagnostic imaging tool capable of providing high-resolution non-destructive insights of biological tissues. Over the years, the technique effectively demonstrated its accuracy in highlighting tissue architecture and hierarchical material structures at multiple length scales. Thus, it was revealed to be a reliable method for the identification of anatomic features and for the assessment of pathological and inflammatory markers in any kind of tissue. By offering a 3D context, this imaging modality can be considered complementary and supportive to the well-known histological procedure, with moreover the potential advantage of guiding tissue physical sectioning. Thanks to its versatility, X-ray virtual histology can be used to complement broad research applications in multimodal frameworks. Here, we will present an overview of X-ray virtual histology case studies carried out at the Phase Contrast Flagship Node located in Trieste, Italy. X-ray virtual histology was achieved by propagation-based phase-contrast microtomography with synchrotron radiation. Illustrative examples will be selected from our multidisciplinary research portfolio, spanning from brain imaging [1] to skin tumor [2], from pulmonary fibrosis [3] to biomaterials for improving ovarian tissue transplantation [4].

[1] J.Y. Lee et al. Frontiers in Physics 11, 1335285 (2023), doi: 10.3389/fphy.2023.1335285
[2] G. Saccomano et al. Skin research and Technology 30, e13801 (2024); doi: 10.1111/srt.13801
[3] L. D'Amico et al. Computers in Biology and Medicine 169, 107947 (2024); doi: https://doi.org/10.1016/j.compbiomed.2024.107947.
[4] M. Spazzapan et al. Bioactive Materials 50, 305-321 (2025) doi: https://doi.org/10.1016/j.bioactmat.2025.03.021

Co-funded by the European Union

Multimodal OCT Across Scales: From Living Organoids to Skin Microvasculature

Richard Haindl, Austrian BioImaging

As the only Optical Coherence Tomography (OCT) unit within Euro-BioImaging, we would like to use our first contribution to the All Hands Meeting to introduce OCT as a versatile, label-free 3D imaging platform for biological and translational research. Rather than showcasing the technology in isolation, we will focus on what OCT makes possible: answering biological questions that are difficult to address with conventional microscopy. How do living 3D models organize internally? How do vascular networks remodel during development and disease? How can structural, functional and molecular contrast be combined without destroying the sample?

The showcase will move across biological scales and application areas. In small animal models, optical coherence photoacoustic microscopy enables co-registered imaging of zebrafish larvae, where OCT resolves morphology while photoacoustic contrast reveals vascular and absorption-based information from endogenous chromophores. In chick embryos, OCT and photoacoustic tomography provide complementary whole-embryo views across developmental stages, linking tissue architecture to vascular development.

Living 3D culture systems form a second focus, because this is where non-destructive volumetric imaging becomes especially powerful. In human placenta-derived trophoblast organoids, ultra-high-resolution OCT reveals internal cavities and scattering bridges associated with trophoblast differentiation. In patient-derived cancer organoids and spheroids, OCT/OCM enables longitudinal tracking of growth and therapy response, while photoacoustic contrast and AI-assisted analysis add functional layers including rare-cell detection, viability classification and single-organoid response heterogeneity. Examples from SARS-infected organoids further illustrate how OCT can support the analysis of host-pathogen-induced tissue changes in complex culture models.

The clinical showcase will focus on skin, where OCT and OCT angiography enable non-invasive imaging of tissue structure and microvasculature. We will present vascular remodeling in chronic venous insufficiency, disease-linked vascular pattern analysis, and dermatological OCTA datasets and pipelines for automated vessel segmentation. Beyond biology, we will also highlight pharmaceutical coating measurements, showing how ultra-high-resolution OCT can provide non-destructive information on coating thickness, homogeneity and multilayer structure for quality control and process development.

Together, these examples position OCT as a bridge between microscopy, preclinical model systems and clinical translation. Looking forward, we aim to expand access within the Euro-BioImaging community through a mobile OCT platform for research sites across Europe very soon. This would make OCT-based imaging available for living, fragile, infectious, clinical or otherwise logistically challenging samples that cannot easily be transported to Vienna.

Co-funded by the European Union

Thursday, 17 September

Breakout Session I – Breakout 2 – Imaging Technology Innovations at Nodes

In situ protein crystallography a light microscopy–guided cryo-FIB pipeline for direct protein structure determination from a single intracellular crystal

Dominik Pinkas, Prague Node

Intracellular crystallisation is an emerging approach in structural biology that bypasses the need for protein purification. In 2024, the InCellCryst pipeline was introduced for structural studies of intracellular crystals using serial X-ray crystallography. However, serial crystallography requires exposure of tens of thousands of cells containing intracellular crystals, precluding high-resolution studies of proteins that crystallize in only a few cells, and it requires access to synchrotron facilities, which significantly limits the availability of this approach.

We have developed IncelluloED, a method that leverages light and fluorescence microscopy–guided cryo-FIB lamella preparation to access intracellular crystals for in situ 3D electron diffraction. The approach relies on expression of a fluorescence marker in the cytoplasm of transfected cells, exclusion of this marker from the crystals to enable crystal localization and on cell surface imaging with reflected light to target the region of interest for FIB. In the ideal case, IncelluloED achieves high-resolution structures from a single crystal within a single cell. Experiments on a microcrystal of the HEX-1 protein from Magnaporthe grisea, grown inside an insect cell, yielded a structure at 1.9 Å resolution from an exposed volume of ~1.6 μm^3. By comparison, serial X-ray crystallography achieved 1.8 Å resolution from more than 50,000 crystals, corresponding to a multimillion-fold gain in efficiency.

IncelluloED uses widely available cryo-EM tools and brings high-resolution structural biology into laboratories without access to large-scale infrastructure. All the necessary pieces for sample processing and data acquisition are now available at the electron microscopy core facility of the IMG in Prague and are accessible through the Czech-BioImaging and Euro-BioImaging research infrastructures.

The work was supported by MEYS CR (LM2023050) and the European Regional Development Fund (No. CZ.02.1.01/0.0/0.0/18_046/0016045, No. CZ.02.01.01/00/23_015/0008205), MEYS CR (LM2023042) and the European Regional Development Fund (Project “Innovation of Czech Infrastructure for Integrative Structural Biology”; No. CZ.02.01.01/00/23_015/0008175), European Regional Development Fund (No. CZ.02.1.01/0.0/0.0/15_003/0000441), Czech Science Foundation (GACR) project No. 24-10671S, and by a grant from the Johannes Amos Comenius Programme of the MEYS CR through the SENDISO project No. CZ.02.01.01/00/22_008/0004596, HORIZON EUROPE framework program for research and innovation (Grant Agreement No. 101094299 “IMPRESS”) and the German Federal Ministry for Education and Research (BMBF; grant 05K18FLA). The synchrotron diffraction data was collected at the P14 beam line operated by EMBL Hamburg at the PETRA III storage ring (DESY, Hamburg, Germany).

Co-funded by the European Union

Micro-stepping extended focus reduces photobleaching and preserves structured illumination super-resolution features

Xian Hu, NorMIC Node

Despite the progress made in fast scan units, confocal systems still have insufficient temporal resolution for many volume imaging requirements, such as tracking movement of membrane vesicles in live cells. Researchers might sacrifice certain imaging modalities to achieve better performance in temporal resolution. This may result in imaging artifacts such as undersampling artifacts and limit the amount of analyzable data.

We propose an imaging modality producing fast projections from the field of depth which will shorten the imaging time by approximately an order of magnitude compared to volume imaging. The implementation requires merely a minimum two synchronized control signals that drive a piezo stage and trigger the camera exposure, a third, optional signal, blanks the laser output when the stage is in motion which mildly improves the stability and repeatability of the exposure. The device generating the signals has been tested on spinning disk confocal as well as on instant structured-illumination-microscopy (iSIM) microscopes.

Our calibration images show that the approach provides highly repeatable and stable imaging conditions and does enable photometric measurements of the acquired data, in both the regular spinning disk setup as well as in the iSIM configuration.While light sheet microscopes can provide even faster projections of the same volume, the presented method provides more homogeneous optical sectioning and maintains the structured illumination characteristics.

Co-funded by the European Union

Unlocking Spatial Multi-OMICS: Combining imaging-based transcriptomics and proteomics

Anna Wedl, Austrian BioImaging

Protein regulation occurs on transcriptional, translational or posttranslational level. Therefore, spatial colocalization of RNA, proteins and protein modifications represent a biologically relevant readout for functional tissue analysis. Spatial transcriptomics technologies (e.g. Xenium Analyzer) allow for deep spatial insights into gene expression in Fresh-Frozen and FFPE-preserved tissue sections. Multiplex immunofluorescence imaging (e.g. cyclic staining with MACSima) delivers highly multiplexed protein detection. Challenges in combining both include Xenium slide compatibility issues with MACSima autofocus, decreasing tissue integrity in long imaging cycles, potential epitope loss, and image co-registration.

Here, we try to overcome those challenges and present a refined workflow for integrated acquisition, analysis, and visualization of spatial transcriptomic and proteomic data from the same tissue section. This approach links gene expression with protein localization in situ, providing functional insights into tissue biology and advancing multimodal spatial analysis for future applications. Our integrated workflow will soon be offered to users at the Core Facilities of the Medical University of Vienna.

Co-funded by the European Union

Cellular-Scale Imaging of Theranostic Radiopharmaceutical Uptake with a Lensless Radiomicroscopy Sensor

Nicola Belcari, MMMI Italian Node

We present a low-cost lensless radiomicroscopy system for cellular-scale imaging of theranostic radiopharmaceutical uptake using a commercial CMOS image sensor. The device enables simultaneous brightfield and β-emission imaging with sub-10 μm spatial resolution, allowing direct correlation between morphology and radionuclide distribution. The system was validated using β^--emitting 111Ag and β^+-emitting 18F-FDG sources, demonstrating quantitative linearity and accurate radioactive decay measurements. Live-cell experiments on MDA-MB-231 breast cancer cells showed detectable intracellular uptake of 111Ag, while imaging of U87 glioblastoma spheroids revealed spatially localized 18F-FDG accumulation in a warm background environment. These results demonstrate the potential of lensless radiomicroscopy as a compact and affordable platform for quantitative in vitro evaluation of theranostic agents at single-cell and multicellular levels.

Co-funded by the European Union

From Ideas to Impact I: Strengthening Industry Collaboration

Mutual Learning from Experts: Industry Job Shadowing Pilot

Frederik Siegmann, PicoQuant & Claudia Pfander, Euro-BioImaging

The EU-funded EVOLVE project piloted an industry job shadowing programme to strengthen long-term partnerships between Euro-BioImaging research facilities and industrial partners. Through targeted matchmaking, six facilities and five companies engaged in tailored site visits and online exchanges, gaining insights into each other's working environments, challenges, and strategic priorities. The pilot generated tangible outcomes, including internship collaborations, community workshops, technical working groups, shared technology requirements, and joint activities around new instruments and user experience. The consistently positive feedback highlights the value of precise matchmaking and direct dialogue in building mutual understanding and identifying opportunities for sustained collaboration. We will hear examples from Industry Board Co-Chair Frederik Siegmann and several facilities. The results demonstrate how structured knowledge exchange can help transform traditional research–industry interactions into meaningful, long-term partnerships.

Co-funded by the European Union

Expanding the Volume Imaging Toolbox: Array Tomography, Serial Sectioning, and Adaptive Plasma FIB Imaging

Rebecca Thompson, Thermo Fisher Scientific

Room-temperature volume imaging in electron microscopy is enabling new opportunities for three-dimensional characterization across biological science applications and beyond. This presentation will highlight complementary approaches for volumetric imaging including array tomography, Auto Slice & View serial sectioning, and plasma FIB spin milling with adaptive scanning strategies for efficient, large-area data acquisition. Together, these approaches provide a versatile toolkit for multiscale volume imaging at room temperature.

