

# The Missing Link in Bioimage AI? Empowering Experimental Scientists to Generate and Share FAIR Data

Caterina Strambio-De-Castillia



Shenzhen Bay Laboratory + SMART  
Shenzhen, 3/18/2026



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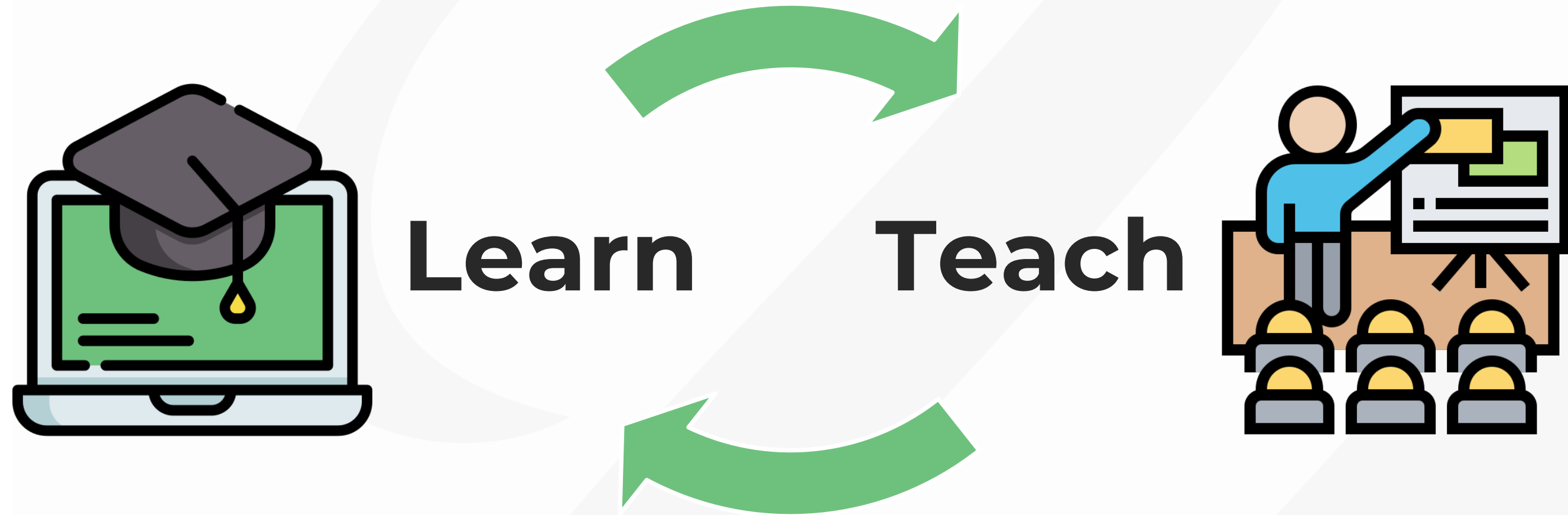


# Advancing science and technology together by building bridges





# Why I love being here!



# Why I love being here!

Walking in  
each other  
shoes... and  
helping each  
other!

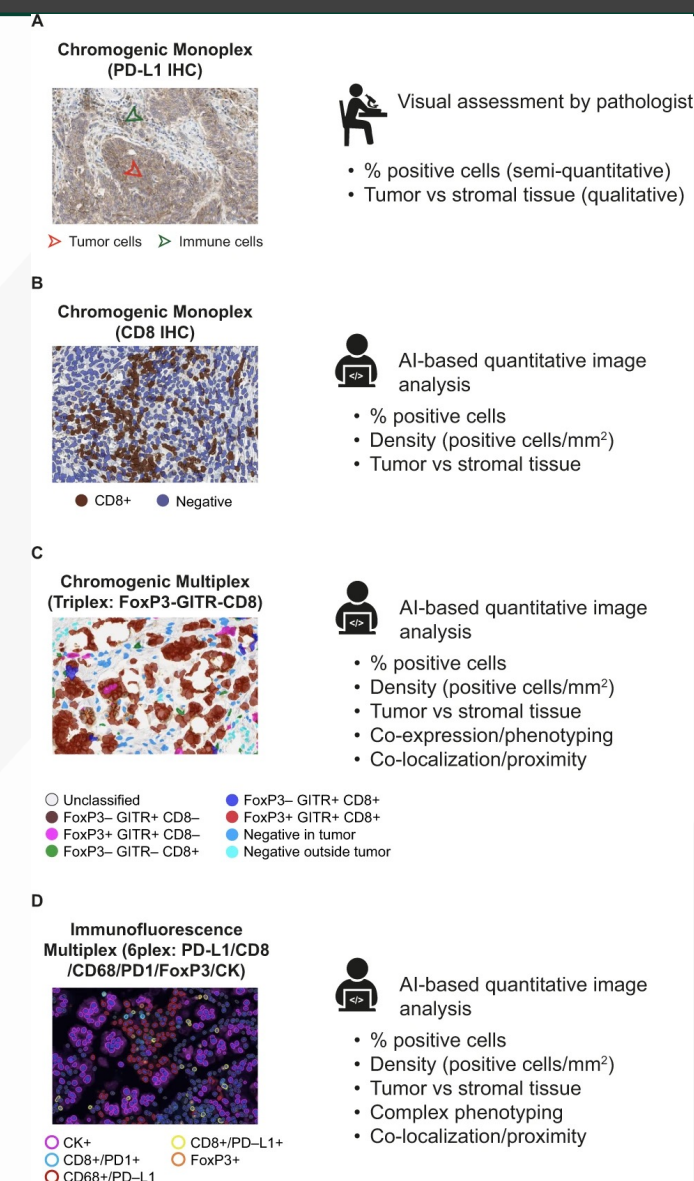
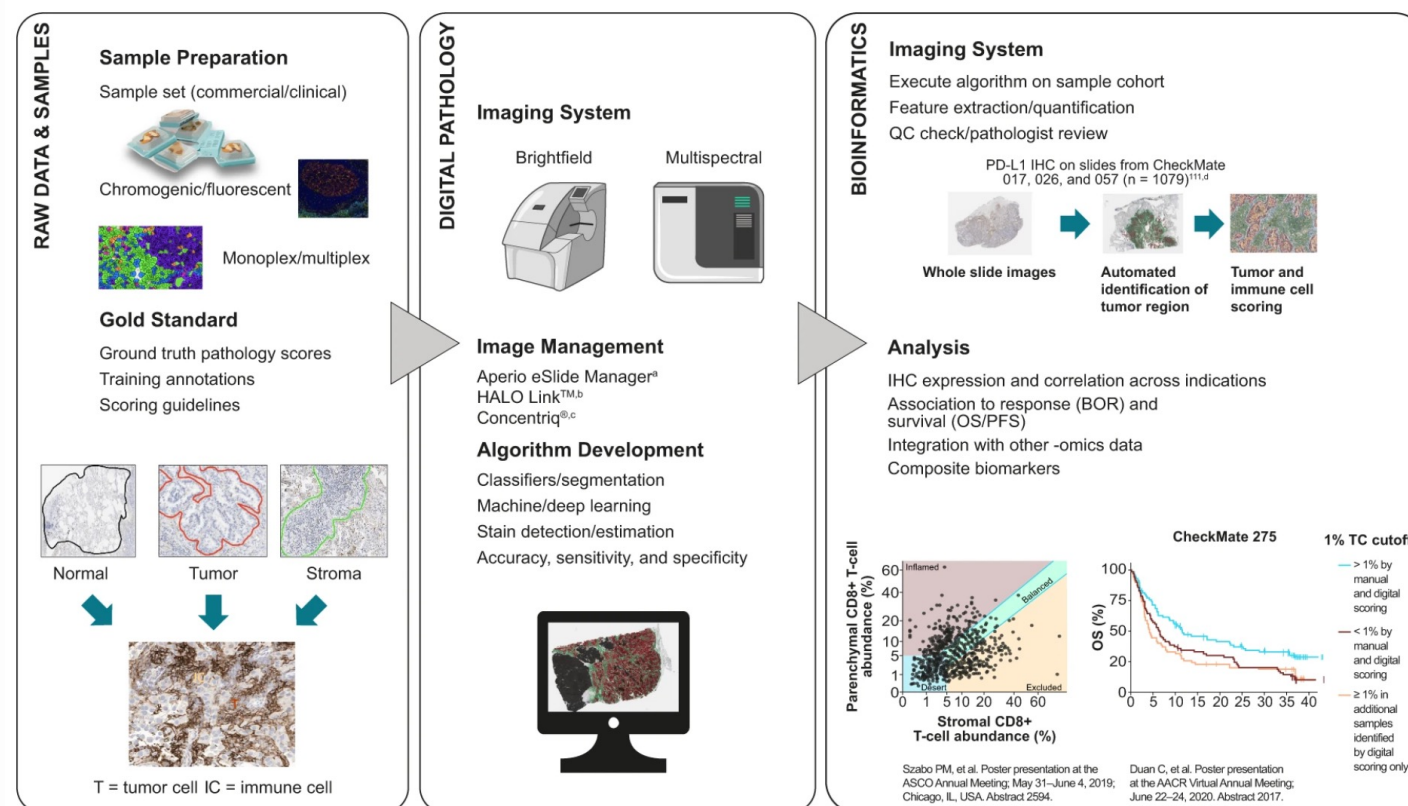


# AI has huge potentials in bioimaging

## Digital pathology and artificial intelligence in translational medicine and clinical practice

[Vipul Baxi](#) , [Robin Edwards](#), [Michael Montalto](#) & [Saurabh Saha](#)

[Modern Pathology](#) **35**, 23–32 (2022) | [Cite this article](#)



# AI has huge potential in image-based spatial-omics...

- Enhancing data analysis
- Facilitating the integration of diverse data types
- Enabling 3D reconstruction

Comment | Published: 09 August 2024

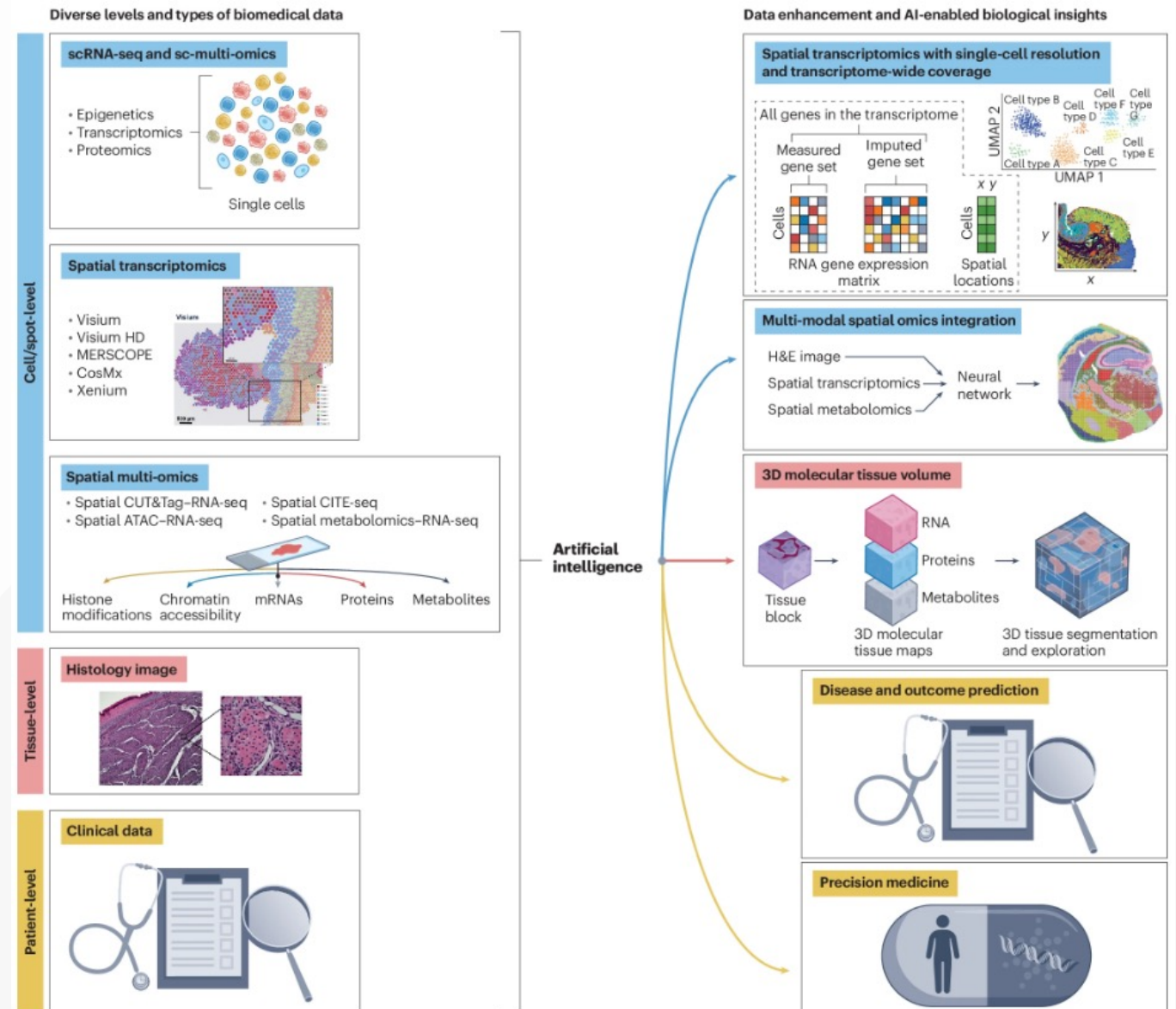
## Unlocking the power of spatial omics with AI

[Kyle Coleman](#), [Amelia Schroeder](#) & [Mingyao Li](#) 

[Nature Methods](#) 21, 1378–1381 (2024) | [Cite this article](#)

8696 Accesses | 37 Altmetric | [Metrics](#)

<https://doi.org/10.1038/s41592-024-02363-x>





# AI models can be shared but they required standards

**AI MODELS AND METHODS FOR THE LIFE SCIENCES**

Research services and infrastructure to support life scientists in the adoption of machine learning solutions that improve the utility and interpretability of image data – the key to future biological and biomedical research.

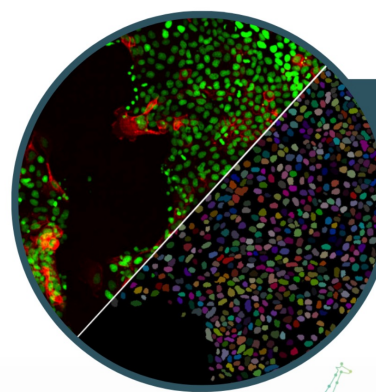
**BRIDGING THE LIFE & COMPUTER SCIENCE COMMUNITIES**



**AI4Life**

LIFE SCIENCE COMMUNITY | SOFTWARE | AI MODELS | STANDARDS | AI METHODS | COMPUTER SCIENCE COMMUNITY


**OPEN CALL**  
for BioImage Analysis Support



**SGEF, a RhoG-specific GEF, regulates lumen formation and collective cell migration in 3D epithelial cysts**

Madeline Lovejoy and Rafael Garcia-Mata (PhD)  
The University of Toledo, Garcia-Mata Lab

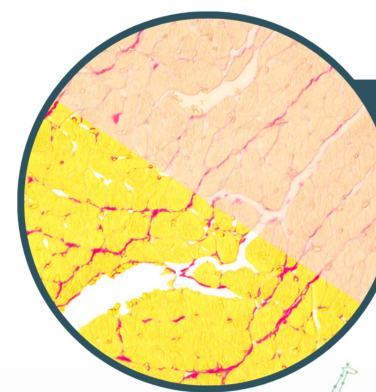
tracking instance segmentation



**AI4Life**

ai4life.eurobioimaging.eu | ai4life@eurobioimaging.eu


**OPEN CALL**  
for BioImage Analysis Support



**Treat Chronic Kidney Disease**

Nathalie Gayraud, Juliana Boukhaled, Irene Cortijo  
RD Néphrologie (France)

semantic segmentation quantification



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**OPEN CALL** BioImage Analysis Support



**Apply by December 10**

Do you need help applying Deep Learning to your research?

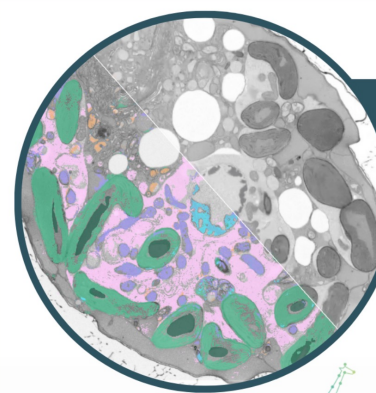


**AI4Life**

ai4life.eurobioimaging.eu | <https://bit.ly/AI4Life-3rd-open-call> | ai4life@eurobioimaging.eu

Funded by the European Union


**OPEN CALL**  
for BioImage Analysis Support



**Atlas of microalgae in plankton symbioses revealed by 3D electron microscopy**

Johan Decelle, Ananya Rao Kedige, Gaëlle Toullec  
LPCV, CNRS (France)

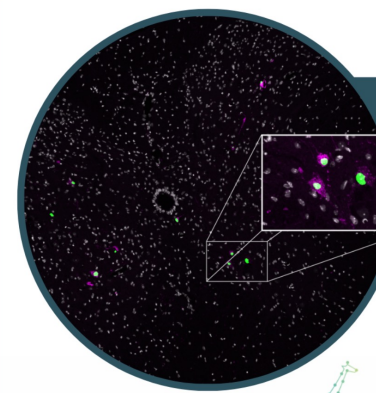
semantic segmentation 3D images



**AI4Life**

ai4life.eurobioimaging.eu | ai4life@eurobioimaging.eu


**OPEN CALL**  
for BioImage Analysis Support



**Identifying senescent cells through fluorescent microscopy**

Ana Filipa Isidro  
Instituto de Medicina Molecular João Lobo Antunes (Portugal)

detection instance segmentation quantification



**AI4Life**

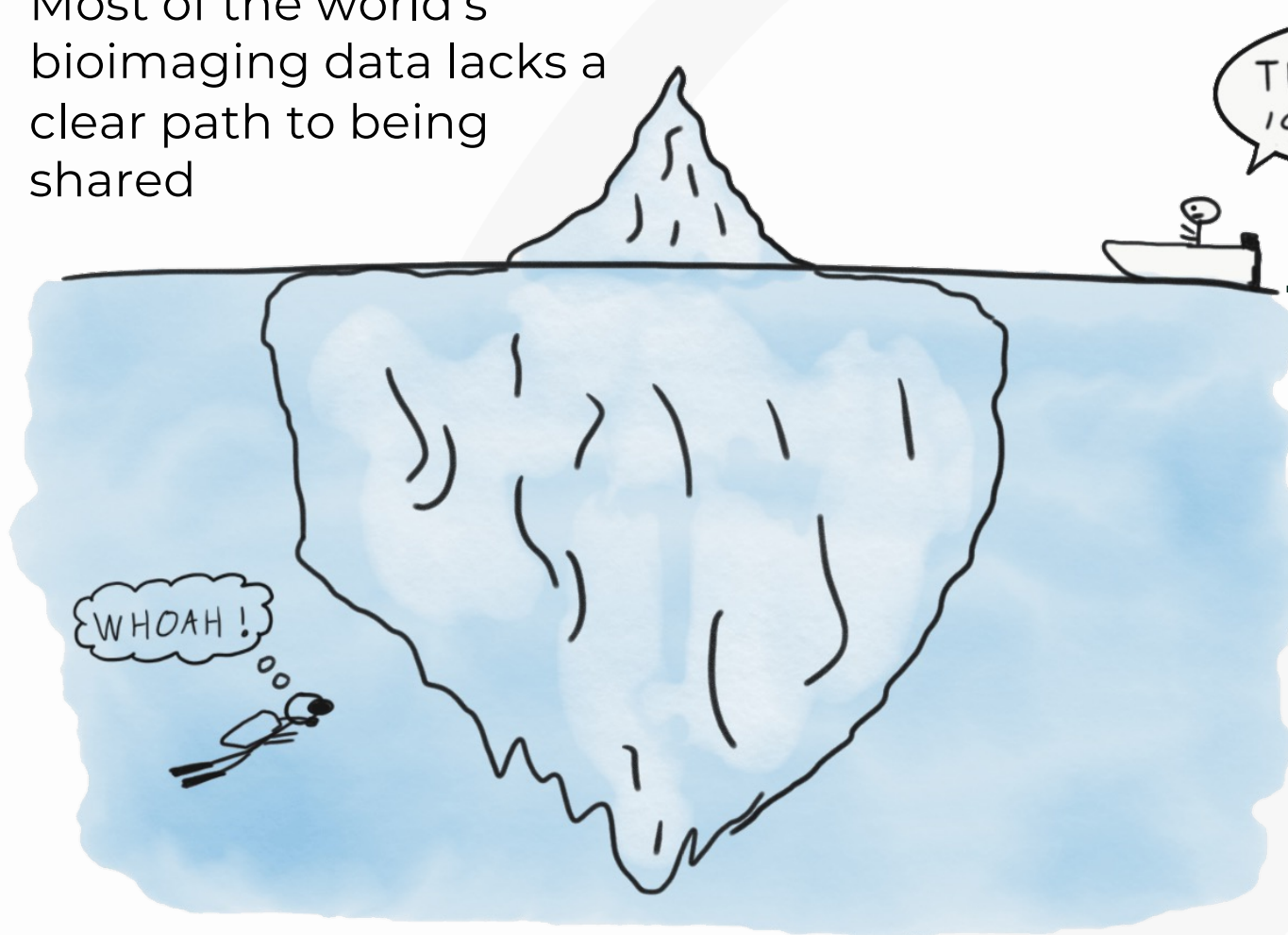
ai4life.eurobioimaging.eu | ai4life@eurobioimaging.eu

<https://ai4life.eurobioimaging.eu/>

<https://ai4life.eurobioimaging.eu/create-your-website-with-blocks/open-calls/use-cases/>

# Bioimaging AI dirty little secret: without Findable Accessible Interoperable Reusable (FAIR) data is just fancy math

Most of the world's bioimaging data lacks a clear path to being shared



## AI implementation ...

### ... Data requirements for AI

- Restricted access to biological images and their metadata inhibits the development of robust and generalizable models,
- This decreases the accuracy and performance of AI applications in bioimaging
- There are rarely comprehensive metadata associated with image data
- The lack of semantic data integration means AI can't assign meaning to bioimages.



# Research Data Management and Sharing for Images: make it possible and make it easy

**OPEN 2018** <https://doi.org/10.1038/s41592-018-0195-8> **comment**

**2021** <https://doi.org/10.1038/s41592-021-01113-7> **Check for updates**

**nature methods**  
**Perspective** <https://doi.org/10.1038/s41592-024-02585-z>

## Enabling global image data sharing in the life sciences

Received: 12 February 2024  
Accepted: 3 December 2024  
Published online: 28 March 2025  
**Check for updates**

**Peter Bajcsy**<sup>1</sup>, **Sreenivas Bhattiprolu**<sup>2</sup>, **Katy Börner**<sup>3</sup>, **Beth A. Cimini**<sup>4</sup>, **Lucy Collinson**<sup>5</sup>, **Jan Ellenberg**<sup>6</sup>, **Reto Fiolka**<sup>7</sup>, **Maryellen Giger**<sup>8</sup>, **Wojtek Goscinski**<sup>9</sup>, **Matthew Hartley**<sup>10</sup>, **Nathan Hotelling**<sup>11</sup>, **Rick Horwitz**<sup>12</sup>, **Florian Jug**<sup>13</sup>, **Isabel Kemmer**<sup>14</sup>, **Anna Kreshuk**<sup>5</sup>, **Emma Lundberg**<sup>15,16</sup>, **Aastha Mathur**<sup>14</sup>, **Kedar Narayan**<sup>17,18</sup>, **Shuichi Onami**<sup>19</sup>, **Anne L. Plant**<sup>1</sup>, **Fred Prior**<sup>20</sup>, **Jason R. Swedlow**<sup>21</sup>, **Adam Taylor**<sup>22</sup> & **Antje Keppler**<sup>14</sup>✉

Cornell University

We gratefully acknowledge support from member institutions

**arXiv** > q-bio > arXiv:2401.13022

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**Quantitative Biology > Other Quantitative Biology**

[Submitted on 23 Jan 2024 (v1), last revised 30 Aug 2024 (this version, v5)]

## Harmonizing the Generation and Pre-publication Stewardship of FAIR Image Data

Nikki Bialy, Frank Alber, Brenda Andrews, Michael Angelo, Brian Beliveau, Lacramioara Bintu, Alistair Boettiger, Ulrike Boehm, Claire M. Brown, Mahmoud Bukar Maina, James J. Chambers, Beth A. Cimini, Kevin Eliceiri, Rachel Errington, Orestis Faklaris, Nathalie Gaudreault, Ronald N. Germain, Wojtek Goscinski, David Grunwald, Michael Halter, Dorit Hanein, John W. Hickey, Judith Lacoste, Alex Laude, Emma Lundberg, Jian Ma, Leonel Malacrida, Josh Moore, Glyn Nelson, Elizabeth Kathleen Neumann, Roland Nitschke, Shuichi Onami, Jaime A. Pimentel, Anne L. Plant, Andrea J. Radtke, Bikash Sabata, Denis Schapiro, Johannes Schöneberg, Jeffrey M. Spraggins, Damir Sudar, Wouter-Michiel Adrien Maria Vierdag, Niels Volkmann, Carolina Wählby, Siyuan (Steven) Wang, Ziv Yaniv, Caterina Strambio-De-Castillia

Together with the molecular knowledge of genes and proteins, biological images promise to significantly enhance the scientific understanding of complex cellular systems and to advance predictive and personalized therapeutic products for human health. For this potential to be realized,

Federated  
Network of Image  
Data Repositories

**Ecosystem  
for FAIR  
Image Data**

Generation of  
bioimage data that  
is FAIR from the  
ground-up



**BioImaging  
North America**

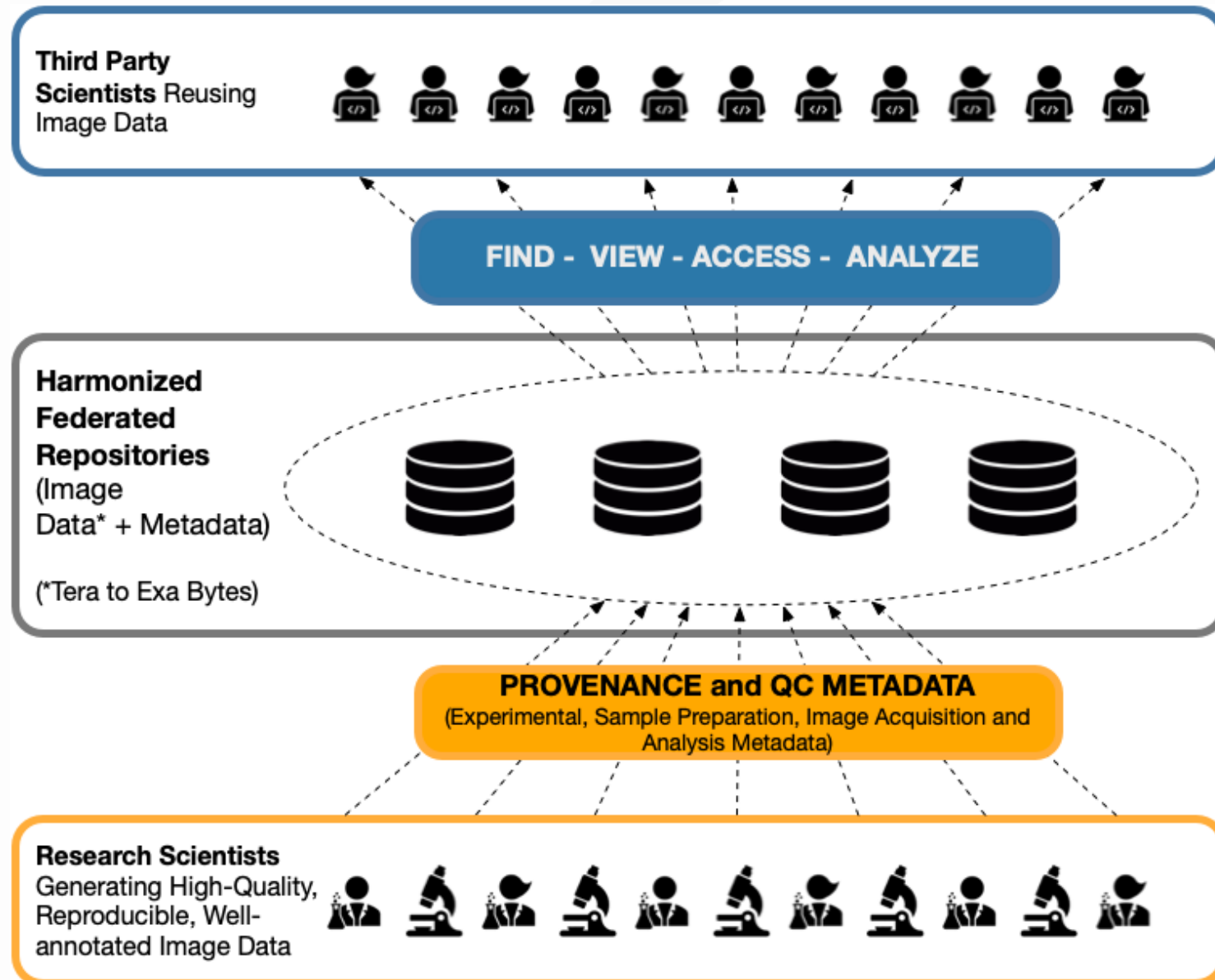


**foundingGIDE**

**GLOBAL  
BIOIMAGING**  
growing collaboration



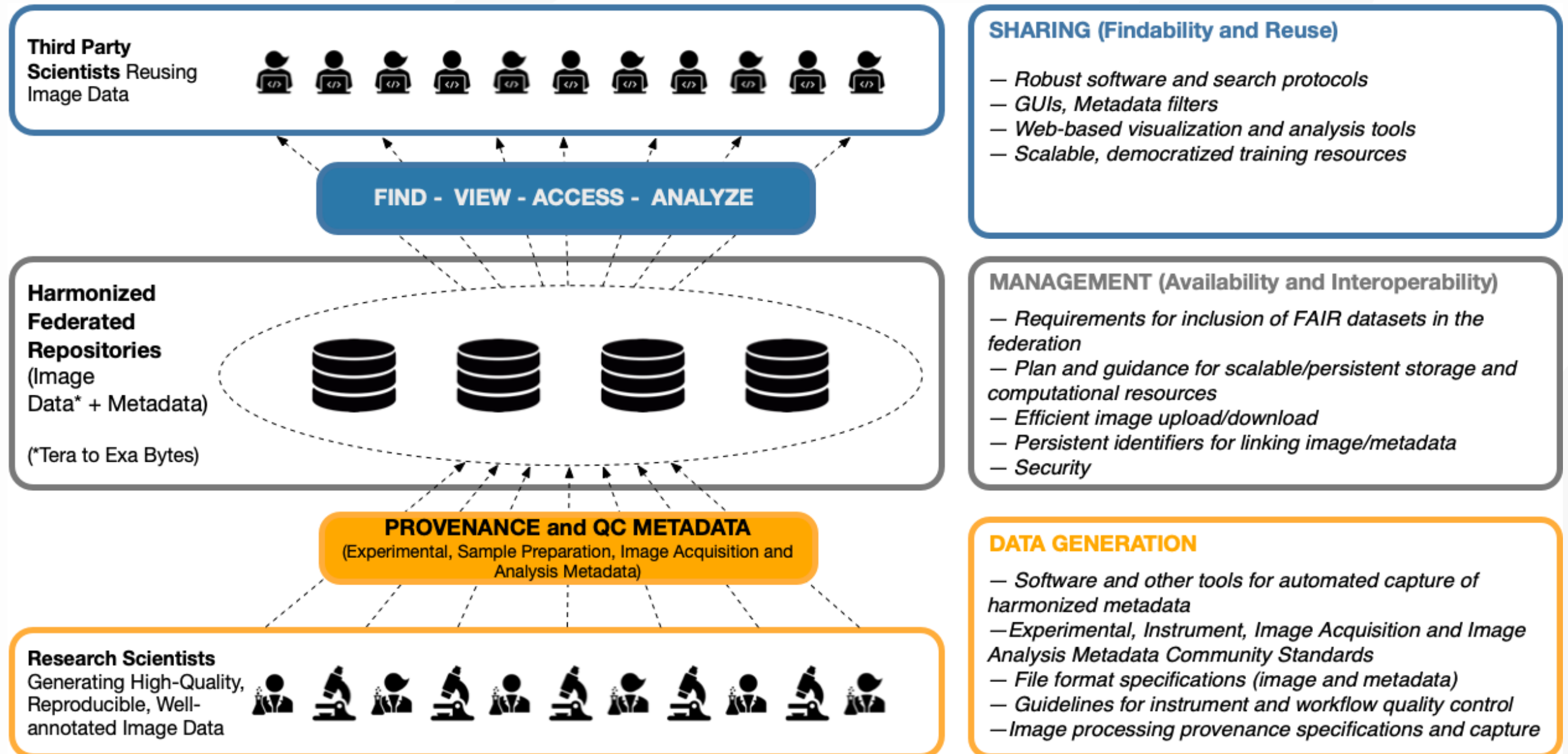
# Building a Global Ecosystem for FAIR Image Data: the vision



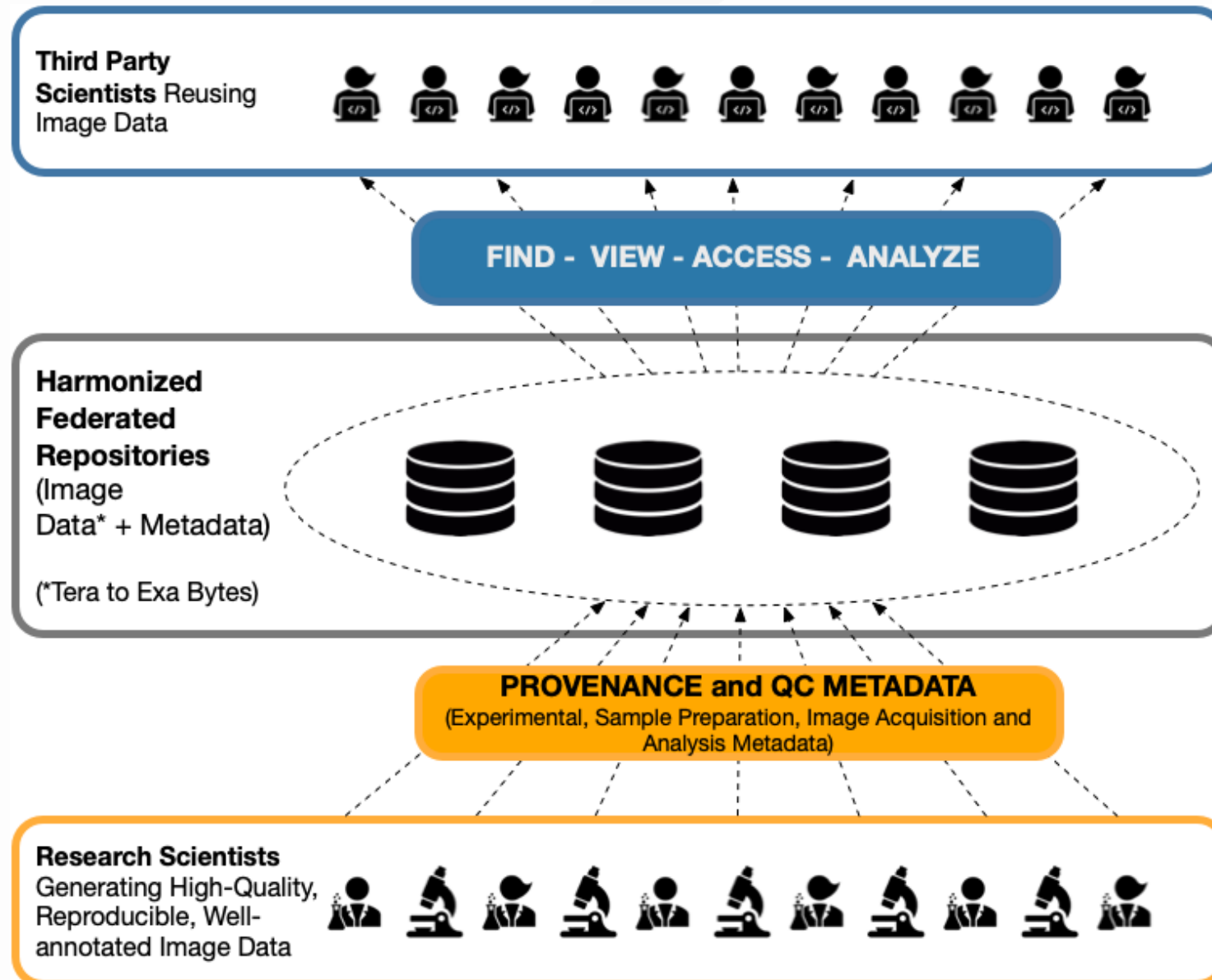
*Make biological images widely accessible and reusable by establishing a Global Image Data Ecosystem built on FAIR (Findable, Accessible, Interoperable, Reusable) principles.*

