Poster Abstract Book

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

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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 foundation 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.

2. Founding GIDE ROCrate Profile: GIDE search portal development

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Part of the Founding GIDE project has been to create a combined search system over the databases of SSBD, IDR (Image Data Resource), and BIA (BioImage Archive) in order to enable researchers to efficiently find relevant data across all three repositories. To do so, we described database entries using detached ro-crate (research object crate) documents with a unified schema (an ro-crate profile). RO-crate is a community standard to describe the outputs of research to help users make their research FAIR (Findable, Accessible, Interoperable, and Reusable). It defines a standard for a linked-data json manifest that describes the files and datasets outputted by research projects, and the context of their creation. While ro-crates typically exist as part of file system structure, detached ro-crates are a way to remotely describe datasets on the web. In order to create a profile describing the shared structure we needed to use relevant RDF (resource description framework) properties for describing linked data on the web. This poster covers the details of the structure of the profile we developed, the ontologies and schemas from which re-used terms, and the design decisions we made prioritising Findability of the datasets.

3. Metadata harmonization for cross-repository discovery in bioimaging data resources

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As part of the foundingGIDE project, we have been working toward metadata harmonization across major bioimaging data resources to improve interoperability and cross-resource discovery. To date, we have conducted a comparative analysis of metadata components used by the BioImage Archive (BIA), the Image Data Resource (IDR), and the SSBD:database. Through this analysis, we identified overlaps and gaps among metadata models and defined key requirements for harmonizing bioimaging metadata across heterogeneous repositories. The outcomes of this work are reported in foundingGIDE Deliverable D6.1, which is publicly available on Zenodo (https://zenodo.org/records/16794787). Building on these results, we have also started an experimental effort to enable cross-repository search at the Study level across BIA, IDR, and SSBD (including both SSBD:repository and SSBD:database). In this activity, studies registered in SSBD are being described using the RO-Crate framework, providing a machine-readable and interoperable representation of study-level metadata. This work is being carried out under the lead of EMBL-EBI and aims to explore practical approaches for federated metadata exchange. In addition, SSBD:database is actively progressing the conversion and sharing of imaging data in the OME-Zarr format, supporting scalable access to large bioimaging datasets and aligning with cloud-native data practices. Together, these activities demonstrate concrete steps toward a harmonized bioimaging data ecosystem within foundingGIDE.

4. Depositing biological segmentation datasets FAIRly

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Key Techniques: volume electron microscopy; electron tomography; X-ray tomography
Keywords: Segmentation; annotation; artificial intelligence

Segmentation of biological images identifies regions of an image which correspond to specific features of interest, which can be analysed quantitatively to answer biological questions. This task has long been a barrier to conducting large-scale biological imaging studies as it is time- and labour-intensive. Modern artificial intelligence segmentation tools can automate this process, but require high quality segmentation data for training, which is challenging to acquire. Biological segmentation data has been produced for many years, but this data is not often reused to develop new tools as it is hard to find, access, and reuse. Recent disparate efforts [1-4] have been made to facilitate deposition and reuse of these valuable datasets, but more work is needed to increase reusability. This work reviews the current state of publicly available annotation and segmentation datasets and makes specific recommendations to increase reusability following FAIR (findable, accessible, interoperable, reusable) principles [5] for the future.

We found that amongst software papers, only 40% of surveyed publications used data collected in other studies, which was surprisingly low considering that software tools are generally developed for an established use case, so segmentation data likely already exists for the specific segmentation problem. Segmentation data was found in 32 different online repositories and 12 different file formats, complicating interoperability of these datasets as added effort is required to integrate the data into existing pipelines or combine different datasets for the same segmentation problem. Segmentation data which were most likely to be reused came from challenges. Of the 50 studies which reused data, 9 of them used the same challenge dataset (ISBI 2012 and SNEMI3D [6-7]), suggesting that challenges with clearly defined scopes, performance metrics, and easily accessible raw and label data have the most potential for reuse.