Co-funded by the European Union

Streamlining High-Plex Spatial Biology with an Automated Multiplex Imaging Workflow

Emmanuelle Steib, Leica Microsystems

Understanding the interactions between tumor cells and the surrounding tumor microenvironment (TME) is essential for advancing cancer research and accelerating the development of new therapeutics. The functional state and spatial organization of immune and tumor cell populations can influence disease progression, therapeutic response, and clinical outcomes. The complexity of the TME often requires highly multiplexed imaging approaches capable of measuring numerous biomarkers while preserving spatial context. When combined with advanced image analysis, these technologies enable researchers to extract meaningful information from tissue datasets, revealing biomarker expression patterns, spatial relationships, and phenotypes. While multiplexed imaging technologies can generate detailed datasets, the time and expertise required for sample preparation, image acquisition, and analysis can create bottlenecks in large-scale studies. Furthermore, validation and performance of antibody staining reagents can add significant challenges to study design. Here, we present a novel automated multiplex imaging solution which provides a flexible platform for high-plex spatial biology studies. By combining walk-away multiplexed imaging, pre-validated ATTOAuriga panels, and analysis workflows, researchers can explore tissue architecture, investigate cellular heterogeneity, and uncover biologically relevant signatures that may be missed using other approaches. This streamlined workflow supports a deeper understanding of complex biological systems and enables new opportunities for discovery in cancer, immunology, and other areas of life science research.

Co-funded by the European Union

Taming the Data Deluge

Alain Pitiot, TissueGnostics

Exposé is TissueGnostics's all-in-one platform for the acquisition, management, visualisation, and analysis of biological data.

It makes it possible to prepare and run complete, end-to-end workflows in a single homogeneous environment, e.g. from scanning slides to statistically characterising cell populations, to preparing plots and figures for publication.

Exposé was developed from the ground up as a flexible and adaptable platform, capable of interoperating with other data management and analysis tools, e.g. OMERO or CellPose. This flexibility enables users to leverage the power of Exposé without disrupting their existing environment.

In this talk, we will discuss how to explore and restructure on the fly large quantities of potentially large data and how to visualise them in Exposé's fast GPU-powered viewer. We will cover Exposé's multi-paradigm approach to data analysis, from code-free point & click, to visual flow programming, to intelligent notebooks running Julia and Python code. Finally we will demonstrate Exposé's bridges to third-party applications and algorithms, such as CellPose.

Co-funded by the European Union

From Ideas to Impact II: Strengthening Industry Collaboration

Academia-Industry Collaborations: Ideas for Joint Action within Europe

Ingo Kleppe, ZEISS

AI now touches every step of science, and the vision of the autonomous, closed-loop lab is arriving fast. But the more autonomous the loop becomes, the more it is bound by one thing: what — and how well — we can measure. As reasoning models consolidate into a handful of non-European players (over 90% of frontier models came from industry in 2025), the scarce and strategic resource becomes trustworthy measurement: traceable, calibrated, information-honest — and generated inside Europe's research infrastructures.

This talk argues that the Euro-BioImaging network is Europe's distributed measurement layer, and is uniquely positioned to set the standard for trusted, AI-ready data — before it is set for them. It puts data ownership and hosting at the center as a European concern: if Europe cannot own the reasoning layer, it must own the measurement layer - and above all the data it creates. Drawing on the roadmap toward autonomous labs, it proposes concrete joint action: a shared provenance-and-uncertainty standard that travels with every dataset, sovereign federated hosting that keeps node data under European governance, a distributed benchmark to catch AI hallucination and leakage, and an open, co-defined instrument–agent interface. The aim is a frank discussion — who owns the data, where it lives, who sets the terms of reuse, and who pays for trust — feeding directly into the panel on strategic collaboration for imaging innovation.

Co-funded by the European Union

Collaborative Research with Companies: Opportunities and Challenges

Mikko Kettunen, Finnish Biomedical Imaging Node

Kuopio Biomedical Imaging Unit is a part of Finnish Biomedical Imaging Node with a focus in advanced preclinical magnetic resonance imaging techniques, in particular silent zero echo time fMRI, and possibility to perform preclinical studies at 0.7 T, 3 T, 7 T and 9.4 T. In addition to academic users, node performs both service and collaborative research with companies. Here, we present two case studies in working with biomedical companies. Both involved development of novel MR imaging techniques to study animal models brought in by the company. In the first project, the company was interested in testing novel MRI methods for detecting changes during demyelination and remyelination and elucidating the underpinnings of myelin MRI readouts from molecular to cellular and tissular scales. The project involved adapting existing structural and awake fMRI techniques from rats to mice and combining fMRI with histological analysis. In the second project, the company was interested in establishing fMRI techniques to research pain in rat monosodium iodoacetate model of osteoarthritis pain with an aim to use it as a tool for drug therapy discovery [MK1.1]. The project involved combining fMRI and behavioural testing.

In our experience, collaboration with commercial users can be beneficial from both economic and scientific point of view. The companies contacting us are not interested in running bulk studies (there are research companies that can do that more efficiently) but want to explore more experimental approaches that may be later translated to bulk studies elsewhere. This aligns well with academic projects and limited resources available in the node. Experimental approach requires a heavy involvement of the node, so a collaborative approach allowing funding of staff (e.g. doctoral researcher) working specifically on the research project has been successful, but finding a suitable legal framework (confidentiality agreements etc.) may take time. The projects usually involve development of novel imaging techniques that will remain in the node allowing expansion of available know-how and technical renewal, sometimes in completely new directions.

Co-funded by the European Union

Academic Research, Innovation, Industrialization: The Success Story of the EIC Pathfinder RE-IMAGINE-CROPS Project

Nicola D'Ascenzo, RE IMAGING

Researchers in applied sciences face a persistent dual challenge: the pressure to produce high-impact, fundamental research suitable for top-tier journals, versus the drive to conduct translational, closed-loop research that culminates in commercial, socially beneficial products. Balancing these parallel paths requires distinct support systems. Academic excellence thrives on cutting-edge infrastructure and collaborative, cross-disciplinary communities. Conversely, commercial viability and industrial impact demand scalable technology demonstrations and dedicated business acceleration pathways.

This presentation shares the journey of the EIC Pathfinder project RE-IMAGINE-CROPS, illustrating with a real example how the Euro-BioImaging ecosystem successfully bridged these two paradigms. We will explore how the concept of advanced plant imaging for precision agriculture gained momentum and resonated across the scientific community through Euro-BioImaging's extensive network and the Expert Group on Plant Imaging, where basic research has been shared across several Nodes. Furthermore, we will show how novel imaging technologies developed within this framework paved the way for the creation of RE IMAGING, a spin-off SME dedicated to scaling these innovations to an industrial level. We will report the challenges experienced during this innovative pathway, in which academia and industry need to conciliate different perspectives, and the solutions found. Through this success story, we offer a scalable model for transforming high-level academic research into tangible industrial innovation.

Co-funded by the European Union

Friday, 18 September

AI Opportunities for and from Euro-BioImaging Nodes

Taming the Publication Monster – Opportunities for Euro-BioImaging Nodes

Guillaume Jacquemet, Finnish Advanced Microscopy Node

Community efforts such as QUAREP-LiMi have done an excellent job of defining what should be reported in light microscopy. Yet a checklist does not always solve the practical problem of finding that information. When a paper is being written, instrument specifications may be on a facility website (or unavailable), acquisition settings inside image files, quality-control records in facility logs, and the correct acknowledgement in another document. Users may not know the exact names of the components they used, while facility staff may be asked to reconstruct an experiment months or even years later. The information exists, but it is scattered and difficult to reuse.

In this talk, I will present a GitHub-based dashboard that we are developing at AIC Turku (https://github.com/AIC-Turku/AIC-Turku-database) to bring this information together. Instrument configurations are recorded using shared templates, while controlled vocabularies keep the names of modalities, components and imaging methods consistent. Automated checks show what is complete and what is still missing. The same structure can hold quality-control and maintenance records, linking an instrument's description to its condition and performance over time.

From this common source, the dashboard creates instrument pages that also serve as our public webpages, draft methods text based on QUAREP-LiMi recommendations, and the correct facility and funding acknowledgements. The information can also be exported in a machine-readable form. Users can then ask an LLM about the facility's inventory and receive preliminary suggestions on which microscope to use for their experiments. LLMs can also help extract acquisition settings from metadata exported with Fiji/ImageJ, although the results must always be checked.

For individual Euro-BioImaging Nodes, this strategy offers a way to maintain information once and reuse it across user support, quality control and publications. Our strategy is fully reusable and can be used as a template.

Co-funded by the European Union

From Question to Result: An AI Agent Interface to Scalable Bioimage Analysis

Nils Mechtel, Swedish NMI Node

Modern bioimaging research infrastructures host rapidly growing volumes of imaging data, but discovering the right datasets and turning them into analysis-ready results still demands substantial technical expertise. As part of the EU RI-SCALE project, we are developing a generative AI-powered assistant that lets researchers explore, analyze, and learn from bioimaging data through natural language.

The assistant connects a conversational agent to the BioImage Archive for data discovery and to BioEngine—a scalable, distributed platform for serving and training AI models—deployed within RI-SCALE. Through a single chat interface, users can search for relevant datasets, apply AI models such as Cellpose for tasks like cell segmentation, and receive visual, downloadable results, with computation transparently dispatched to shared GPU infrastructure. The same platform underpins adapting and training models on archive-scale data, opening a path toward assistants that not only find and analyze data but also help improve the models behind them.

We will present the current system, early lessons from deploying it on federated research infrastructure, and our vision for a unified, AI assistant serving the bioimaging community.

Co-funded by the European Union

An Alternative Route to Clinical Care: Medical Imaging Software as an in-house MDRCertified Medical Device

Jon Bregman, Erasmus MC, Population Imaging Flagship Node Rotterdam

In recent years, the amount of research output in the field of medical image processing has exploded, including new neural network architectures, machine learning methods, and large-scale datasets. However, developed methods and tools usually stay within the research domain and are rarely used as part of clinical care. This is partially because the Medical Device Regulation (MDR) that became active in May 2021 explicitly considers software to be a medical device. This means that before the methods and tools resulting from research can be used in patient care, they must undergo an extensive certification process. Additionally, the research may not always be viable for commercialization, making it impossible to find commercial partners to implement the software. In case there are no commercial options available, the MDR has a provision for in-house development that allows hospitals to create medical devices for their own in-house use. Through this route, the Population Imaging Flagship Node Rotterdam is bringing machine learning research into clinical practice. The new lung disease quantification web application incorporates a worklist, study manager interface, and annotation viewer which is partly automated using machine learning. The talk will highlight this new tool, as well as explain which phases are necessary to the MDR process, what extra documentation is needed, how this aligns with standard software engineering practices, and give an overall overview of the extra time/effort needed for receiving the MDR certification.

Co-funded by the European Union

UK-BIAS: A New National, Distributed Service Exclusively for Bioimage Analysis

David Barry, The UK Node

Expert image analysis has become a critical bottleneck in life science research - one that only deepens as imaging technologies continue to advance. Some imaging core facilities employ their own dedicated analysts, but access to dedicated bioimage analysis teams or facilities is rare.

We introduce the UK Network of BioImage Analysts (UK-BIAS): a new, open, distributed national service dedicated exclusively to bioimage analysis, and the first such service within the UK Node of Euro-BioImaging. Inspired by similar initiatives elsewhere, F-BIAS in particular, UK-BIAS unites analysts across ten UK institutions to complement instrument access with shared analysis capacity, supporting the full experimental life cycle from initial consultation to bespoke pipeline development. As strong advocates of the FAIR principles, we release all outputs as open source, while researchers retain full ownership of their raw data.

We set out our operating model - how requests are received, triaged and allocated to analysts across sites; how we coordinate a federated team with resources equivalent to roughly two full-time analysts; and how we are approaching the questions every node service wrestles with, such as sustainability, governance and quality control.