*The vision is to build a federated network of high-quality, publicly available FAIR image repositories,*

# Building a Global Ecosystem for FAIR Image Data: what is needed



# Building a Global Ecosystem for FAIR Image Data: stakeholders



- Research Scientists
- Imaging Scientists
- Core Facilities
- Manufacturers
- Standards Organizations
- Institutions
- Funders

**Strong Community Efforts**



# Towards a Global Image Data Ecosystem



A CORNERSTONE IN BIOIMAGE DATA SHARING

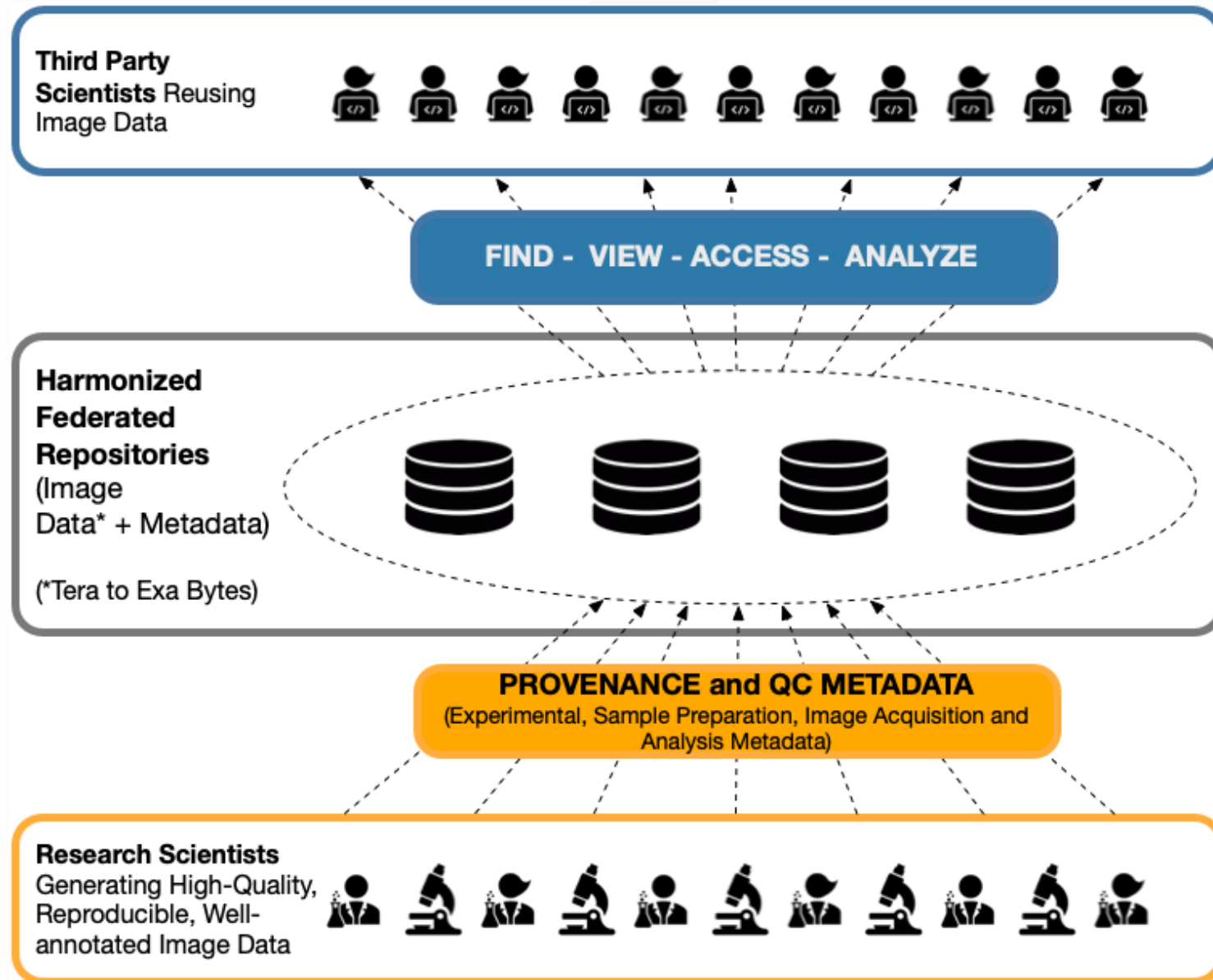
## Founding a Global Image Data Ecosystem

foundingGIDE is enabling bioimage data exchange based on global coordination of technical developments among data infrastructures and communities

Shuichi Onami, RIKEN  
Aastha Mathur, EU-Bioimaging  
Josh Moore, German BioImaging  
Matthew Hartley, EMBL-EBI

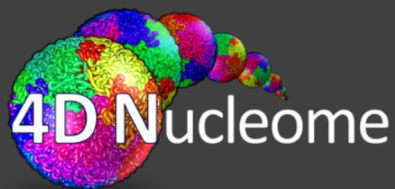


# Building a Global Ecosystem for FAIR Image Data: my role



1. Development of data exchange and integration formats
2. Community Development and Education
3. Image Metadata Standards and Software
4. Persistent Identifiers
5. Development and adoption of easy to use local RDMS cyberinfrastructure

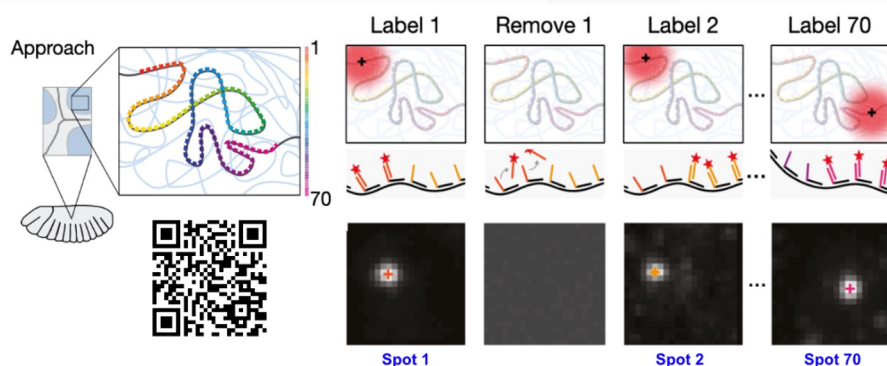




# Standardizing and Sharing value: 4DN use case

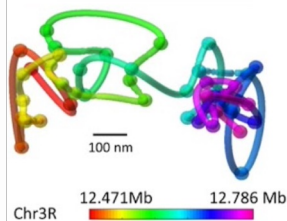


## MULTIPLEXED FISH CHROMATIN TRACING

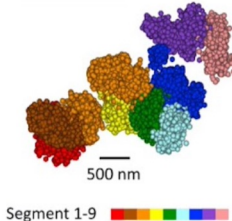


Mateo et al.,  
<https://doi.org/10.1038/s41586-019-1035-4>

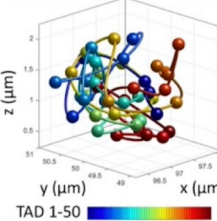
Drosophila Chr3R - 330 kb trace by ORCA:



Human Chr19 - 8.19 Mb trace by OligoSTORM:



Murine Chr19 - 58 Mb trace by MINA:

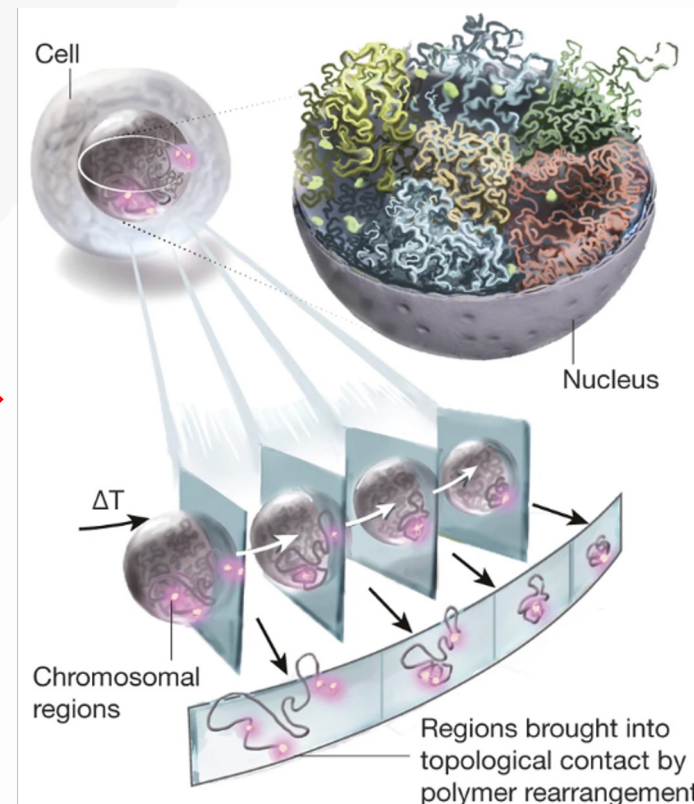


## FOF-CT Data and Metadata Exchange Format

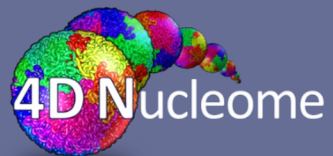
```
##FOF-CT_version=v0.1
##Table_namespace=4dn_FOF-CT_core
##genome_assembly=GRCh38
##XYZ_unit=micron
#lab_name: Siyuan Yale
#experimenter_contact: siyuan.wang@yale.edu
#Software_Title: MINA Analyst
#Software_Type: MATLAB
#Software_Authors: Siyuan Wang
#Software_Description: Custom written software
#Software_Repository: https://campuspress.yale.edu/wanglab/mina-analyst/
#Software_Preferre 2667-2697 (2021). https://doi.org/10.1038/s41596-021-00518-0
#additional_tables: 4dn_FOF-CT_cell 4dn_FOF-CT_bio
##columns=(Spot_ID Trace_ID X Y Z Chrom Chrom_Start Chrom_End Cell_ID)
```

Spot_ID	Trace_ID	X	Y	Z	Chrom	Chrom_Start	Chrom_End	Cell_ID
1	1	110.573964	129.244672	1.79925511	19	4190000	4290000	411
2	1	110.262885	129.093298	2.31765925	19	5890000	5990000	411
3	1	109.743291	129.745431	1.363418	19	7195510	7295510	411
4	1	109.165345	129.784738	0.91529473	19	8055510	8155510	411
5	1	109.176669	129.793967	0.7188798	19	9255510	9355510	411

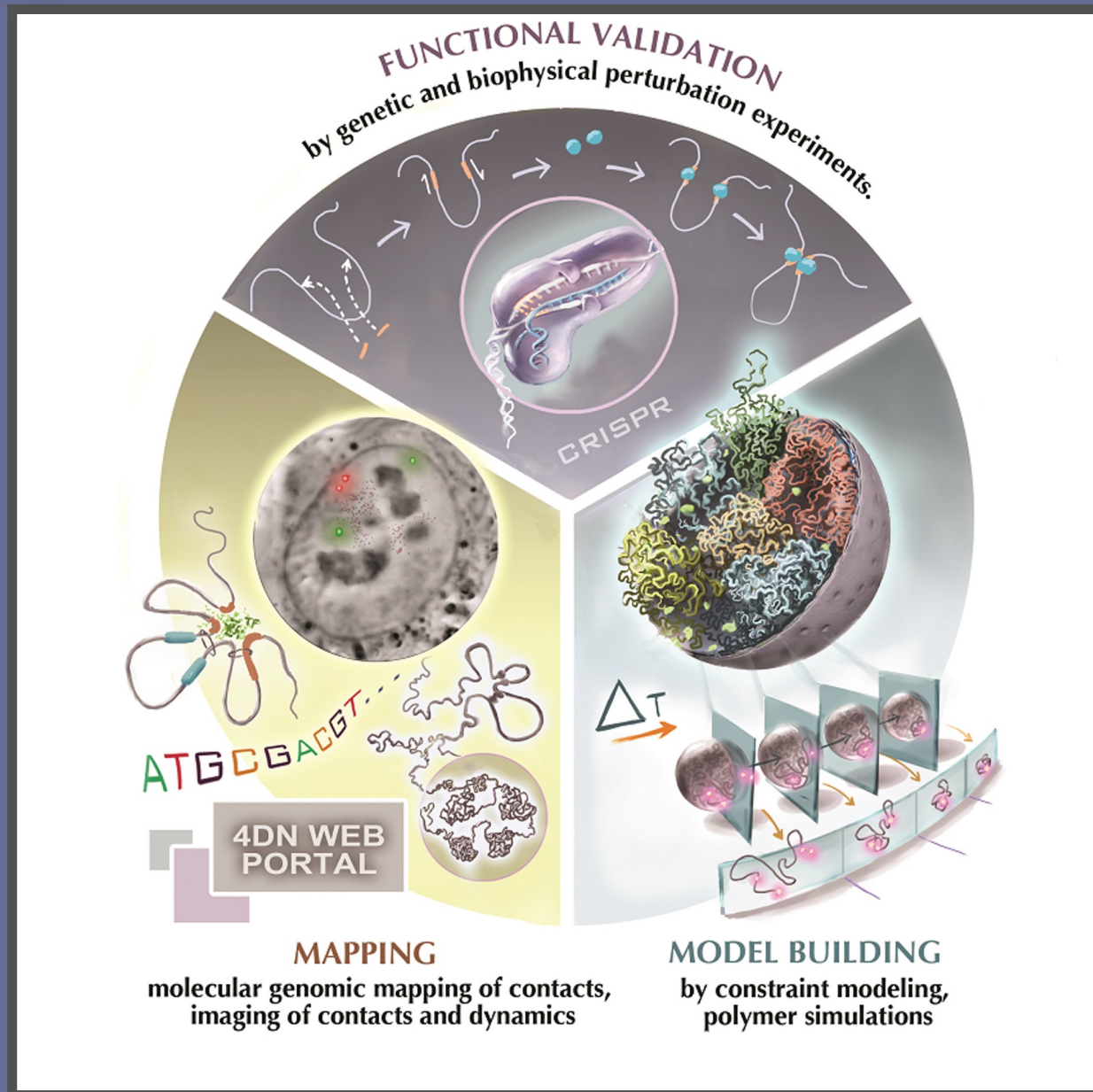
## PREDICTIVE MODELING/ AND MECHANISMS



<https://doi.org/10.1038/nature23884>



# NIH 4D Nucleome Initiative



- Phase 1: 2015-19
- Phase 2: 2020-25
- 4DN Data Portal  
<https://data.4dnucleome.org/>
- Dekker et al. Current state and future aims of the 4D nucleome project. *Molecular Cell*.  
<https://doi.org/10.1016/j.molcel.2023.06.018>





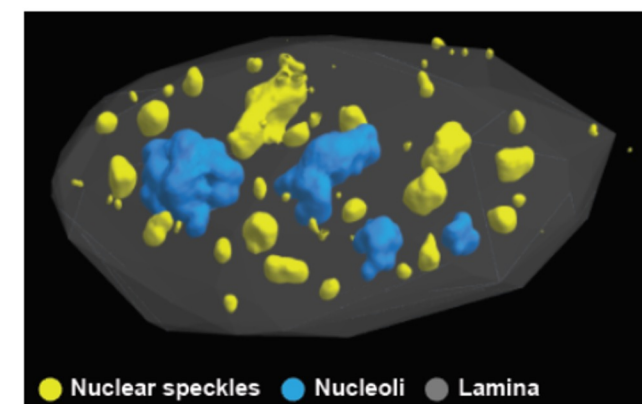
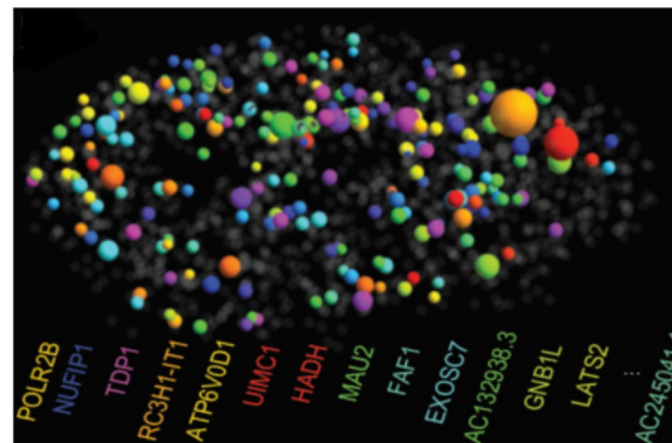
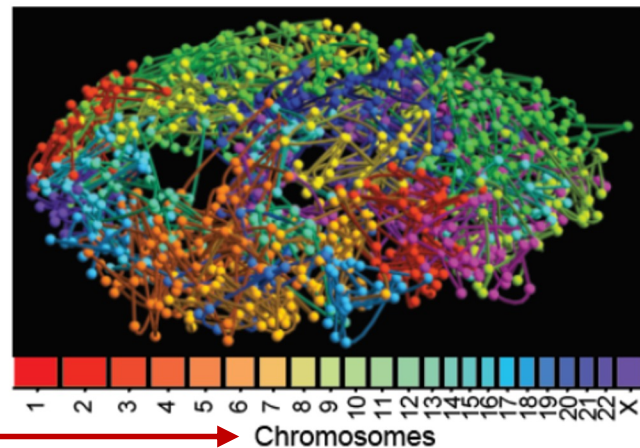
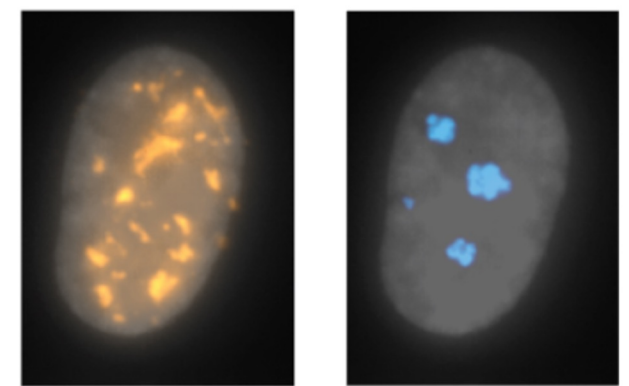
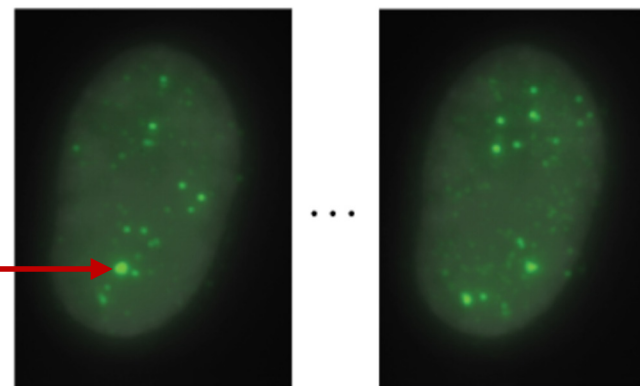
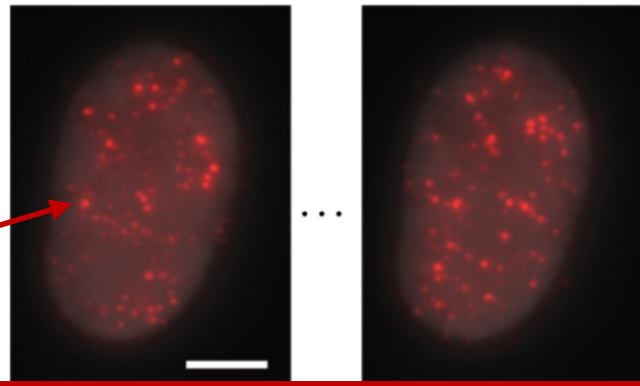
# Imaging Working Group focusing on Data Formats & Standards for multiplexed DNA, RNA, and protein imaging

Multiplexed DNA imaging

Multiplexed RNA imaging

Protein imaging

Need to record  
3D (x,y,z)  
coordinates  
of DNA  
RNA  
&  
genomic  
information



Gene name (RNA)

Figure from Bogdan Bintu's Lab website: <https://b.bintulab.com/research/>  
Su, J.H., ...Bintu, B.\* and Zhuang, X\*. *Cell* 2020, 182(6), pp.1641-1659.

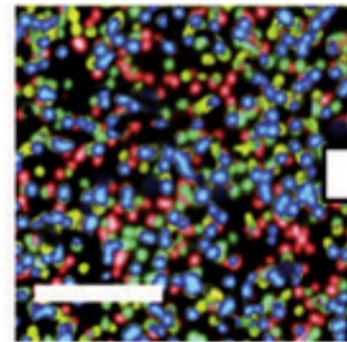
**We need a common data format for imaging DNA&RNA spots in cells!**

**Imagine not having a common fastq files and each of your trainees has to deal with the raw images from sequencer:**

### **Illumina Flow Cell Raw Data**

for one round of sequencing,  
Colors: A,T,C,G incorporation  
each spot is a cluster

(from review Lakdawalla...Fan  
Molecular Oncology 2013)



Images

lane	tile	x	y	A	C	G	T
6	40	355	115	478	392	4264	385
6	40	215	866	4230	2829	238	185
6	40	154	281	521	508	3200	545
6	40	115	153	432	577	264	614
6	40	717	392	2294	1520	294	135
6	40	154	364	318	48	3902	105
6	40	542	168	87	70	226	189
6	41	591	75	5003	4021	391	605
6	41	458	726	55	73	392	535
6	41	642	529	61	560	354	338
6	41	286	659	151	19	2227	925

Intensities

144	555	TAGCAG
235	556	GGCGTA
277	843	AAATAG
291	365	GGTCTC
113	228	ACCCTG
27	451	TCAGAT
135	931	TATACC
282	437	GGCTCA
263	770	CCAGTG
109	471	GGGCBT

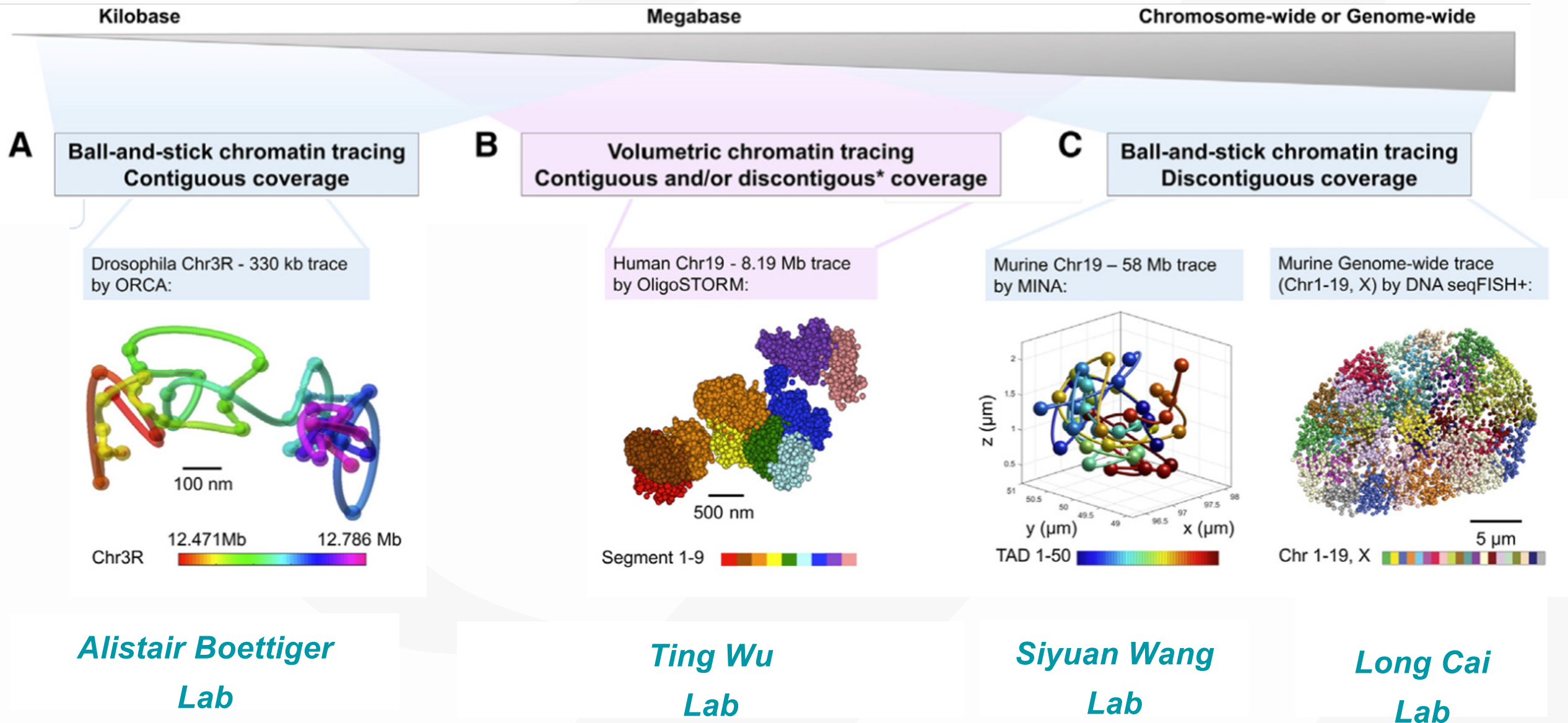
Base calls

**But instead they have pipelines that give them back nice files, like  
fastq, bam, with sequencing reads or counts.**

**fastq released over 20 years ago!!!**

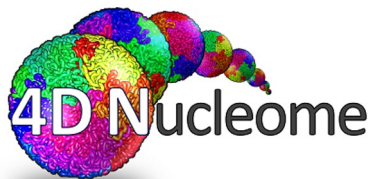
**Can use any shared datasets without having to write/rewrite code.**

# Where to start: multiplexed DNA FISH, FISH Omics Chromatin Tracing

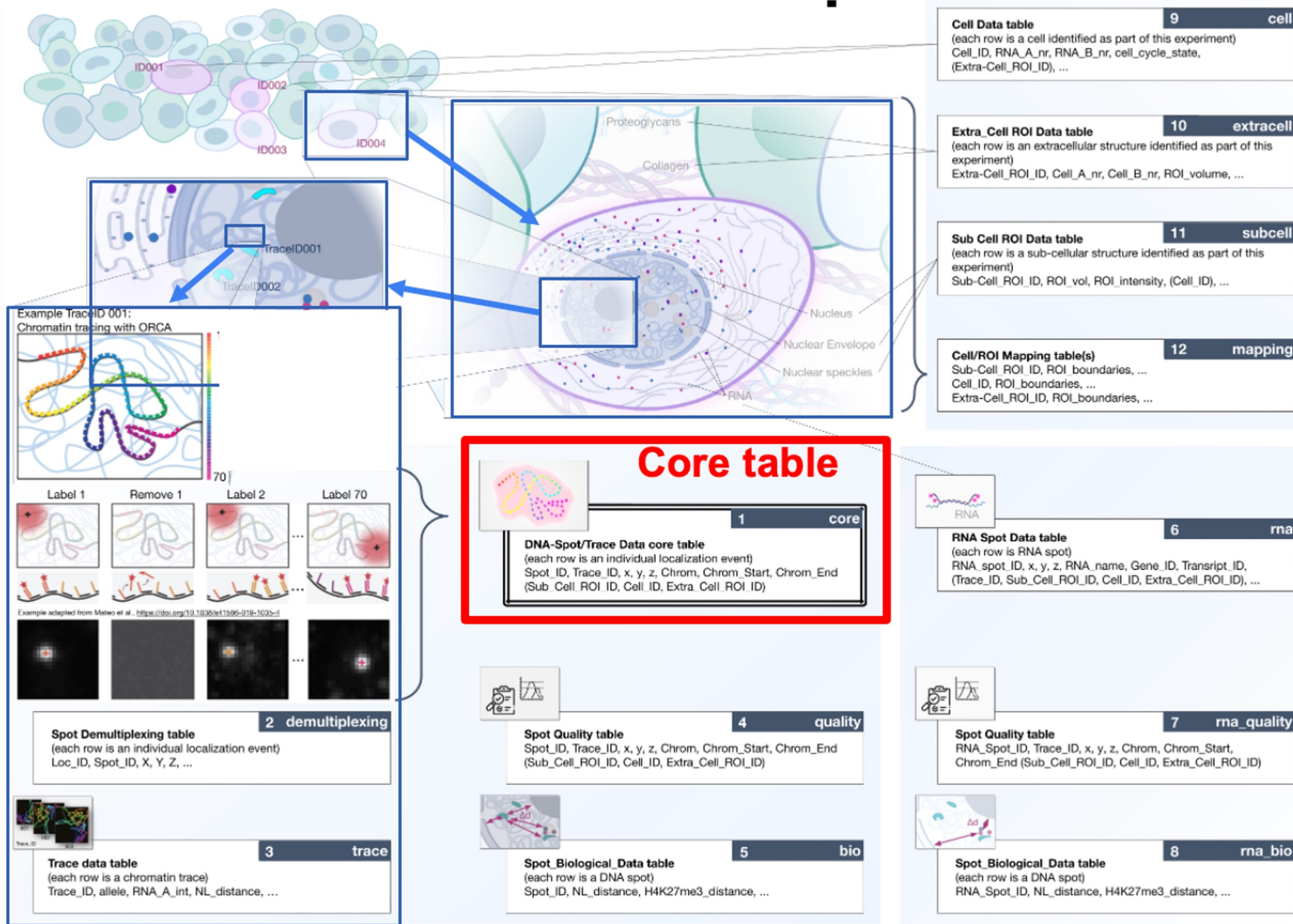


Figure, by Sarah Aumfcolk, adapted from: Spatial and temporal organization of the genome: Current state and future aims of the 4D nucleome project, Dekker et al, Mol Cell. 2023 (<https://doi.org/10.1016/j.molcel.2023.06.018>)

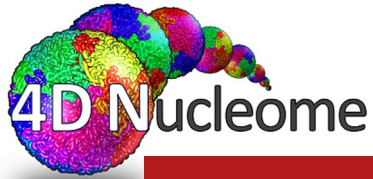




# 4DN FISH Omics Format for Chromatin Tracing: modular architecture







# 4DN FISH Omics Format for Chromatin Tracing: modular architecture

arXiv > q-bio > arXiv:2508.13255

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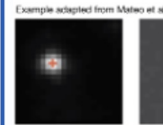
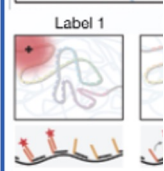
Quantitative Biology > Other Quantitative Biology

[Submitted on 18 Aug 2025 (v1), last revised 17 Dec 2025 (this version, v3)]

## FAIR sharing of Chromatin Tracing datasets using the newly developed 4DN FISH Omics Format

Rahi Navelkar, Andrea Cosolo, Bogdan Bintu, Yubao Cheng, Vincent Gardeux, Silvia Gutnik, Taihei Fujimori, Antonina Hafner, Atishay Jay, Bojing Blair Jia, Adam Paul Jussila, Gerard Llimos, Antonios Lioutas, Nuno MC Martins, William J Moore, Yodai Takei, Frances Wong, Kaifu Yang, Huaiying Zhang, Quan Zhu, Magda Bienko, Lacramioara Bintu, Long Cai, Bart Deplancke, Marcelo Nollmann, Susan E Mango, Bing Ren, Peter J Park, Ahilya N Sawh, Andrew Schroeder, Jason R Swedlow, Golnaz Vahedi, Chao-Ting Wu, Sarah Aufmkolk, Alistair N Boettiger, Irene Farabella, Caterina Strambio-De-Castillia, Siyuan Wang

In recent years, multiplexed Fluorescence In Situ Hybridization (FISH) or FISH-omics methods have rapidly expanded, enabling the quantification of chromatin organization in single cells, often in conjunction with measurements of RNA and protein. These approaches have deepened our understanding of how 3D chromosome architecture relates to transcriptional activity and cell states in health and disease. Despite these advances, results from Chromatin Tracing FISH-omics experiments remain challenging to share, reuse, and analyze due to the absence of standardized data exchange specifications. Building on the release of microscopy metadata standards, we introduce the FISH Omics Format–Chromatin Tracing (FOF–CT), a community–developed standard for processed results from diverse imaging modalities. We describe the FOF–CT file format and present a curated collection of datasets deposited in the 4DN Data Portal and the OME Image Data Resource (IDR). We also highlight their potential for reuse, integration, and modeling by outlining example analysis pipelines and illustrating biological insights enabled by standardized, FAIR–compliant Chromatin Tracing datasets. While this manuscript focuses on the representation of ball–and–stick Chromatin Tracing, the format is designed to be extensible to volumetric Chromatin Tracing.



Trace data table  
(each row is a chromatin trace)  
Trace\_ID, allele, RNA\_A\_int, NL\_distance, ...

3

trace



Spot Biological Data table  
(each row is a DNA spot)  
Spot\_ID, NL\_distance, H4K27me3\_distance, ...

5

bio



Spot Biological Data table  
(each row is a DNA spot)  
RNA\_Spot\_ID, NL\_distance, H4K27me3\_distance, ...