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5. IndiaBioimaging: The growing bioimaging network in India

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IndiaBioimaging as a community has made significant efforts in providing access to cutting edge microscopy facilities to everyone in India and has worked towards the standardization of microscopy training across India. Revitalized in 2024, it has made incredible progress in the last 2 years through the main and sub working group (WG) activities. The main working group has been instrumental in supervising different activities of the IBI including conducting the 1st IBI annual meeting at Mysore in December 2025 and registration of the Bioimaging Society, India in January 2026. The outreach and communications WG have been successful in highlighting the IBI activities and efforts on social media as well as developing a culture and capacity for bioimaging in India by initiatives such as Fluorescent Fridays and IBI webinar series. The training and workshop WG have contributed to conducting of basic and advanced microscopy courses across the country. In 2026, IBI plans to conduct 4 different microscopy courses in different parts of India including the “train the trainers” course for the very first time. In the next phase of its progress IBI is striving to consolidate academia-industry partnerships in the Indian ecosystem as well as continue to work on the democratization of imaging and microscopy in India.

6. Indian Biological Data Centre: Life Science Data Hub for Diverse Data Types

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Abstract

India's first national repository, the Indian Biological Data Centre (IBDC), manages, preserves, and shares various life science data for the scientific community. Rapid advancements in high-throughput technology generate massive amounts of heterogeneous data in several fields such as healthcare, genomics, proteomics, structural biology, metabolomics, bioimaging, phenomics, agriculture, and livestock studies. Effective data management requires a centralized infrastructure for uniform submission, curation, storage, and access. In 2022, the Department of Biotechnology (DBT), Government of India (GOI) formed the IBDC to address those requirements. The center is situated at the Regional Centre for Biotechnology (RCB) in Faridabad, Haryana, India. The IBDC is a life science data hub that supports many data types through domain-specific repositories (e.g., INDA, ICPD, IMDA, IPD, ISDA, IBIA, IPR, IADA). The center allows data sharing at national and international levels, adhering to international norms. The center is also creating tools for data curation, visualization, annotation, and analysis to improve the usefulness of stored datasets. To promote capacity building and community participation, IBDC offers guidelines, training materials, and assistance for researchers using high-performance computing (HPC). The effort is crucial for encouraging open science, reproducibility, and collaboration in life science fields. IBDC is a major step towards a strong national infrastructure for biological data management, expediting scientific discovery, and promoting data-driven innovation in healthcare, agriculture, and biotechnology. The IBDC website is available at https://ibdc.dbt.gov.in/.

7. Automated extraction of ontologies ID code from ontology web-based repositories based on metadata value

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Introduction: In data management, ontologies are critical for enhancing data interoperability, integration, and analysis across various domains and platforms [1]. This work presents a Python-based tool for the automatic mapping of metadata fields to standardized ontology terms.

Methods: We developed a Python-based tool using Flet to support the mapping of metadata extracted from a predefined Microsoft Excel template to ontology terms retrieved through the BioPortal Search API [2]. The system implements a three-step workflow. First, an Excel file containing metadata values (e.g., imaging modality, image coverage) is uploaded to the application. Second, each metadata value is queried against BioPortal to retrieve candidate ontology terms. Finally, the selected ontology codes and associated synonyms are exported into output files.

Results/Discussion: The implemented workflow generates a list of candidate ontology terms for each metadata term, from which users select the ontology code that best matches the context of the dataset. This approach supports more consistent ontology mapping. By combining automatic term retrieval with expert validation, the workflow simplifies the assignment of ontology codes to metadata terms, reducing mapping time while maintaining reliability and consistency.

Conclusion: The present tool aims to improve the findability and accessibility of preclinical image datasets by identifying and selecting a set of ontology codes and their synonyms that are useful to describe the variety and multi-domain information contained within the biomedical images, hence implementing the FAIR principles [3].