In keeping with the meeting's "Connecting the Communities" theme, UK-BIAS is itself an exercise in connection: drawing together a national community of analysts who were previously, in many cases, working in isolation, and linking the UK Node's analytical capacity into the wider Euro-BioImaging network. We reflect on what this offers both the broader scientific community and the analysts within UK-BIAS.

Co-funded by the European Union

Implementing the EQIPD Quality System in an Academic Preclinical Imaging Core Facility: A Practical Framework for Reproducibility and FAIR Data Management

Sara Neyt, Flanders BioImaging

Preclinical imaging core facilities operate in complex research environments characterized by multimodal workflows, large imaging datasets, multidisciplinary collaborations, and high expectations regarding reproducibility and translational relevance. To address these challenges, Core ARTH Infinity initiated implementation of the EQIPD (Enhancing Quality in Preclinical Data) Quality System.

The implementation aimed to establish a sustainable quality culture supporting reproducibility, traceability, transparency, and research integrity across multiple imaging modalities, including PET, SPECT, CT, MRI, optical imaging, ultrasound, and small-animal radiotherapy. The EQIPD Quality System was adapted to the operational realities of an academic core facility, with strong emphasis on practicality, scalability, and integration into daily workflows, rather than a focus on a stringent implementation compared to other quality systems.

A particular challenge within academic core facilities is the diversity of users and study types. At Core ARTH Infinity, workflows were therefore structured according to three service concepts, each providing full or partial EQIPD implementation. Full-service studies are conducted in accordance with the EQIPD framework. In assisted studies, researchers are supported during their work by the staff, while maintaining EQIPD-compliant documentation and traceability procedures. In self-service studies, EQIPD implementation cannot be enforced, the facility ensures FAIR-aligned data storage, backup procedures, and infrastructure-level documentation.

Implementation focused on the 18 EQIPD core requirements and included development of SOPs, well-documented onboarding and training procedures, risk assessment workflows, documentation plans, and continuous improvement strategies. Particular attention was given to data integrity and FAIR data management. A digital infrastructure based on Microsoft Teams, SharePoint, and an electronic laboratory notebook (ELN) was developed to centralize SOPs, quality documentation, metadata capture, and communication. The ELN enables unique study and experiment identifiers, version tracking, linkage between raw and processed imaging data, and long-term traceability of experimental workflows.

Early implementation outcomes are being evaluated using practical quality indicators, including SOP availability, completeness of metadata capture, implementation of training procedures, and traceability of imaging datasets. Initial observations indicate improved workflow standardization, enhanced documentation consistency, and increased awareness of reproducibility-related practices among facility staff and users.

This work demonstrates that quality systems can be successfully integrated into imaging core facilities using existing institutional digital tools, providing a practical framework for more reproducible, transparent, and trustworthy preclinical imaging research.

Co-funded by the European Union

Bridging the Translation Gap in Medical AI

Paula Doria Borrell, Radiology and Medical Imaging Valencia Node

The rapid evolution of AI and medical imaging is generating a vast influx of research outputs, novel algorithms, and expanding infrastructures. However, a critical challenge persists: transforming these fragmented technological milestones into trusted, scalable, and clinically integrated solutions. To deliver meaningful healthcare benefits, medical AI must move beyond theoretical publications. It must be translated into validated clinical workflows, backed by the rigorous evidence and trust required for medical adoption. Crucially, these solutions can no longer operate in isolation; they must leverage fully interoperable architectures aligned with the European Health Data Space (EHDS) and federated data models to enable large-scale deployment across Europe.

To address this paradigm, we present the operational model and strategic evolution of the Radiology and Medical Imaging Valencia Node, spearheaded by the Biomedical Imaging Research Group (GIBI230) at the Health Research Institute Hospital La Fe. Over the past decade, our unique position in integrating an embedded research workflow within a major tertiary hospital alongside our own dedicated imaging equipment for research has enabled us to build an extensive, high-quality repository of medical imaging data. Supported by our own Data Processing Centre optimized for advanced AI development, this foundation has positioned our node as a key player in major European initiatives. Notably, we co-lead the development of landmark infrastructures such as EUCAIM, while actively validating third-party imaging prototypes and proprietary tools to accelerate their translation to the clinical market.

Navigating this evolving landscape introduces critical operational challenges, particularly the need to adapt established institutional governance to the emerging requirements of the EHDS and federated ecosystems. By showcasing our ecosystem's strategy for overcoming socio-technical barriers, our Node provides a scalable, real-world blueprint for EuroBioImaging nodes aiming to maximize the tangible impact of digital health technologies in Europe.

Co-funded by the European Union

Posters

List of posters and number assignments

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#2 Maria Mirza
#3 Ramish Bibi
#4 Mezida Saeed
#5 Sanjana Singh
#6 Gleb Grebnev
#7 Katie Holden
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#38 Szilvia Barkó

Co-funded by the European Union

#1

Euro-BioImaging/EVOLVE Scientific Ambassador Programme: Scaling Outreach Through Community Connectors

Marianna Childress Poli, Euro-BioImaging

Research Infrastructures (RI) have a number of ways to measure impact. Beyond publications, citations and technological advances, their true value comes from how they connect communities, inspire innovation, shape policy, build talent and expand access to cutting-edge technologies. To reach further into diverse scientific domains and local research communities and amplify impact, Euro-BioImaging ERIC launched a Scientific Ambassador Programme in 2024. The Ambassadors, more than 20 outstanding Early Career Researchers embedded in institutes and disciplines across Europe, act as trusted connectors, enabling a greater understanding of Euro-BioImaging services in communities we may not otherwise be able to reach, and making imaging technologies more accessible for everyone. In turn, Euro-BioImaging helps the Ambassadors grow their networks, gives them visibility, and helps them build new skills. A win-win situation that defies traditional metrics, but provides real-world impact, one person at a time.

From Spring 2024 - Spring 2025, we ran the first cohort of our Ambassador programme, with twelve selected Scientific Ambassadors, who carried out impactful activities: attended conferences, organised seminars & outreach events, published articles in scientific journals and on online platforms, and contributed to diverse outreach campaigns. In addition, Ambassadors served on the EVOLVE Job Shadowing Selection Committee and the EVOLVE Call for Event Proposals Selection Committee, taking an active role in Euro-BioImaging's operations, providing valuable external viewpoints that enrich decision-making.

The programme's scalability is clear: in December 2024, the second call for Ambassadors attracted significant interest, with 78 applications from 29 countries. The newly selected cohort of 11 Ambassadors further increases geographic and gender diversity, embedding Euro-BioImaging more deeply in regional communities. By participating in events, engaging peers at their institutes and domains, visiting Euro-BioImaging Nodes to interview technical staff and raising awareness about the opportunities available through Euro-BioImaging and of the diversity of careers in imaging core facilities, the Ambassadors multiply the impact of outreach and strengthen the Euro-BioImaging network.

This poster will explore the development of the Euro-BioImaging Scientific Ambassador programme, from its conception to implementation to daily operations. We will share a few of our favourite moments, highlight some lessons learned, and expose some ways we are measuring the impact of this programme – both for Euro-BioImaging's visibility and for the Ambassadors' professional growth.

EVOLVE is co-funded by the European Union grant agreement no. #101130986.

Co-funded by the European Union

#2
Founding a Global Image Data Ecosystem

Maria Mirza, Euro-BioImaging

The 2.5-year foundingGIDE project established the foundations for a Global Image Data Ecosystem (GIDE) to address fragmentation of biological and preclinical imaging data across international repositories.

A key outcome is the GIDE Stack, an open, multi-layered technical architecture for improving the findability, accessibility, interoperability, and reuse of imaging datasets across distributed resources. It combines harmonised metadata models, domain-specific ontology recommendations, and indexing and search APIs with reference web portals. These components support cross-database discovery across repositories including the BioImage Archive, Image Data Resource (IDR), and Systems Biology Image Database (SSBD).

foundingGIDE also addressed the community and organisational requirements for interoperability. Researchers, repository developers, imaging facility staff, and policymakers contributed through international Community Events in Japan (2024), Australia (2025), and Germany (2026), as well as technical workshops and hackathons.

The project concluded in June 2026. Its tools, standards, and reusable resources remain available to support continued development and adoption of interoperable imaging data infrastructure.

Co-funded by the European Union

#3

A Python-Based Image Analysis Pipeline for Volume Electron Microscopy of Plasmodium falciparum Ookinetes

Ramish Bibi[1], Junel Solis[1], Irina Belaia[1], Pablo Suárez-Cortés[2], Týč Jiří[3], Pasi Kankaanpää[1]
[1] Turku BioImaging, Åbo Akademi University and the University of Turku
[2] Max Planck Institute for Infection Biology
[3] Institute of Parasitology, Biology Centre of the Czech Academy of Sciences

Malaria remains a global health challenge, with *Plasmodium falciparum* causing the most severe infections. A critical stage in its transmission cycle occurs in the mosquito midgut, where ookinetes initiate infection. Understanding the ookinete stage requires high resolution, three dimensional imaging, yet the data volumes generated by volume electron microscopy (vEM) are massive, often exceeding terabytes. Traditional image analysis tools struggle with the scale and complexity of such data. To meet this challenge, we successfully developed an end to end image analysis pipeline that blends classical computational workflows with advanced image analysis methods to extract meaningful insights.

Raw vEM data—composed of tens of thousands of 2D tiles—are first stitched into contiguous slices using a fully automated Python interface to the ImageJ Grid/Collection Stitching plugin. These slices are converted to the OME Zarr format to enable memory efficient parallel access. Where needed, AI-based denoising models are applied to enhance contrast and suppress imaging artefacts, followed by automated cropping to focus on regions containing the parasite. A semi automated Z registration workflow aligns the slices into coherent 3D volumes. The reconstructed volumes are segmented using a combination of manual annotations and an AI powered segmentation network, which accelerates the delineation of parasite membranes and sub cellular structures by learning from sparse labels. Quantitative features such as sizes, volumes, surface areas and organelle spatial distributions are computed directly from the segmentation masks.

This image analysis workflow demonstrates a scalable and efficient approach for managing, processing, and analyzing large-scale vEM data while reducing manual workload and increasing reproducibility.

Acknowledgments: The project was designed as a collaborative effort between three institutions; Max Planck Institute for Infection Biology, Euro-BioImaging Prague ALM & EM Node and the Finnish Advance Microscopy Node (Turku BioImaging) funded by ISIDORe (Integrated Services for Infectious Disease Outbreak Research) through Euro-BioImaging.

Co-funded by the European Union

#4

Imaging Across Scales: The Birmingham Example

Mezida Saeed, The UK Node

The University of Birmingham Advanced Imaging Facilities provide open access to a highly integrated, multi-modal bioimaging environment spanning fluorescence microscopy from single molecules to cells, tissues and whole organisms. The Facilities offer expertise in ultrafast single-molecule and functional imaging, super-resolution microscopy, light-sheet and deep-tissue imaging, multiphoton microscopy, advanced sample preparation and quantitative image analysis. Users are supported across the full experimental workflow, from project design, sample preparation and training through to data acquisition, analysis and interpretation. Embedded within Birmingham's interdisciplinary research environment, including the Centre of Membrane Proteins and Receptors (COMPARE), clinical research infrastructure and computational expertise, the Facilities provide a collaborative platform where advanced microscopy, probe development, custom imaging technologies and quantitative analysis can be applied to biological and biomedical discovery.