8

rna\_bio



Example Track ID 001  
Chromatin tracing with

Help | Advanc

**Spot Demultiplex**  
(each row is an  
Loc\_ID, Spot\_ID)

**Trace data tab**  
(each row is a c  
Trace\_ID, allele,

---

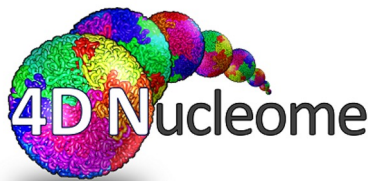
# Under revision in Nature Methods

# Nature Methods

**Trace data table**  
(each row is a chromatin trace)  
Trace ID, allele, RNA A int, NL distance, ...

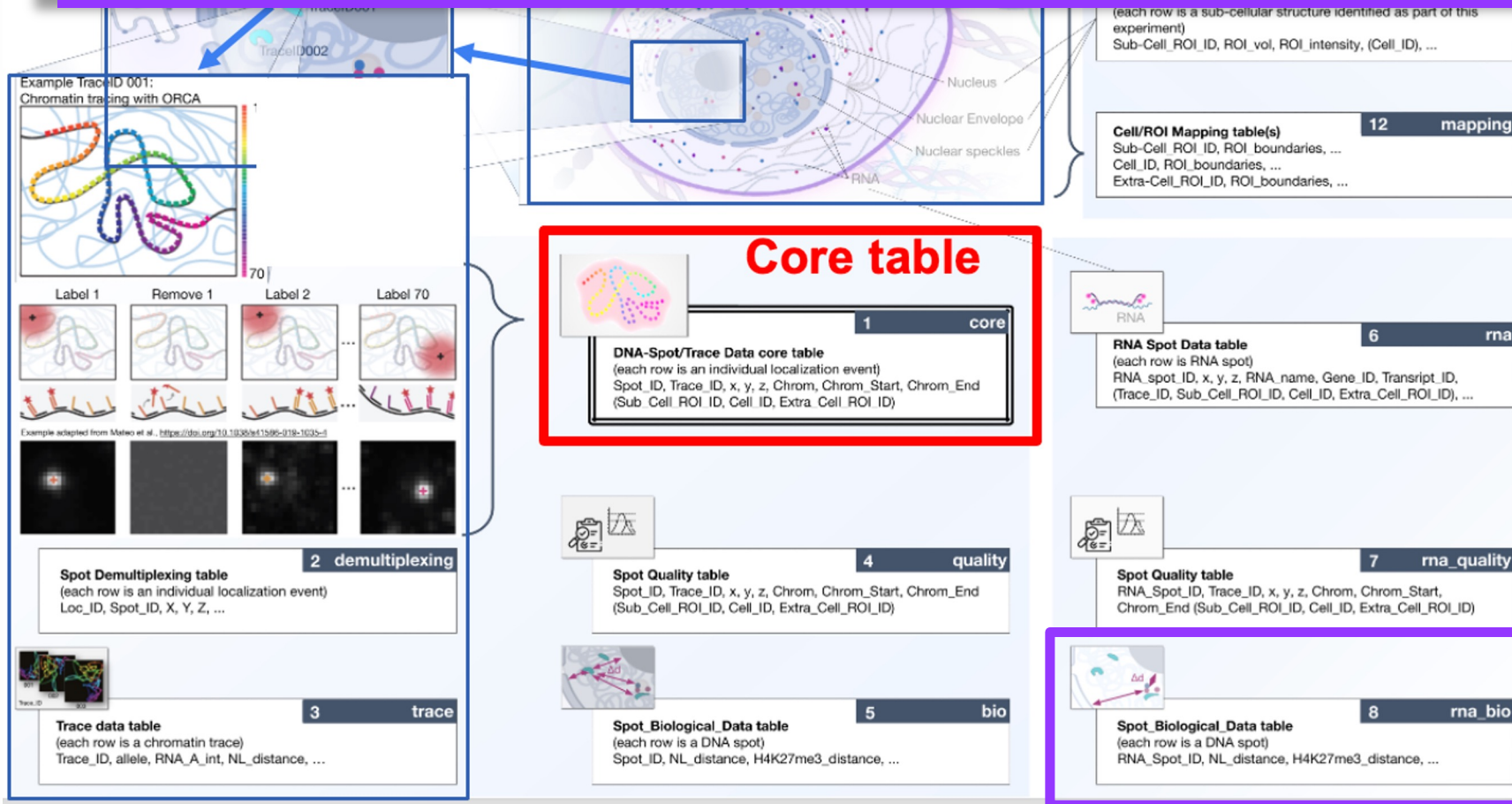
**Spot\_Biological\_Data** table  
(each row is a DNA spot)  
Spot\_ID, NL\_distance, H4K27me3\_distance, ...

**Spot\_Biological\_Data** table  
(each row is a DNA spot)  
RNA Spot ID, NL distance, H4K27me3 distance, ...



# 4DN FISH Omics Format for Chromatin Tracing: modular architecture

From arbitrary XYZ coordinates to a biologically significant Nuclear Common Coordinate Framework (CCF)





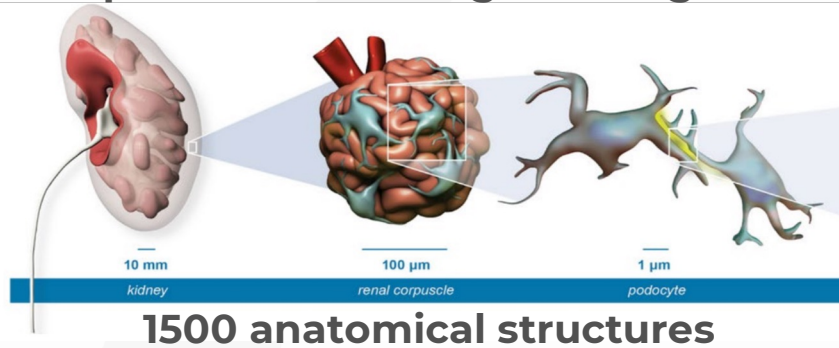


# Standardizing and Sharing value: HuBMAP use case



Katy Borner  
Indiana U.

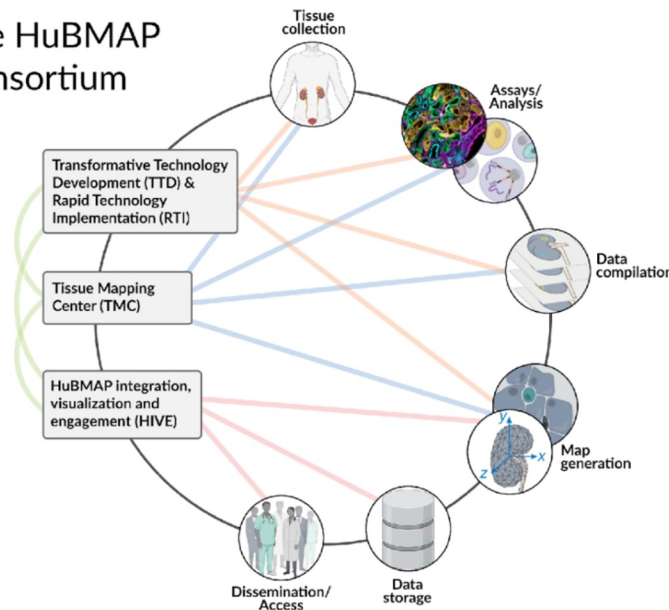
## Common Coordinate Framework for Spatial and Ontological Integration



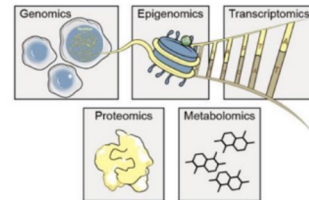
Data Resource Center @



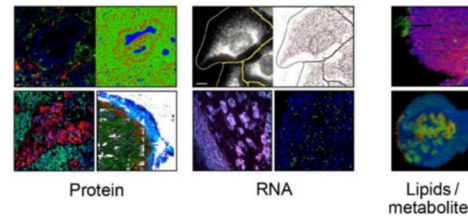
## The HuBMAP Consortium



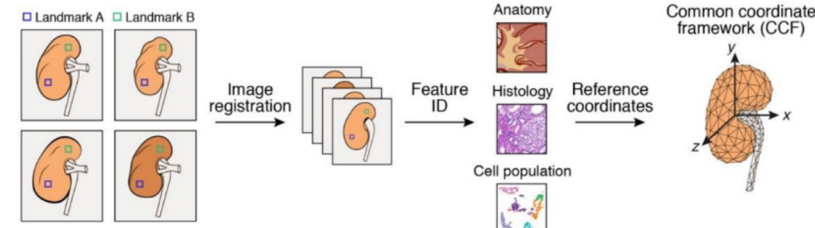
### Single cell and 'omics assays



### Multiplexed spatial assays



### Map assembly and data query

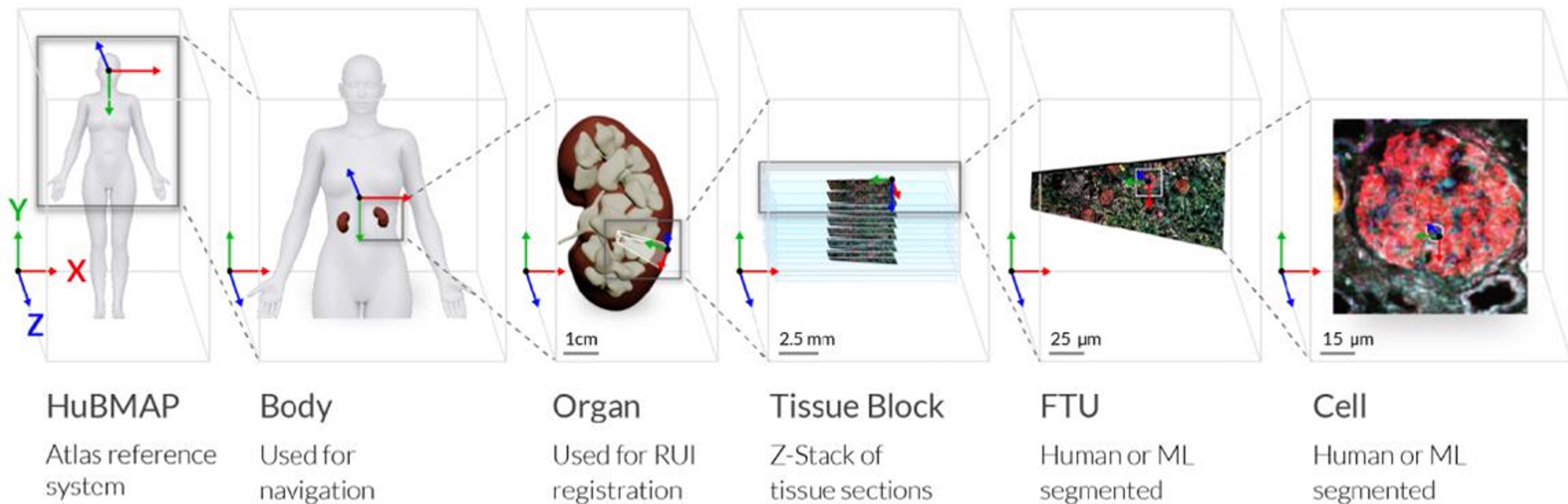


HuBMAP Paper package

<https://www.nature.com/immersive/d42859-023-00019-y>



# Standardizing and Sharing value: HuBMAP use case

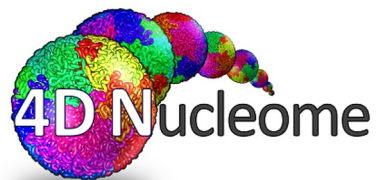






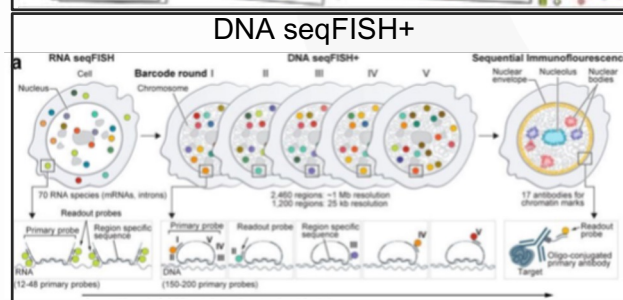
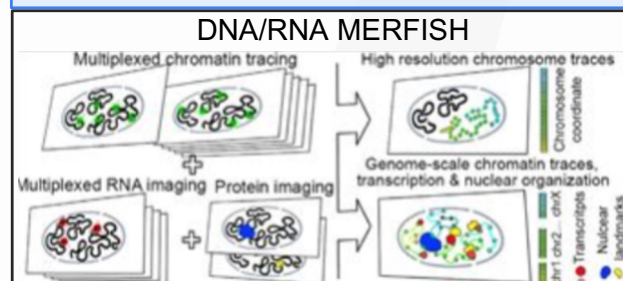






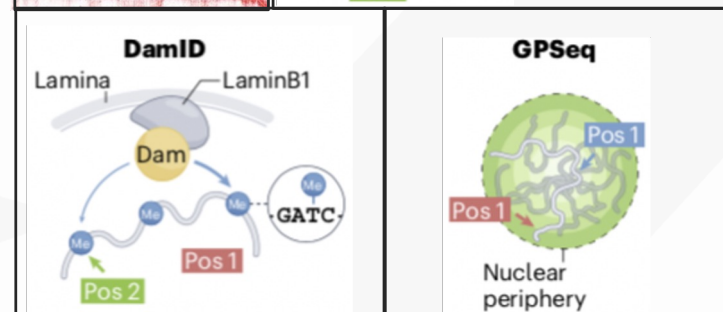
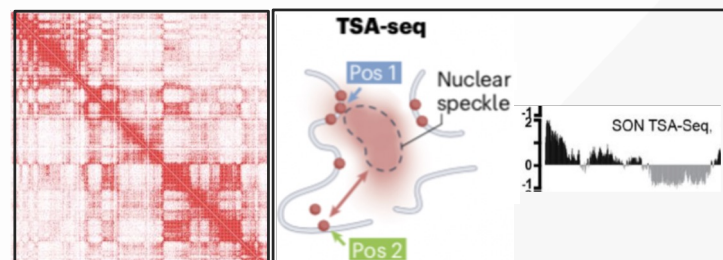
# Development of a Nuclear Common Coordinate Framework

**Imaging FISH-Omics**  
(multiplexed FISH)  
and other imaging



etc

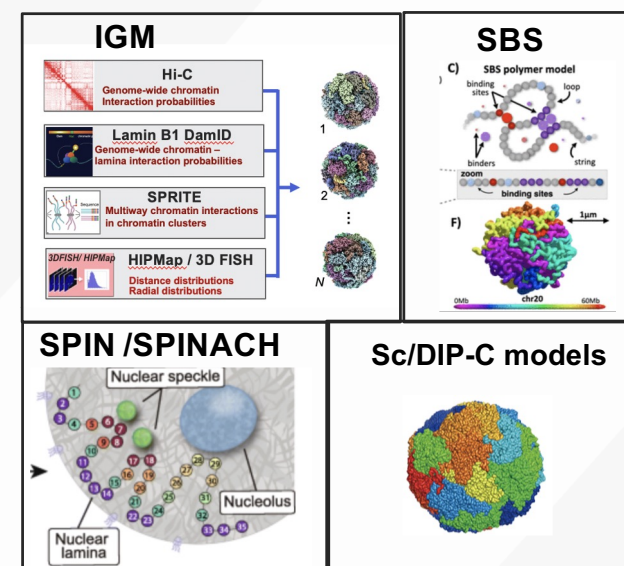
**Single cell and bulk  
genomics data**  
Cytological mapping data



NAD-seq, SPRITE, etc.

etc

**Computational  
models and  
methods**

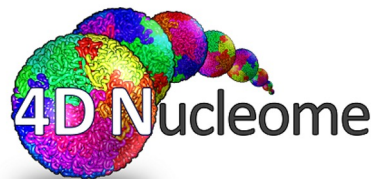


etc

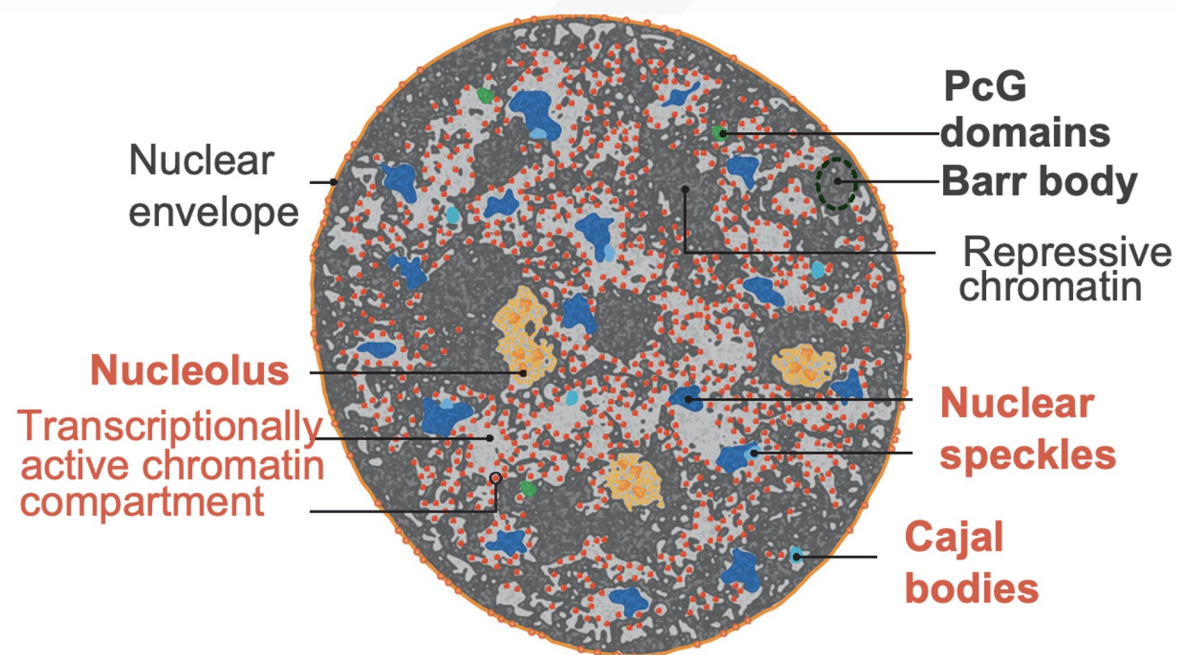


Frank Alber  
UCLA



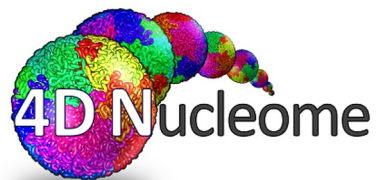


# Why do nuclear coordinates matter?



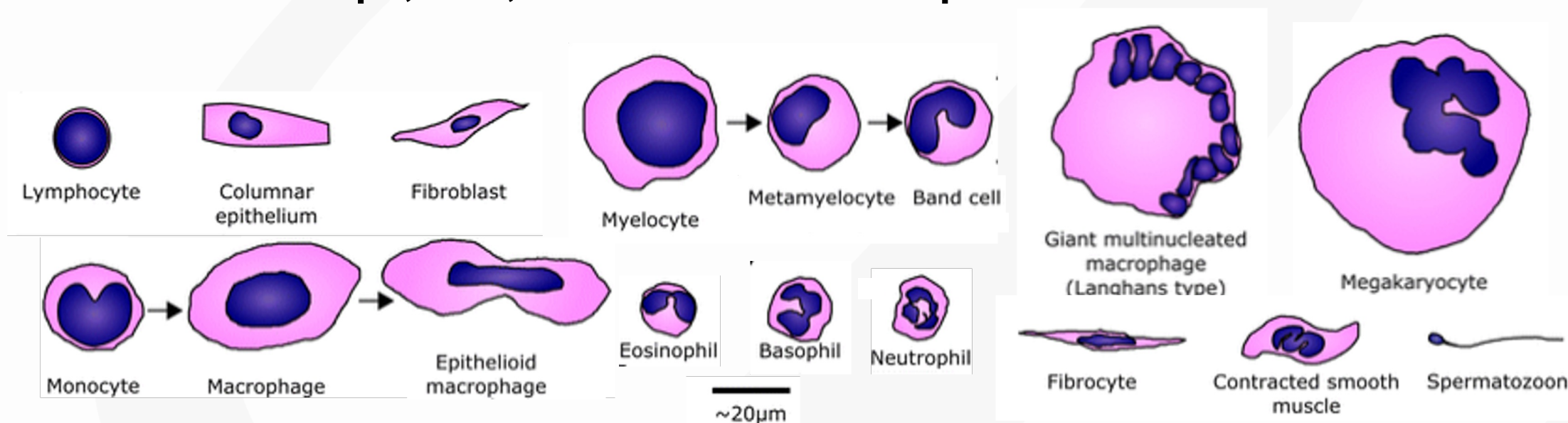
Caudron-Herger et al., Curr.Op.Gen.&Dev. 2012

**The nucleus is organized into functional compartments. The spatial proximity to nuclear compartments and nuclear bodies matters.**



# Why do nuclear coordinates matter?

The nucleus varies largely between cell types, tissues, differentiation state. in terms of shape, size, internal nuclear compartments.



Skinner et al. Chromosoma 2017



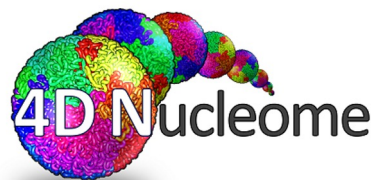
Susanne  
Rafelski  
AICS

**How do we compare data across different cell type and conditions?**

- We need a systematic way to describe the nuclear topography
- We should provide reference information about the nuclear topography

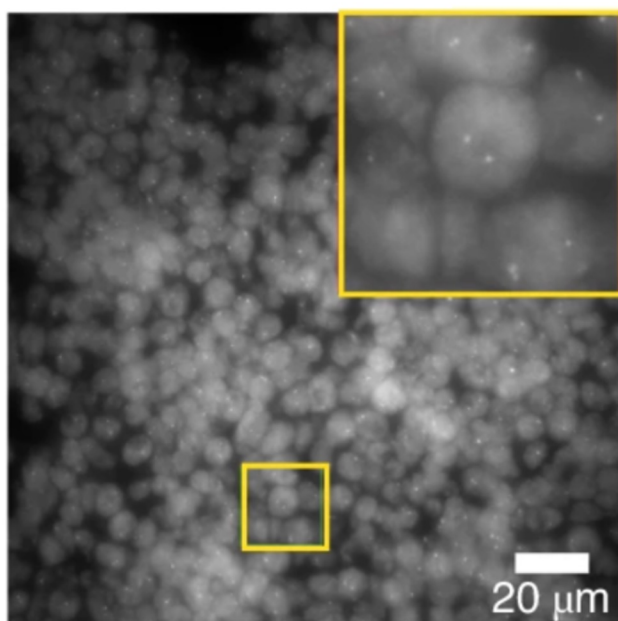
What are the minimum requirements to quantitatively describe the nuclear landscape?  
(e.g., in relation to the nuclear landmarks, compartments)





# 4DN Nuclear Common Coordinate Framework (CCF)

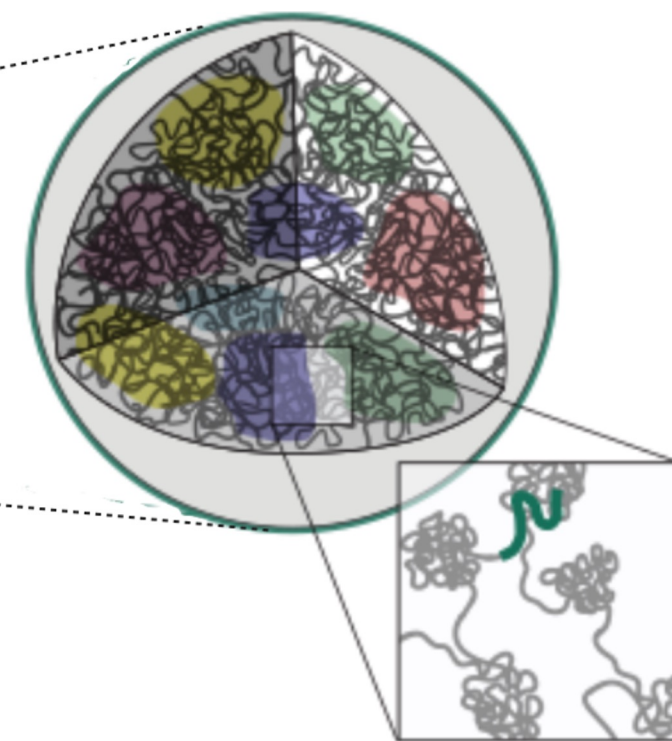
Multiplexed FISH  
basCT



Liu, M., Yang, B., Hu, M. *et al.* (2021). 10.1038/s41596-021-00518-0

The goal is to have a set of recommendations how to measure and store nuclear information together with locations of loci.

Models from  
genomics data (Hi-C)

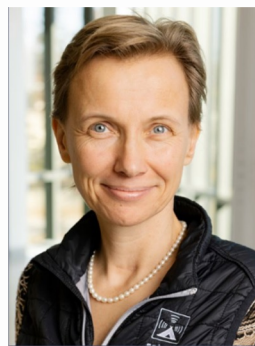


Spot 1 ( $\Delta 1$ ,  $\Delta 2$ ,  $\Delta 3$ ,  $\alpha$ )

An underlying common 'language' for describing and indexing the data in a spatially explicit and semantically consistent way to integrate knowledge from diverse data types (i.e., multiplexed FISH and 3C methods) and sources and build coherent predictive models of 4D Nucleome structure and function

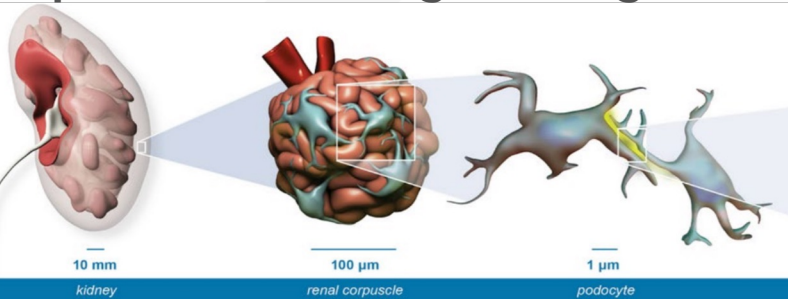


# CCF integration → from whole tissues to chromatin organization



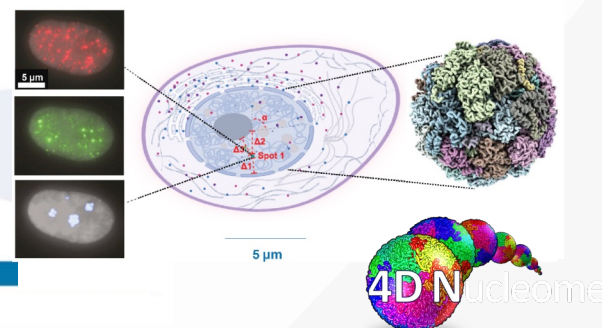
Katy Borner  
Indiana U.

## Common Coordinate Framework for Spatial and Ontological Integration



1500 anatomical structures

## Integration of 4DN FISH Omics



Frank Alber  
UCLA



Susanne Rafelski  
AICS



Yin Shen  
UCSF



Laca Bintu  
Stanford



Quan Zhu  
UCSD

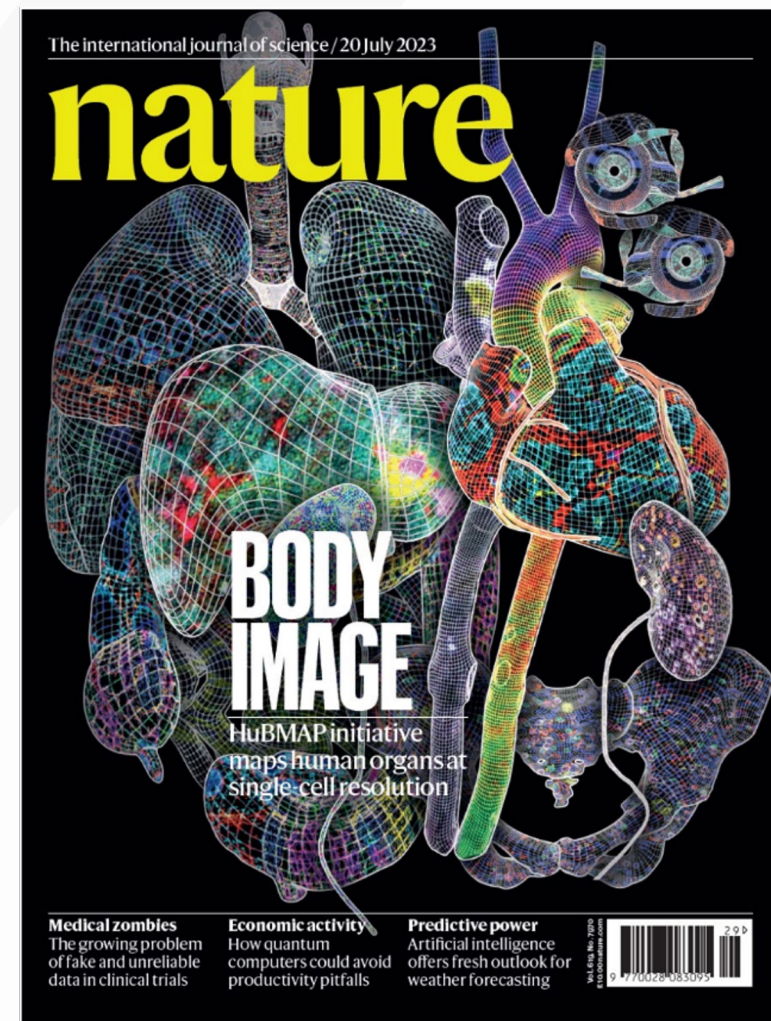


Bogdan Bintu  
UCSD

4DN Integrating and  
Imaging and Omics WG

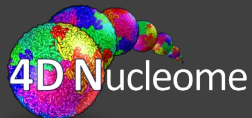
4DN Imaging  
WG

Benchmarking  
Datasets



HuBMAP Paper package

<https://www.nature.com/immersive/d42859-023-00019-y>

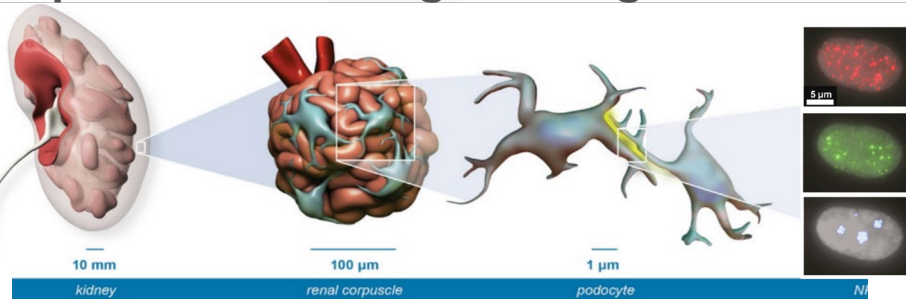


# CCF in action → from single cells to Functional Tissue Units in human lung



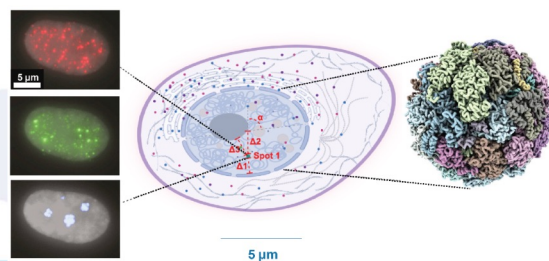
Katy Borner  
Indiana U.

Common Coordinate Framework for  
Spatial and Ontological Integration



1500 anatomical structures

Integration of  
4DN FISH Omics



Frank Alber  
UCLA



Quan Zhu  
UCSD



Bogdan Bintu  
UCSD



Gloria Pryhuber  
Rochester  
Medical School

Integrative  
Modeling

Multimodal  
MERFISH in lungs

Lung physiology  
and pathology

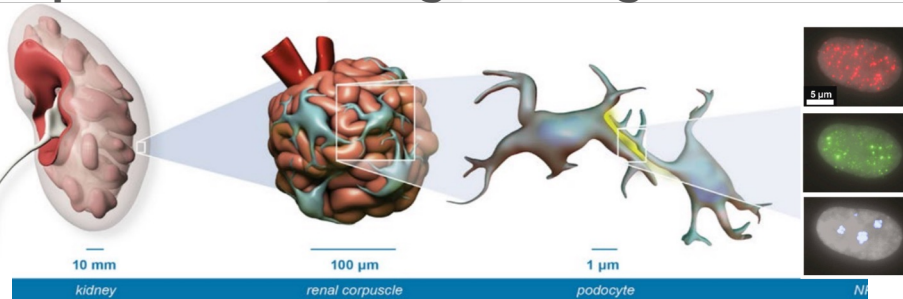


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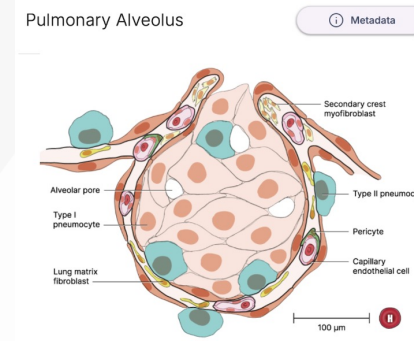
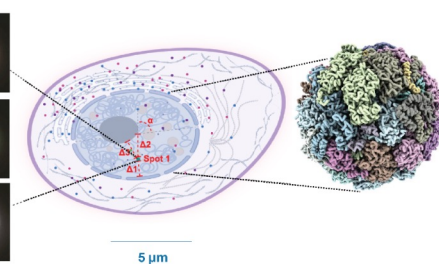
Katy Borner  
Indiana U.