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8. A Reproducible Framework for Preclinical MRI Image Quality Evaluation for theXNAT platform

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Introduction:
Image quality is essential for reliable analysis in preclinical imaging studies. To support standardized and quantitative evaluation, we developed a set of Image Quality Assessment (IQA) tools integrated into the XNAT platform [1], with a focus on usability and seamless interaction for end users.

Methods:
We implemented multiple IQA tools, including Signal-to-Noise Ratio (SNR), Sharpness Index (SI) [2], Mutual Information (MI) [3], and Rician noise estimation for MRI data [4]. The tools were developed in Python and Matlab, and deployed as Docker containers within the XNAT platform. A user-friendly interface was designed to allow users to easily select and run specific IQA tools at either scan or subject level. Outputs are automatically stored within XNAT, ensuring traceability and data organization.

Results:
The outputs of the IQA containers are generated as downloadable PNG plots and Excel files containing summary statistics . All results are directly accessible within XNAT and could be easily downloaded by users for further analysis. The framework was evaluated on a preclinical MRI dataset comprising 2000 DICOM images (T1w, T2w, and CEST). Image quality classification was performed using the interquartile range (IQR) and outlier detection.

Conclusion:
We developed an open-source, XNAT integrated IQA framework tailored for preclinical MRI imaging, with a strong emphasis on ease of use and reproducibility. The platform enables users to efficiently run quality assessment tools, manage outputs, and download results, facilitating standardized image quality evaluation in preclinical research.

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9. The MicroMundo Project: a virtual microscope for everyone

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Most microscopic image repositories are fee-based, in English, or focused on animal or human pathology, which difficult their use in Spanish/Portuguese-speaking educational settings and limits their potential as teaching tools.

MicroMundo started as user-friendly virtual microscopy solution for Chilean secondary schools. This platform already hosts a library of high-resolution digital slides allowing students to zoom, annotate and explore various specimens at multiple magnifications.

We now want to expand this platform, so that it becomes a collaborative public platform for virtual microscopy based on an open, accessible, verified and sustainable repository that enables the conservation, organization and dissemination of biological samples and data not only for schools but also for universities, clinical and environmental health organizations.

At the end of the project, it is expected that the samples available in the repository will be increased and diversified in order to achieve greater reach and relevance over time for both local and regional communities.

10. Small data, big borders: a differentially private federated meta-learning framework for cross-institutional cancer imaging in Southeast Asia

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Abstract:
Southeast Asia carries a rapidly rising cancer burden against a backdrop of fragmented registries, heterogeneous imaging workflows, and strict cross-border data governance. Conventional federated learning architectures assume data-rich, well-harmonised repositories which is a condition rarely met across low-to-middle income country institutions where small patient cohorts, inconsistent metadata schemas, and national data sovereignty regulations preclude centralised model training.

We present PPCR-ML (Privacy-Preserving Cross-Registry Meta-Learning), a federated architecture combining Model-Agnostic Meta-Learning (MAML) with differential privacy (ε-DP) to enable cross-institutional cancer imaging model training without raw data leaving institutional nodes. Each country-cancer-type combination is treated as a distinct meta-learning task; the system learns a globally generalisable initialisation θ that participating institutions rapidly adapt with minimal local data. Differential privacy is enforced at the gradient level (ε=1.0, δ=1e-5), with per-round privacy budget tracked and auditable. This framework is compatible with national data protection regulations across Malaysia, Vietnam, and Thailand.

An MVP deployed on AWS (EC2, SQS, Lambda, S3) uses three placeholder nodes holding population-matched synthetic breast cancer cohorts representing institutional repositories in Malaysia, Vietnam, and Thailand. New sites can be integrated as additional meta-learning tasks without architectural changes or retraining. This work presents a replicable, cloud-native blueprint for privacy-preserving federated AI in underrepresented regional health contexts, with a clear pathway to real institutional deployment.