Co-funded by the European Union

#5

Bridging Molecular and Organismal Scales: IMAGINE-ing Next-Generation Bioimaging Services

Sanjana Singh, Euro-BioImaging

The IMAGINE project (Next generation imaging technologies to probe structure and function of biological specimens across scales in their natural context) aims to develop disruptive, cross-scale imaging technologies that go beyond specialized laboratories and standard models and into routine service provision across European research infrastructures as well as in native field deployment. Its 31-member consortium focuses on advancements in four major technologies: X-ray imaging, cryo-EM, cryo- and dynamic super-resolution microscopy (SRM), and large-volume intravital light microscopy. These advancements are integrated with AI-based image analysis and data-integration tools to support multi-modal workflows and FAIR data sharing via open repositories. Central to IMAGINE's mission is the translation of these innovations into rigorously validated, service-ready offerings across major European Research Infrastructures, including Euro-BioImaging, Instruct-ERIC, and EMBRC. This includes validating technical performance, evaluating user experience, workflow integration and feasibility for routine open access provision. Through staff training and an open innovation ecosystem involving academic and industrial partners, IMAGINE democratizes access to advanced bioimaging. The resulting cross-scale, cutting edge technology made available to a broad research community will position European research to lead global efforts in addressing future challenges.

Co-funded by the European Union

#6

Global BioImaging Supports Capacity Building in Imaging Core Facilities Across the World

Gleb Grebnev, Global BioImaging

Imaging core facilities have become an integral part of life science research institutions around the globe. They provide access to state-of-the-art imaging equipment, scientific services, know-how and expertise in many areas, including sample preparation, image acquisition, and data analysis; all necessary to support researchers and answer scientific questions in health and disease models. Global BioImaging (GBI)[1], an international network of imaging infrastructures and communities, coordinated by European Molecular Biology Laboratory (EMBL)[2], uniquely positions itself to offer training to imaging scientists working in core facilities. Following its conception, GBI offers two distinct, but complementary training opportunities to core facility imaging scientists that includes international courses and the job shadowing program. Each of its courses focuses on one of the following overarching themes: 1) core facility management, 2) image data handling and bioimage analysis, and 3) train-the-trainer. By organizing core facility management and data handling and bioimage analysis courses, GBI aims to increase capacity, especially in communities that are starting to develop their imaging core facilities. With the train-the-trainer format, the aim is to train core facility imaging scientists to run microscopy courses in their core facilities[3]. In addition, GBI courses serve as an excellent platform for networking and establishing international collaborations. Since the start of 2023, thirteen GBI courses have taken place around the world, including in Canada, Mexico, Brazil, Denmark, South Africa, India, Singapore, Japan, and Australia. Another activity as part of the Training Program, the job shadowing involves visiting another imaging core facility where the staff may have more experience, operate different imaging technologies, or have implemented procedures not found at the home facility. This experience helps job shadowing participants learn new aspects related to facility management, bioimage analysis, image data storage, quality management, software tools, user access, and much more. To date, almost 500 core facility imaging scientists from more than 36 countries have participated in GBI courses and the job-shadowing program. In addition, GBI provides two resources for independent learning, including the Virtual Training Platform[4] hosted on the Global BioImaging website and Microtutor[5].

[1] https://globalbioimaging.org/
[2] https://www.embl.org/
[3] https://onlinelibrary.wiley.com/doi/10.1111/jmi.70116
[4] https://globalbioimaging.org/international-training-courses/repository
[5] https://microtutorcourses.org/

Co-funded by the European Union

#7

Imaging and quantification of infection in complex 3D models

Katie Holden, The UK Node

Complex 3D biological models provide powerful systems for studying infection and host–pathogen interactions, but they also present substantial image acquisition and analysis challenges. Large multidimensional datasets, variable morphology, heterogeneous labelling and high background make robust quantification difficult, particularly when pathogen localisation must be interpreted within complex tissue architecture.

At the Cellular Imaging Core Facility, we have combined automated advanced confocal imaging with bespoke analysis pipelines designed within arivis Pro software to provide end-to-end workflows for collaborative projects involving complex 3D infection models. Here we illustrate this approach through three projects. First, in a 3D human urothelial microtissue model of urinary tract infection, confocal imaging and batch analysis were used to quantify intracellular and extracellular uropathogenic *E. coli* following antibiotic, bacteriophage or combined treatment. Second, workflows were developed to quantify *Salmonella* infection in human apical-out gut-derived organoids on a single-cell basis, and to assess bacterial localisation using multi-channel fluorescence reporters. Finally, a live neurosphere imaging assay was developed to study the effects of viral challenge on neuronal development, enabling automated quantification of neural migration, radial glia growth and, more recently, high-temporal-resolution nuclei tracking.

Together, these examples demonstrate how carefully developed model systems combined with advanced imaging and analysis enables scalable, reproducible and biologically meaningful quantification from challenging 3D infection datasets, supporting the transition from advanced imaging to robust quantitative interpretation.

Co-funded by the European Union

#8

Scaling Expertise Across Europe: Measuring the Impact of the EVOLVE Training Framework at Euro-BioImaging

Daniela Aviles Huerta & Victoria Alonso, Euro-BioImaging

Training and capacity building are central to strengthening the European research infrastructure landscape. Within the framework of the EVOLVE Project (Grant Agreement No. 101130986), Euro-BioImaging ERIC has implemented a structured training framework designed to enhance skills, knowledge exchange, and collaboration across its distributed network of Nodes. EVOLVE aims to advance Euro-BioImaging to its next level as a pan-European research infrastructure by reinforcing operational capacity, strategic partnerships, innovation support, and scientific excellence, while aligning with the organisation's Strategic Plan 2024–2028.

A key component of this effort is the EVOLVE Training Framework, built on three complementary pillars: Job Shadowing, Mentoring, and Training Courses. These activities are designed to foster professional development among Node staff, strengthen cross-node collaboration, and disseminate expertise across the Euro-BioImaging community. By March 2026, the programme has supported 153 applications for training, including 55 cross-Node job shadowing visits and international mentoring connections, and 32 endorsed participations in specialised training courses.

To ensure lasting impact, the programme integrates structured knowledge dissemination plans following each mobility activity. Participants are encouraged to transfer newly acquired expertise to their home institutions through local workshops, training materials, and internal capacity-building activities, thereby multiplying the benefits across the network.

One notable initiative is the Train-the-Trainer course organised in 2025, which focused on empowering imaging experts to become effective trainers within the Euro-BioImaging ecosystem. The course addressed pedagogical approaches for teaching imaging techniques, course and workshop design, user training strategies, diverse delivery formats, and collaboration with other Nodes and industry partners. While the course directly trained approximately 30 participants, its multiplier effect is expected to be substantial: if each participant subsequently trains five additional trainers, the initiative could empower more than 150 new trainers across Europe.

This contribution presents the metrics, implementation strategy, and early impact assessment of EVOLVE training activities, highlighting how targeted training, mobility, and mentoring programmes can strengthen distributed research infrastructures. The results demonstrate how structured training frameworks and knowledge dissemination mechanisms can significantly expand expertise, foster collaboration, and enhance the long-term sustainability and impact of European scientific infrastructures.

Co-funded by the European Union

#9
IMG Electron Microscopy Core Facility

Aneta Przybeková & Dominik Pinkas, Prague Node

The Electron Microscopy Core Facility offers services in a wide range of both advanced and routine techniques, focused mainly on biological samples. The team's expertise is supported by state of the art equipment for sample preparation and ultrastructural imaging. Our high-end transmission electron microscope (TEM) operates at up to 200 kV and offers high-resolution TEM, imaging in STEM mode, 3D analysis by TEM- or STEM tomography, cryo-electron microscopy and STEM-EDS elemental analysis. For routine observation, a standard 120kV TEM with a user-friendly Limitless panorama application is used. Recently, we have incorporated a FIB-SEM instrument, which, among other applications, is being used for the development of an original cryo-lamella lift-out workflow.

Standard and advanced techniques are tied up also with the sample preparation. Starting from routine chemical fixation and resin embedding, or negative staining of weakly observable samples, we can proceed to better preservation of natural sample appearance by cryofixation using plunge-freezing or high-pressure freezing, followed by freeze-substitution, cryosectioning or freeze fracture replica labeling. For even more advanced applications we can provide cryoCLEM technique using a specialized microscope. Another field forms pre- and post-embedding immunolabeling techniques using gold nanoparticles of different sizes.

Users as well as potential applicants can think of service processing and imaging of various biological samples – in the core facility we can deal with human and animal cell cultures, plant and animal tissues, worms, microorganisms, lipid micelles, isolated DNA, or purified proteins. We provide development and optimization of sample preparation, based on a long expertise and fruitful collaborations with companies providing equipment for electron microscopy.

The Electron Microscopy Core Facility is part of the IMG Czech-BioImaging node and Prague Euro-BioImaging Node. We provide open access to our technologies and expertise and are ready to welcome users from all fields.

Acknowledgement:
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#10

Advanced Light Microscopy Node Poland - Image Processing & Analysis

Artur Wolny, Advanced Light Microscopy Node Poland

The Advanced Light Microscopy Node Poland provides comprehensive support for microscopy image processing, analysis, and visualization using both commercial and open-source software solutions. Our facility offers expert assistance in selecting appropriate analysis workflows, image restoration, quantitative analysis, automation, and data visualization for a broad range of biological imaging applications.

The commercial software portfolio includes two floating licenses of Imaris for Core Facilities with advanced modules (FilamentTracer, Batch, Cell, Deconvolution, Lineage, Track, and Xt), Imaris Stitcher, SVI Huygens Professional (including Deconvolution Express, Full Restoration and Visualization, AI-based Object Analyzer, Colocalization, Object Tracker, Fusion, Stitcher, Lightsheet Fuser, Workflow Processor, Batch Processing, Image Quality Control, and Abberior Bundle), ZEISS arivis Pro with modules for membrane-based segmentation, blob detection, tiling and stitching, volume fusion, colocalization and distance analysis, tracking, neuron tracing, machine learning and deep learning (Arivis Cloud), and VR visualization tools. Additional vendor-specific software includes ZEISS ZEN Desk, Leica LAS X, and Abberior Lightbox.

Support is also provided for widely used open-source platforms, including ImageJ/Fiji (with macro development and workflow automation) and CellProfiler.

Users can access the software remotely via an online server or locally through dedicated workstations. Computational resources include a high-performance HIVE server equipped with 48 CPU cores (96 threads), 1 TB RAM, and an NVIDIA RTX A6000 professional GPU, complemented by three dedicated image analysis workstations. This infrastructure enables efficient processing and quantitative analysis of large multidimensional microscopy datasets, including high-resolution, lightsheet, and AI-assisted image analysis workflows.

Co-funded by the European Union

#11
Advanced Light Microscopy Node Poland ONI Nanoimager

Emre Hakli, Advanced Light Microscopy Node Poland

The Advanced Light Microscopy Node Poland provides access to the ONI Nanoimager, a single-molecule super-resolution microscopy platform designed for imaging biological samples beyond the diffraction limit. The system supports a wide range of applications requiring nanoscale resolution, enabling visualization of protein organization, molecular interactions, and subcellular structures with high spatial precision.

The ONI Nanoimager is configured for single-molecule localization microscopy (SMLM), supporting techniques including dSTORM and DNA-PAINT. The instrument combines sensitive fluorescence detection, multicolor imaging, environmental control, and integrated acquisition and analysis software within a compact platform. These features enable robust super-resolution imaging while maintaining a streamlined and user-friendly workflow.

The facility provides comprehensive support throughout the entire experimental process, including consultation on experimental design, sample preparation, fluorophore selection, imaging strategy, data acquisition, and image reconstruction. Users receive training on instrument operation as well as guidance in quality assessment and quantitative analysis of super-resolution datasets.

The ONI Nanoimager expands the portfolio of advanced imaging technologies available at the Advanced Light Microscopy Node Poland, providing researchers with access to state-of-the-art super-resolution microscopy for a broad range of life science applications. By combining cutting-edge instrumentation with expert support, the facility enables users to address biological questions at the nanometer scale and facilitates the adoption of SMLM techniques by both experienced and new users.