## Common Coordinate Framework for Spatial and Ontological Integration



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Frank Alber  
UCLA



Quan Zhu  
UCSD



Bogdan Bintu  
UCSD

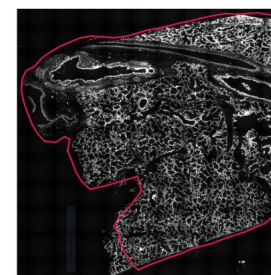
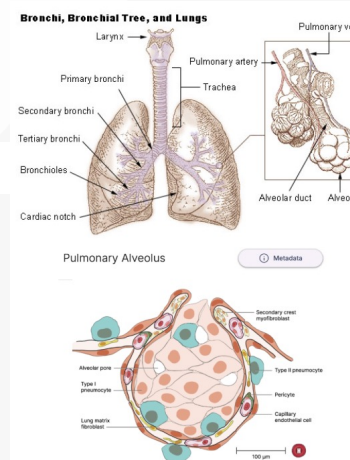


Gloria Pryhuber  
Rochester  
Medical School

Integrative  
Modeling

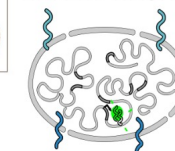
Multimodal  
MERFISH in lungs

Lung physiology  
and pathology

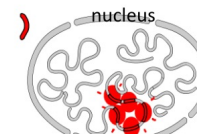


## Multimodal MERFISH Imaging of Human Lung

### RNA-MERFISH

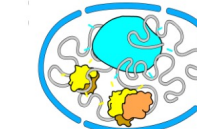


### DNA-MERFISH



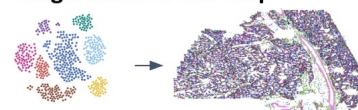
sub-Mb 3D structure of 25 genes and their regulatory landscape

### Iterative immunofluorescence



Integration of  
MERFISH data  
with:

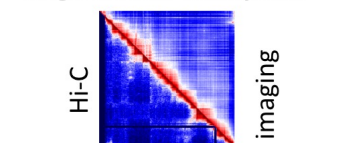
single nucleus RNAseq



single nucleus ATACseq



single nucleus methyl HiC



Hi-C

imaging

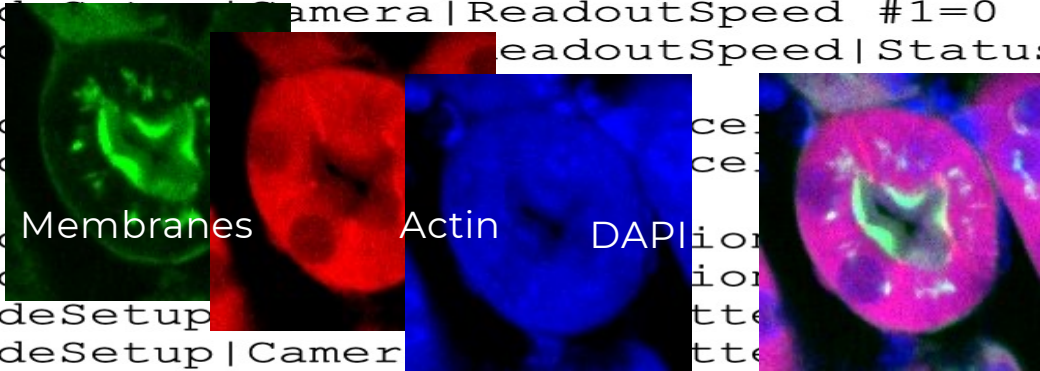
# Biolmage Data

Kidney, 1.5  
microns

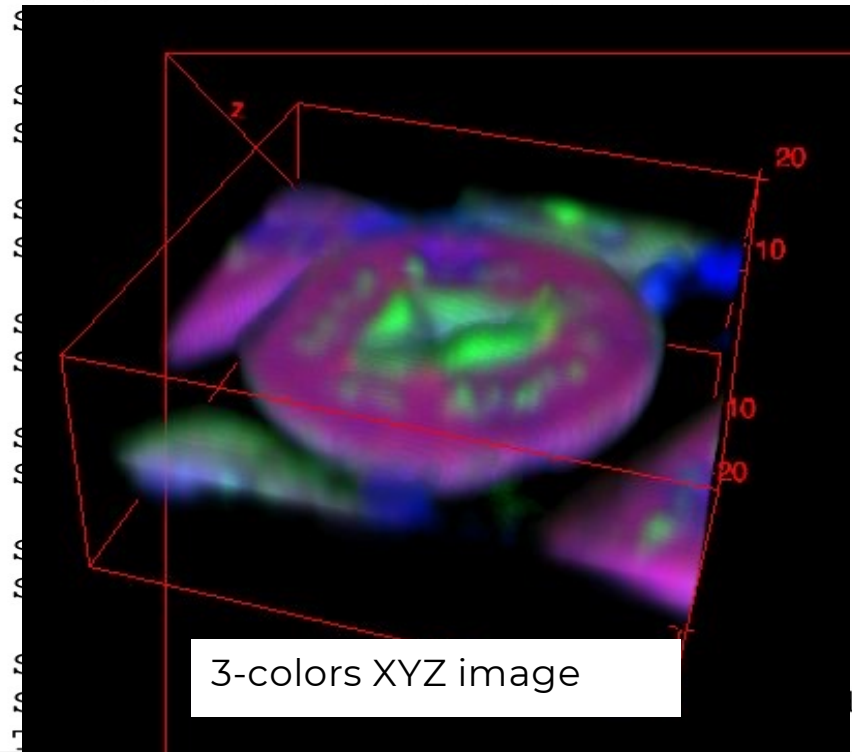
11866 levels of gray

2119 levels of gray

```
Block|AcquisitionModeSetup|Camera|ReadoutPort|Status #1=Valid
Block|AcquisitionModeSetup|Camera|ReadoutSpeed #1=0
Block|AcquisitionModeSetup|Camera|ReadoutSpeed|Status
Block|AcquisitionModeSetup|Camera|ReadoutSpeed|Status #1=3
Block|AcquisitionModeSetup|Camera|ReadoutSpeed|Status #1=Valid
Block|AcquisitionModeSetup|Camera|ReadoutSpeed|Status #1=Valid
Experiment|AcquisitionBlock|AcquisitionModeSetup|Camera|SequenceCount #1=1
Experiment|AcquisitionBlock|AcquisitionModeSetup|Camera|SequenceCount #1=1
```



- Multi-dimensional (XYZCT)
- COMPLEX experimental set-ups
- Proprietary file formats/lack of standards
- TB to PB (continue adding zeros...)
- VISUALIZATION is mandatory
- COMPUTING POWER and SPEED necessary for:
  - 3D VISUALIZATION
  - PROCESSING and ANALYSIS (including AI/ML)
- **METADATA is essential**

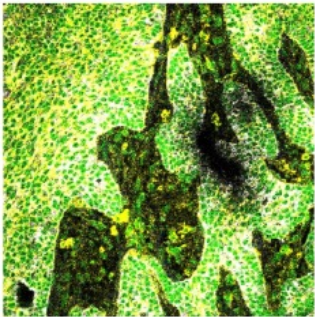


3-colors XYZ image

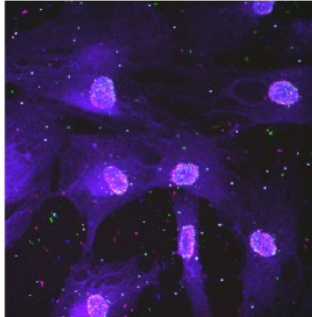


# Bioimages: complex data and metadata

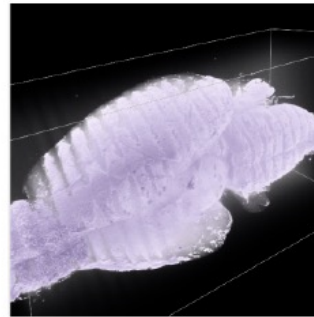
## Diversity in imaging applications/modalities



Multiplexed



Spatial tx



Light-sheet



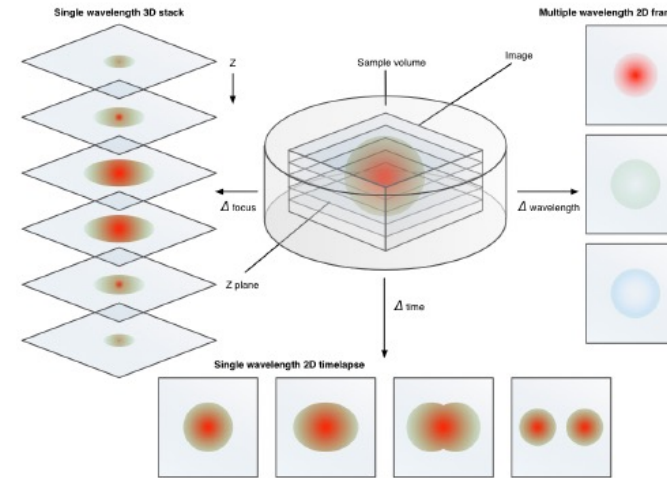
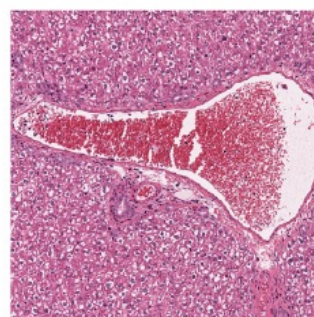
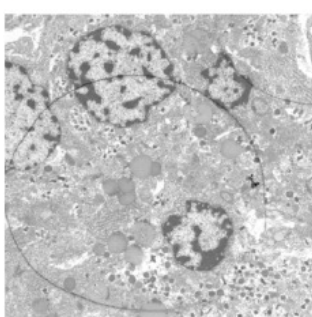
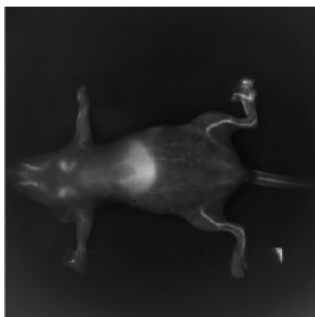
Infrared



Scanning EM



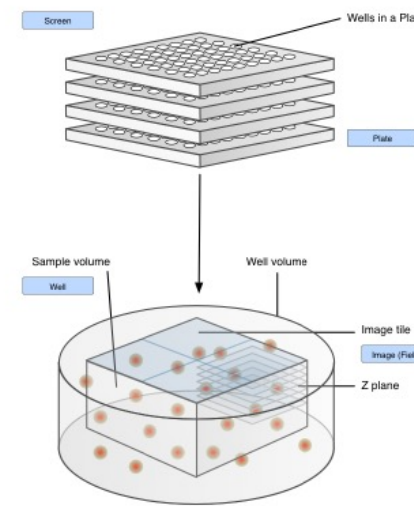
Digital pathology



## 5D Images

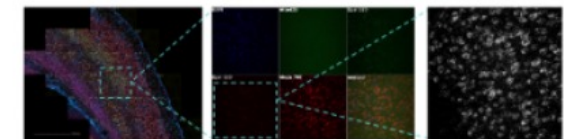
3D, multi-color, movies, or any combination

<https://ome-model.readthedocs.io/>



High-content Screen

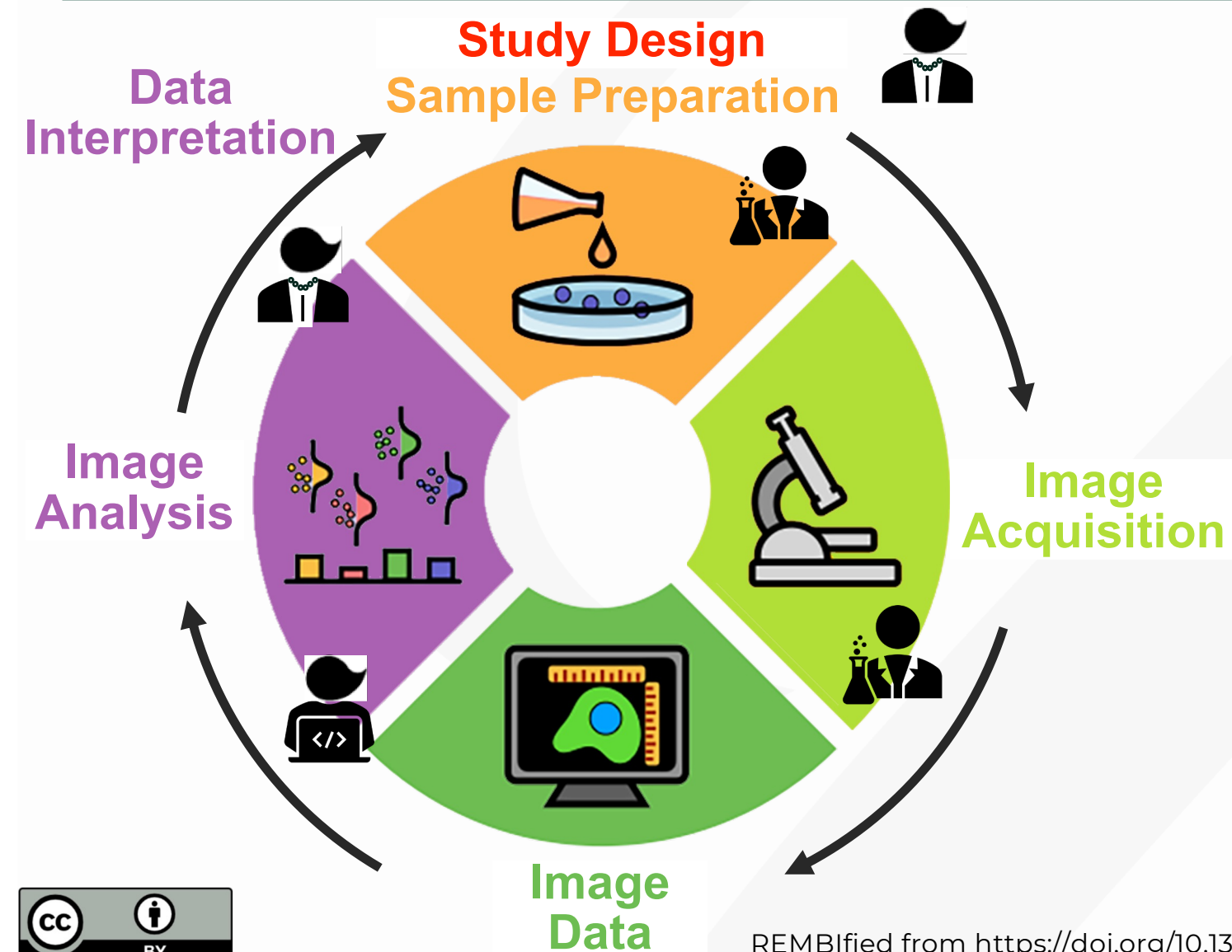
## Complex Acquisitions



Single-cell tissue



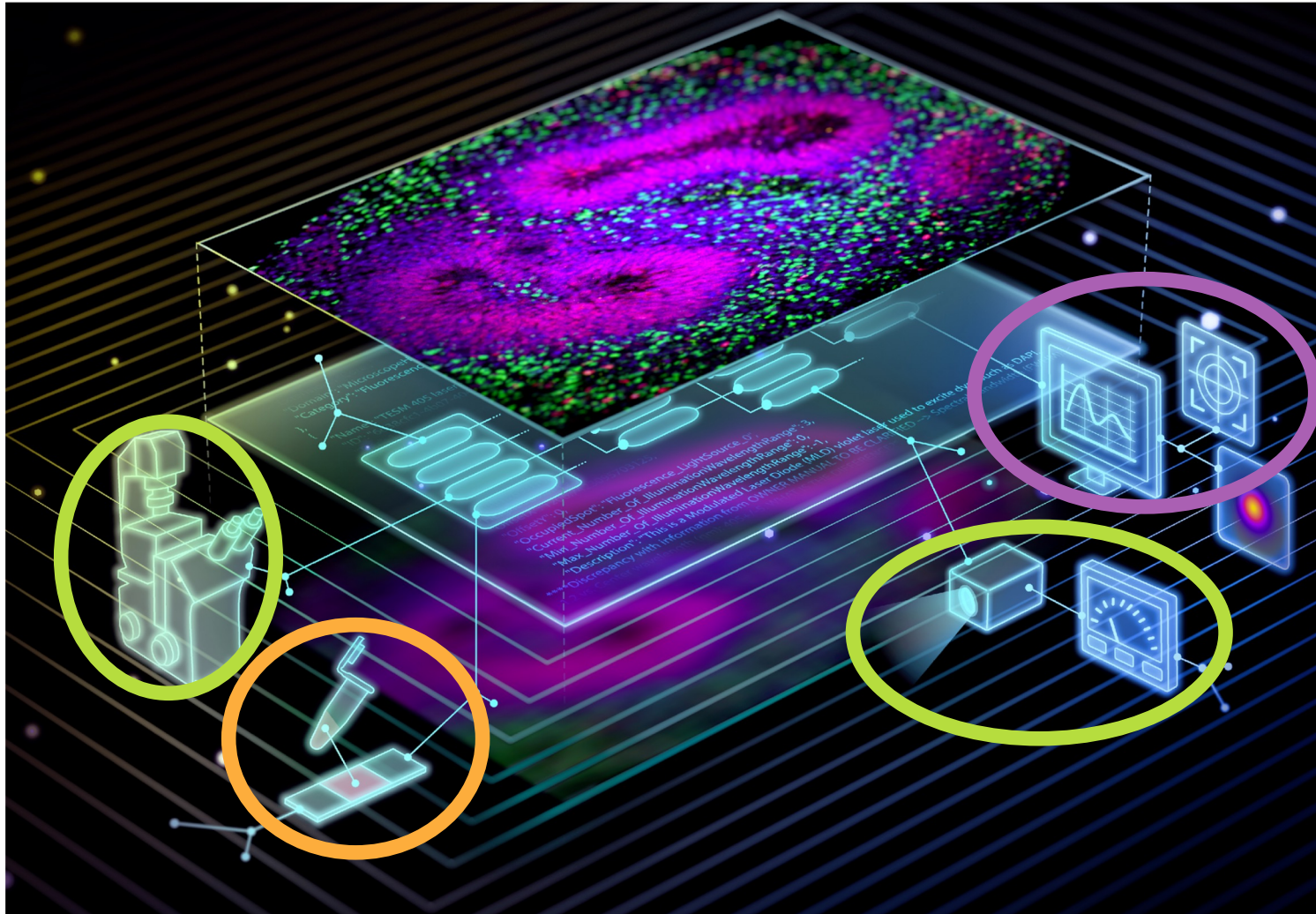
# Imaging experiments contain multiple related steps - starting with **PLANNING**



- Each step produces metadata
- Steps are mutually related
- Data and metadata produced at each step **affect** subsequent steps
- Desired outcomes **determine** how previous steps should be performed



# Image Metadata



All information that is needed to interpret, evaluate the quality reproduce and share microscopy images

- Sample preparation
- Image Acquisition
  - Hardware configuration
  - Acquisition setting
  - Quality Control
- Image data processing and analysis

© Thao Do (Allen Institute, Seattle, WA, USA)

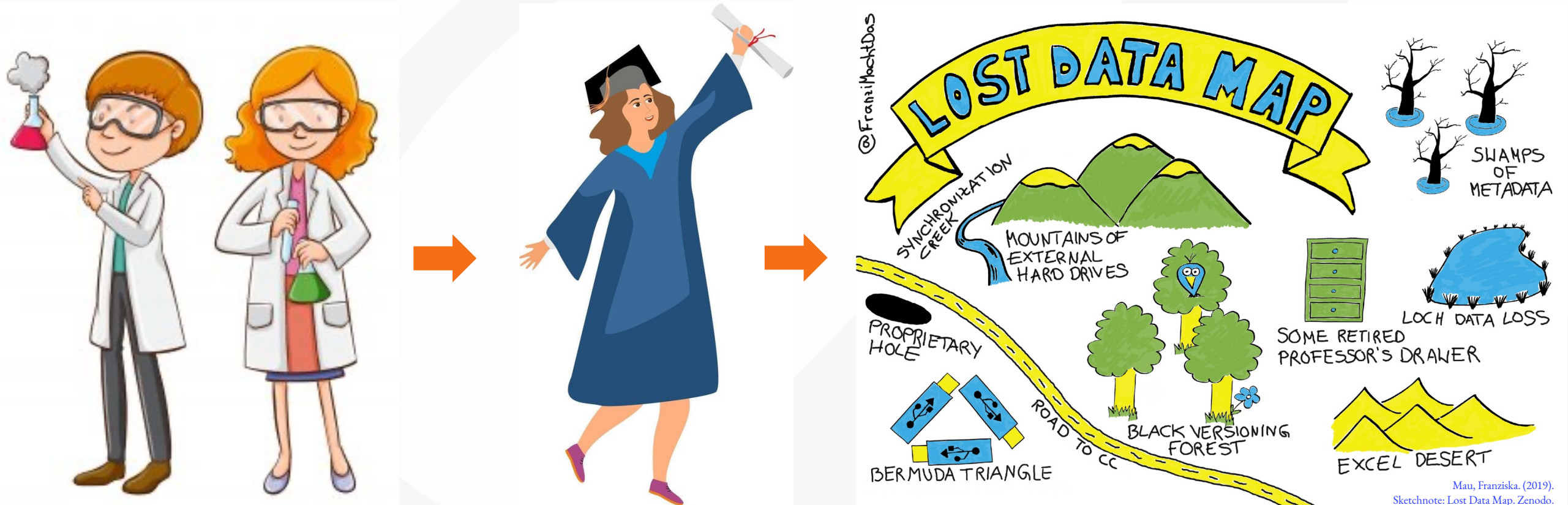
Nature Methods FOCUS issue on Reporting and Reproducibility in Microscopy:

<https://www.nature.com/collections/djicihhjh>





# Challenges for the Researchers

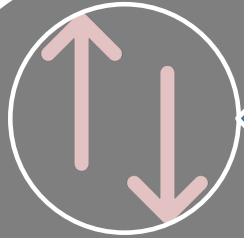


## In addition...

- Lack of affordable institutional storage and backup solution
- Lack of data preservation guidance (How long? Who is in charge?)
- Institutional repository not equipped for image data



# Challenges for the Researchers



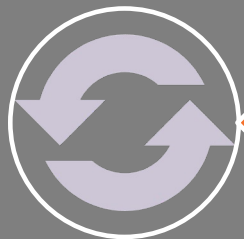
## **SAFE, BACKED-UP AND ORGANIZED DATA**

Easy-to-Find, Metadata-Rich, Reduced Waste, Provenance Tracking



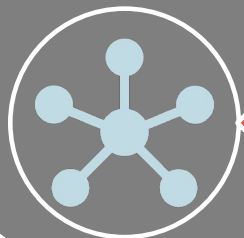
## **QUALITY & RIGOR**

Reliable Data, Supports Study Conclusions, Easier to Analyze



## **REPRODUCIBILITY**

Researchers have sufficient information to repeat experiments with same outcome



## **SHARING VALUE**

Public Archives, Increase impact, Accelerate Scientific Discovery, Quality Management, Documentation

49

Image credit: Claire Brown



# China is leading the global trend towards strong Research Data Management and Sharing (RDMS) policies

## ➤ 2018 - Measures for the Management of Scientific Data *(General Office of the State Council)*

- ❑ Scientific data generated through government funded research MUST BE managed, preserved and shared
- ❑ Data must be **Findable Accessible Interoperable and Reusable (FAIR)**
- ❑ Institutions must establish RDMS systems
- ❑ Promotes development of data repositories and standards
- ❑ Ensures privacy, intellectual property and security

## ➤ 2023 – National Strategic Action Plan for the Development of Scientific Data

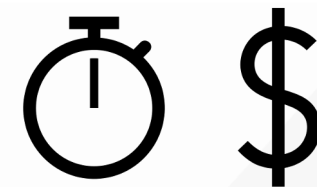
- ❑ 20-30 national scientific data centers
  - ❑ Biotechnology → National Genomic Data Center
- ❑ Develop standardized data management and protocols
- ❑ Enhance sharing with global partners under secure conditions

## ➤ Funding Agencies Requirements

- ❑ **National Science Foundation of China (NSFC)** → Required Data Management Plan and Data Deposition in recognized repositories as a precondition for funding
- ❑ **Ministry of Science and Technology (MOST)** → Oversees data policies for major national R&D projects

### Funding is tied to

- DMS plan
- Complying with the DMS plan.
- Data deposition



# China is leading the global trend towards strong Research Data Management and Sharing (RDMS) policies

## ➤ KEY PRINCIPLES

- ❑ **Openness by Default:** non sensitive data from public funding SHOULD be shared
- ❑ **Data Sovereignty:** emphasizes control over data generated in China
- ❑ **Standardization:** adoption of data formats and metadata standards to ensure interoperability
- ❑ **Ethics and Privacy:** Compliance with laws on personal information protection
- ❑ **Promotion of FAIR principles**



# China is leading the global trend towards strong Research Data Management and Sharing (RDMS) policies

## ➤ KEY FINDINGS

❑ Open Access

❑ Data Check

❑ Statistics

❑ Ethics

information protection

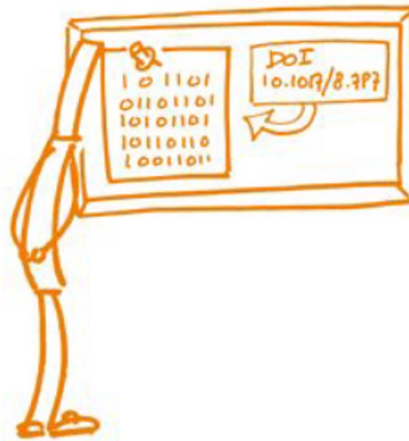
**FAIR Data Principles** provide guidance for producing machine actionable data and metadata



### FAIR DATA PRINCIPLES



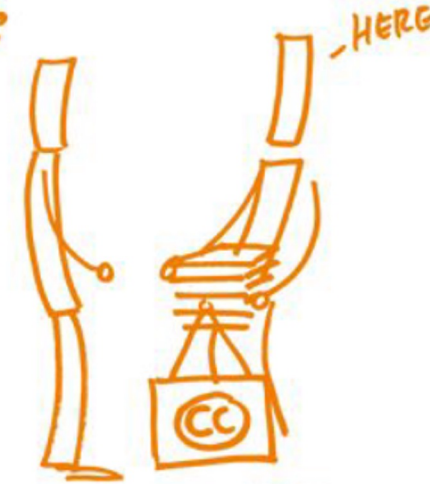
FINDABLE



ACCESSIBLE



INTEROPERABLE



REUSABLE

<https://force11.org/info/the-fair-data-principles/>

Wilkinson et al., *Sci Data* **3**, 160018 (2016).  
<https://doi.org/10.1038/sdata.2016.18>

[10.5281/zenodo.1212496](https://zenodo.org/record/1212496)

funding

erated in

data

al

# China is leading the global trend towards strong Research Data Management and Sharing (RDMS) policies

## ➤ KEY POINTS

❑ Open Access

❑ Data Collection

❑ Statistics

❑ Ethics

information protection

**FAIR Data Principles** provide guidance for producing machine actionable data and metadata



FAIR DATA PRINCIPLES

Where is my data?

FINDABLE

Who can find and use my data and when?

ACCESSIBLE

What does my data mean and what questions can it answer?

INTEROPERABLE

Can my data be used as substrate for AI/ML driven insight?

REUSABLE

<https://force11.org/info/the-fair-data-principles/>

Wilkinson et al., *Sci Data* **3**, 160018 (2016).  
<https://doi.org/10.1038/sdata.2016.18>

[10.5281/zenodo.1212496](https://doi.org/10.5281/zenodo.1212496)

funding

erated in

data

al

# China is leading the global trend towards strong Research Data Management and Sharing (RDMS) policies

## ➤ KEY POINTS

FAIR Data



□ Open

funding

**Ultimately, this is about  
machine readability and  
automation**

in

□ Et

<https://for>

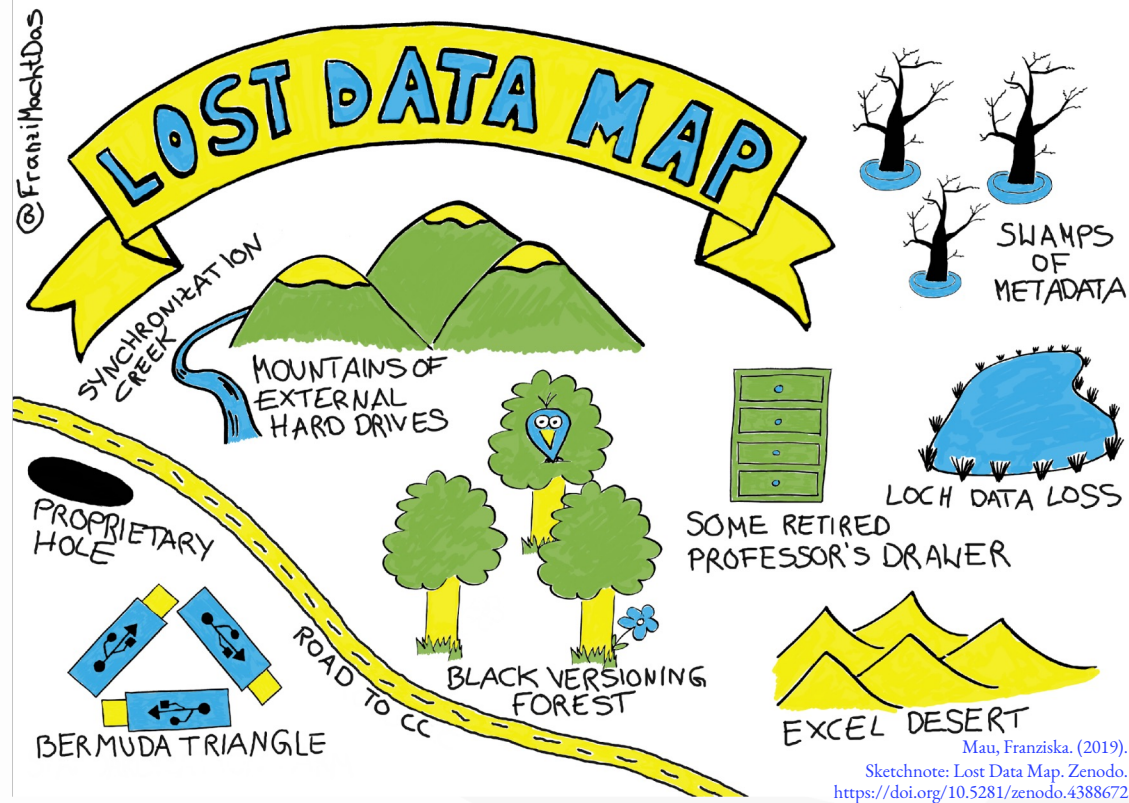
2496

al

information pro



# RDMS → Data **organization** and **preservation**: a gift to your future self!



Information

Storage +  
Management



# RDMS → Data organization and preservation: **3 critical elements**

1. Data must be stored and preserved

- **Hardware**
- **Policies**

2. To be useful data must be found. Labels are essential for organization

- **Metadata standards**
- **Curation**

3. Automation is critical for efficient scientific progress

- **Software Infrastructure + tools**

Content = **Data**





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Content = **Data**

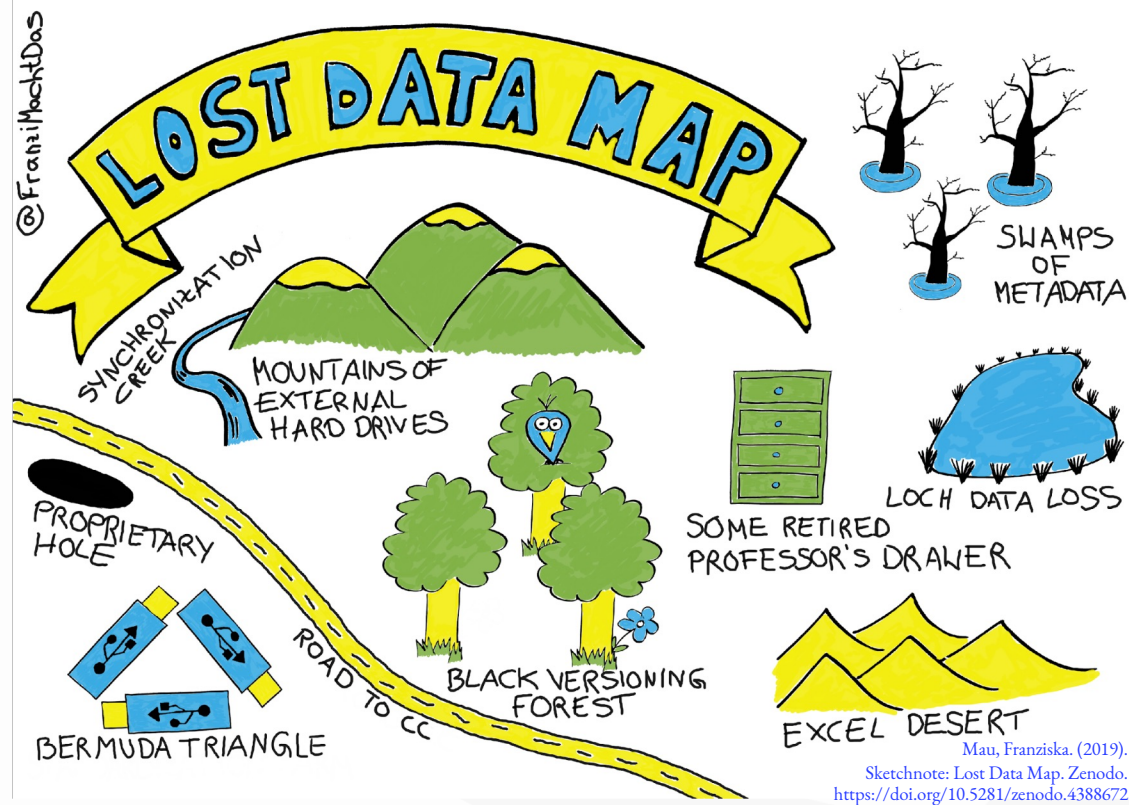
Shelving = **Infrastructure**



Forklift = **Software tools**

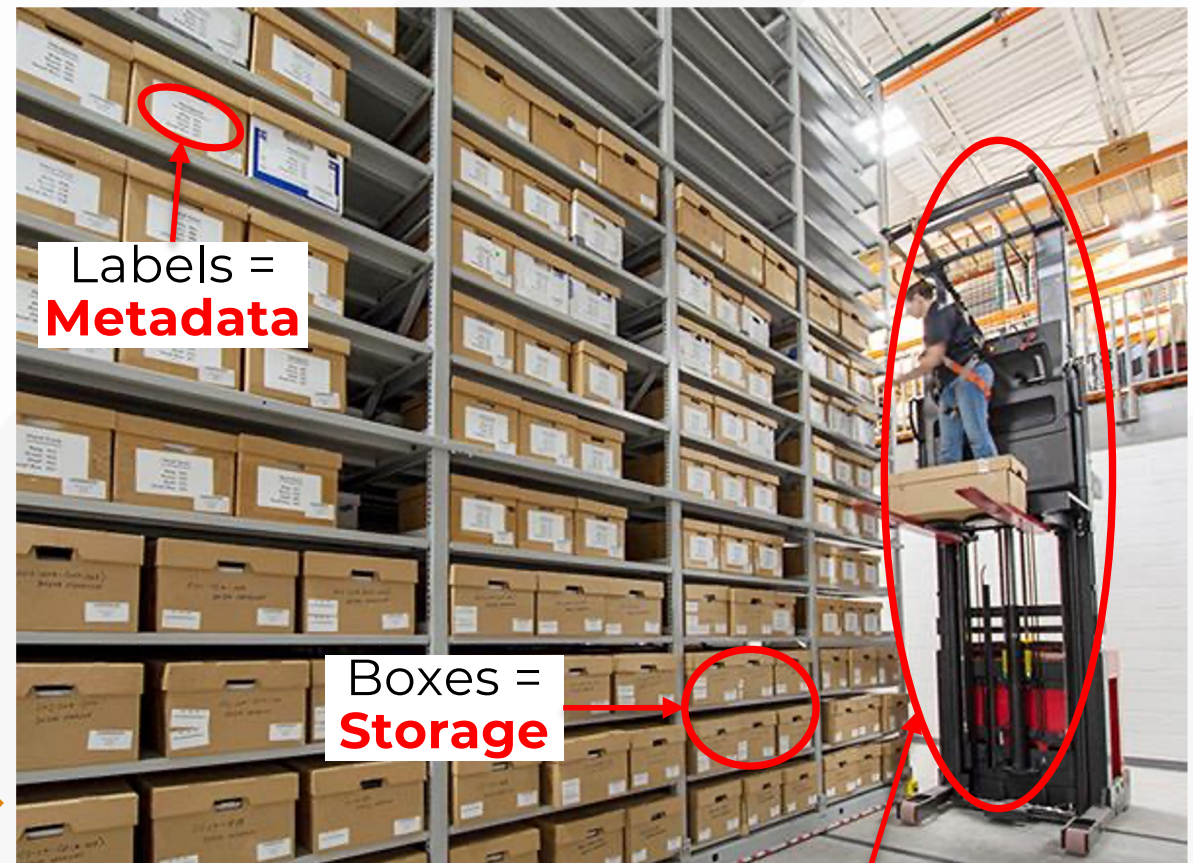


# RDMS → Data organization and preservation: **3 critical elements**



Information  
Storage +  
Management

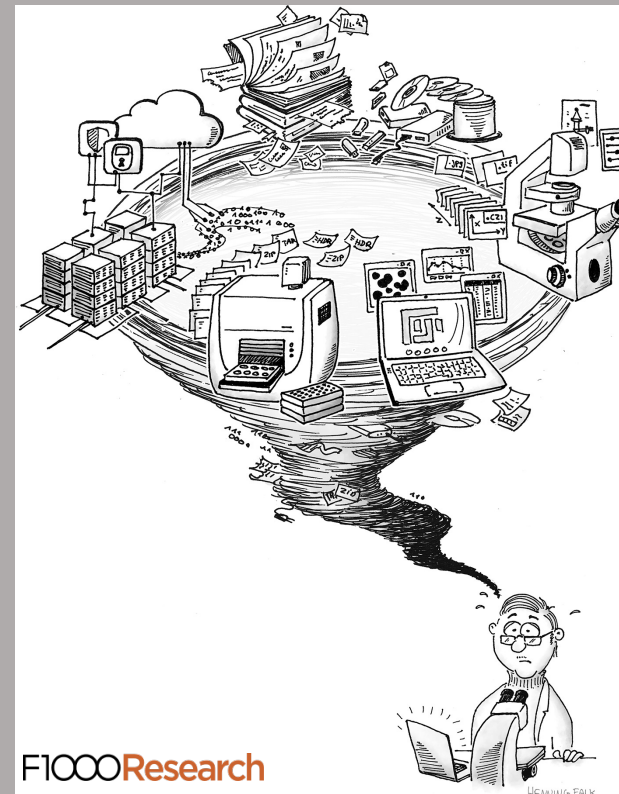
Content = **Data**  
Shelving = **Infrastructure**



# RDMS → Data organization and preservation: **3 critical elements**

**Complex  
Challenging  
Scary  
Time-consuming  
Impossible!**

Content = **Data**  
**Infrastructure**



Forklift = **Software tools**

Storage  
Management

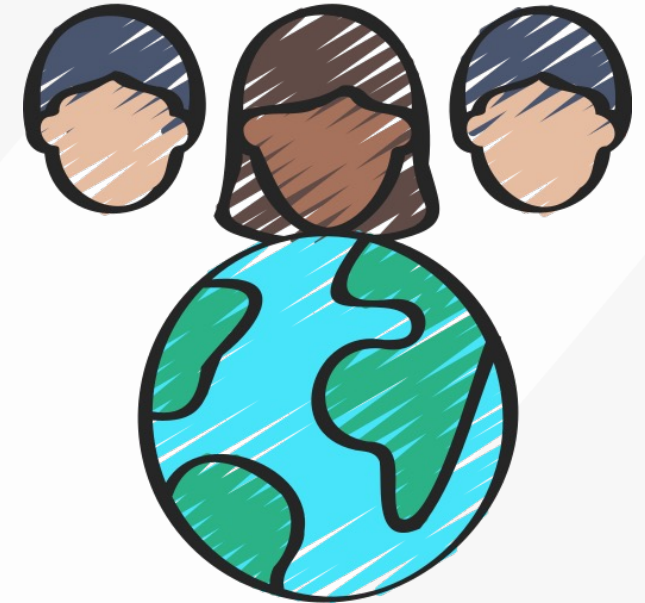


# Take home: data FAIR-ification cannot be done in isolation



Local  
expertise

Community  
Guidelines,  
Specifications  
and Tools



# A network of international organizations spanning the globe



Image credit: <https://quarep.org>



# A network of international organizations spanning the globe





# A network of international organizations spanning the globe



QUAREP-LiMi

News ▾ Organisation ▾ Working Groups ▾ Resources ▾ Events ▾ About ▾



## Quality Assessment and Reproducibility for Instruments & Images in Light Microscopy

The Consortium for Quality Assessment and Reproducibility for Instruments and Images in Light Microscopy (QUAREP-LiMi), *formed* by the global community of practitioners, researchers, developers, service providers, funders, publishers, policy makers and industry related to the use of light microscopy, is committed to democratising access to quantitative and reproducible light microscopy and the data generated by it.