11. Global BioImaging: Driving Global Image Data Practices

Global BioImaging (GBI), coordinated by European Molecular Biology Laboratory (EMBL), connects imaging infrastructures and communities across **70+ countries and 15 partner networks**. As the **"Global" in the Global Image Data Ecosystem (GIDE)**, GBI brings foundingGIDE resources and achievements to a worldwide audience, gathering insights on bottlenecks, challenges, and opportunities for interoperable image data practices.
Through its **International Data Working Group (WG)**, training programs and job shadowing opportunities, GBI develops recommendations, engages with experts and developer communities, and promotes best practices for metadata, formats, and analysis tools. By connecting regional initiatives with global stakeholders, GBI fosters solutions that are practical, inclusive, and ensure that image datasets remain reusable, reproducible, and accessible across borders.
GBI'Spotlight 2026 launches this year with a focus on **"Managing Image Data is a Marathon: Ten Simple Steps for Running Durable and Sustainable Research Data Management in Bioimaging"**. The initiative provides a *live platform* across two time zones to share experiences, advance training, and strengthen global collaboration in image data management.

12. Creating an AI-Powered Ecosystem for Open Science in Mexico

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Newly founded, one of Mexico Bioimaging's first priorities is promoting the creation The International Hub for Data Science, starting with a Bioimaging Node at the Centro Internacional de Ciencias in Morelos, Mexico. Early priorities for this initiative are to integrate AI into open scientific workflows with tools for metadata enrichment, reproducible analysis, and collaborative knowledge discovery, supported by robust education, interdisciplinary networks, and FAIR principles. By addressing critical infrastructure and workforce gaps, the Hub will empower Latin American researchers to build a cohesive, globally connected scientific community.

13. PIDAR: A FAIR Metadata Repository with Ontology-Driven Search and XNAT Integration for preclinical image datasets

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Introduction:

Preclinical imaging datasets are increasingly hosted on XNAT instances, yet their contextual metadata remains scattered and poorly standardized, limiting their reuse and interoperability. We developed PIDAR (Preclinical Image DAtaset Repository), a FAIR-compliant web platform that addresses both challenges: it catalogs richly structured, ontology-coded metadata for preclinical imaging datasets and provides a dedicated interface for browsing datasets deposited in connected XNAT instances.

Methods:

An ontology landscape analysis was conducted, from which 14 ontologies were selected to standardize key metadata fields, including NCIT (imaging modality, species, genotype), ChEBI (drugs, anesthetics, contrast agents), DOID (disease models), CLO (cell lines), EFO (strains), UBERON (organs/tissues), OBI (procedures), GO (genes), and MP (immune status). A XNAT integration pilot web page has been developed to query public projects in two XNAT instances.

Results:

PIDAR currently indexes 28 datasets covering 601 subjects across 218 metadata fields. The ontology-aware search allows users to query datasets using standard codes or synonyms across all 14 ontologies. The XNAT integration page enables researchers to browse public projects from XNAT instances and navigate directly to their associated PIDAR metadata entries. The platform is publicly available at https://pidar.hpc4ai.unito.it.

Conclusion:

PIDAR combines a structured ontology schema, derived from a systematic landscape analysis, with a live connection to world-wide accessible XNAT instances. This repository makes preclinical imaging datasets more findable, better described, and directly linkable to their raw data, advancing FAIR principles across the preclinical imaging community.