Co-funded by the European Union

#12

OSCARS-FIESTA: FAIR Image Analysis Across Sciences

Beatriz Serrano Solano, Euro-BioImaging

Imaging techniques have become increasingly popular across scientific fields due to their ability to provide rich and comprehensive information. These images, image series, and videos are invaluable resources, offering researchers a wealth of information to explore and analyse. Despite the widespread use of imaging, the practice of extracting quantitative information from image data remains fragmented across scientific communities. Scientists often work in isolated silos, resulting in limited cross-talk and collaboration. This isolation can lead to redundant work and inefficient resource utilisation, as experts in different domains may duplicate efforts unknowingly. The rise of AI and machine learning further complicates this landscape, with access to the necessary tools and computational resources becoming a significant bottleneck for researchers.

The "FAIR Image Analysis Across Sciences" project addresses these challenges by developing reusable image analysis workflows that can be shared across disciplines such as bioimaging, environmental sciences, and astrophysics.

Co-funded by the European Union

#13

AI-based bioimage analysis in Euro-BioImaging

Beatriz Serrano Solano, Euro-BioImaging

Advances in microscopy are driving an unprecedented growth in biomedical image data, making automated and reproducible analysis essential for scientific discovery. While Artificial Intelligence (AI) and Machine Learning (ML) offer powerful solutions, access to these methods remains fragmented and technically challenging for many researchers.

Euro-BioImaging helps bridge this gap by contributing to a pan-European ecosystem for AI-based bioimage analysis, enabling its Nodes and users to move from manual workflows towards AI-supported discovery for faster, more impactful biological and medical discoveries.

Co-funded by the European Union

#14

Advanced Light Microscopy Node Poland – expanding access to next-generation bioimaging technologies

Jędrzej Szymański, Advanced Light Microscopy Node Poland

The Advanced Light Microscopy Node Poland, coordinated by the Nencki Institute of Experimental Biology, Polish Academy of Sciences, is the Polish node of the Euro-BioImaging research infrastructure. The node provides open access to advanced imaging technologies, expert scientific consultation, user training, image analysis support, and collaborative research for academic and industrial users from Poland and abroad.

Our mission is to enable researchers to address challenging biological questions by providing access to state-of-the-art microscopy platforms together with comprehensive methodological support, from experimental design and sample preparation to image acquisition, quantitative analysis, and data management.

Over the last few years, the node has substantially expanded its technological portfolio, creating one of the most comprehensive collections of advanced light microscopy systems in Central and Eastern Europe. Newly established platforms include:

- Revvity Opera Phenix Plus high-content screening system for automated multiparametric imaging and phenotypic analysis;
- ZEISS LSM 990 equipped with Airyscan 2 and Lightfield 4D for high-speed, low-phototoxicity confocal imaging with enhanced sensitivity and resolution;
- Bruker Luxendo InVi SPIM Lattice Pro for advanced light-sheet microscopy of living specimens with minimal photobleaching and phototoxicity;
- Olympus SpinSR spinning-disk super-resolution microscope for fast live-cell imaging;
- Abberior MIRAVA super-resolution microscope providing STED and RESOLFT imaging capabilities;
- Olympus VS200 digital slide scanner with automated slide loader and Speckle Illumination Acquisition (SILA) technology for high-throughput pathology and whole-slide imaging;
- Femtonics Atlas Plug-and-Play multiphoton microscope supporting deep-tissue imaging, neuroscience applications, and functional in vivo studies.

Together with our existing instrumentation, these platforms enable workflows ranging from high-content screening, live-cell and intravital imaging, super-resolution microscopy, multiphoton imaging, and light-sheet microscopy to digital pathology, whole-organ imaging, and advanced quantitative image analysis.

The continuous development of the node reflects our commitment to providing the Euro-BioImaging community with cutting-edge imaging technologies, interdisciplinary expertise, and an open-access environment that fosters scientific excellence, collaboration, technology transfer, and innovation. More information about the Advanced Light Microscopy Node Poland is available at amf.nencki.edu.pl.

Core facility at the Nencki Institute is part of the infrastructure of the Polish Euro-BioImaging Node. Polish Node is supported by the project co-financed by the Minister of Science based on contract No 2022/WK/05 (Polish Euro-BioImaging Node “Advanced Light Microscopy Node Poland”).

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#15

Integrated Cell and Tissue Imaging Infrastructure at the University of Eastern Finland

Hanna Grobe, Eastern Finland BioImaging

Imaging has been a vital and valuable part of biomedical research for decades and an increasing number of publications feature microscopy methods to visualize and emphasize research findings. However, new method developments and techniques that appear on an almost weekly basis can be especially challenging for research groups whose focus is not primarily microscopy. Here is where the Cell and Tissue Imaging Unit (CTIU) has established relevant infrastructure for the researchers at the University of Eastern Finland by providing support and services for the full experimental pipeline, from sample preparation to data sharing. Our idea is that the CTIU functions as a classical core facility as well as a comprehensive service provider, depending on the researcher's needs.

With our on-site histology laboratory, we can both support and provide sample preparation, including fixation, embedding, sectioning and staining which ensures high-quality, standardized specimens suitable for downstream imaging workflows. Our imaging systems, that range from widefield microscopes to a high-throughput spinning disc confocal microscope can then be used directly by the researches or can be operated by the CTIU staff to image samples according to the researchers instructions and thereby deliver image data to research groups that lack the resources, time or knowledge to get familiar with the system. The same principle is applied to the downstream image analysis and data sharing where the CTIU provides support through workshops and courses as well as one-to-one training or offers to perform the analysis and/or data deposition according to the researcher's specifications. In practice, an imaging experiment can go from our histology lab where the tissue is prepared and slides are automatically stained in a newly purchased automatic staining System to the Leica Thunder where the researcher images the stained slides and analyzes the obtained images. After publication the user can then employ the CTIU to share the data in a relevant repository. With this modular pipeline approach we aim to give every user [KK1.1] the option to outsource individual steps or entire imaging pipelines depending on their needs and expertise. We thereby hope we can lower technical barriers and enable access to advanced methodologies to research groups that lack specialized resources.

Co-funded by the European Union

#16

Introducing SYLI – the Living Biobank-Cancer Laboratory

Kirsi Ketola, Eastern Finland BioImaging

Translating discoveries in cancer research into clinical and societal impact requires coordinated interaction between basic science, technology development and medical innovation. SYLI, the Living Biobank–Cancer Laboratory, has been established to accelerate this process by integrating multidisciplinary expertise, biobank resources and advanced technologies into a unified translational research infrastructure.

The aim of SYLI is to combine existing equipment, specialized expertise and key new investments into a new RDI infrastructure, the Cancer Laboratory. This infrastructure will support the development of an operating concept and a comprehensive service model for close collaboration between the University of Eastern Finland (UEF), clinical partners and regional businesses. The long-term goal is to create a service package for translational cancer research in North Savo for both academic and industrial users. These new RDI services will strengthen the existing research infrastructure at UEF, create opportunities for business-oriented innovations and potentially benefit healthcare through improved cancer research workflows.

The SYLI umbrella spans multiple departments at the Faculty of Health Sciences and the School of Medicine, including the A.I. Virtanen Institute, the Institute of Biomedicine and Pathology. It brings together three core facilities - the Cell and Tissue Imaging Unit, the Single Cell Genomics Core and the Bioinformatics Center - together with the Biobank of Eastern Finland. SYLI provides access to high-end technologies for academic and industry partners and enables a seamless workflow from biobank-derived cancer samples to advanced molecular and imaging analyses, including high-content imaging, single-cell sequencing and spatial transcriptomics, followed by bioinformatic analysis and reporting to support data-driven decision-making.

By promoting the use of advanced technologies and shared infrastructure, SYLI supports both industry partners and academic users of UEF core facilities and service providers. The close collaboration between core facilities, research groups, biobank resources and regional stakeholders will generate long-term benefits for the cancer research community and strengthen translational cancer research in Eastern Finland.

Co-funded by the European Union

#17

Expanding Access to Advanced Imaging Across Biological Scales: New Services at the EMBL Imaging Centre

Virginia Pierini, EMBL

Understanding biological systems requires imaging technologies that can capture structure, dynamics, and mechanical properties across multiple spatial and temporal scales while preserving native physiological conditions. To address this challenge, the EMBL Imaging Centre (IC), as part of the EMBL Node, has expanded its portfolio with three advanced imaging services: serialised lift-out for cryo-electron tomography (cryo-ET), Oblique Plane Microscopy (OPM), and Brillouin microscopy.

Serialised lift-out is a transformative cryo-focused ion beam (cryo-FIB) workflow that enables high-resolution cryo-ET of thick vitrified specimens, including tissues and whole organisms prepared by high-pressure freezing. Building on recent developments in Serial Lift-Out and SOLIST methodologies[1,2], the approach allows sequential extraction of multiple lamellae from a single specimen, substantially increasing throughput while preserving native cellular context. This enables molecular-scale investigation of complex biological systems that were previously difficult to access by cryo-ET.

To complement structural imaging, the EMBL IC is introducing Oblique Plane Microscopy (OPM), a high-speed light-sheet fluorescence microscopy technique that combines illumination and detection through a single objective lens. OPM enables rapid, low-phototoxic volumetric imaging of living samples in conventional inverted microscope configurations, providing high-resolution visualisation of dynamic cellular processes in three dimensions[3,4].

In parallel, Brillouin microscopy offers label-free mapping of biomechanical properties such as stiffness and viscosity in living biological specimens. Integrated with confocal fluorescence microscopy, the system enables correlative measurements of tissue mechanics, molecular organisation, and cellular architecture within the same sample[5,6].

Together, these complementary technologies provide researchers with unprecedented opportunities to connect molecular architecture, cellular dynamics, and mechanical function across scales. By combining near-native structural analysis, live volumetric imaging, and quantitative biomechanical measurements, the EMBL IC continues its mission of providing the life-science community with access to state-of-the-art imaging technologies and expert support.

References:

[1]Schiøtz et al., 2024, https://doi.org/10.1038/s41592-023-02113-5
[2]Nguyen et al., 2024, https://doi.org/10.1038/s41592-024-02384-6
[3]Dunsby, 2008, DOI: 10.1364/oe.16.020306
[4]Sapoznik et al., 2020, https://doi.org/10.7554/eLife.57681
[5]Scarcelli et al., 2015, https://doi.org/10.1038/nmeth.3616
[6]Bevilacqua et al., 2019, DOI: 10.1364/BOE.10.001420

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#18

Opera Phenix System with Harmony Software for studying tissues, cells and vesicles in Euro-BioImaging Advanced Light Microscopy Node Poland

Agnieszka Strzelecka-Kiliszek, Advanced Light Microscopy Node Poland

Laboratory of Imaging Tissue Structure and Function operates as an imaging core-facility at the Nencki Institute of Experimental Biology of the Polish Academy of Sciences. We provide training, support and advice for internal and external users. The facility is also a part of Euro-BioImaging Advanced Light Microscopy Node Poland.

We offer our new Opera Phenix™ Plus microscopy (Revvity) of confocal solution for most demanding high-content applications with liquid handling option and Harmony™ analysis software (Revvity). The system is designed for high-throughput imaging assays, phenotypic screening, assays using complex disease models, such as live cells, primary cells and microtissues, and fast-response assays, such as Ca2+ flux. It is also heavily utilized for studying extracellular vesicles (EVs). It provides the high sensitivity and spatial resolution needed to visualize and quantify these nanoscale biological messengers. [1, 2]

Researchers typically use the system to study EVs in the following ways:

- Internalization Assays: tracking and quantifying how EVs are taken up by recipient cells over time, often using fluorescently labeled vesicles. [1, 3]
- High-Throughput Analysis: high-content imaging of 96- or 384-well plates, allowing for fast, automated screening of EV uptake or functional effects on cell lines. [3]
- Quant Integration: combining specialized gel immobilization assays with the confocal microscope to automatically count and characterize EVs in biofluids (like urine, blood or lymph). [2]
- Phenotypic Profiling: evaluating how EV cargo (proteins, miRNA) induces biological responses like cell adhesion, migration, directionality, angiogenesis, polarization or extracellular matrix deposition. [1, 4]

For more details on its automated imaging capabilities, you can visit the official Opera Phenix Plus High-Content Screening System page.