Our mission is to provide a comprehensive set of community-agreed guidelines, protocols, automation procedures and other resources to improve quality control, quality assurance, and instrument/method calibration. The stakeholders advocate for the use of the highest level of reproducibility for data generated by light microscopy methods in scientific research and biotechnology applications. To support the achievement of its mission, QUAREP-LiMi:

QUAREP-LiMi operates a [NextCloud](#) and an OMERO server, which serve as a central repository and exchange point for our collective work. These platforms facilitate collaboration and data sharing between our members.

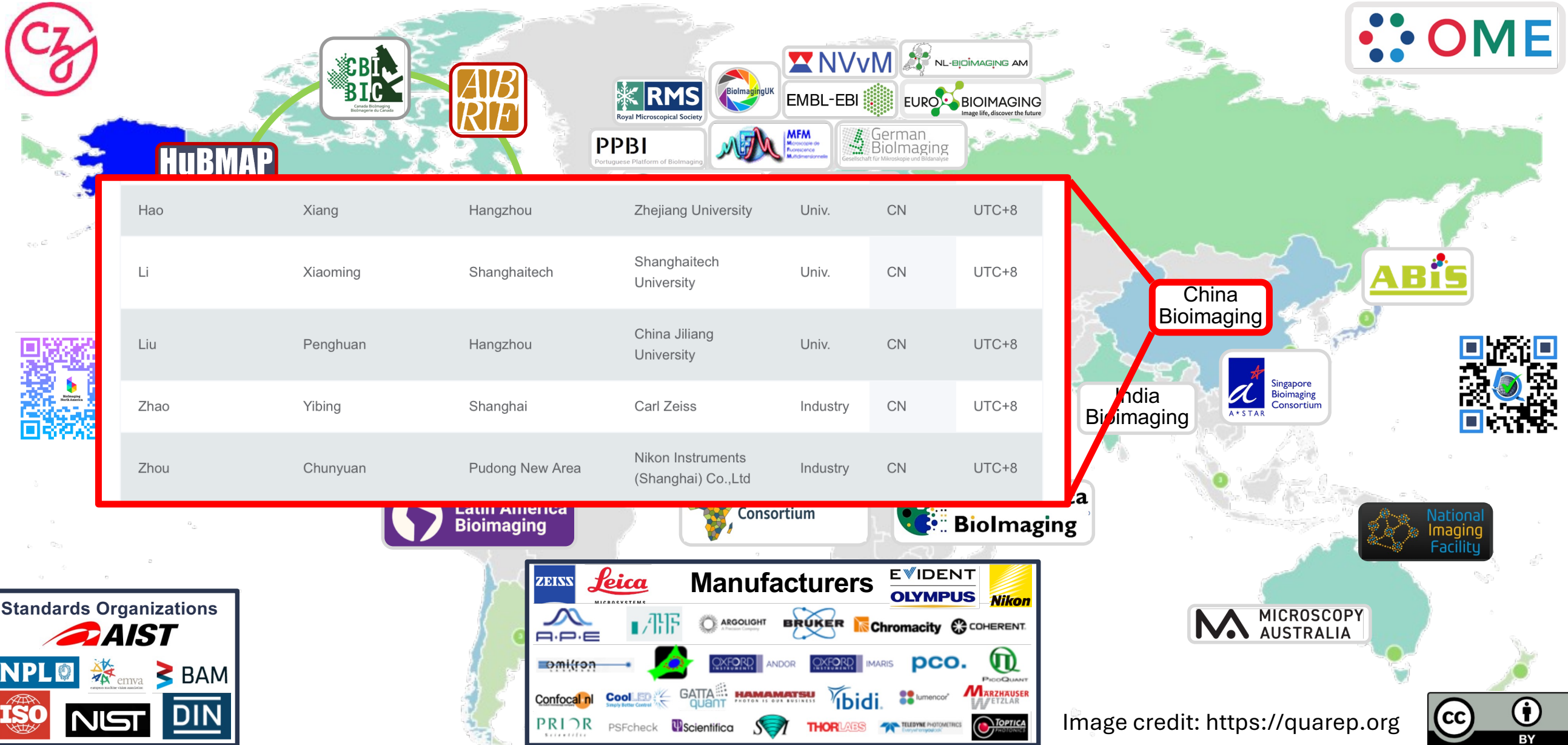
QUAREP-LiMi is open to new members, and we look forward to your contribution. If you are interested in joining our initiative, please fill out our [membership form](#). If you would like to change your Working Group (WG) or join a new WG, please use our [form](#). For any further questions, please [contact us](#).



Standards Organ



# A network of international organizations spanning the globe



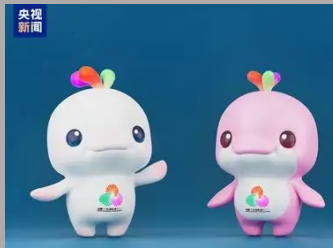


# A network of international organizations spanning the globe



**HuBMAP**

Hao	Xiang	Hangzhou	Zhejiang University	Univ.	CN	UTC+8
Li	Xiaoming				CN	UTC+8
Liu	Pe				CN	UTC+8
Zhao	Yibing				CN	UTC+8
Zhou	Chunyuan	Pudong New Area	(Shanghai) Co.,Ltd	Industry	CN	UTC+8



**Please Join Us!**

**China Bioimaging**

**India Bioimaging**



Image credit: <https://quarep.org>





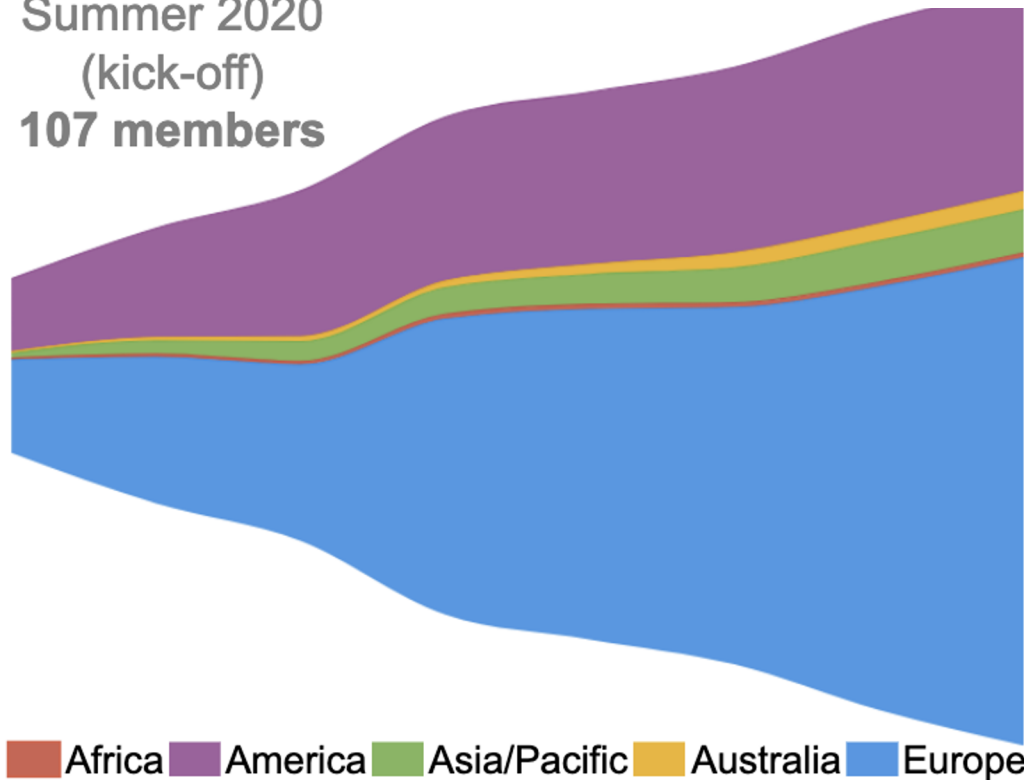
# QUAREP-LiMi: industry and academia to promote quality, reproducibility and sharing-value



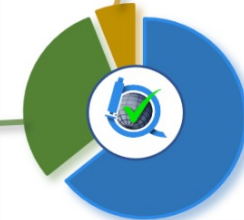
## Membership growth

2026  
> 700 members

Summer 2020  
(kick-off)  
107 members



## Membership composition





# BioImaging North America (BINA)



**Mission:** Engaging bioimaging scientists across North America by creating an inclusive and supportive community to share, advance and succeed together.



Events and Newsletter each month!

8 Working Groups: **Builders**, **Communications**, **Corporate Partners**, **Diversity, Equity & Inclusion**, **Early Career**, **Image Informatics**, **Quality Control & Data Management**, **Training & Education**



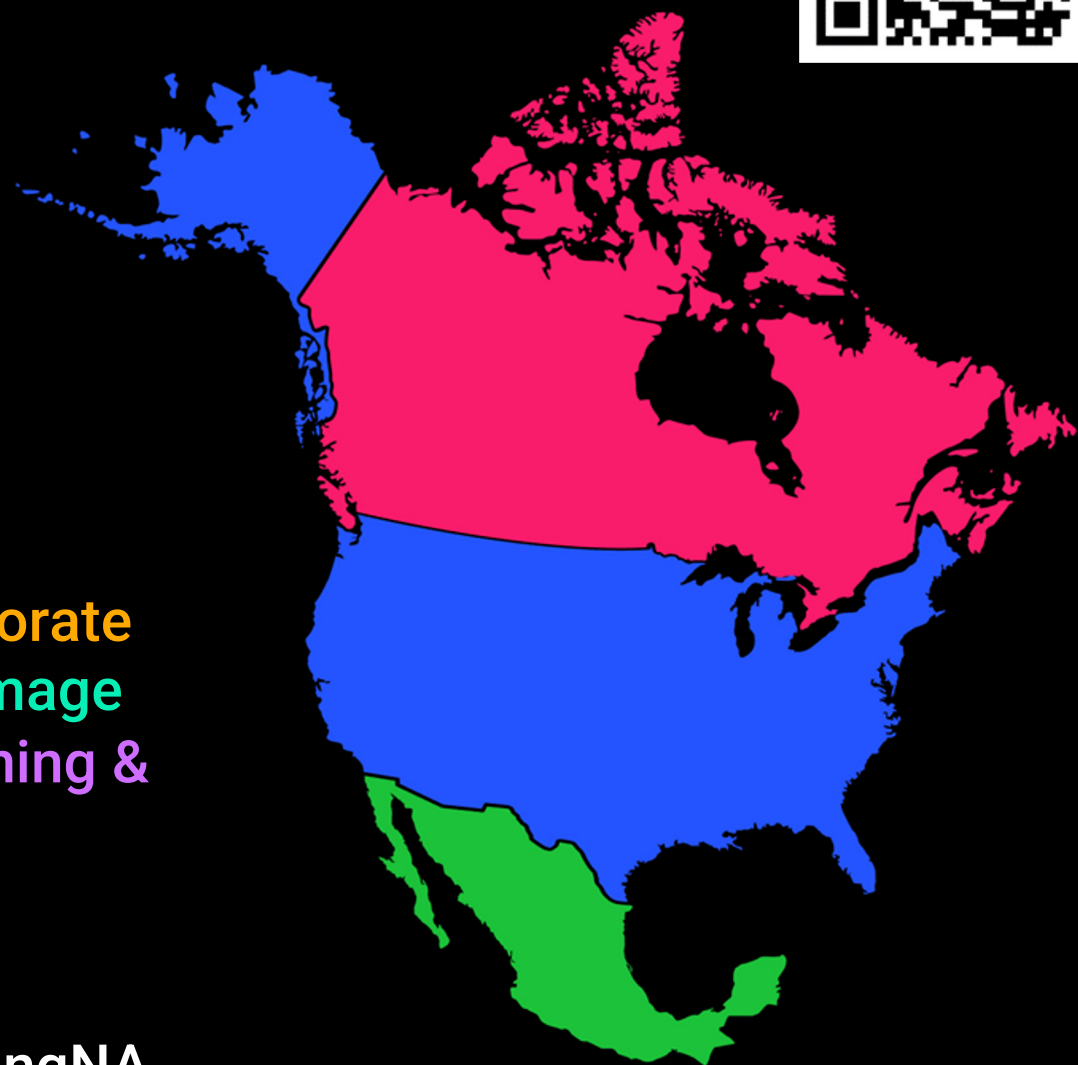
[www.BioImagingNorthAmerica.org/join](http://www.BioImagingNorthAmerica.org/join)



[contact@bioimagingna.org](mailto:contact@bioimagingna.org)



[@BioimagingNA](https://twitter.com/BioimagingNA)





# Quality Control & Data Management Working Group



**Caterina Strambio De Castillia** >  
*Chair*  
UMass Chan Medical School



**Claire Brown** >  
*Board Liaison*  
McGill University



**Eduardo Brito Alarcón** >  
*Member*  
Universidad Nacional Autónoma de México, Cuernavaca



**James Chambers** >  
*Member*  
University of Massachusetts, Amherst



**Alex Corbett** >  
*Member*  
University of Exeter



**Nathalie Gaudreault** >  
*Member*  
Allen Institute for Cell Science



**Adán Guerrero** >  
*Member*  
Universidad Nacional Autónoma de México, Cuernavaca



**Judith Lacoste** >  
*Member*  
MIA Cellavie Inc.



**Glyn Nelson** >  
*Member*  
Newcastle University



**Michael Halter** >  
*Member*  
National Institute of Standards and Technology (NIST)



**Caroline Miller** >  
*Member*  
Histology, Imaging, and Image Analysis Consultant



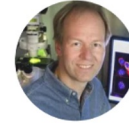
**Roland Nitschke** >  
*Member*  
University of Freiburg



**Arturo Pimentel** >  
*Member*  
Universidad Nacional Autónoma de México



**Kurt Weiss** >  
*Member*  
University of Wisconsin-Madison



**Damir Sudar** >  
*Member*  
Oregon Health Science University

- Quantitative assessment and calibration of microscope performance,
- Rigorous record-keeping of data generation and processing conditions
- Connection of imaging dataset with machine-readable metadata describing its “provenance.”







# Pop-Up EoE: taking the fear out of RDMS



**Beth  
Cimini**



**Vanessa  
Orr**



**Nikki  
Bialy**

Past Events

[Pop-Up EoE, @ BINA 2022](#) October 2022  
Woods Hole, MA

[Pop-Up EoE, @ ABRF](#) (Association of  
Biomolecular Resource Facilities) May 2023,  
Boston, MA

[Pop Up EoE at LABIxBINA](#): BioImaging Across  
the Americas Sep 2023, Morelos, Mexico

## Quotes from Past Exchange of Experience Participants:

- “Wonderful experience! Thank you so much for organizing!” ~Anonymous, PoP-Up EoE participant
- “Thank you for an amazing two days!” ~Anonymous, PoP-Up EoE participant
- “This was a wonderful experience and I really appreciate the organizing staff for their thoroughness and thoughtfulness.” ~Anonymous, PoP-Up EoE participant
- “It was an amazing experience and I am very grateful for being part of this community. I learned a lot, not only during the conference, but watching [the communications] and logistics.” ~Anonymous, PoP-Up EoE participant



# BINA RDMS User Group

Judith  
Lacoste



MIA Cellavie  
/ CBI / BINA  
/ QUAREP

- Customization
- Usability
- Added value
- Automation

## Automated Image Management and Metadata Annotation (AIMM) User Group



Experimental &  
Sample Metadata



Microscopy  
Metadata



Analysis &  
Visualization Metadata

The AIMM User Group brings together researchers to share experiences to enable rapid dissemination and uptake of best practices and tools for the automated management and metadata annotation of image data



BioImaging  
North America

1st Friday of the month,  
every other month



Goal for this year: harmonizing the use of REMBI metadata collection templates



# Community momentum: Nature Methods FOCUS issue, Nature Methods Editorials, Guidelines, etc., etc.

nature methods

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Publish with us

nature > nature methods > focus

Focus 03 December 2021

## Reporting and reproducibility in microscopy

This Focus issue features a series of papers offering guidelines and tools for improving the tracking and reporting of microscopy metadata with an emphasis on reproducibility and data re-use.

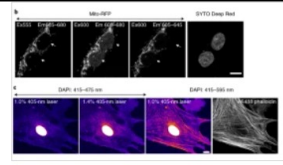
<https://doi.org/10.1038/s41592-021-01342-y>



### Best practices and tools for reporting reproducible fluorescence microscopy methods

Comprehensive guidelines and resources to enable accurate reporting for the most common fluorescence light microscopy modalities are reported with the goal of improving microscopy reporting, rigor and reproducibility.

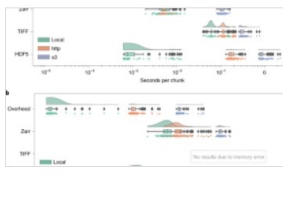
Paula Montero Llopis, Rebecca A. Senft ... Michelle S. Itano



### OME-NGFF: a next-generation file format for expanding bioimaging data-access strategies

OME's next-generation file format (OME-NGFF) provides a cloud-native complement to OME-TIFF and HDF5 for storing and accessing bioimaging data at scale and works toward the goal of findable, accessible, interoperable and reusable bioimaging data.

Josh Moore, Chris Allan ... Jason R. Swedlow



### A global view of standards for open image data formats and repositories


Imaging technologies are used throughout the life and biomedical sciences to understand mechanisms in biology and diagnosis and therapy in animal and human medicine. We present criteria for globally applicable guidelines for open image data tools and resources for the rapidly developing fields of biological and biomedical imaging.

Jason R. Swedlow, Pasi Kankaanpää ... Shuichi Onami

### QUAREP-LiMi: a community endeavor to advance quality assessment and reproducibility in light microscopy

The community-driven initiative Quality Assessment and Reproducibility for Instruments & Images in Light Microscopy (QUAREP-LiMi) wants to improve reproducibility for light microscopy image data through quality control (QC) management of instruments and images. It aims for a common set of QC guidelines for hardware calibration and image acquisition, management and analysis.

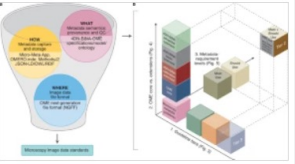
Ulrike Boehm, Glyn Nelson ... Roland Nitschke



### Towards community-driven metadata standards for light microscopy: tiered specifications extending the OME model

Rigorous record-keeping and quality control are required to ensure the quality, reproducibility and value of imaging data. The 4DN Initiative and BINA here propose light Microscopy Metadata Specifications that extend the OME Data Model, scale with experimental intent and complexity, and make it possible for scientists to create comprehensive records of imaging experiments.

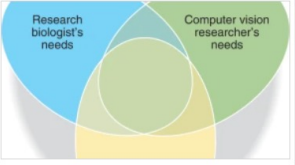
Mathias Hammer, Maximiliaan Huisman ... Caterina Strambio-De-Castillia



### REMBI: Recommended Metadata for Biological Images—enabling reuse of microscopy data in biology

Bioimaging data have significant potential for reuse, but unlocking this potential requires systematic archiving of data and metadata in public databases. We propose draft metadata guidelines to begin addressing the needs of diverse communities within light and electron microscopy. We hope this publication and the proposed Recommended Metadata for Biological Images (REMBI) will stimulate discussions about their implementation and future extension.


Ugis Sarkans, Wah Chiu ... Alvis Brazma



### Micro-Meta App: an interactive tool for collecting microscopy metadata based on community specifications

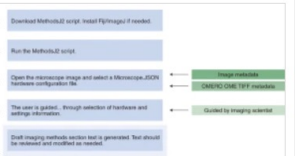
Micro-Meta App is an intuitive, highly interoperable, open-source software tool designed to facilitate the extraction and collection of relevant microscopy metadata as specified by recent community guidelines.

Alessandro Rigano, Shannon Ehmsen ... Caterina Strambio-De-Castillia




### MethodsJ2: a software tool to capture metadata and generate comprehensive microscopy methods text

Joel Ryan, Thomas Pengo ... Claire M. Brown



### MDEmic: a metadata annotation tool to facilitate management of FAIR image data in the bioimaging community

Susanne Kunis, Sebastian Hänsch ... Stefanie Weidtkamp-Peters





# Community standards: Best practices for fluorescence microscopy methods



Perspective

7 Jun 2021

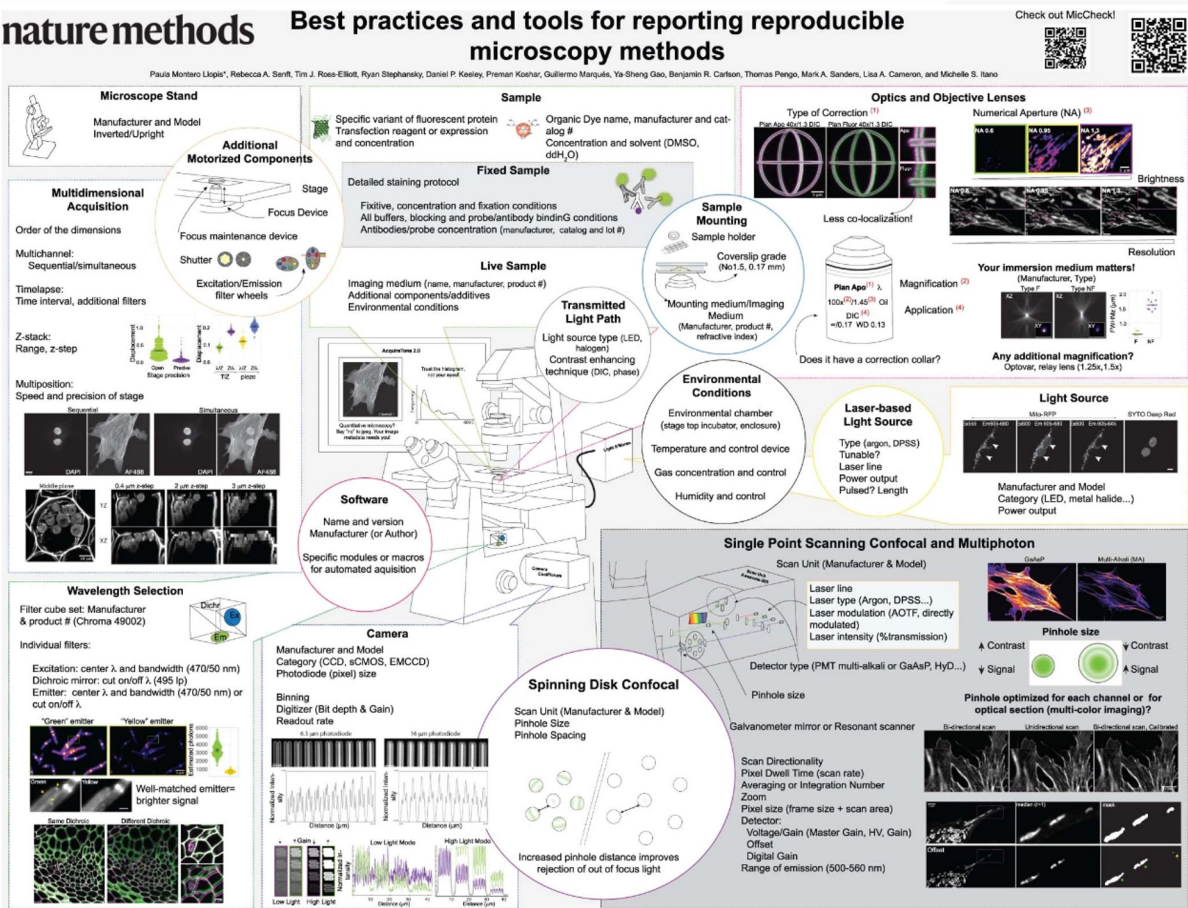
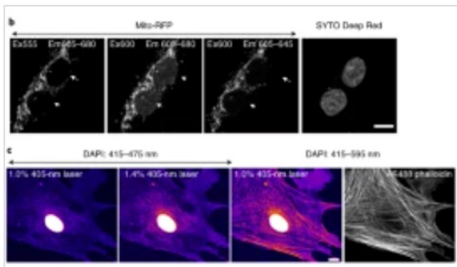
[Nature Methods](#)



## Best practices and tools for reporting reproducible fluorescence microscopy methods

Comprehensive guidelines and resources to enable accurate reporting for the most common fluorescence light microscopy modalities are reported with the goal of improving microscopy reporting, rigor and reproducibility.

Paula Montero Llopis, Rebecca A. Senft ... Michelle S. Itano



**BioImaging  
North America**



**QUAREP-LiMi**



# Community standards: Cloud optimized OME-Next-Gen File Format (2021) OME-Zarr (2023)



## OME-NGFF: a next-generation file format for expanding bioimaging data-access strategies

OME's next-generation file format (OME-NGFF) provides a cloud-native complement to OME-TIFF and HDF5 for storing and accessing bioimaging data at scale and works toward the goal of findable, accessible, interoperable and reusable bioimaging data.

Josh Moore, Chris Allan ... Jason R. Swedlow

[Home](#) > [Histochemistry and Cell Biology](#) > [Article](#)

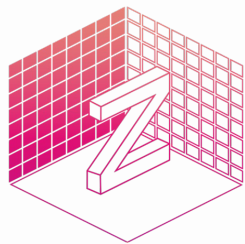
## OME-Zarr: a cloud-optimized bioimaging file format with international community support

[Original Paper](#) | [Open access](#) | Published: 10 July 2023

Volume 160, pages 223–251, (2023) [Cite this article](#)

OME

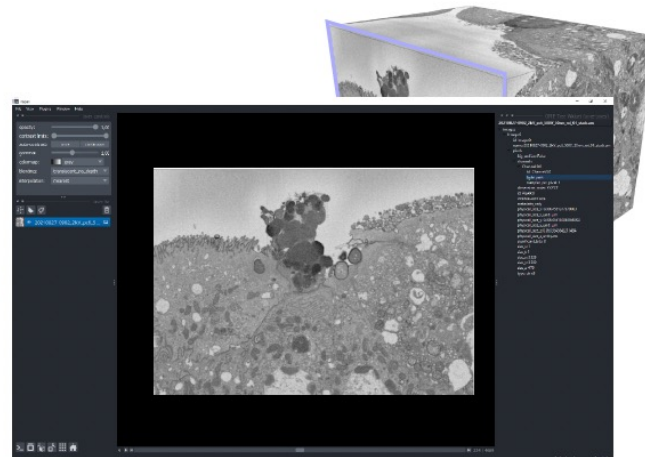
Zarr



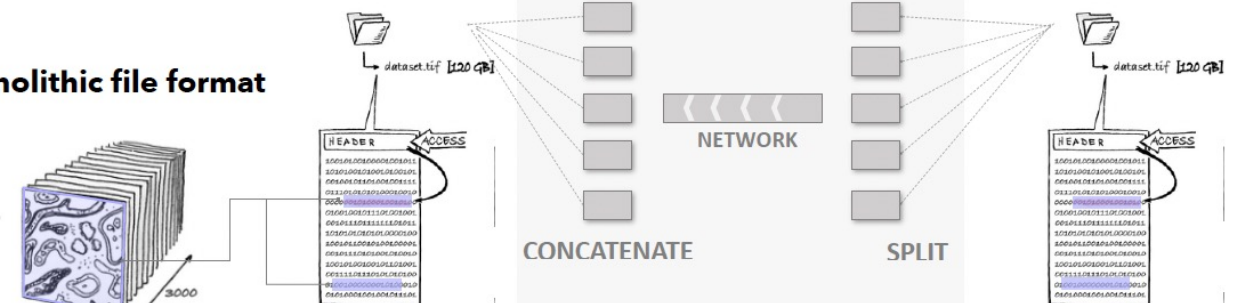
viewed in



napari



### Monolithic file format

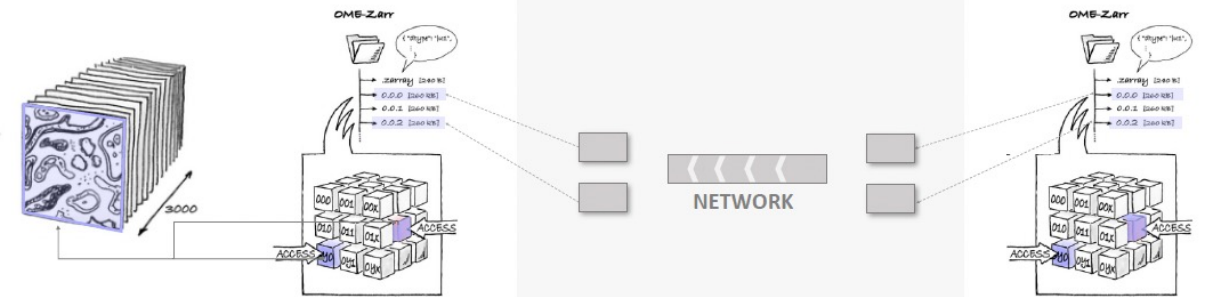


Local computer

Access via network

External data storage

### Chunkable file format ("Cloud-optimized")





# Community-developed checklists for publishing images and image analysis



Perspective | [Published: 14 September 2023](#)

## Community-developed checklists for publishing images and image analyses

[Christopher Schmied](#) , [Michael S. Nelson](#), [Sergiy Avilov](#), [Gert-Jan Bakker](#), [Cristina Bertocchi](#), [Johanna Bischof](#), [Ulrike Boehm](#), [Jan Brocher](#), [Mariana T. Carvalho](#), [Catalin Chiritescu](#), [Jana Christopher](#), [Beth A. Cimini](#), [Eduardo Conde-Sousa](#), [Michael Ebner](#), [Rupert Ecker](#), [Kevin Eliceiri](#), [Julia Fernandez-Rodriguez](#), [Nathalie Gaudreault](#), [Laurent Gelman](#), [David Grunwald](#), [Tingting Gu](#), [Nadia Halidi](#), [Mathias Hammer](#), [Matthew Hartley](#), ... [Helena Klara Jambor](#)  [+ Show authors](#)

[Nature Methods](#) **Community-developed checklists for publishing images and image analyses**

### Acquisition of microscopy images

Image, microscope setup, experimental design

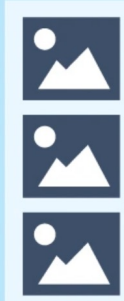


### Foundation

Experimental design and good scientific practice

### Publishing of microscopy image figures and image analyses

#### Microscopy images



- Image processing
- Qualitative analysis
- Quantitative analysis
- Analysis workflows

#### Results

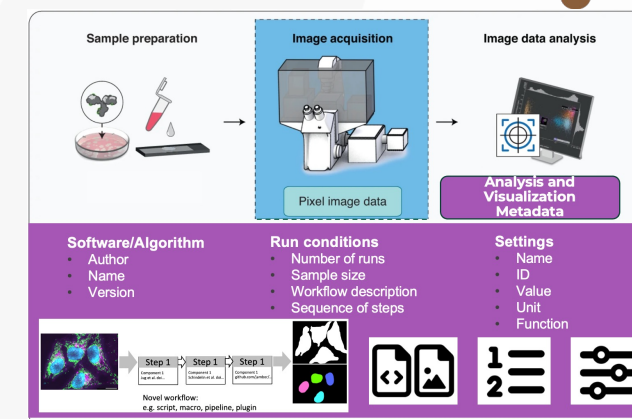


Image figure

Cell	Area	Circ.
1	102	0.6
2	210	0.3
3	150	0.7

Measurements

Image data storage and availability



### Checklists for publication of image-analysis workflows

#### Machine learning workflows

- |  |  |  |
|--|--|--|
|  | Cite original method                   | <input type="checkbox"/> Minimal (all models)                    |
|  | Access to model                        | <input type="checkbox"/>   |
|  | Example or validation data             | <input type="checkbox"/>   |
|  | Training and testing data and metadata | <input type="checkbox"/> Recommended (pretrained and new models) |
|  | Code available                         | <input type="checkbox"/>   |
|  | Limitations                            | <input type="checkbox"/>   |
|  | Cloud hosted or container              | <input type="checkbox"/>   |
|  | Standardized format                    | <input type="checkbox"/> Ideal (new models)                      |



# Community-developed recommendations for promoting reproducible bioimage analysis



PERSPECTIVE | 30 OCTOBER 2024

## The crucial role of bioimage analysts in scientific research and publication

In collection: Imaging

Beth A. Cimini , Peter Bankhead , Rocco D'Antuono , Elnaz Fazeli , Julia Fernandez-Rodriguez , Caterina Fuster-Barceló , Robert Haase , Helena Klara Jambor , Martin L. Jones , Florian Jug , Anna H. Klemm , Anna Kreshuk , Stefania Marcotti , Gabriel G. Martins , Sara McArdle , Kota Miura , Arrate Muñoz-Barrutia , Laura C. Murphy , Michael S. Nelson , Simon F. Nørrelykke , Perrine Paul-Gilloteaux , Thomas Pengo , Joanna W. Pylvänäinen , Lior Pytowski , Arianna Ravera , Annika Reinke , Youss Rekik , Caterina Strambio-De-Castillia , Daniel Thédié , Virginie Uhlmann , Oliver Umney , Laura Wiggins , Kevin W. Eliceiri 



**BioImaging  
North America**

**GLOBAL  
BIOIMAGING**  
growing collaboration



### Barriers to bioimage analysis

#### Personal

**Getting started**  
Lack of awareness of the benefits of quantitative image analysis  
Pressure to publish  
Lack of software documentation

**Career**  
Lack of career progression opportunities for bioimage analysts  
Lack of well-defined roles

#### Scientific community

**Peer pressure**  
Not feeling legitimate enough to contribute, scrutiny from the community

**Governance principles**  
Choosing a model: e.g. community led or a small team of developers?

**Moral incentive**  
Researchers who have benefited from open-source tools should contribute to the open-source ecosystem.