Acknowledgements:

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14. Czech BioImaging Data Repository as an international BioImage Data Infrastructure Node

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Under the umbrella of the European Open Science Cloud (EOSC) we are establishing a new repository for FAIR-sharing of biological image data. Initiated with the Czech BioImaging community, it will eventually serve all researchers in the Czech Republic integrating their outputs into the international bioimage data infrastructure. During development we prioritized metadata conceptualization as a critical step to ensure consistency and cross-domain interoperability. We adopted the Czech Core Metadata Model[1] (CCMM), an application profile based on DCAT-AP with native DataCite support. This enables seamless metadata harvesting from local repositories into the National and European Open Data Catalogues. To address domain-specific needs, we extended CCMM[1] with elements based on the Recommendations for Metadata in Biological Imaging[2], utilizing the Dataspecer[3] tool to maintain the linked data approach for semantic web operability. Our application profile treats metadata as provenance information using “activity“ as a core element. Combined with hierarchical structure inspired by the ISA framework, this allows for both horizontal and vertical organization of records. To ensure persistent identification, we implement a dual-identifier system: ePIC identifiers for granular technical records and DOIs for comprehensive datasets and scientific studies. In this poster, we demonstrate how this model ensures high-quality, interoperable, and FAIR-compliant data management for biological imaging.

This output was developed with financial contributions from the EOSC CZ initiative through the National Repository Platform for Research Data project (CZ.02.01/00/23_014/0008787), funded by the Operational Programme Johannes Amos Comenius of the Ministry of Education, Youth and Sports of the Czech Republic.

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15. Data generation for whole-body super-resolution imaging across entire vertebrate bodies

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Achieving nanoscale-resolution imaging across entire vertebrate bodies remains a major challenge in biological imaging. While conventional microscopy can capture molecular or anatomical information at high resolution within limited fields of view, it is difficult to extend this capability to whole organisms or large developmental specimens. This limitation is especially pronounced in embryos and neonatal animals, where body size, tissue density, and anatomical complexity change rapidly during development. In this talk, I will introduce a new imaging technique, termed whole-body expansion microscopy, that enables nanoscale-resolution imaging of anatomical structures across entire vertebrate bodies. This approach allows uniform expansion of whole mouse embryos, as well as tissue slices from neonatal mice. A key innovation is the use of cyclic digestion, with the number of digestion cycles adjusted according to developmental stage. During mouse embryonic development, body weight and size increase dramatically from day to day. Tissue composition also changes substantially, including a marked increase in skeletal and other dense structures. To enable uniform expansion across such diverse specimens, we developed a cyclic digestion strategy in which each cycle consists of proteinase K treatment followed by collagenase treatment. This cycle is repeated as needed, with only the number of cycles varied according to embryonic age. Using this approach, we show that anatomical structures in mouse embryos and neonatal mice can be imaged at nanoscale resolution across entire bodies.

16. Standardising electron microscopy acquisition metadata

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- European Molecular Biology Laboratory, https://ror.org/03mstc592
- VIB Leuven, https://ror.org/045c7t348
- CEA Grenoble, https://ror.org/02mg6n827
- Delft University of Technology, https://ror.org/02e2c7k09
- EMBL European Bioinformatics Institute, https://ror.org/02catss52
- Frederick National Laboratory for Cancer Research, https://ror.org/03v6m3209

The imaging community aims to make data FAIR at all levels of the data life cycle. This involves transitioning from proprietary to open-source data and metadata formats. OME-Zarr is the prefered choice but requires metadata standardisation for different imaging modalities. Together with imaging data specialists from EMBL, NIH, VIB and VolumeEM community, we launch a project on standardising electron microscopy acquisition metadata. The goal is to collect examples of raw metadata from different instruments to develop a minimal schema ready for implementation in future OME-Zarr 1.0, compliant with BioImage Archive REMBI schema. Consequently, we aim to submit a technical article manuscript and an OME-Zarr RFC by the end of 2026. Meanwhile we welcome any suggestions, collaborations and synergies.

17. **BioImage Archive and EMPIAR:** Making bioimaging data FAIR, explorable, and reusable

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The BioImage Archive (BIA) and the Electron Microscopy Public Image Archive (EMPIAR) are complementary EMBL-EBI resources that support open biological imaging data across modalities and scales. BIA covers biological image data broadly, while EMPIAR focuses on electron microscopy image data supporting 3D cryo-EM maps, tomograms, volume EM and X-ray tomography datasets. Together, these resources underpin reproducibility, method development, benchmarking, training, and the growing reuse of imaging data for AI and machine learning.