References:

1. Cell Commun Signal. 2025 Dec 3;24:10. doi: 10.1186/s12964-025-02571-8
2. Sci Rep. 2021 Oct 21;11:20760. doi: 10.1038/s41598-021-00289-4
3. J Extracell Vesicles. 2023 Jan 3;12(1):12297. doi: 10.1002/jev2.12297
4. eLife 2025. https://doi.org/10.7554/eLife.90375.2

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#19

Global BioImaging: the international network of imaging facilities and communities

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Global BioImaging (GBI) is an international network connecting imaging scientists, facility managers, and technical staff in more than 70 countries across all inhabited continents. Through working groups, annual meetings, and training workshops designed specifically for imaging core facility staff, GBI connects local expertise and initiatives internationally. Our work focuses on strengthening imaging facilities and the communities around them, with particular attention to equitable access to imaging technologies, long-term funding, dedicated career paths, and training opportunities for the workforce that supports researchers with imaging expertise. As GBI marks its 10th anniversary, this poster highlights initiatives developed by the network around open access, image data management, FAIR data practices, and career development for imaging scientists. GBI's Annual Meeting 2026 will bring these topics together under the theme "Open Access to Imaging Around the Globe", with discussions on equitable access, data sharing, and collaborative approaches to imaging infrastructure.

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#20

Euro-BioImaging Finland as a Lighthouse Research Infrastructure for Science and Innovation

Irina Belaia[1], Tiina Saanijoki [1], Pasi Kankaanpää[1]

[1]Euro-BioImaging Finland

Euro-BioImaging Finland (www.eurobioimaging.fi) consists of two Euro-BioImaging Nodes, Finnish Advanced Microscopy Node and Finnish Biomedical Imaging Node. Altogether, Euro-BioImaging Finland consists of imaging facilities from 7 universities and 3 university hospitals, and it is one of Finland's largest research infrastructures. Euro-BioImaging Finland has 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 demonstrable 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.

Euro-BioImaging Finland is led by Turku BioImaging, which has in addition received European Regional Development Funding and national regional development funding to develop open access image analysis services for industry-academia collaboration, digital agriculture, marine biology, and environmental protection. This type of development is increasingly important for the broad impact of imaging, and very relevant 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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#21

Automated and integrated data flow at ACAM

Marlies Verschuuren[1,2,3], David D'Haese[1,2,3], Sofie Thys[1,2,3], Isabel Pintelon[1,2,3], Jean-Pierre Timmermans[1,2,3], Winnok H. De Vos[1,2,3]

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The Antwerp Centre for Advanced Microscopy (ACAM, www.acam-uantwerpen.be), part of the Flanders BioImaging node, develops data-driven microscopy approaches to gain insight in and expose novel therapeutic targets for human aging diseases like cancer and neurodegeneration. To facilitate user access and follow-up, we established an integrated workflow within our core facility, covering sample intake and imaging as well as data delivery and invoicing. Central to this workflow is an in-house developed software that connects a dedicated administrative database with acquisition computers and analysis servers. This enables seamless data transfer and storage, ensures data integrity and traceability across the different microscopy setups and users, facilitates consistent metadata annotation throughout as well as timely invoicing. In addition, we are developing an analysis pipeline editor that allows users to execute custom image analysis scripts independent of the underlying programming languages. The design was purposefully made modular, low-tech and low-cost, rendering this infrastructure adaptable to other imaging core facilities and providing a practical framework for implementing automated data management workflows.

Co-funded by the European Union

#22

Grand Challenge: An End-to-End Platform for AI Algorithm Development in Medical imaging and beyond

Miriam Groeneveld, Challenges Framework Flagship Node, the Netherlands

The growing volume and complexity of medical (imaging) data have created a pressing need for robust, reproducible, and collaborative tools to develop and validate AI algorithms in healthcare. Grand Challenge is a cloud-based platform, developed and maintained by the Diagnostic Image Analysis Group (DIAG) at Radboud University Medical Center since 2012, that supports the full lifecycle of AI algorithm development, from data curation to algorithm deployment, all within a single secure environment.

The platform is built around four core services. Archives allow researchers and data managers to centrally store, organize, and share data. A wide range of file formats is supported, including DICOM, MHA, NifTI for medical images, PDF, JSON, and plain text, with images viewable across multiple synchronized viewports. This service is designed with FAIR data principles in mind, helping ensure that datasets remain findable, accessible, interoperable, and reusable well beyond a single study.

Reader studies support structured annotation and evaluation workflows for both research and educational purposes. Study designers can build custom question sets, including multiple choice and free-text items, alongside annotation types such as bounding boxes, polygons, and binary or multi-label segmentations. Ground-truth answers can be uploaded to enable automated performance monitoring, making reader studies a flexible tool for training annotators as well as collecting expert-labeled data.

Challenges give organizers the tools to design and run benchmarking competitions with standardized, transparent evaluation metrics. This addresses well-documented concerns in the literature around the fairness and interpretability of competition rankings, offering a more rigorous alternative to *ad hoc* benchmarking efforts.

Algorithms can be containerized and deployed directly on the platform, allowing developers to share fully executable models rather than static code repositories. This lowers the barrier for others to test and validate algorithms on new data, supporting reproducibility across the community.

With over 100,000 users and 390+ public and private challenges hosted to date, Grand Challenge serves a broad community of researchers, students and clinicians. This poster presents an overview of these services and offers practical guidance for setting up archives, reader studies, challenges, and algorithms on the platform. We invite you to stop by the poster to see these features in action and discuss how they might fit your own research or infrastructure needs. For those interested in a closer look, we are happy to arrange a live demo of the platform's services.

Co-funded by the European Union

#23

AI-Enabled Data Exploitation for Research Infrastructures through the RI-SCALE project

Dorothea Dörr, Euro-BioImaging

Research Infrastructures (RIs) generate vast and highly valuable datasets that are essential for advancing data-driven science. However, their full exploitation is often constrained by fragmented access, limited computational scalability, and the technical complexity of applying advanced AI methods. The Horizon Europe RI-SCALE project addresses these challenges by federating RI data holdings with scalable AI, compute, and data services through Data Exploitation Platforms (DEPs).

RI-SCALE brings together thematic RIs, e-infrastructure providers, and data space initiatives to co-design and deploy trusted, scalable environments that enable seamless data access, AI-driven analysis, and reuse.

Within this framework, Euro-BioImaging contributes two complementary AI-driven use cases that address key challenges in biological and biomedical imaging. The first explores the development of foundational models for heterogeneous bioimage data to enable reuse across diverse imaging modalities. By learning generalisable representations, these models aim to support multiple downstream applications, such as categorisation, similarity search and derived measurements.

The second use case focuses on a generative AI-powered assistant for data discovery and analysis, embedded within the BioImage Archive image data repository. The assistant is designed to simplify dataset exploration and enable intuitive access to advanced image analysis capabilities, lowering technical barriers for users while streamlining user support workflows.

Together, these use cases demonstrate how RI-SCALE Data Exploitation Platforms can empower RIs to transform complex data holdings into accessible, AI-ready resources, accelerating scientific discovery and enabling sustainable, user-centric data services across research domains.

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#24

SCIANCE: Establishing the Foundations for a European AI in Science Agenda and Ecosystem

Dorothea Dörr, Euro-BioImaging

SCIANCE is a European coordination initiative establishing the foundations for the Resource for Artificial Intelligence (AI) Science in Europe (RAISE). The project promotes interdisciplinary collaboration to integrate AI into scientific research by enabling streamlined access to trustworthy data repositories, computing resources, and research infrastructures across Europe. Bringing together leading research infrastructures, scientific organisations, and AI centres of excellence, SCIANCE develops a Strategic Research and Innovation Agenda (SRIA) through an iterative co-creation process. The project mobilises expertise across five scientific pilot areas: life sciences, fundamental physics and astronomy, materials science, earth sciences, and social sciences and humanities. Within this framework, Euro-BioImaging ERIC coordinates the life sciences contributions, ensuring that the community's strategic priorities and research requirements are comprehensively represented in the European AI-in-science agenda.

Building on an AI-in-science landscape analysis, the SRIA identifies long-term research challenges where AI can accelerate discovery and defines cross-domain AI research and innovation priorities, focusing on open, trustworthy, and frugal AI methods for science. A roadmap for infrastructure upgrades and cooperation mechanisms supports its implementation, translating scientific research and innovation priorities into coordinated action.

To consolidate the European AI-in-science ecosystem, SCIANCE pilots the RAISE Secretariat, supported by the RAISE Digital Hub, community-building events at annual AI in Science (AIS) Summits, and the RAISE Academy, providing a continuous framework for engagement, capacity building, knowledge sharing, and cross-domain collaborations. By combining scientific domain expertise with AI research and infrastructure knowledge, SCIANCE delivers robust, evidence-based guidance that is strategically aligned with European Union objectives, laying the foundations for future collaborative, AI-enabled science in Europe.

Co-funded by the European Union

#25

Introducing the University of Oxford Advanced Microscopy Core: a multi-site Euro-BioImaging Node for advanced light microscopy

James Bancroft, The UK Node

The University of Oxford Advanced Microscopy Core brings together complementary open-access imaging facilities across the Medical Sciences Division to provide a coordinated route into Oxford's advanced light microscopy infrastructure. The founding partners are the Micron Bioimaging Facility in the Department of Biochemistry, the Cellular Imaging Core Facility at the Centre for Human Genetics, and the Oxford-ZEISS Centre of Excellence for Biomedical Imaging at the Kennedy Institute of Rheumatology and Institute of Developmental and Regenerative Medicine. The Core is structured around three major areas of expertise. Micron provides nationally leading super-resolution capability, including SIM, TIRF-SIM, iSIM, TauSTED and SMLM, supported by expertise in reconstruction, chromatic alignment, localisation microscopy and quantitative super-resolution workflows. The Oxford-ZEISS Centre of Excellence provides advanced dynamic and functional imaging, including lattice light-sheet microscopy for fast, gentle volumetric imaging, alongside FCS, FCCS, FLIM and complex ZEISS-based workflows. The Cellular Imaging Core Facility provides high-content and long-term live-cell imaging in complex biological models, with strengths in organoids, iPSC-derived systems, infection biology, CL2/CL3-compatible workflows, automated microscopy and advanced 3D/4D analysis. Beyond instrument access, the Oxford Core offers an integrated sample-to-data support model. Users can access tissue-culture and wet-lab facilities, assay and sample-preparation advice, supervised acquisition, remote and hybrid access, high-performance analysis workstations, secure data storage and bespoke image-analysis pipeline development using commercial and open-source platforms. The Core also benefits from strategic partnerships with major microscope manufacturers and software developers, including ZEISS, Leica, Evident, arivis and Aivia, supporting early evaluation of emerging technologies and collaborative method development. Training and community engagement are central to the Oxford model. The participating facilities contribute to the Oxford BioImaging Network, deliver the OxMIC microscopy course, specialist super-resolution training, one-to-one user support, image-analysis teaching and outreach activities. This presentation will introduce the structure, specialisms and user support model of the Oxford Core, highlighting how a distributed but connected node can provide users with access to specialist technologies, expert methodological support and end-to-end imaging workflows.

Co-funded by the European Union

#26

Advanced cryo-workflows at the IMG Electron Microscopy Core Facility

Pavla Molínová, Prague Node

Continual advancements in cryo-electron microscopy (cryo-EM) have established it as the method of choice for reliable analysis of biological samples in their close-to-native state. Our facility consistently updates cryo-workflows to provide professional solutions for current scientific demands.