#### Structural

**Publishing**  
Publishing tools is difficult due to lack of interest from journal editors. Publication metrics do not reflect the usefulness of the tool.

Effectively addressing a wide range of problems can mean that results are less impressive on specific established benchmarks.

Non-open-source algorithms can claim novelty without responsibility, making it harder to publish truly open, user-friendly alternatives.

Original software publications do not represent the contributions of people who join the project later.

There is a lack of rules and guidelines for publishing software dependencies.

**Funding**  
Lack of dedicated funding for software  
Lack of funding for software maintenance and documentation

### What can we do? What do we need?

#### Bioimage analysis community

**Define standards**

- Communication, usability and visibility of BIA tools
- File formats and metadata
- New metrics for evaluation of impact
- Training and curriculum

**Catalog resources**

- BIA tools and workflows
- Training materials
- Events (conferences, courses, hackathons)

**Adopt best practices**

- Software engineering and FAIR standards
- Didactics
- Licensing

**Disseminate standards**

- Publications with guidelines
- Policies
- Training materials

**How-to guides**

- Challenges for specific biological applications
- Example workflows
- Computational environments for testing

**Training**

- Events (conferences, courses, hackathons)
- Train-the-trainer courses
- Undergraduate courses

#### Policy makers and funders

**Provide dedicated funding**

- BIA specialists
- Existing platforms and repositories
- Software engineers
- Software development and maintenance (focus on tool usability)

**Support publications**

- BIA tools
- BIA workflows

**Recognize non-standard scientific contributions**

- New metrics for evaluation of impact
- Career pathways

### A Image analysis

- Theoretical knowledge (e.g. filtering, segmentation, feature extraction, ML, AI)
- Technical knowledge (e.g. image analysis software, microscopy, statistics, ML, AI)
- Context (e.g. biology, biophysics)

### B Implementation

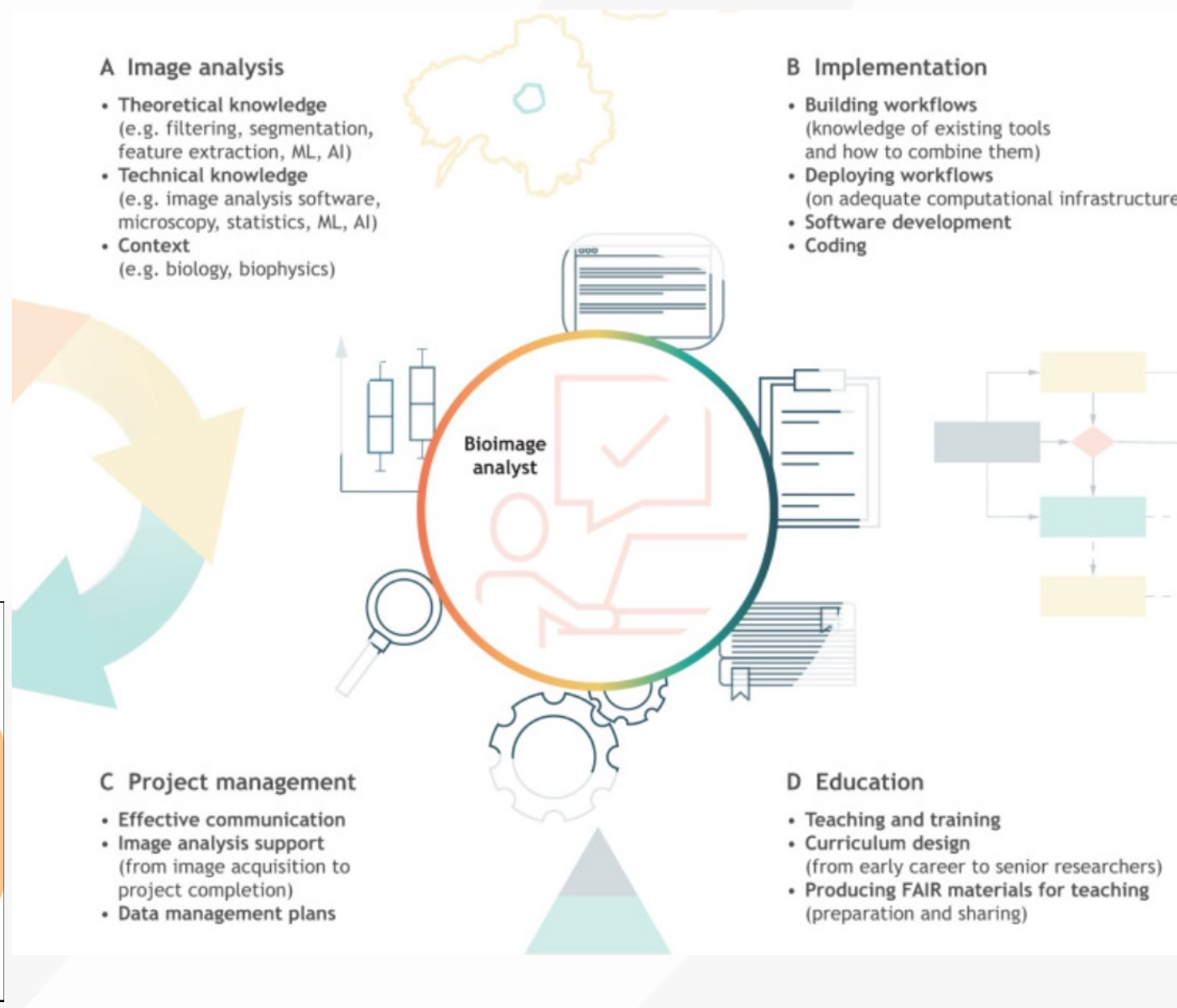
- Building workflows (knowledge of existing tools and how to combine them)
- Deploying workflows (on adequate computational infrastructure)
- Software development
- Coding

### C Project management

- Effective communication
- Image analysis support (from image acquisition to project completion)
- Data management plans

### D Education


- Teaching and training
- Curriculum design (from early career to senior researchers)
- Producing FAIR materials for teaching (preparation and sharing)



# Community-developed checklists for microscopy methods reporting



Rockefeller University Press ▾ JCB JEM JGP JHI LSA ↗



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Volume 225, Issue 3  
2 March 2026


















































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## Article Contents


Introduction

Viewpoint | Reproducibility | February 25 2026



### Better reporting is better science: Community-defined minimal reporting requirements for light microscopy

Paula Montero Llopis , Chloë van Oostende-Triplet , Nathalie Gaudreault , Caterina Strambio De Castillia , Julia Fernandez-Rodriguez , Gabriel Martins , Alison North , Luis Acevedo , Sergiy Avilov , Cristina Bertocchi , Ulrike Boehm , Lisa Cameron , Michael Cammer , Aurélie Cleret-Buhot , Steffen Dietzel , Orestis Faklaris , David Gaboriau , Thomas Guilbert , David Grunwald , Tingting Gu , Nadia Halidi , Mathias Hammer , Hella Hartmann , Janosch Heller , Helena Jambor , Ayse Aslihan Koksoy , Judith Lacoste , DeLaine Larsen , Sylvia Emmanuelle Le Dévédec , Penghuan Liu , Josh Moore , Glyn Nelson , Michael Nelson , Nils Norlin , Adam Parslow , Alexander L. Payne-Dwyer , John Peterson , Santosh Podder , Andrea Ravasio , Eduardo Rosa-Molinari , Britta Schroth-Diez , Olaf Selchow , Sathya Srinivasan , Douglas Taatjes , Kirstin Vonderstein , Christa Walther , Roland Nitschke 

+ Author and Article Information

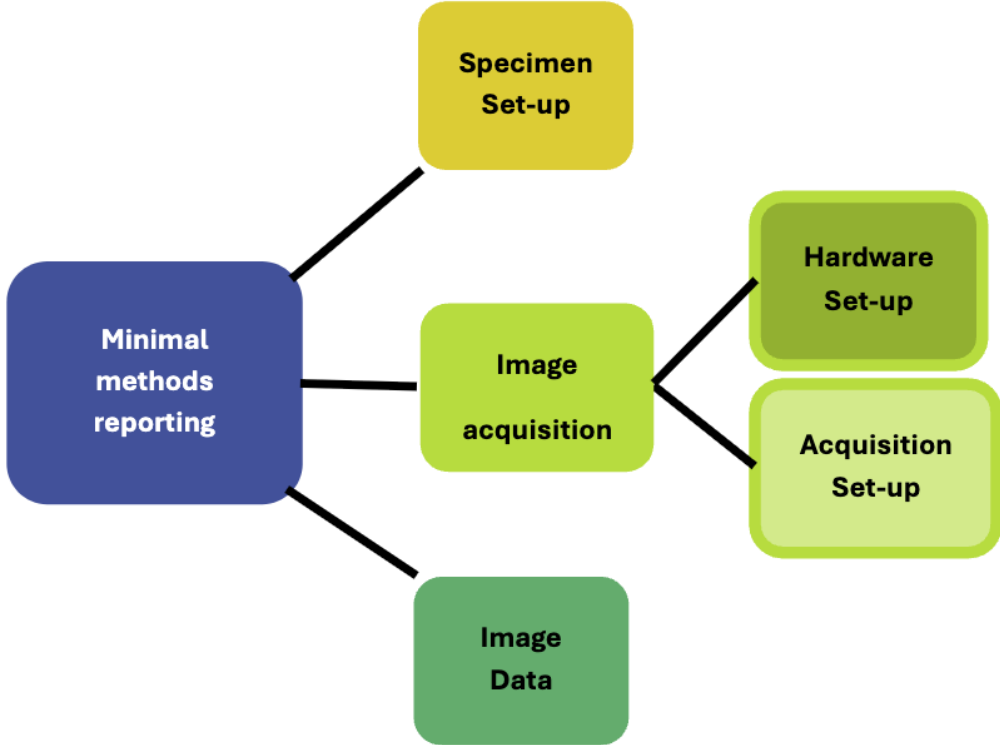
 Check for updates

*J Cell Biol* (2026) 225 (3): e202601032. <https://doi.org/10.1083/jcb.202601032>

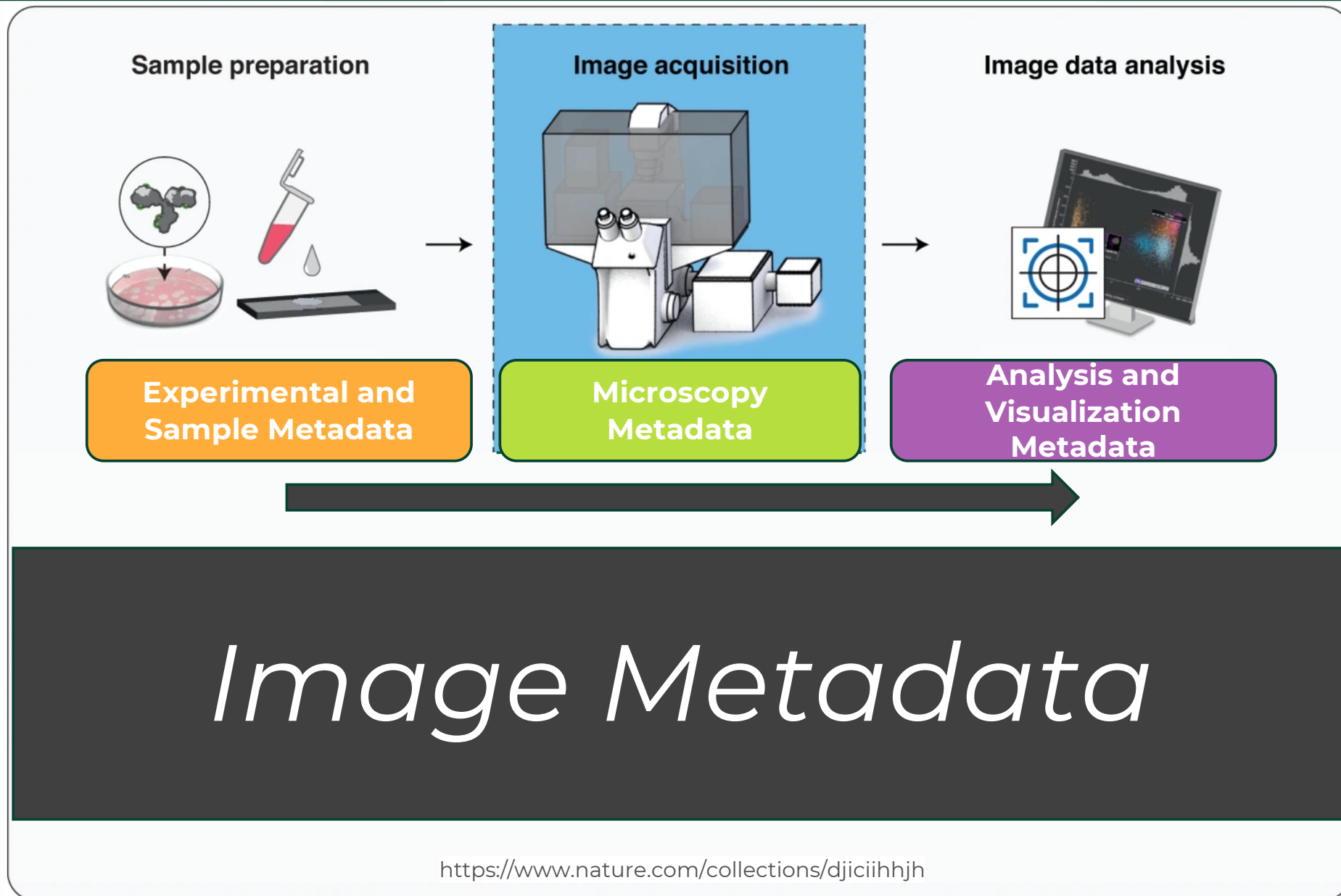
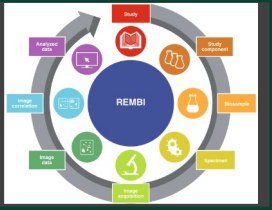
 Split-Screen  PDF  Share ▾  Tools ▾

Incomplete reporting of microscopy methods undermines transparency, reproducibility, and data reuse. Despite recent initiatives, comprehensive, broadly endorsed, and accessible reporting guidelines are still lacking. Here, we present a bare minimal microscopy reporting requirements checklist that integrates human- and machine-readable input to provide clear, actionable guidance for researchers, reviewers, and publishers and to advance community standards in microscopy.

Categories		Examples	Machine readable NBO-Q* alignment
Specimen set-up			
Sample mounting	Cover glass (cover glass number or thickness; coating)	Samples were grown on #1.5H cover glass (Martenfeld), coated with 1 mg/ml collagen type I (Sigma, C8919).	CoverGlass/CoverGlassNo CoverGlass/Thickness CoverGlass/Coating
	Mounting medium or imaging medium (name and manufacturer)	Prior to imaging, samples were mounted in Slowfade Glass mounting medium (ThermoFisher).	MountingMedium/Model MountingMedium/Manufacturer
Sample labelling*	Fluorescent protein (specific variant or probe)	mGFPmu3, GCaMP6f	
	Dye (name, manufacturer and concentration)	MitoTracker Green at 1 µg/ml final Secondary antibody conjugated to AlexaFluor 647	
Hardware set-up			
Microscope stand	Description (manufacturer; model; inverted or upright)	Microscopy imaging experiments were performed on a Nikon Ti2 inverted microscope stand.	MicroscopeStand/Manufacturer MicroscopeStand/Model MicroscopeStand subtype (Inverted, Upright)
Modalities and modules/add-on	Specify the modalities and modules used**	Microscope stand was equipped with a Yokogawa spinning disk CSU-W1 and a SORA module.	Pixels/Channel/IlluminationType (Wide-field_Fluorescence, Confocal_Fluorescence_array-raster-scan, Confocal_Fluorescence_spinning disk)
		For phase contrast imaging, we used a phase contrast objective and a respective phase plate in the condenser.	
		Fluorescent images were captured on a Zeiss Observer.Z1 widefield microscope equipped with an Apotome module.	

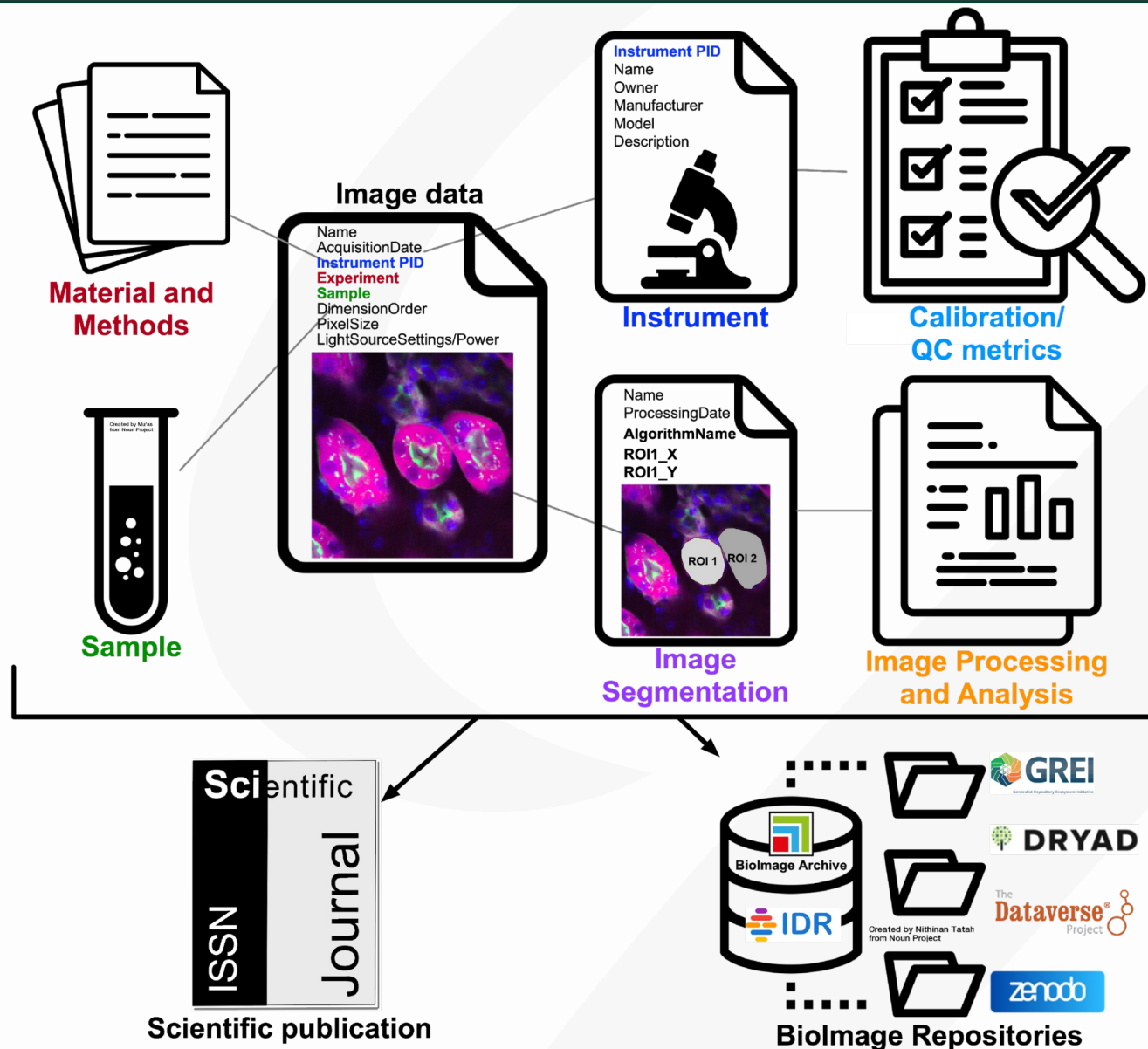


# Image Metadata is key for producing high-quality FAIR data

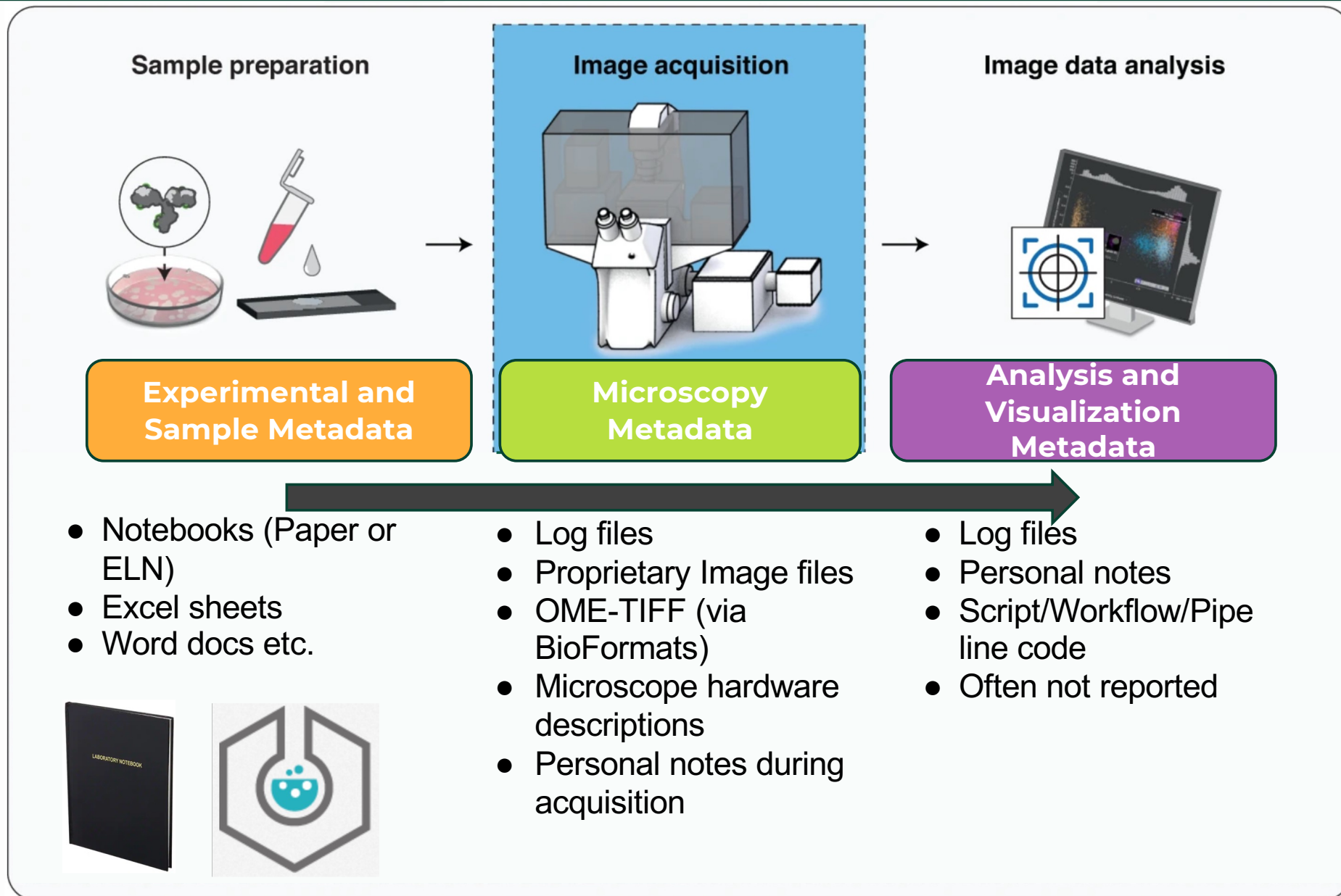
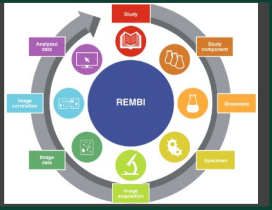




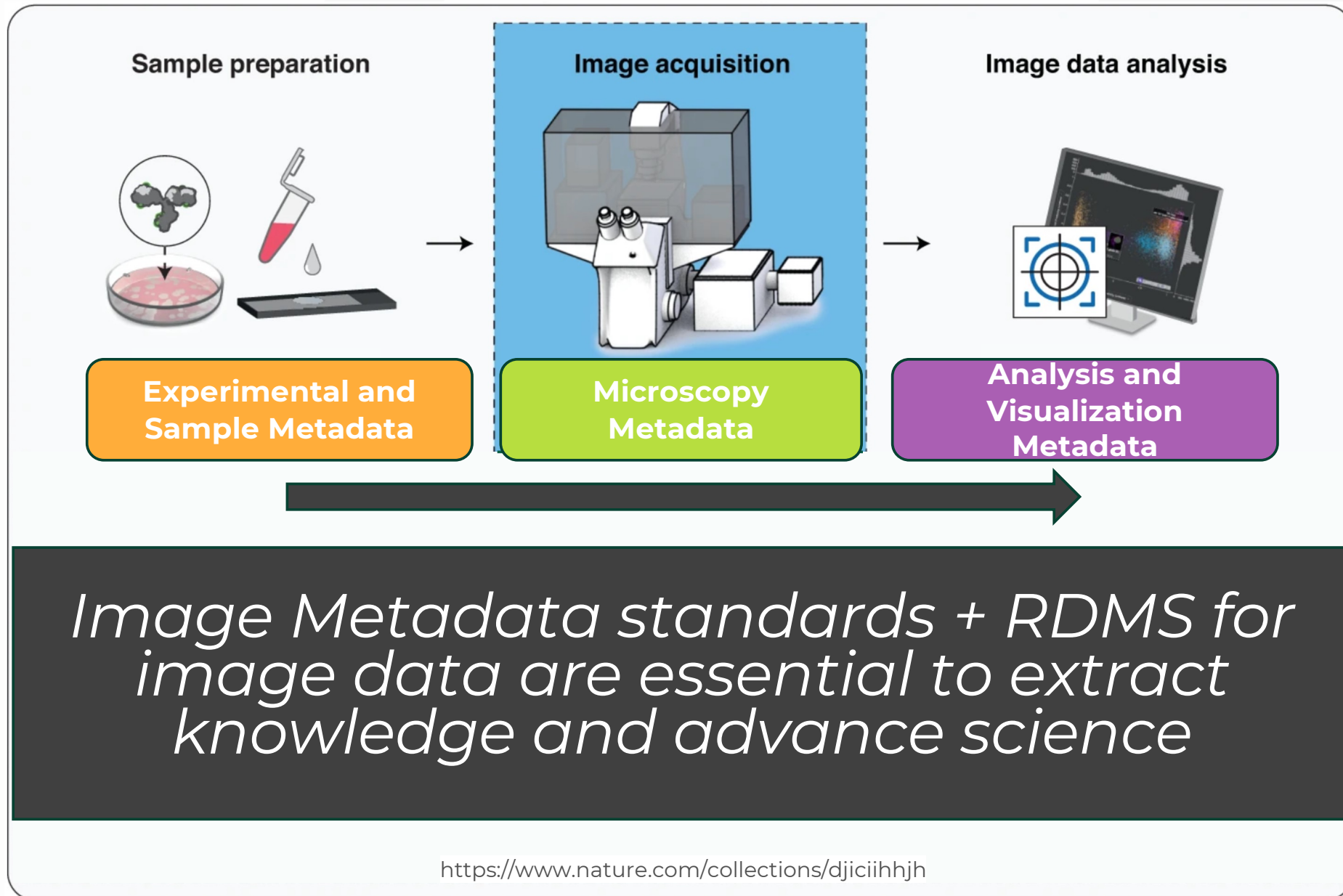
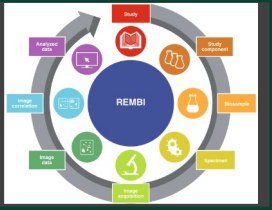
# Where is bioimage metadata?



# Fragmentation is the enemy

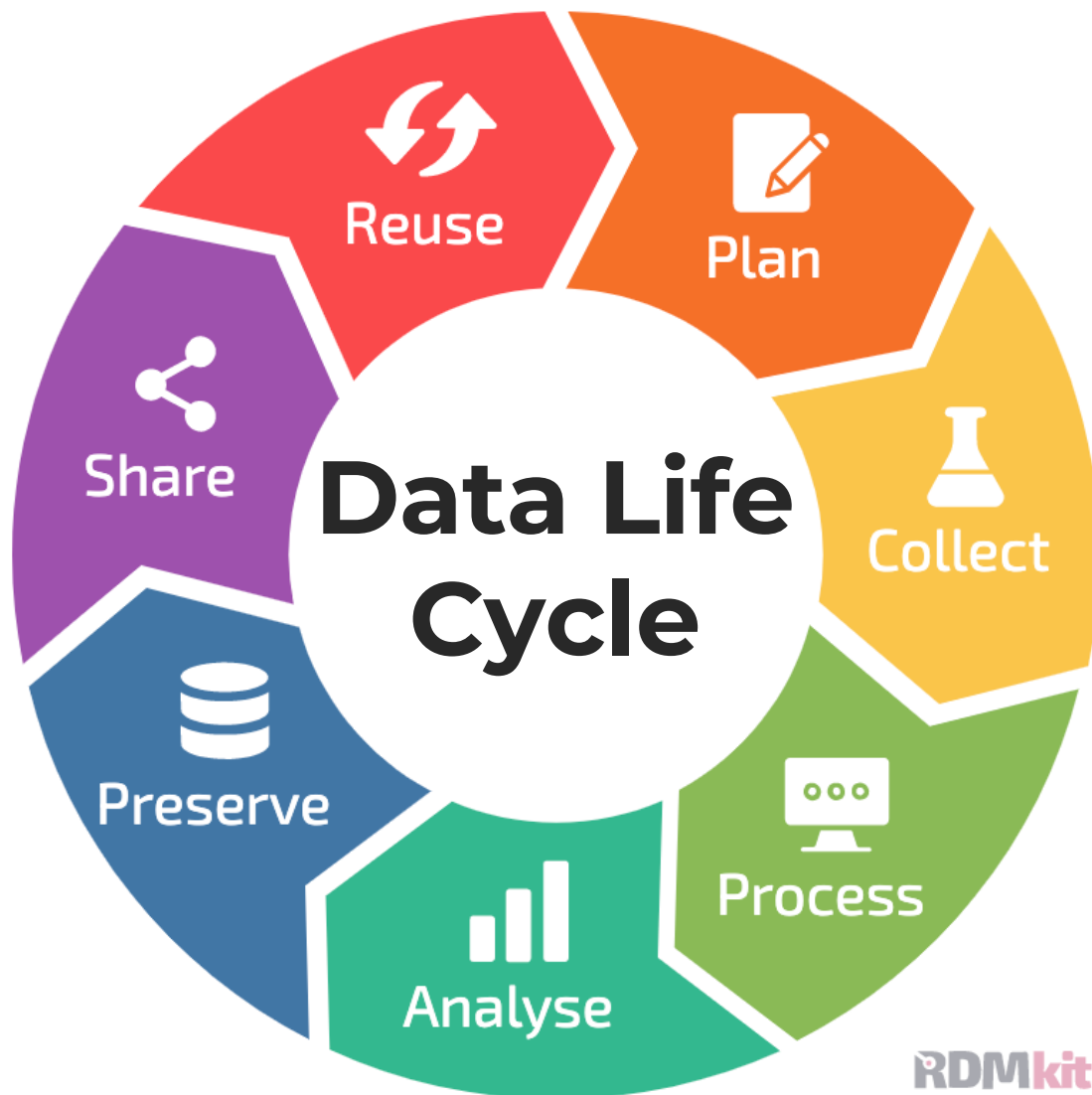


# Image Metadata is key for producing high-quality FAIR data





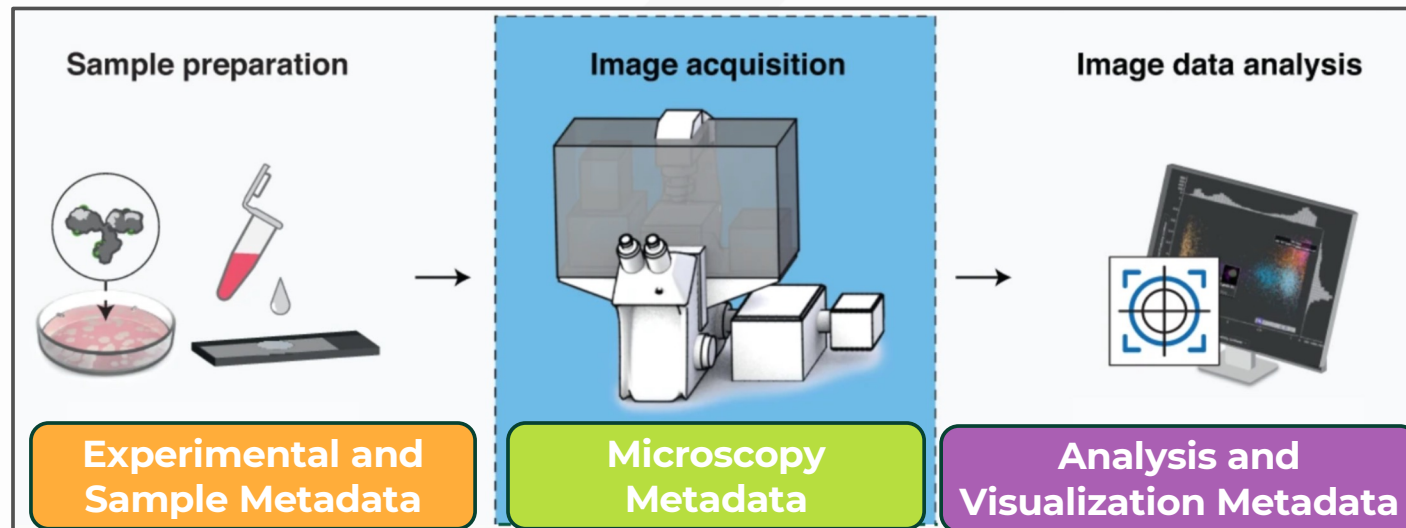
# What is FAIR Research Data Management and Sharing (RDMS)?