A recent beta release of the BioImage Archive places greater focus on visual exploration of datasets. Selected datasets were converted to OME-Zarr, enabling cloud-based streaming and interactive viewing in the browser. This allows users to inspect and assess image data visually, without requiring local high-performance computing, before deciding which datasets to download or analyze further. The updated platform also strengthens data discovery through improved search and image-centered browsing, including galleries that organize datasets of particular interest, such as AI-ready and spatial omics data.

Beyond deposition and access, BIA and EMPIAR also support community training through openly available tutorials and materials covering discovery, visualization, submission, metadata standards and reuse. Together, these resources illustrate how imaging archives can go beyond repositories of record into more explorable, interoperable, and AI-ready infrastructure for the life sciences.

18. EDAM Bioimaging: enabling findability and provenance of image data and image analysis tools

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EDAM Bioimaging is an ontology dedicated to bioimage informatics, and imaging in general [1]. It has been developed in an open global collaboration, involving consortia such as ELIXIR Europe and the NEUBIAS and COMULIS projects, members of Euro-BioImaging, Global BioImaging, Australian BioCommons, and numerous experts from diverse subdomains of bioimaging.

Following the input from QUAREP-LiMi and the foundingGIDE hackathon in 2024, the hierarchy of imaging modalities in EDAM has received major improvements and refinements. After the *alpha* release towards a full-production version in 2025, we have been in the process of further polishing and recently finally assigning persistent identifiers to all concepts, and hoping for an additional community review during the foundingGIDE hackathon 2026. EDAM Bioimaging will continue evolving in the future, with a growing and diversifying community of contributors. It is used for example in BIII, the registry of bioimage analysis tools, workflows, and training materials [2], and recommended as one of the essential ontologies for image metadata in REMBI (Recommended Metadata for Biological Images) [3].

EDAM Bioimaging is crucial for FAIR image data, imaging services, software, publications, data, workflows, and learning materials. By enabling findability and provenance of all such kinds of resources related to bioimaging, EDAM contributes to fostering open science and reproducible image analysis.

The latest release of EDAM Bioimaging is always browsable on the NCBO BioPortal. The very latest, unreleased “collaborative development” version can be viewed and commented on WebProtégé (free registration required). New contributors are very warmly welcome!

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19. Microscopy Australia: OPEN ACCESS INSTRUMENTS AND EXPERTS

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Microscopy Australia, established in 2007, is a consortium of university-based microscopy facilities united by values of collaboration, accessibility, excellence and innovation. Each year, over 4,000 researchers from universities and industry use our instruments and expertise in facilities around Australia. Over 50,000 trainee microscopists around the world use our online training tools each year: Myscope.

Microscopy Australia (ROR ID: https://ror.org/042mm0k03) is enabled by the National Collaborative Research Infrastructure Strategy (NCRIS), state governments and participating institutions. We report high-impact science outcomes from this investment in our annual Research Highlights and online news. We also engage the public in science with unique exhibitions and learning resources.

Microscopy Australia enables access to an array of high-end microscopy platforms and associated scientific expertise in strategic locations to efficiently service Australia's microscopy needs. Microscopy Australia provides professional development opportunities for our scientific staff, and has formal connections with a range of other specialised linked laboratories.

Keywords: Network; Collaboration; Australia

20. Euro-BioImaging Image Data Services

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 standardised community driven data and metadata formats 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 these activities place Euro-BioImaging in a unique position to influence, adopt and disseminate practices that make the data and data handling processes ready to interface with cutting edge AI methods. Together with the community, our aim is to create an ecosystem of FAIR image data and services and foster interactions among various stakeholders to shape the field.