Our 200 kV Jeol JEM-F200 transmission electron microscope, equipped with a cryo polepiece, cold field emission gun, Volta phase plate, Gatan Alpine direct electron detector and a 4k CMOS camera (TVIPS XF-416), is optimized for diverse cryoTEM applications. These include observing dehydration-sensitive small objects (e.g., small organisms, DNA origami), quality checks of purified protein samples before SPA, collecting diffraction patterns from frozen protein crystals, and cryo-electron tomography of subcellular structures.

The core facility now offers a complete cryo-TEM tomography workflow for frozen hydrated lamellae, developed through a collaboration with TESCAN Company. This optimized on-grid workflow involves plunge freezing (Leica EM GP2), quality checks (Leica THUNDER cryo-CLEM), sample mounting and transfer to TESCAN Amber Cryo FIB-SEM for lamella fabrication, and final transfer to cryoTEM for tilt series acquisition. Larger samples vitrified via high-pressure freezing (Leica EM ICE HPF with light-stimulation) can also be imaged in a frozen hydrated state after cryo FIB lift-out, or processed into resin blocks following freeze-substitution (Leica EM AFS2). This workflow has successfully enabled observations and volume reconstructions of subcellular structures in *C. elegans*, *S. cerevisiae*, *Chlamydomonas*, *Chlorella* and HeLa cells.

Additionally, our facility provides other specialized vitrification-based workflows: freeze-fracture replica immunolabeling (Leica EM ACE900), cryo-CLEM imaging with reliable image correlation, and cryo-sectioning followed by immunolabeling after Tokuyasu.

As part of Czech-BioImaging and Euro-BioImaging, the EM Core Facility offers open access to all described technologies with professional support throughout user projects.

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#27

Spatial Organization of Urothelial Cells

Samo Hudoklin[1,*], Tim Zaveršek[1], Maja Deutsch[1], Aleksandar Janev[1], Urška Dragin Jerman[1], Nataša Resnik[1], Daša Zupančič[1], Andreja Erman[1], Rok Romih[1], Mateja Erdani Kreft[1], Peter Veranič[1]

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*SiMBION Node

The ultrastructural organization of cells and their spatial arrangement within tissues are fundamental determinants of organ function in both health and disease. The urinary bladder represents a unique biological system in which the coordinated interplay of nervous, muscular, connective, and epithelial tissues enables urine storage while maintaining a highly effective blood–urine permeability barrier and accommodating substantial changes in volume during the micturition cycle.

The permeability barrier is primarily established by epithelial cells known as urothelial cells. During urothelial differentiation, these cells develop specialized membrane domains termed urothelial plaques. Located on the apical plasma membrane of luminal urothelial cells, urothelial plaques, together with tight junctions, constitute the molecular basis of the permeability barrier. However, the spatial organization of cellular organelles involved in urothelial plaque formation and maintenance in both normal and damaged urothelium remains incompletely understood. Even less is known about the ultrastructure and spatial organization of cells within the lamina propria, which contribute to signal transduction and form a sensory network within the urinary bladder.
The aim of this work is to present our recent progress toward elucidating the spatial organization of urothelial and underlying bladder cells using volume electron microscopy, particularly serial block-face scanning electron microscopy (SBF-SEM), in combination with complementary microscopy techniques.

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#28

Cell dynamics using microfluidic assays

Juliana Manosalva Pérez, Smart Optical Microscopy (SOM) Node, Spain

Introduction:

Microfluidics has emerged as a powerful tool to study cell dynamics, enabling precise control over the cellular microenvironment for real-time evaluation. Researchers typically choose between syringe pumps, pneumatic pressure systems, and advanced closed-loop controllers, each offering specific benefits and drawbacks. Syringe pumps provide precise flow and ease of use, making them cost-effective for long-term cell imaging. However, they lack the rapid response and pulsation-free flow of pressure-driven systems, which may impact sensitive intracellular dynamics. Nevertheless, a wide variety of assays can be performed with this setup, including cellular response to treatments and biofilm phenotyping. Here, we adopt two different approaches integrating microfluidics with live-cell imaging: first, to study cell dynamics in response to treatments, and second, for biofilm phenotyping.

Cell dynamics assay:

For microfluidic experiments involving cytoplasmic-to-nuclear protein translocation, we used the U-2 OS human osteosarcoma cell line transfected with a FOXO3-GFP plasmid. FOXO3 is a transcription factor involved in aging and cancer that moves from the cytoplasm to the nucleus upon activation. The cells were seeded in a six-channel µ-slide suitable for flow experiments. This device was connected to a syringe pump using sterile tubing, taking care to avoid air bubble formation. Subsequently, stimulation was performed with culture medium containing different stimuli to induce FOXO3 translocation. Finally, the stimuli were washed away. The treatment stage provides information regarding the kinetics of translocation, while the washout period indicates the binding stability of the transcription factor.

Biofilm phenotyping:

Candida parapsilosis is a common cause of opportunistic infections, and its incidence has risen in recent years. Here, we use microfluidic experiments to characterize the colonization and spreading potential of various *C. parapsilosis* strains, including both fungicide-susceptible and non-susceptible variants. In this assay, cells were seeded using the syringe pump at a constant flow rate. The different *C. parapsilosis* strains were capable of adhering to a plastic surface under dynamic conditions. During the washing period, however, the non-susceptible strains formed unstable aggregates that were washed away, whereas the susceptible strains formed aggregates that remained adhered to the plastic surface. This provides insights into the spreading potential of different strains in clinical environments.

Conclusion:

Our results demonstrate that microfluidic-based assays provide a robust and versatile platform for the real-time monitoring of complex biological processes. By enabling precise control over environmental conditions and stimulus exposure, this approach overcomes the limitations of traditional static cultures.

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#29

Smart Optical Microscopy Node Madrid: A New Imaging Infrastructure for Advanced Biological Microscopy and Image Analysis

Diego Megias, Smart Optical Microscopy (SOM) Node, Spain

The Smart Optical Microscopy Node (SOM) is a new Euro-Bioimaging node that brings together three complementary institutions: the “Instituto de Salud Carlos III (ISCIII)”, the Spanish National Cancer Research Centre (CNIO), and the “Universidad Carlos III de Madrid (UC3M)”.
This multi-site node aims to provide researchers with access to advanced optical microscopy technologies, image analysis services, training activities, and expert support throughout the whole imaging workflow.

One of the main strengths of the node is the combination of advanced microscopy with automated acquisition systems, multiplex fluorescence imaging, and artificial intelligence-based image analysis.
Users will have access not only to imaging instruments but also to dedicated image-analysis workstations, GPU computing resources, and expert support for quantitative analysis of large, complex datasets.

The node will offer a wide range of imaging techniques, including confocal microscopy, live-cell imaging, fluorescence lifetime imaging (FLIM), STED super-resolution microscopy, holographic tomography, tissue imaging, and high-content screening platforms. These technologies will support applications in cell biology, cancer research, tissue analysis, and other areas of biomedical research.

The node will also provide support in experimental design, sample preparation, image processing, data management, and training. By combining the expertise available at ISCIII, CNIO, and UC3M, the node aims to help researchers obtain reliable and reproducible results and make better use of advanced imaging technologies.

The creation of this node in Madrid will help fill an important geographical gap in the Spanish Euro-Bioimaging landscape. It will increase access to advanced imaging infrastructure for the large biomedical research community located in central Spain and promote new collaborations between academia, healthcare institutions, and industry partners.

Co-funded by the European Union

#30

Imaging Beyond Observation: Molecular Organisation, Dynamics and Mechanics at OCTOPUS

Esther Garcia, The UK Node

Modern biological questions increasingly demand more from imaging than a sharper picture of where something is. Researchers also need to know how structures are organised at the molecular scale, how they behave over time and space, and how they respond mechanically to their environment. OCTOPUS, at the UK Central Laser Facility gives academic and industry users access to a broad portfolio of advanced optical and electron imaging technologies together with the expertise to match technique to biological questions, and, where useful, to combine methods.

This poster showcases a set of case studies developed with our user community, organised around three imaging dimensions. Organisation: super-resolution methods including STED, STORM, SIM and MINFLUX resolve nanoscale molecular arrangement, while FIB-SEM and cryo-FIB-SEM extend this to ultrastructural context at the whole-cell scale — revealing distributions and architectures invisible to conventional confocal microscopy. Dynamics: the same technologies can be repurposed across temporal scales to capture changes over time. Light-sheet microscopy follows cellular and developmental processes over long timescales, while confocal and super-resolution imaging resolve equivalent dynamics over shorter, faster experiments with finer spatial detail. FLIM and FLIM-FRET add a temporal dimension to molecular interactions, and fluorescence fluctuation-based methods report on molecular dynamics such as diffusion. Mechanics: optical tweezers enable controlled manipulation of fluorescent objects and quantification of mechanical properties, while the same fluctuation- and lifetime-based methods quantify the resulting membrane biophysical response, including tension, lipid order and metabolic state.

Rather than a catalogue of instruments, OCTOPUS is a diverse technological toolkit paired with the expertise to adapt and combine methods for problems that resist a single conventional approach.

We hope these examples spark discussion on pushing established imaging technologies beyond their conventional applications, and we welcome discussion on opportunities for collaboration and technique-sharing across Nodes.

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#31

Image Data Services at Euro-BioImaging

Aastha Mathur, Euro-BioImaging

Euro-BioImaging ERIC is a European Research Infrastructure that democratises access to world-class imaging services ranging from nano to macroscopic scales. As of April 2026, it provides open access to over a hundred different state-of-the-art biological and biomedical imaging technologies through more than 295 individual imaging facilities hosted by national research institutions and universities across Europe. 18 European countries and the international organization EMBL have committed to jointly operate this pan-European research infrastructure. Euro-BioImaging ERIC - in addition to its imaging technology services - provides access to Image Data Services, which include coordinating user access for data services through Nodes, participation in data related European projects, community engagement, support for technical developments, including around uptake of NGFFs in imaging facilities, and image data stewardship. Euro-BioImaging plays a key role in representing the interests of the bioimaging community on a policy level as well as in the European Open Science Cloud (EOSC), while mediating the participation and uptake of the EOSC by imaging scientists. Together with the community, the aim is to create an ecosystem of FAIR image data and services and foster interactions among various stakeholders to shape the field.

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#32

Supporting the Preclinical Imaging Community: Euro-BioImaging's Open Tools for FAIR Animal Imaging Data

Feriel Ramdhane, Euro-BioImaging

Preclinical image datasets obtained from biomedical imaging modalities lack uniform standards and centralized platforms, making it challenging to query, find and aggregate data across studies. The FAIR principles are therefore scarcely implemented in the preclinical imaging domain while open access to research data is a priority for the European Commission. Consequently, the inability to effectively find and reuse datasets reduces the overall research efficiency and hampers the advancement of knowledge. Euro-BioImaging aims at facilitating the FAIRification of preclinical image datasets by developing and providing to researchers several open tools to address these issues.

We developed a containerized framework for quantitative MRI quality control, designed for scalable and reproducible assessment of large imaging datasets. The tool can be executed via command line using Docker or deployed within an XNAT instance as a containerized tool. The framework computes four quantitative image quality metrics and it has been validated in several preclinical projects of MRI datasets involving 72 subjects with 583 scans. Results are accessible through an integrated XNAT dashboard or as structured output files when running in standalone mode.

The XNAT for Preclinical Imaging Centers (XNAT-PIC), a free and open-source application to streamline the management of preclinical image data, has been improved to facilitate the upload of multi-modal imaging studies to the XNAT platform and by integrating editable custom forms to allow users to easily annotate information at subjects level. The XNAT-PIC tools have been packaged into a Windows desktop application and exploited for uploading and annotating 26 preclinical projects with a total of 140 subjects and 164 imaging sessions uploaded to our XNAT instance. We have developed several standardized, open-source tools for uploading, storing, querying metadata and analyzing/processing preclinical image datasets, providing valuable resources for the large preclinical imaging community.