- Streamlined annotation, organization, integration, analysis storage, preservation, and sharing of data
- Pre-Publication: Everyday **Handling of Active Data** (includes local storage)
- Post-Publication: Long-term **Data Storage, Preservation, and Sharing**

# Pre-publication vs. Post-publication Research Data Management and Sharing (RDMS)

## Pre-publication

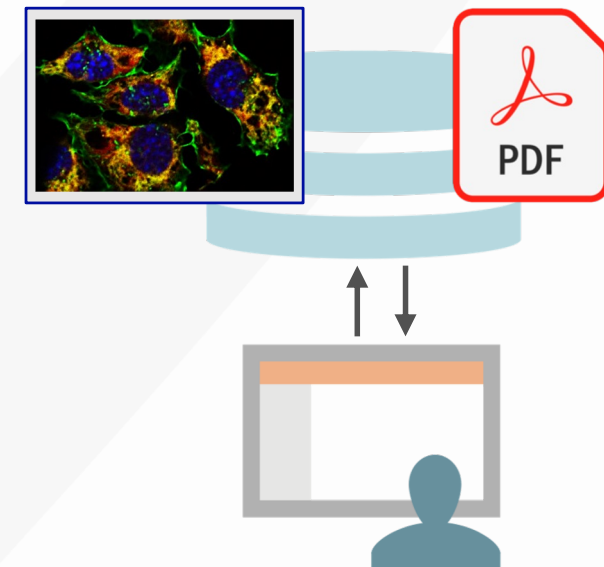


*Data Organization during research project*

***Benefits data producers***

*Image Data Resources  
= OMERO*

## Post-publication



*FAIR Data Sharing*

***Benefits data producers  
+ re-users***

*(mostly) Image Data Repositories  
= BioImage Archive*

# Pre-publication vs. Post-publication Research Data Management and Sharing (RDMS)

Pre-publication

Post-publication



**Pre-Publication RDM is the Missing Link to extract knowledge from FAIR bioimage data**

Data Organization

**Benefits data producers**

*Image Data Resources  
= OMERO*

**+ re-users**

*(mostly) Image Data Repositories  
= BioImage Archive*





# RDMS cyberinfrastructure for images: beautiful fountains require ugly piping!

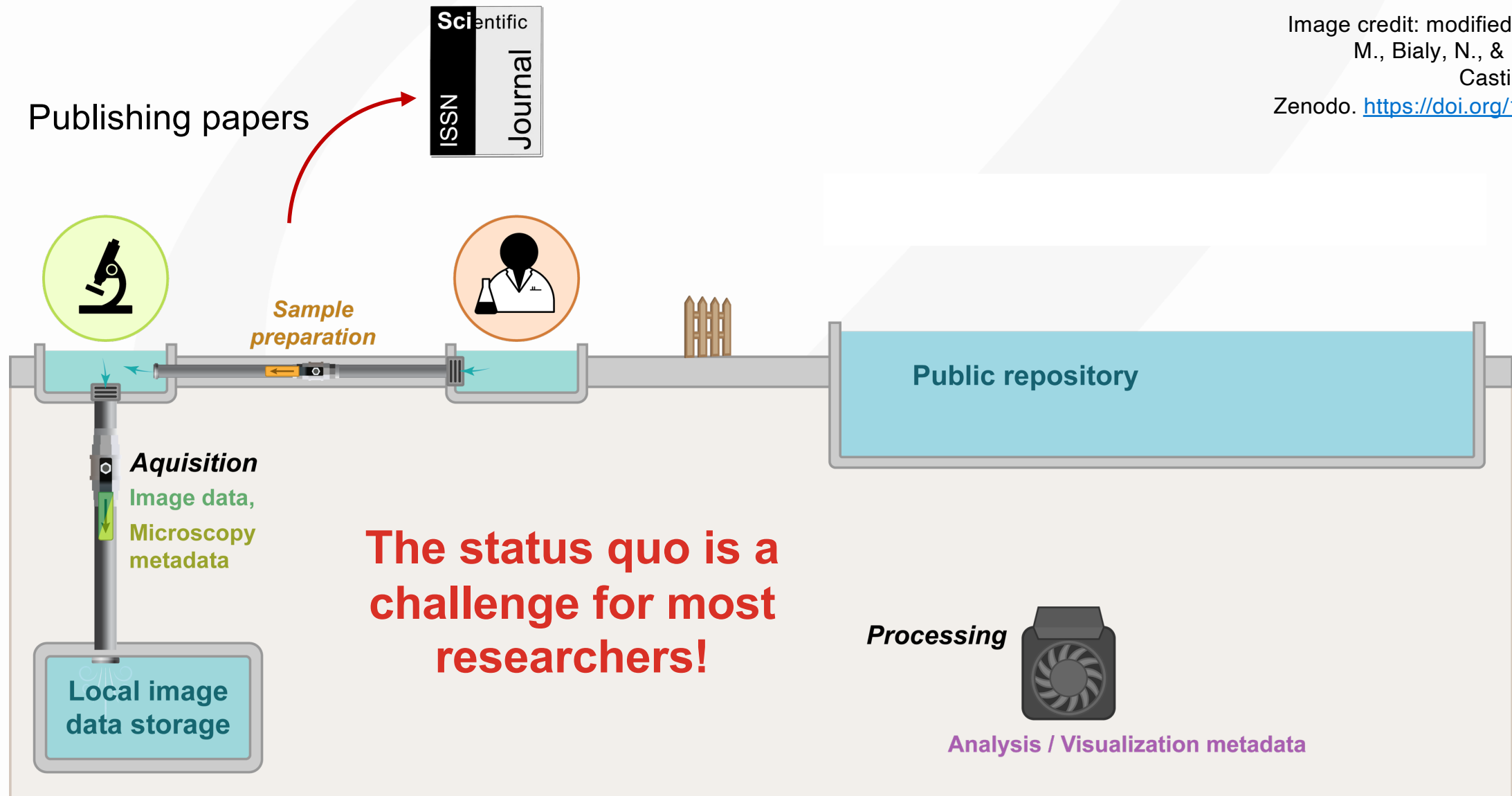


Image credit: modified from Stefely, M., Bialy, N., & Strambio-De-Castillia, C. (2024). Zenodo. <https://doi.org/10.5281/zenodo.14020675>

# RDMS cyberinfrastructure for images: beautiful fountains require ugly piping!

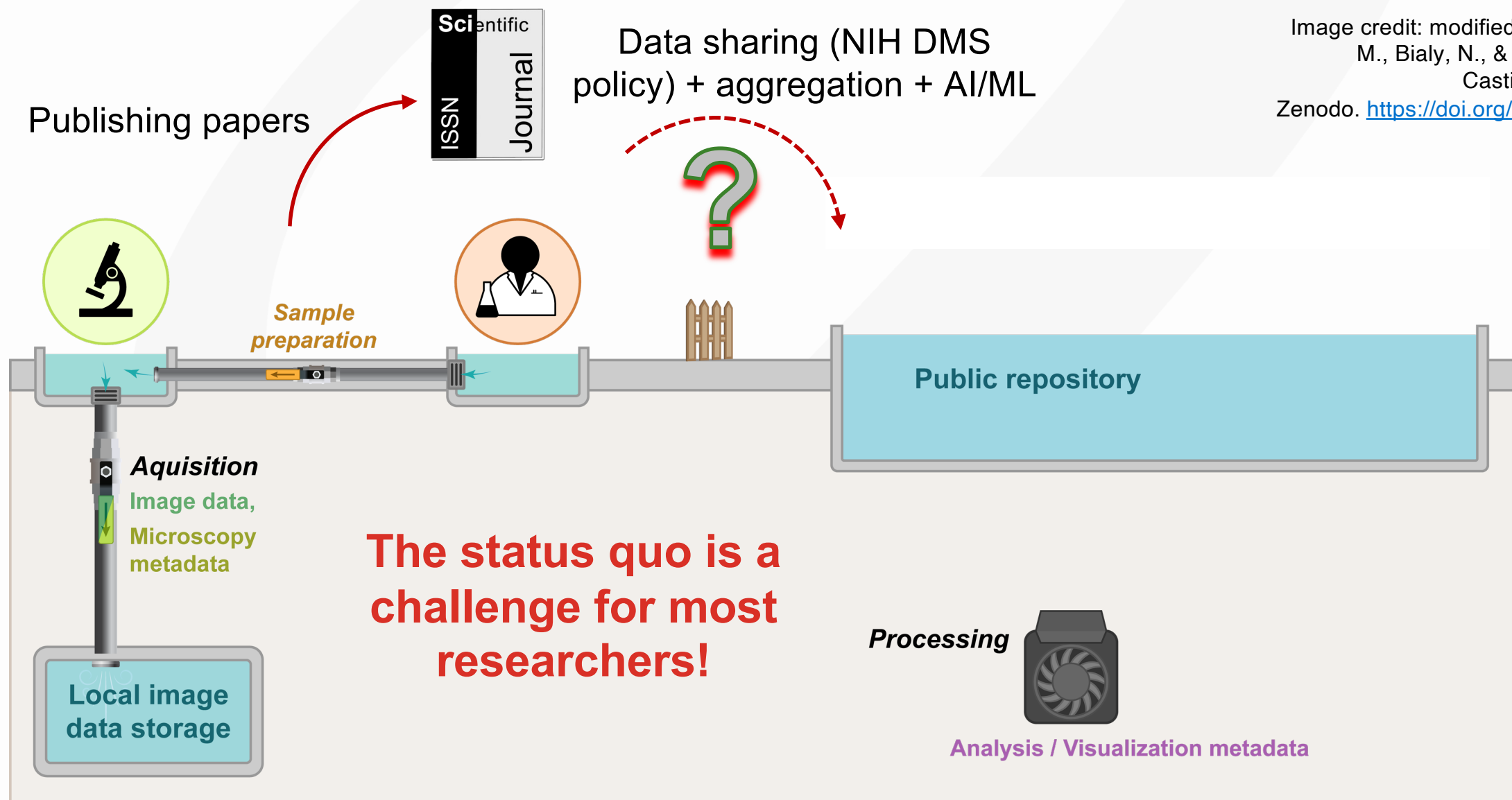


Image credit: modified from Stefely, M., Bialy, N., & Strambio-De-Castillia, C. (2024). Zenodo. <https://doi.org/10.5281/zenodo.14020675>

# RDMS cyberinfrastructure for images: beautiful fountains require ugly piping!

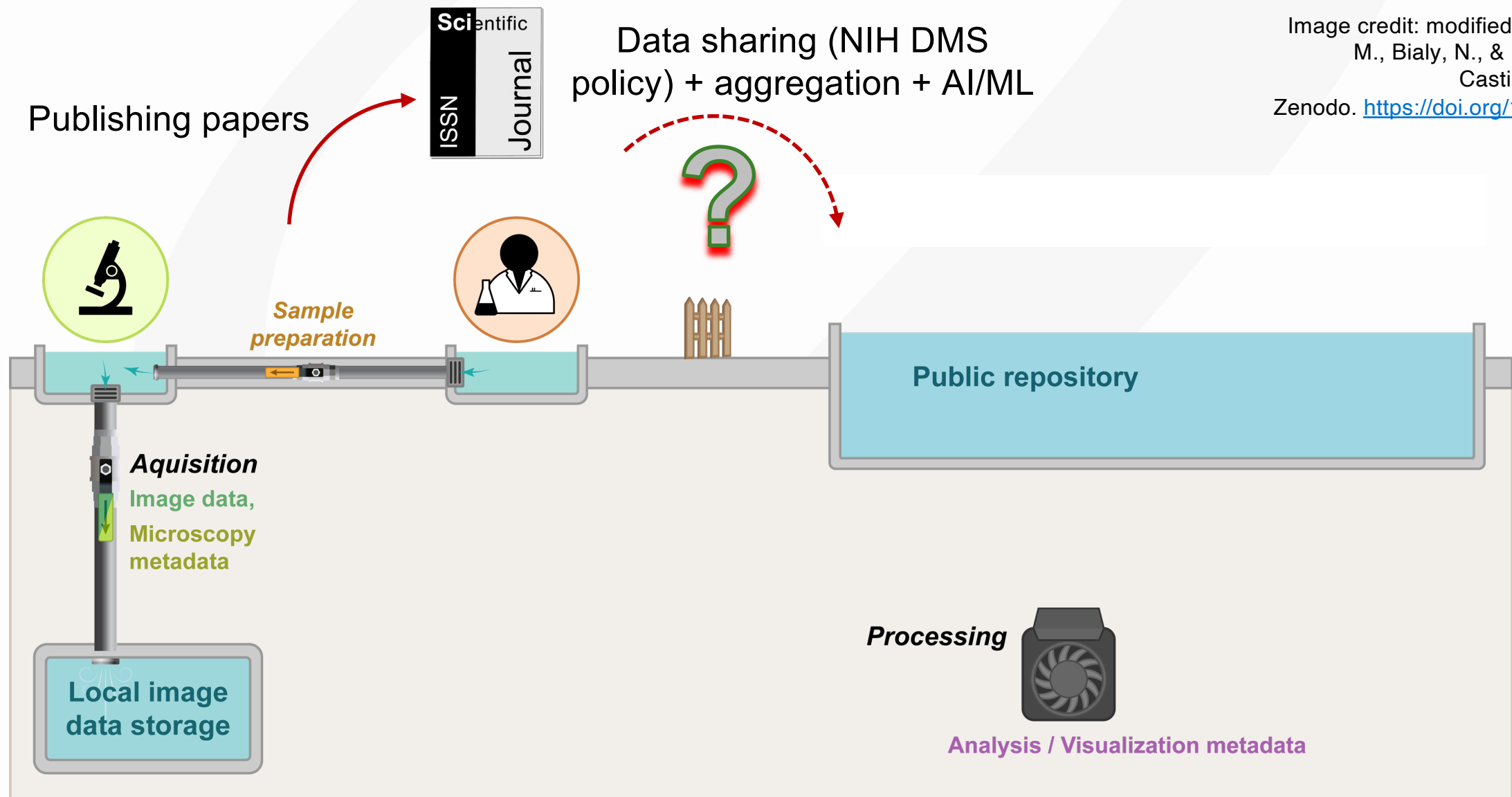


Image credit: modified from Stefely, M., Bialy, N., & Strambio-De-Castillia, C. (2024) Zenodo. <https://doi.org/10.5281/zenodo.14020675>



# RDMS cyberinfrastructure for images: beautiful fountains require ugly piping!

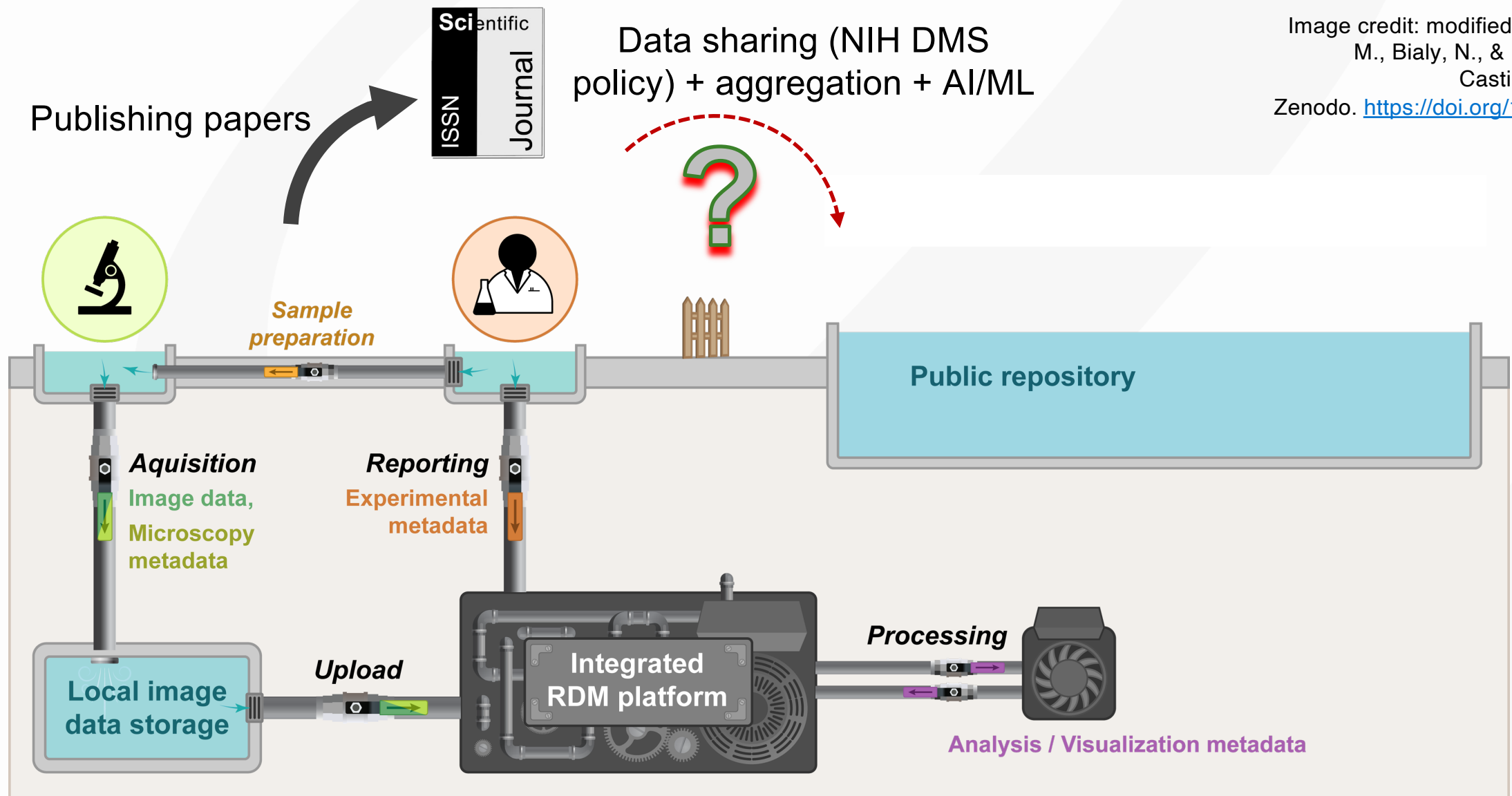
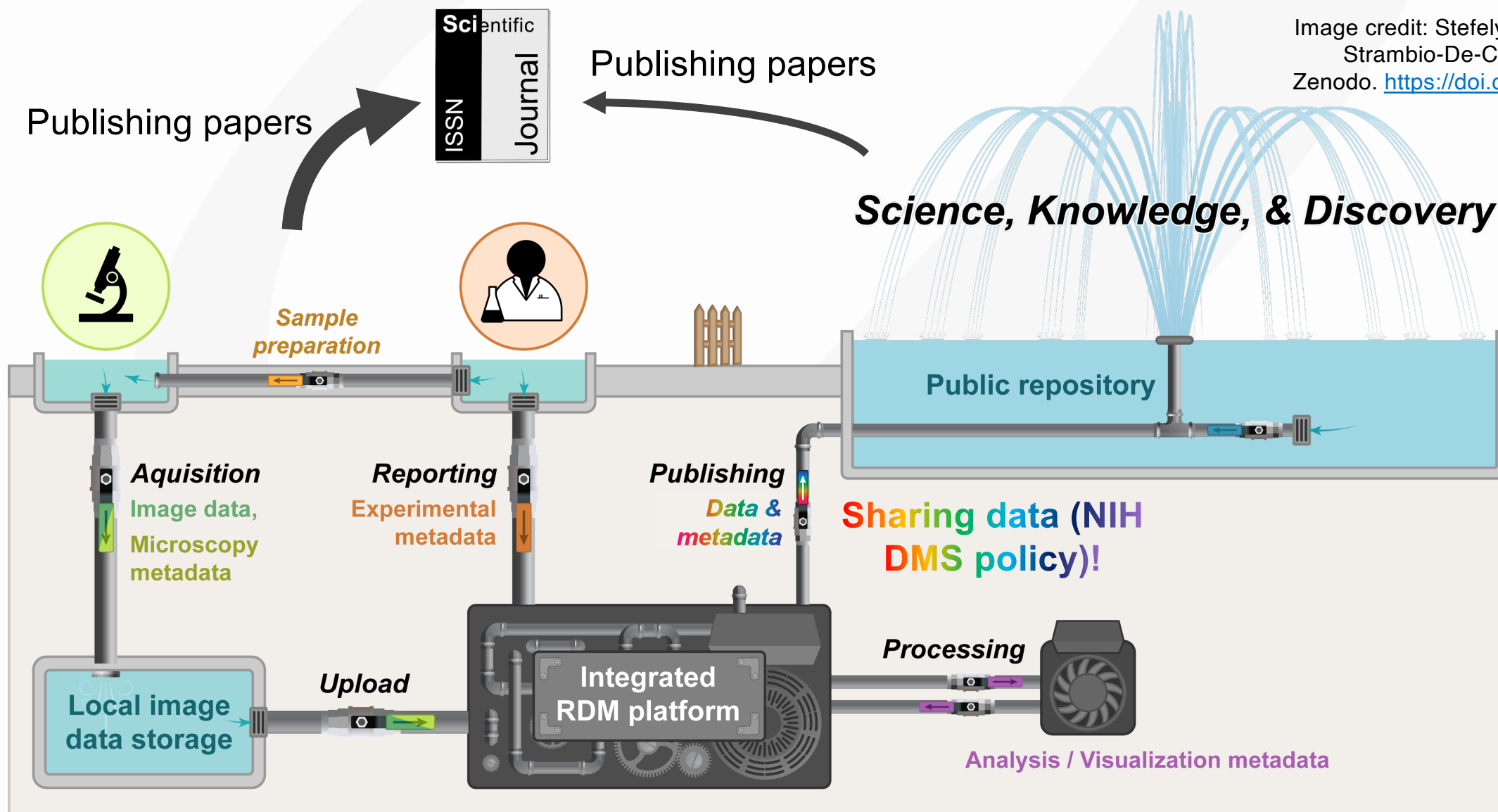


Image credit: modified from Stefely, M., Bialy, N., & Strambio-De-Castillia, C. (2024) Zenodo. <https://doi.org/10.5281/zenodo.14020675>

# RDMS cyberinfrastructure for images: beautiful fountains require ugly piping!



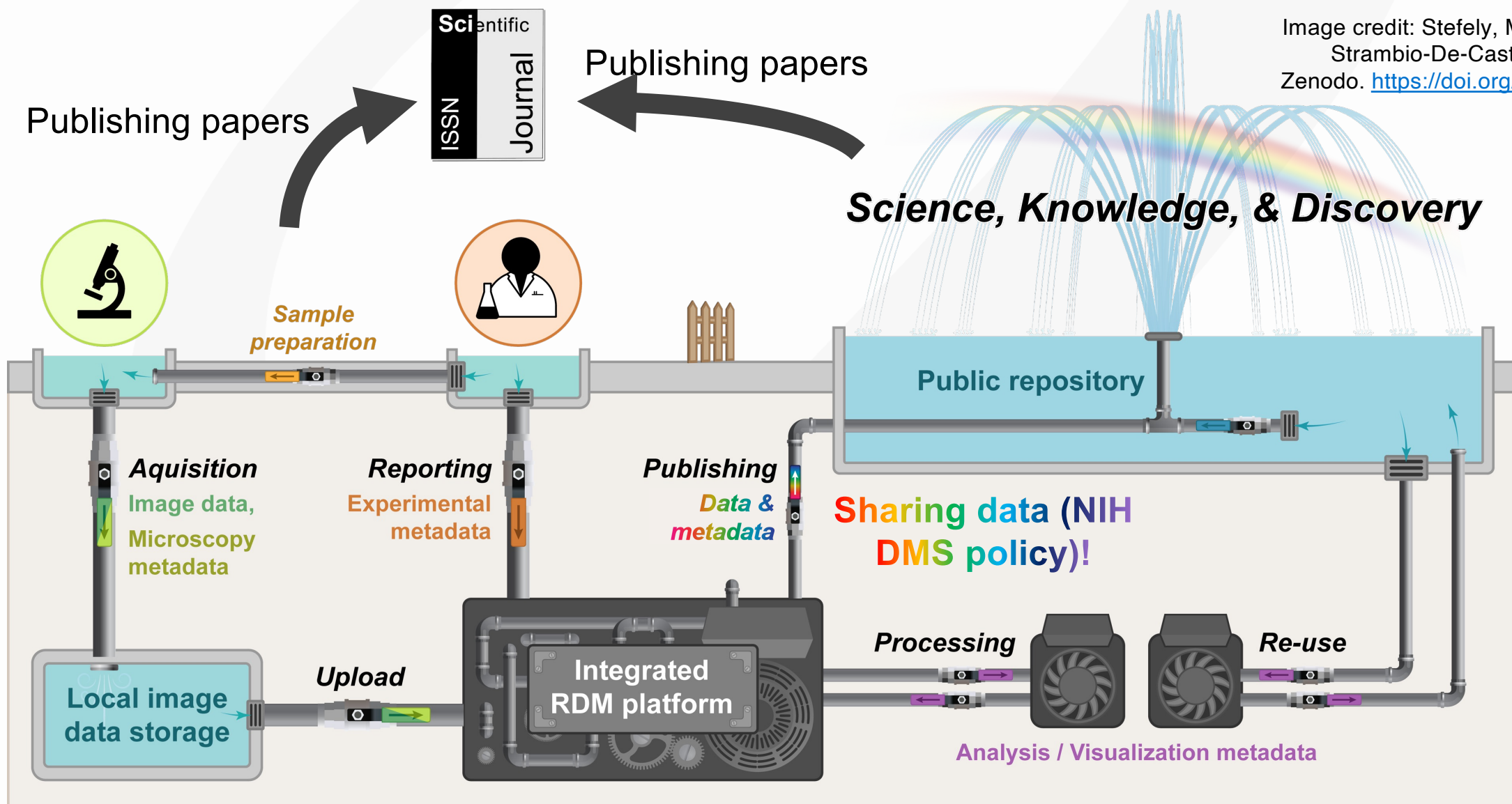
Image credit: Stefely, M., Bialy, N., &  
Strambio-De-Castilla, C. (2024)  
Zenodo. <https://doi.org/10.5281/zenodo.14020675>



# RDMS cyberinfrastructure for images: beautiful fountains require ugly piping!

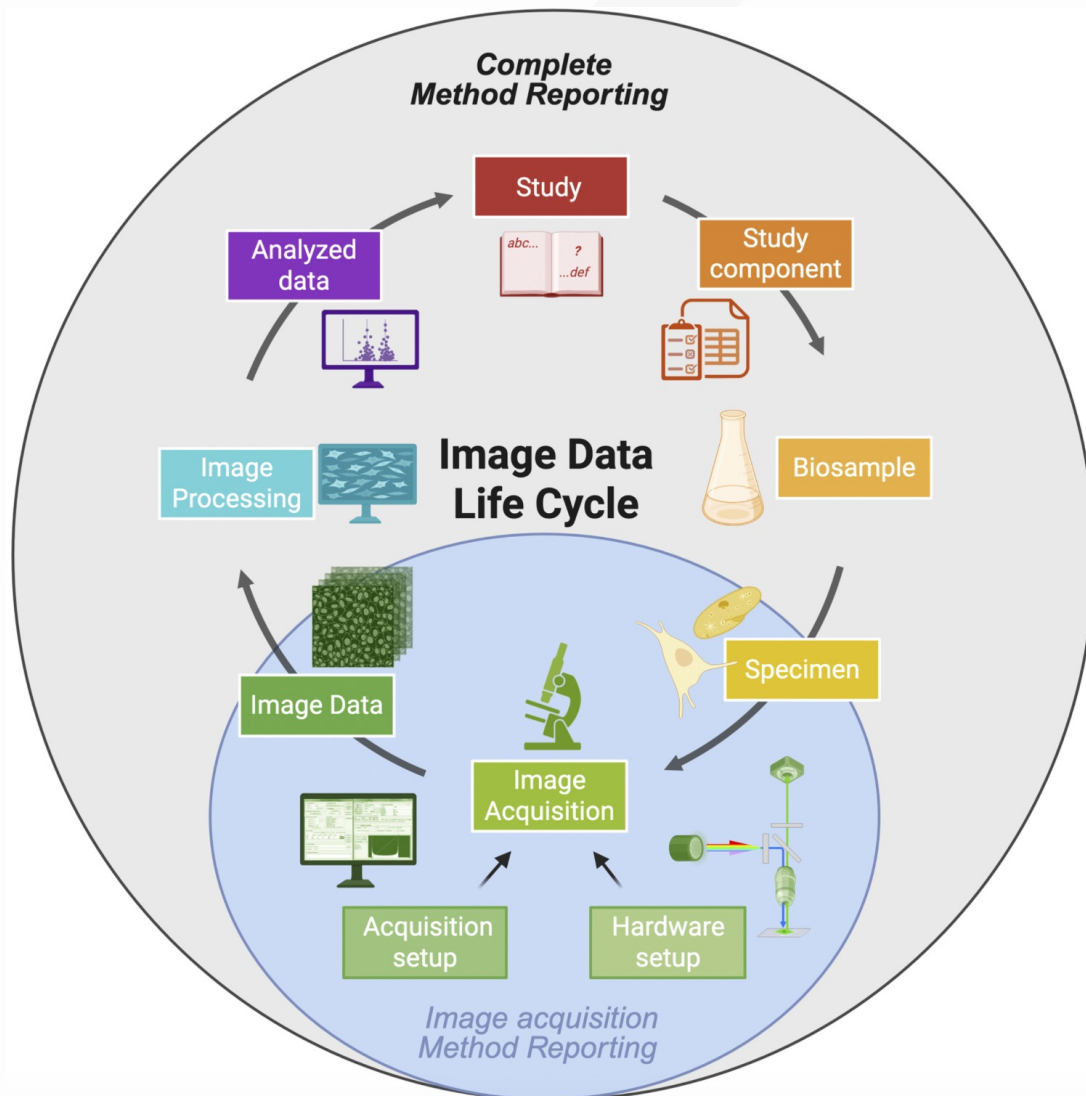


Image credit: Stefely, M., Bialy, N., &  
Strambio-De-Castilla, C. (2024)  
Zenodo. <https://doi.org/10.5281/zenodo.14020675>



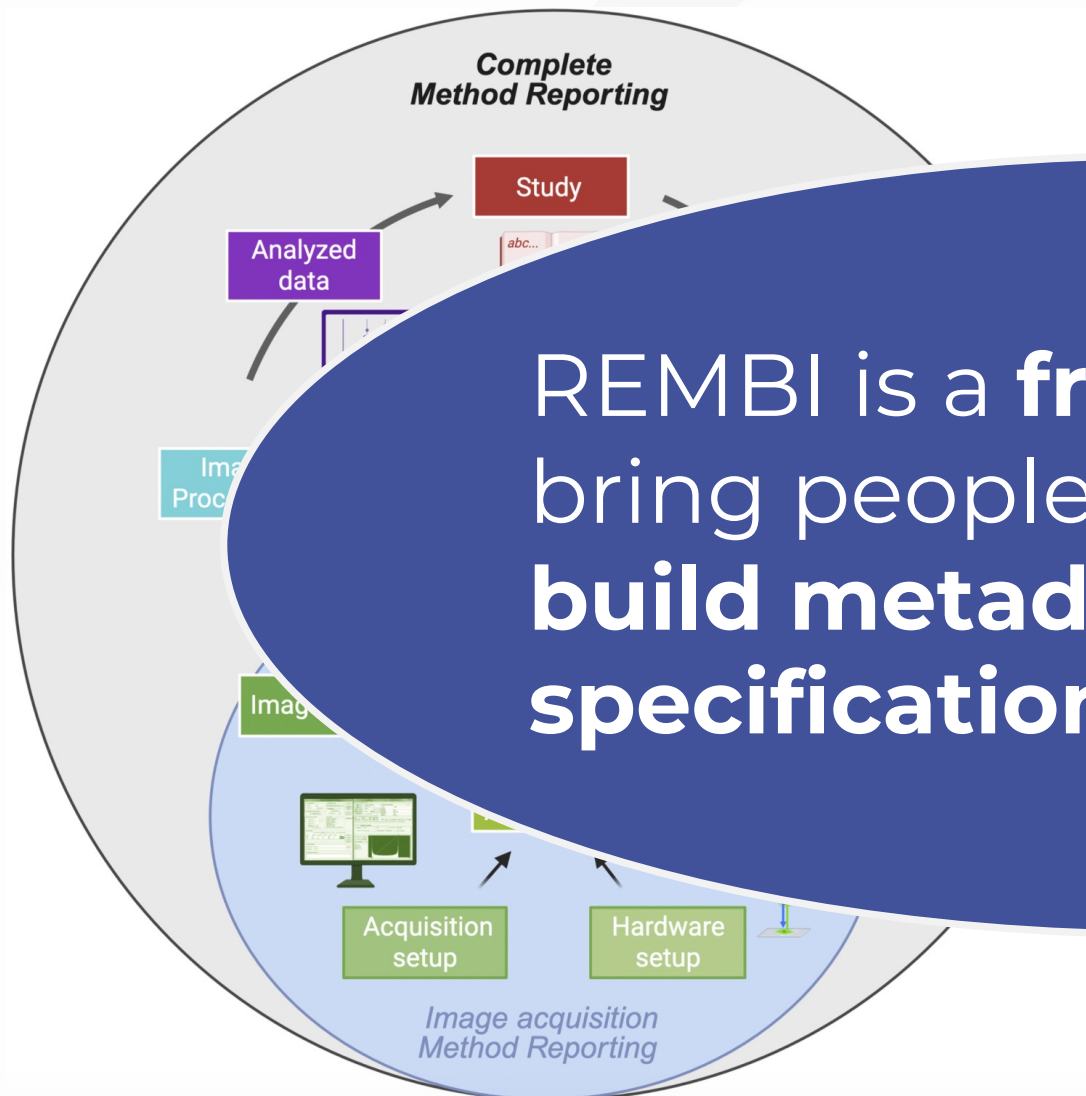


# Recommended Metadata for Biological Images (REMBI) helps to keep track of all necessary metadata



- The REMBI metadata cycle follows the bioimage data life cycle
- Each REMBI module is used to collect metadata for a specific step of the data life cycle
- Each REMBI module is also used to organize the subsequent metadata modules

# Recommended Metadata for Biological Images (REMBI) helps to keep track of all necessary metadata



REMBI is a **framework** to bring people together to **build metadata specifications**

- The REMBI metadata cycle is used to track the bioimage data life cycle



is used to track the bioimage data life cycle

is also

the  
modules

# REMBI as a framework for gathering the community



## Community-developed checklists for publishing images and image analyses

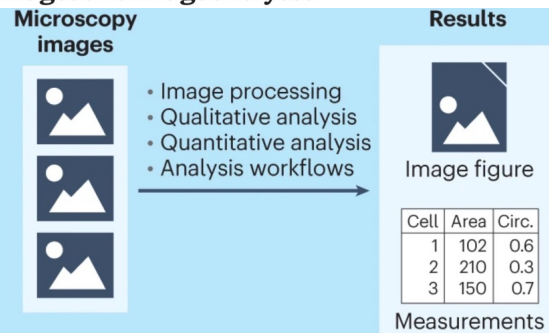
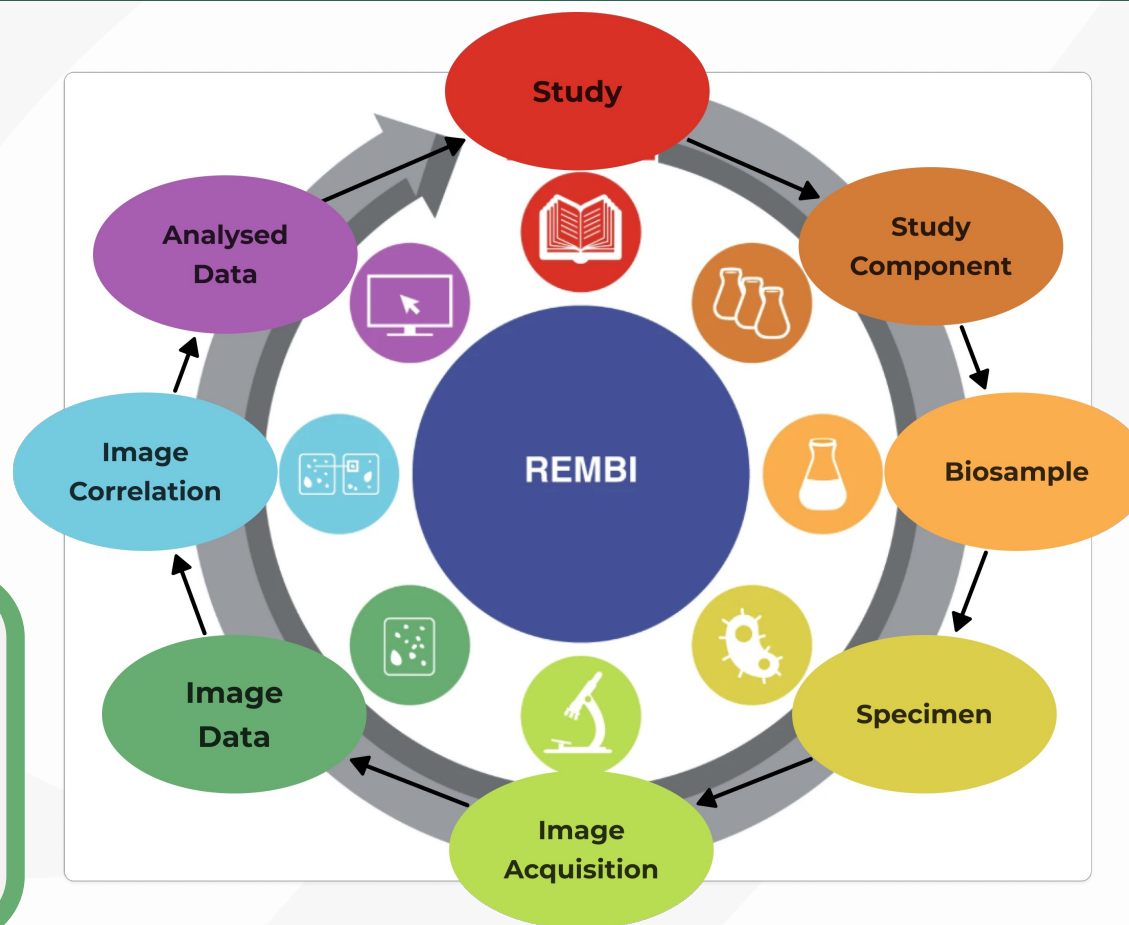


Image data storage and availability



OME-Data Model  
BioFormats  
OME-Zarr metadata



3D-MMS, MITI  
MIHCSME,  
SSBD metadata  
model,  
NIH CFDE  
metadata  
model  
(CFDE C2M2),  
Canada BI - UMass



Many more....