Moreover, we developed PIDAR (Preclinical Image Dataset Repository), a public platform that collects and organizes metadata about preclinical imaging datasets linked to peer-reviewed publications to facilitate their findability. It covers all biomedical imaging modalities and uses a structured system built on 14 specialized ontologies to keep information consistent and searchable, covering everything from imaging techniques, animal species, and disease models to drugs, organs, genes, and cell lines. The platform also includes a pilot feature that lets users search public projects across different XNAT instances directly from the interface. The PIDAR repository is currently storing 28 preclinical imaging datasets that include 601 subjects and 218 metadata entries. Our open-source tools empower the preclinical imaging community to manage, share, and process animal imaging data across modalities.

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#33

Imaging 4 All: Global BioImaging Initiative Helps Expand Access to Imaging Expertise, Technologies and Training

Deniz Saltukoglu, Global BioImaging

Access to advanced imaging technologies and specialist expertise remains unevenly distributed worldwide, limiting the ability of many researchers to use bioimaging effectively in their scientific work. To help address this gap, Global BioImaging, with funding from the Wellcome Trust, established Imaging 4 All (i4A), a global mobility funding programme for researchers and imaging professionals affiliated with not-for-profit institutions in low- and middle-income countries (LMICs).

Imaging 4 All provides three complementary funding tracks—Access, Pro and Training—designed to respond to different scientific and professional development needs. Through these tracks, researchers can access imaging instrumentation and expertise for experimental projects, undertake hands-on training in imaging technologies and sample preparation at host facilities worldwide, or participate in specialised imaging courses.

Beyond supporting individual research and training activities, the programme aims to strengthen imaging capacity by connecting scientists in resource-limited settings with imaging facilities, experts and training providers across the international bioimaging community. The mobility-based model also creates opportunities for knowledge exchange, the development of new collaborations and the transfer of imaging expertise back to researchers' home institutions.

This poster will provide an overview of the i4A funding model and its three funding tracks, illustrate how the programme enables access to imaging technologies, expertise and training across international host institutions, and highlight examples of the different types of activities supported through the initiative.

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#34

Identification of SynGAP1 Missense Variant–Induced Deficits and Drug Screening Using Rodent Neuronal Imaging and Developed Image Analysis Algorithm

Dulashini Udawatta, Finnish Advanced Microscopy Node

In SynGAP1-related non-syndromic intellectual disability (NSID), loss of function of SynGAP1 leads to impaired synaptic development and disrupted cognitive processes. SynGAP1 is highly enriched in the postsynaptic density and plays a central role in regulating synaptic plasticity through dynamic localization. While truncation mutations lead to loss of function because nonsense-mediated decay will remove the affected mRNA, most mutations lead to a missense variation. Typically, however, it is unclear whether missense mutations lead to loss of function, and these are clinically categorized as “variants of uncertain significance” or VUS even when the affected patients have the symptoms of SynGAP1-NSID. These patients do not receive a diagnosis or mechanism for their symptoms and will be excluded from expression boosting therapies under development. Therefore, one unmet clinical need is disease-modifying therapies for pathogenic missense variants of SynGAP1 and a second is improving the clinical classification of VUS.

This study investigates the effects of SynGAP1 missense mutations on protein expression, subcellular localization, synaptic enrichment, and activity-dependent regulation. A total of 24 missense variants were selected from patient databases, spanning several functional domains of SynGAP1, including the PH, C2, GAP, CC, and PBM regions.

SynGAP1 variants are assessed using high-throughput image-based phenotyping, mechanistic assays, and advanced data analysis pipelines. Candidate repurposed drugs and a pilot library of compounds are screened to identify molecules capable of restoring healthy neuronal function. Hit identification and validation are performed using image analysis, incorporating developed analytical algorithms, and machine learning approaches to detect and quantify phenotypic changes.

High-throughput staining in 384-well format is performed to facilitate the direct correlation of live-cell phenotypes with molecular readouts of synaptic structure. By integrating functional and structural analyses, this approach is expected to provide deeper insight into the dominant-negative effects of pathogenic SynGAP1 variants at the cellular level.

As a mechanistic assay, an in-cell Bioluminescence Resonance Energy Transfer (BRET) assay was performed to evaluate the oligomerization ability of SynGAP1 variants located in the C-terminal region.

This study can support the development of more effective therapies, while analyzing pathogenic variants alongside VUS will generate evidence to contribute to internationally accepted clinical classification for disease diagnosis.

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#35

Tampere Imaging Facility – Advanced Light Microscopy Services for Research and Industry

Jenni Karttunen, Tampere Imaging Facility

Tampere Imaging Facility – Light Microscopy Core unit of Tampere University (Tampere, Finland) provides state of the art light microscopy services for academic and industrial users. The facility hosts various high quality imaging systems and offers expert user training as well as contributions to teaching at Tampere University. Our instrumentation includes five confocal microscopes, six widefield systems, and several specialized modalities such as TIRF, FLIM, and SIM. Typical application areas span 2D and 3D imaging of (bio)materials, organoids, body on chip systems, tissue sections, and small model organisms (zebrafish and Drosophila melanogaster).

The facility currently supports more than 200 active users representing over 30 research groups. In 2024–2026, we have also contributed to the project “A collaborative platform for accelerating biomedical research and development through providing advanced microscopy services”, funded by the European Regional Development Fund. The project strengthens collaboration between companies in the region and Tampere University’s light microscopy services, expanding access to advanced imaging technologies and expertise. Tampere Imaging Facility is also part of a national roadmap infrastructure Euro BioImaging Finland, uniting nine imaging organizations across seven universities and three university hospitals in Finland.

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#36

From Screening to Opportunistic Imaging: Hospitals as Imaging Data Ecosystems

Aikaterini Vraka, Radiology and Medical Imaging Valencia Node

The Radiology and Medical Imaging Valencia Node contributes to the development of imaging-based approaches for cancer screening, early detection and risk stratification by leveraging routinely acquired clinical imaging data. Through participation in local and European initiatives, the Node supports the creation and use of multicenter imaging repositories, longitudinal cohorts, screening studies and AI-assisted image analysis pipelines.

This poster highlights representative activities demonstrating how MRI and CT examinations acquired during routine clinical care can be repurposed beyond their original diagnostic indication. Particular emphasis is placed on opportunistic imaging, where quantitative image analysis and artificial intelligence enable the extraction of imaging biomarkers and predictive information from scans acquired for unrelated clinical purposes. These approaches expand the value of existing imaging data while supporting more proactive and personalized strategies for cancer detection.

The poster also showcases the Valencia Node's involvement in collaborative imaging infrastructures that promote harmonized datasets, reproducible AI development and multicenter validation of imaging biomarkers. These activities are aligned with ongoing European efforts to improve interoperability, data sharing and trustworthy clinical translation, while addressing challenges including data heterogeneity, annotation, governance and validation across institutions.

Overall, the poster illustrates how the Radiology and Medical Imaging Valencia Node contributes to transforming routine clinical imaging into a strategic resource for AI-enabled oncology research and future screening paradigms.

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#37

AI4Access: Connecting Research Questions with Euro-BioImaging Technologies, Expertise and Data Services

Sudeep Das, Euro-BioImaging

Finding the right imaging approach can be challenging, particularly for researchers unfamiliar with the available technologies. AI4Access aims to make Euro-BioImaging's services easier to discover and access, helping researchers connect their scientific questions with the technologies, expertise and support available across the network.

The project will develop the Research Navigator, an AI-powered conversational assistant which will transform the Euro-BioImaging Access Portal. Researchers will be able to describe their needs in everyday language and receive tailored, evidence-based guidance on suitable imaging methods, facilities, image analysis and data services, and training opportunities. By drawing on information validated by Nodes, scientific literature and previous research use cases, the Navigator will support users from initial exploration through to preparing access applications. Community participation will be central: researchers, Node staff and Hub teams will help identify user needs, contribute and validate service information, and test the Navigator through practical use cases. Through this collaborative approach, AI4Access will build on the network's collective expertise to strengthen access, support more effective use of imaging resources and help shape future services around emerging research needs. Transparency, explainability and expert oversight will underpin its development.

AI4Access aims to lower barriers for new users, broaden participation across disciplines and shorten the journey from research idea to experiment. Nodes and facilities will benefit from greater visibility of their services and expertise, better alignment between user requests and available capabilities, and support for preparing more complete access proposals.

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#38

Latest results from Nano-Bio-Imaging Core Facility

Szilvia Barkó[1], Krisztina Bánfai[1], Henriett Halász[1], Nikolett-Kis Bicskei[1], Géza Makkai[2], Tibor Jánosi[2] and András Lukács[1]

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We would like to report on two studies conducted in collaboration with the István Ábrahám Nanobioimaging Center. Both are associated with the Department of Biophysics in Pécs, where microbiological and optogenetic research is being performed that is likely to be of great interest in the future.

One topic relates to the bacterial cytoskeleton. As has been known for nearly thirty years, prokaryotes also possess a cytoskeletal protein like actin in eukaryotes, which is called MreB. In our experiments, we studied this protein using spectroscopic and microscopic methods and were able to provide a detailed description of a new interaction between this protein and an antibiotic—specifically, vancomycin.

The results are significant for two reasons. First, because they describe a completely new target for this antibiotic. Second, because the specific inhibition of this MreB protein makes Gram-negative bacteria—which are highly prevalent among multidrug-resistant bacteria—vulnerable to attack. Direct MreB-vancomycin binding was characterized using a fluorescently labeled vancomycin analog, through a series of microscopic and spectroscopic assays. Our SIM images clearly show that MreB, which is depolymerized in A22 *E. coli* cells, exhibits a fundamentally altered pattern compared to the control. In our opinion, this is the reason why the synergistic effect of the two agents inhibits bacterial growth even at very low concentrations, since without an intact cell wall, bacterial cells are unable to divide.

The other topic we would like to discuss is a new set of optogenetic tools that we believe will attract significant interest, much like GFP, and may even replace traditional fluorophores in some areas.
AvicFP and AausFP are families of fluorescent-protein (FP) homologs from jellyfish in the genus *Aequorea*, discovered in a study that looked beyond the canonical avGFP. The names refer to the source species: AvicFP is from *Aequorea victoria* and AausFP is from *Aequorea cf. australis*.
The particularly interesting member is AausFP1, because it has a quite different property from conventional GFP. AausFP1 is remarkable. It has a quantum yield of 0.97, meaning almost every absorbed photon that can produce fluorescence does so. Together those make it roughly 5× brighter per molecule than GFP. In our experiments, we fused this protein to the actin-binding Lifeact protein, and we observed that, compared to a classic (mCherry) fusion protein, although its localization is identical, this fluorescent protein is indeed quite unique in terms of its brightness.

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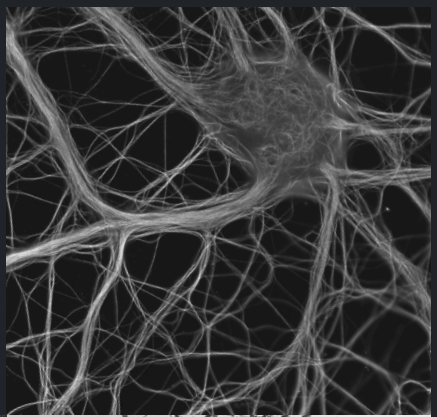

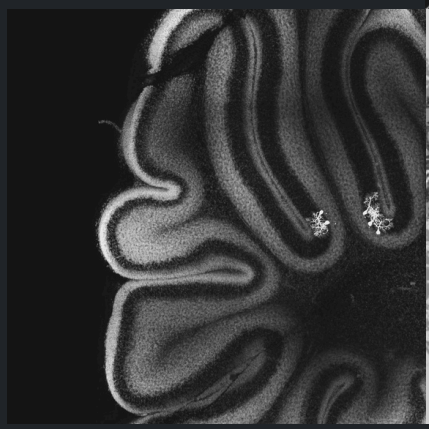

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