Light Microscopy

NBO-Q

BioImaging  
North America



Volume  
EM





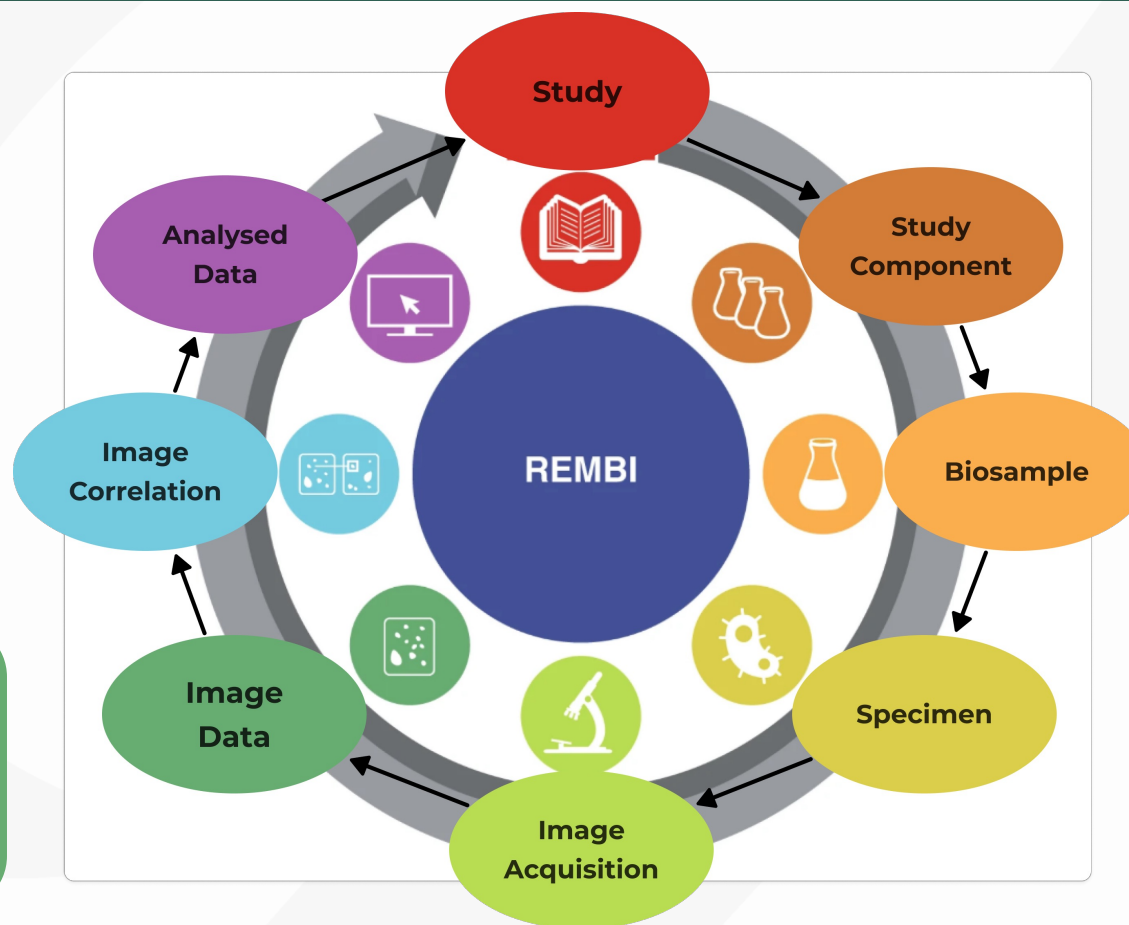
# REMBI as a framework for gathering the community: governance?

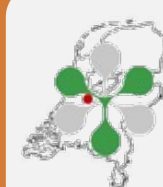


 **BioImaging  
North America**

  
**QUAREP-LiMi**

 **OME  
Community**



 **MIHCSME**  
NL-BIOIMAGING AM

**SSBD metadata model**  


many more...

 **QUAREP-LiMi**

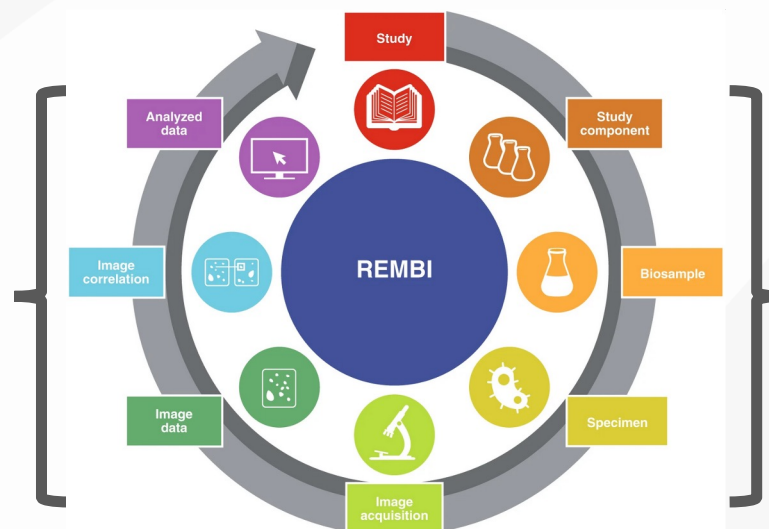
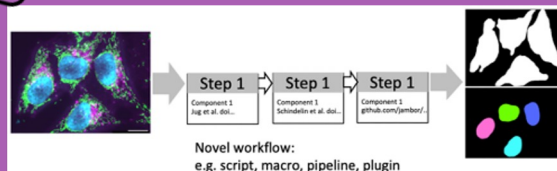
**Volume EM  
community**



# REMBI: aligns with the major image data life cycle steps



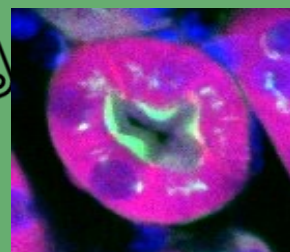
## Image Analysis



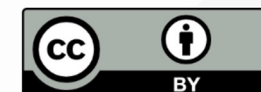
## Sample Description



## Image Data



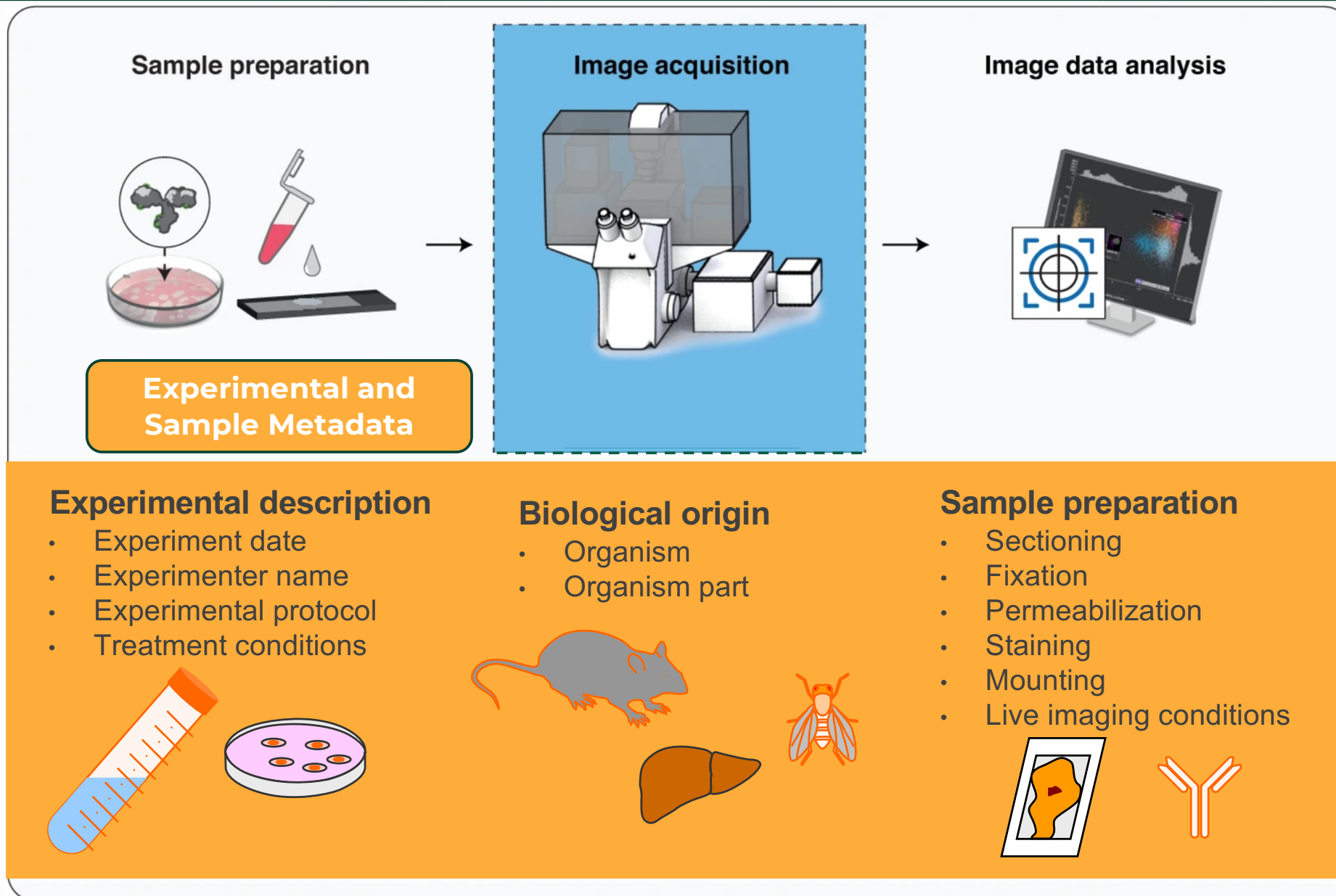
## Image Acquisition



<https://www.nature.com/articles/s41592-021-01166-8>

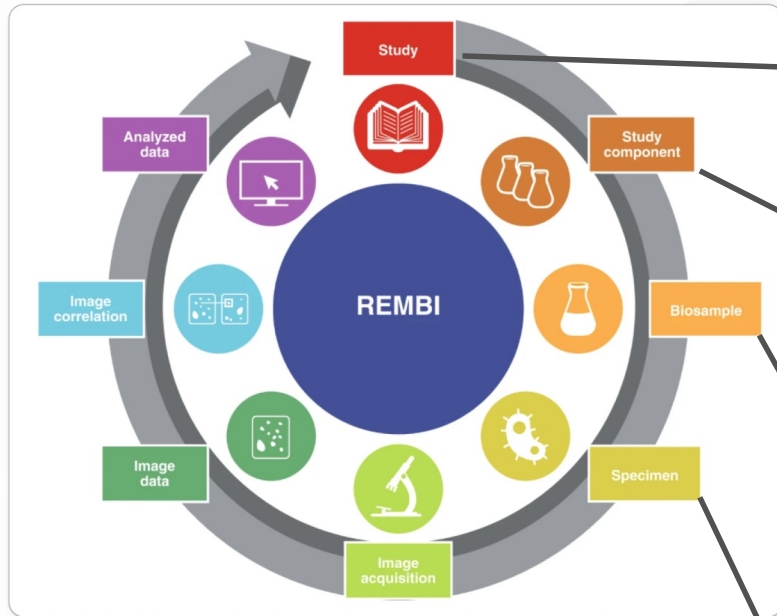
<https://www.ebi.ac.uk/bioimage-archive/rembi-model-reference/>

# Part 1: Experimental and Sample preparation Metadata





# Experimental metadata captured using REMBI-compatible modular spreadsheets



- Customized based on user needs
- Ontology-enriched
- Controlled vocabularies

Study:

**Study**

Study_ID	pazour001_STUCK_mutant-analysis
Study_Description	xyz
Study_Title	Mutant Analysis
Study_Type	Fixed sample imaging
Study_Type_term_accession	<a href="https://purl.bioontology.org/ontology/EDAM-">https://purl.bioontology.org/ontology/EDAM-</a>
Data_Publisher_Principal_Investigator	Pazour
Data_Publisher_Department	Molecular Medicine
Data_Publisher_Institution	UMass Chan Medical School
Contributor	Michael Stuck
Repository	UMass Chan OMERO
Licence	CC BY-NC-SA 4.0

SC:

**Study Component**

Study_Component_Name	0001a_Live-imaging
Study_Component_Description	xyz
Study_Component_Type	Fixed cell imaging
Date	XXXX-XX-XX
Experimental_Replicate_Number	1
Experimenter_name	Lyu Bo
Experimenter_contact_info	Bo.Lyu@umassmed.edu

Biosample:

**Biosample**

Biological_Organism	Homo sapiens
Biological_Organism_Term_Accession	<a href="http://purl.obolibrary.org/obo/NCBITaxon_9606">http://purl.obolibrary.org/obo/NCBITaxon_9606</a>
Biological_Entity_Status	fixed cells
Biological_Entity_Status_term_accession	<a href="http://purl.obolibrary.org/obo/MI_0348">http://purl.obolibrary.org/obo/MI_0348</a>
Biological_Entity_Tissue_Origin	kidney
Biological_Entity_Tissue_Origin_term_accession	<a href="http://purl.obolibrary.org/obo/UBERON_0002113">http://purl.obolibrary.org/obo/UBERON_0002113</a>
Biological_Entity_Cell_Type	cell line
Biological_Entity_Cell_Type_term_accession	<a href="http://purl.obolibrary.org/obo/CLO_0000019">http://purl.obolibrary.org/obo/CLO_0000019</a>
Biosample_Intrinsic_Variable	
Biosample_Extrinsic_Variable	
Biosample_Experimental_Variable	

Specimen:

**Specimen**

Specimen_Experimental_Status	Test
Fixation_condition	2% PFA 15 min
Embedding_Condition	
Section_Thickness	
Antigen_Retrieval	0.05% SDS 5 minutes
Number_of_Channels	3
Counterstaining_Channel	1
DNA_counterstain	DAPI

# Exchanging REMBI modules key/value pair sets: Experiment 1



Study Design



Sample Preparation



Image Acquisition



Image Data

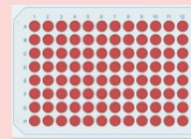


Image Analysis



Data Interpretation

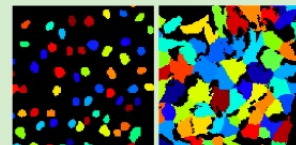
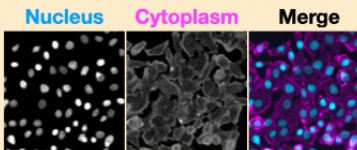
What effect does drug X have on cancer cell proliferation?



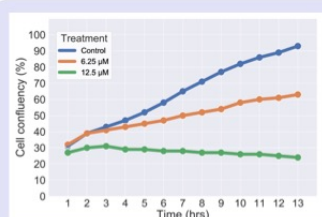
Live human colon cancer cell line HT29 grown on plastic, treated with drug X and vehicle control. Organic dyes Hoechst labels DNA (nucleus) and Phalloidin labels actin (cytoplasm).



High-throughput live cell imaging



Measurements  
Cell Count  
% Area occupied



Treatment with increasing concentrations of drug X has a negative effect on cell proliferation, as determined by measuring cell confluency

SC:  
HT cell proliferation assay

Biosample:  
*H. Sapiens*  
Colon  
HT29

Specimen:  
Live cells  
Treated  
Vital staining

Image Acquisition:  
Widefield fluorescence

Image Data:  
2-colors

Image Analysis:

Segmentation

# Exchanging REMBI modules key/value pair sets: Experiment 2



## Study Design

Sample Preparation

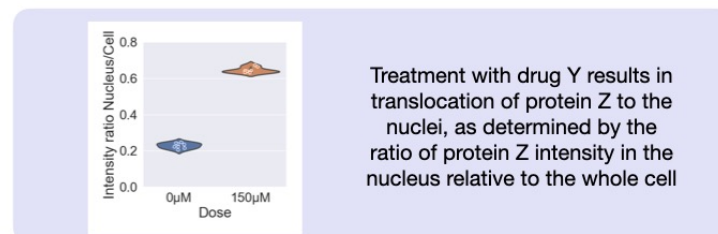
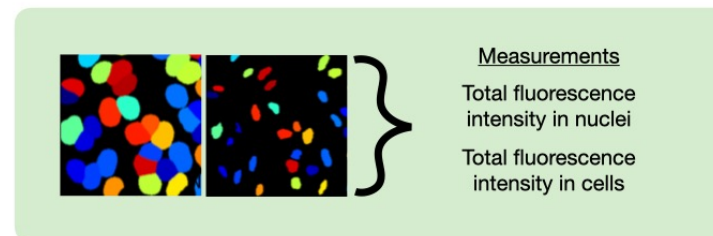
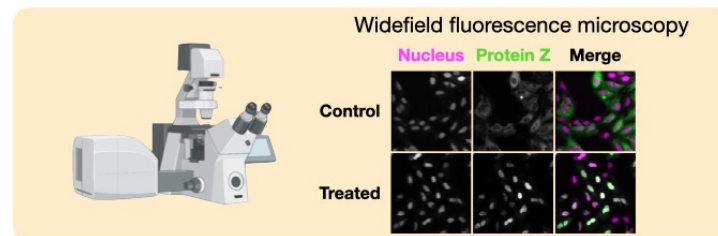
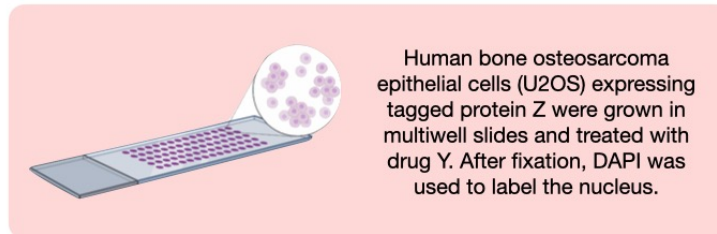
Image Acquisition

Image Data

Image Analysis

Data Interpretation

What effect does drug Y have on protein Z localization?



SC:  
Protein translocation assay

Biosample:  
*H. Sapiens*  
Bone  
U2OS

Specimen:  
Fixed cells  
Treated  
IF staining

Image Acquisition:  
Widefield

Image Data:  
2-colors,  
Z-stack

Image Analysis:  
Segmentation



# Exchanging REMBI modules key/value pair sets



- Customized based on user needs
- Ontology-enriched
- Controlled vocabularies



**Marteen Paul**



**Katy Wolstencroft**



**Judith Lacoste**

 [NL-BioImaging / ISA-REMBI-Metadata-Modules](#) Public

**Contributors** 2



**strambc** Caterina Strambio De Ca...



**maartenpaul** Maarten Paul



# Customized Community-Standards-compatible tools to capture experimental metadata

Study (Project) - METADATA

Study_ID	pazour001_STUCK_mutant-analysis
Study_Description	xyz
Study_Title	Mutant Analysis
Study_Type	Fixed sample imaging
Study_Type_term_accession	https://purl.bioontology.org/ontology/EDAM-
Data_Publisher_Principal_Investigator	Pazour
Data_Publisher_Department	Molecular Medicine
Data_Publisher_Institution	UMass Chan Medical School
Contributor	Michael Stuck
Repository	UMass Chan OMERO
Licence	CC BY-NC-SA 4.0

Image-level METADATA

Image_Name	Image Path (relative to root)	LightSource_Trigger_Type	Illumination_Dose
t1-200.txt	TTL\1340uWx1060ms\GFP\	TTL	1340uWx1060ms
t201-400.txt	TTL\1340uWx1060ms\GFP\	TTL	1340uWx1060ms
t400.txt	TTL\1340uWx1060ms\ROS\	TTL	1340uWx1060ms
t0.txt	TTL\1340uWx1060ms\ROS\	TTL	1340uWx1060ms
t200.txt	TTL\1340uWx1060ms\ROS\	TTL	1340uWx1060ms
t400.txt	TTL\1340uWx1060ms\ROS\	TTL	1340uWx1060ms
t1-200.txt	TTL\31300uWx48ms\GFP\	TTL	31300uWx48ms
t201-400.txt	TTL\31300uWx48ms\GFP\	TTL	31300uWx48ms
t0.txt	TTL\31300uWx48ms\ROS\	TTL	31300uWx48ms
t200.txt	TTL\31300uWx48ms\ROS\	TTL	31300uWx48ms

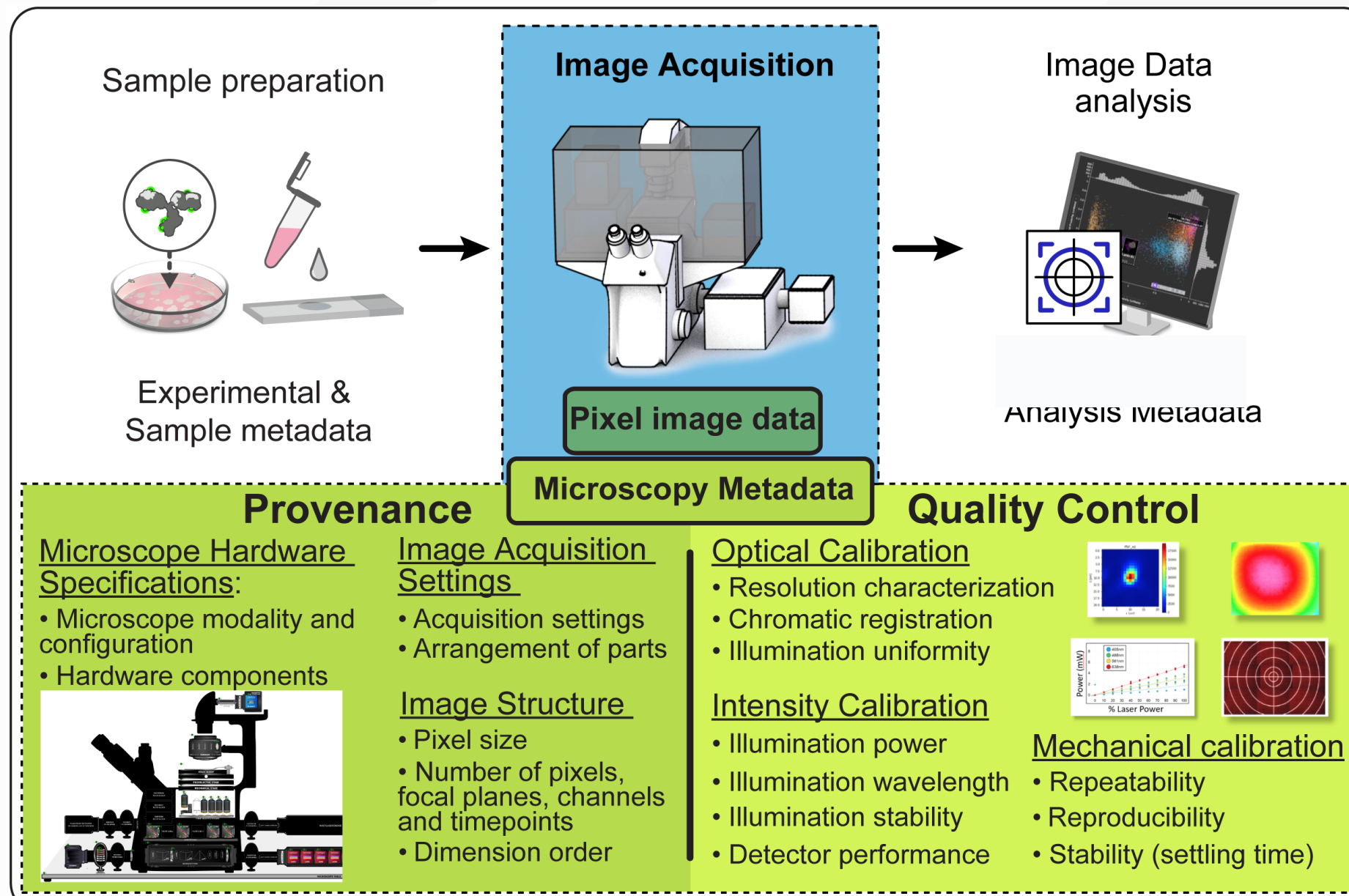
Study Component (Experiment) - Sample - Specimen METADATA

Study Component	Study_Component_Name	0001a_Live-imaging
	Study_Component_Description	xyz
	Study_Component_Type	Fixed cell imaging
	Date	XXXX-XX-XX
	Experimental_Replicate_Number	1
Biosample	Experimenter_name	Lyu Bo
	Experimenter_contact_info	Bo.Lyu@umassmed.edu
	Biological_Organism	Homo sapiens
	Biological_Organism_Term_Accession	http://purl.obolibrary.org/obo/NCBITaxon_9606
	Biological_Entity_Status	fixed cells
	Biological_Entity_Status_term_accession	http://purl.obolibrary.org/obo/MI_0348
	Biological_Entity_Tissue_Origin	kidney
Specimen	Biological_Entity_Tissue_Origin_term_accession	http://purl.obolibrary.org/obo/UBERON_0002113
	Biological_Entity_Cell_Type	cell line
	Biological_Entity_ID	
	Biological_Entity_Cell_Type_term_accession	http://purl.obolibrary.org/obo/CLO_0000019
	Biosample_Intrinsic_Variable	
	Biosample_Extrinsic_Variable	
	Biosample_Experimental_Variable	
	Specimen_Experimental_Status	Test
	Fixation_condition	2% PFA 15 min
	Embedding_Condition	
Image acquisition	Section_Thickness	
	Antigen_Retrieval	0.05% SDS 5 minutes
	Number_of_Channels	3
	Counterstaining_Channel	1
	DNA_counterstain	DAPI
Image acquisition	Instrument_Type	Laser Scanning Confocal
	Instrument_Quality_Control	

- REMBI compatible
- Customized based on user-needs
- Facilitate user-input with drop-down lists
- **Examples available**

Inspired by/modified from Thomas Zobel – Uni Münster - Münster Imaging Network  
<https://confluence.uni-muenster.de/display/WWUIMW/Adding+Key-Value+Pairs>

# Part 2: Image Acquisition Metadata





# Community standards: Light Microscopy (LiMi) Metadata to expand the OME model



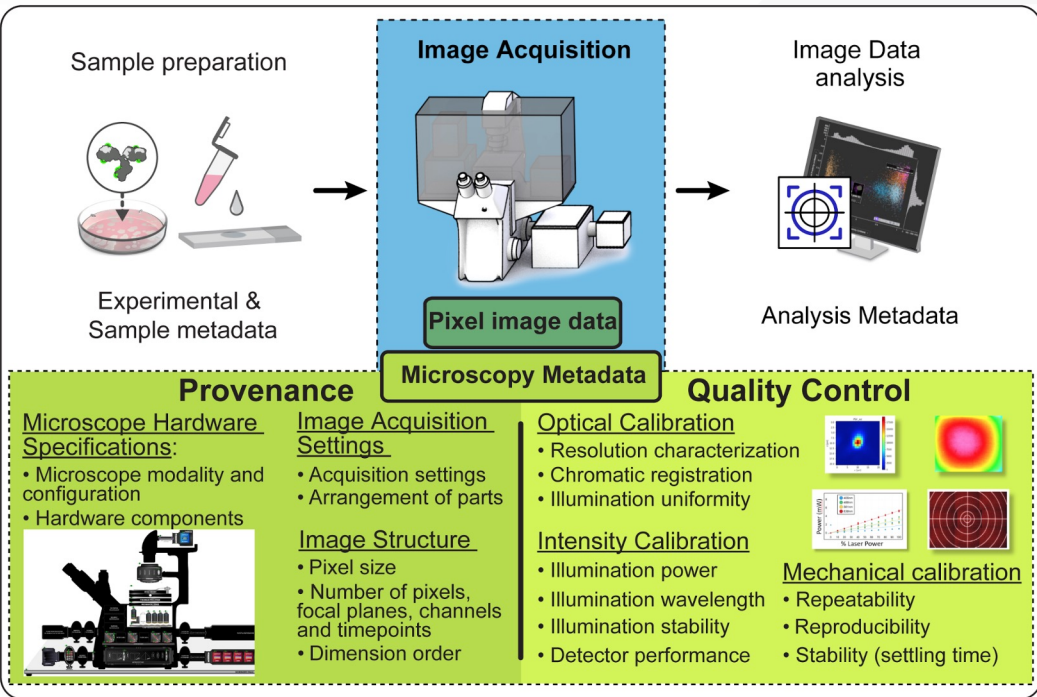
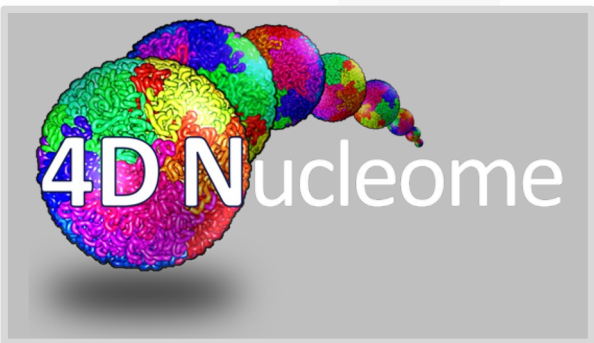
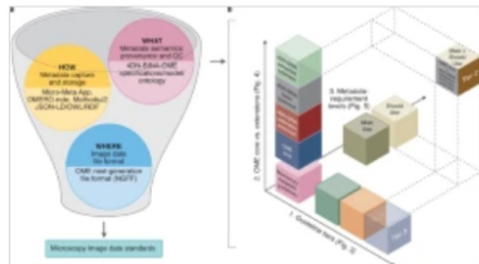
Comment  
3 Dec 2021  
[Nature Methods](#)



## Towards community-driven metadata standards for light microscopy: tiered specifications extending the OME model

Rigorous record-keeping and quality control are required to ensure the quality, reproducibility and value of imaging data. The 4DN Initiative and BINA here propose light Microscopy Metadata Specifications that extend the OME Data Model, scale with experimental intent and complexity, and make it possible for scientists to create comprehensive records of imaging experiments.

Mathias Hammer, Maximiliaan Huisman ... Caterina Strambio-De-Castillia



Hammer et al. (2021) *Nat Methods*;  
<https://doi.org/10.1038/s41592-021-01327-9>



# Community standards: Light Microscopy (LiMi) Metadata to expand the OME model



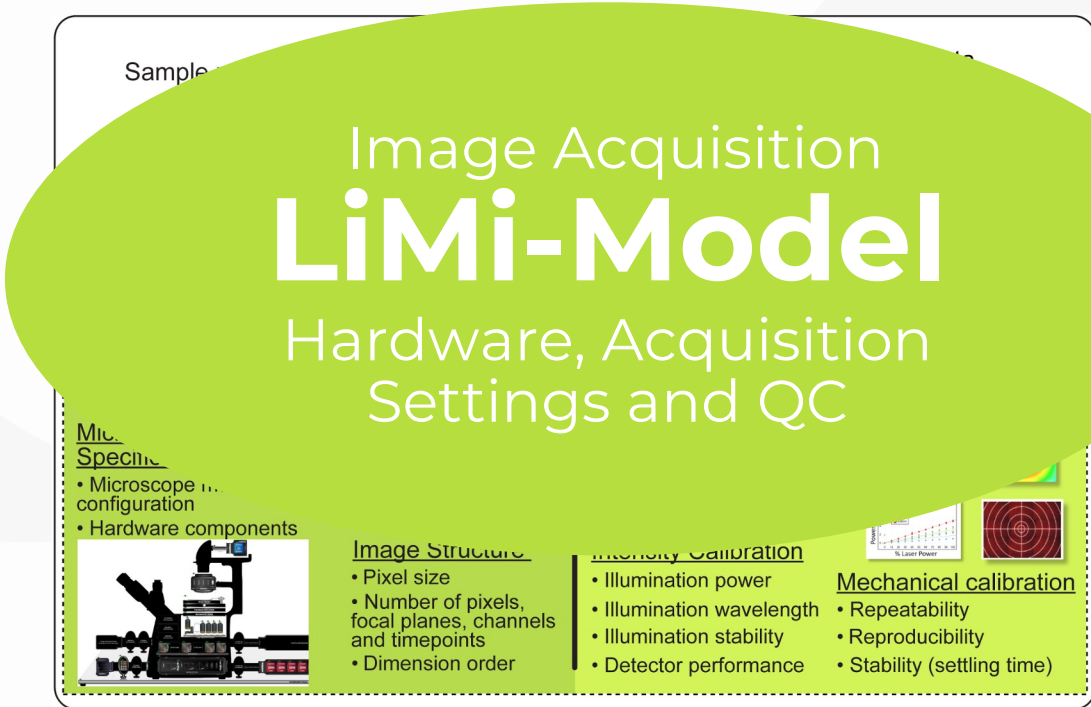
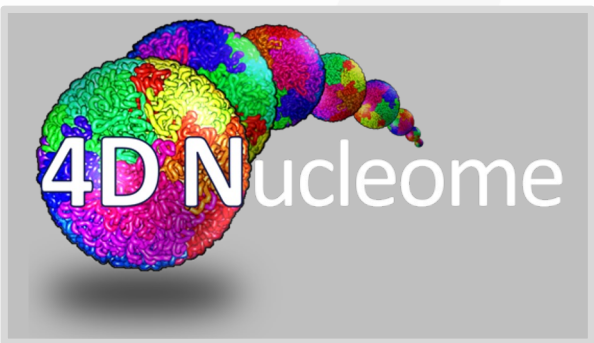
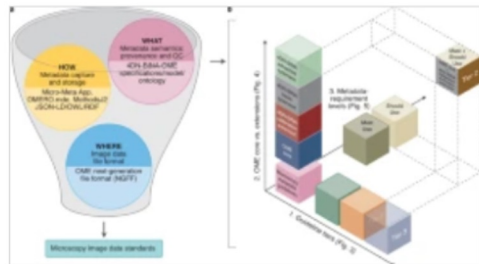
Comment  
3 Dec 2021  
[Nature Methods](#)



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Mathias Hammer, Maximiliaan Huisman ... Caterina Strambio-De-Castillia

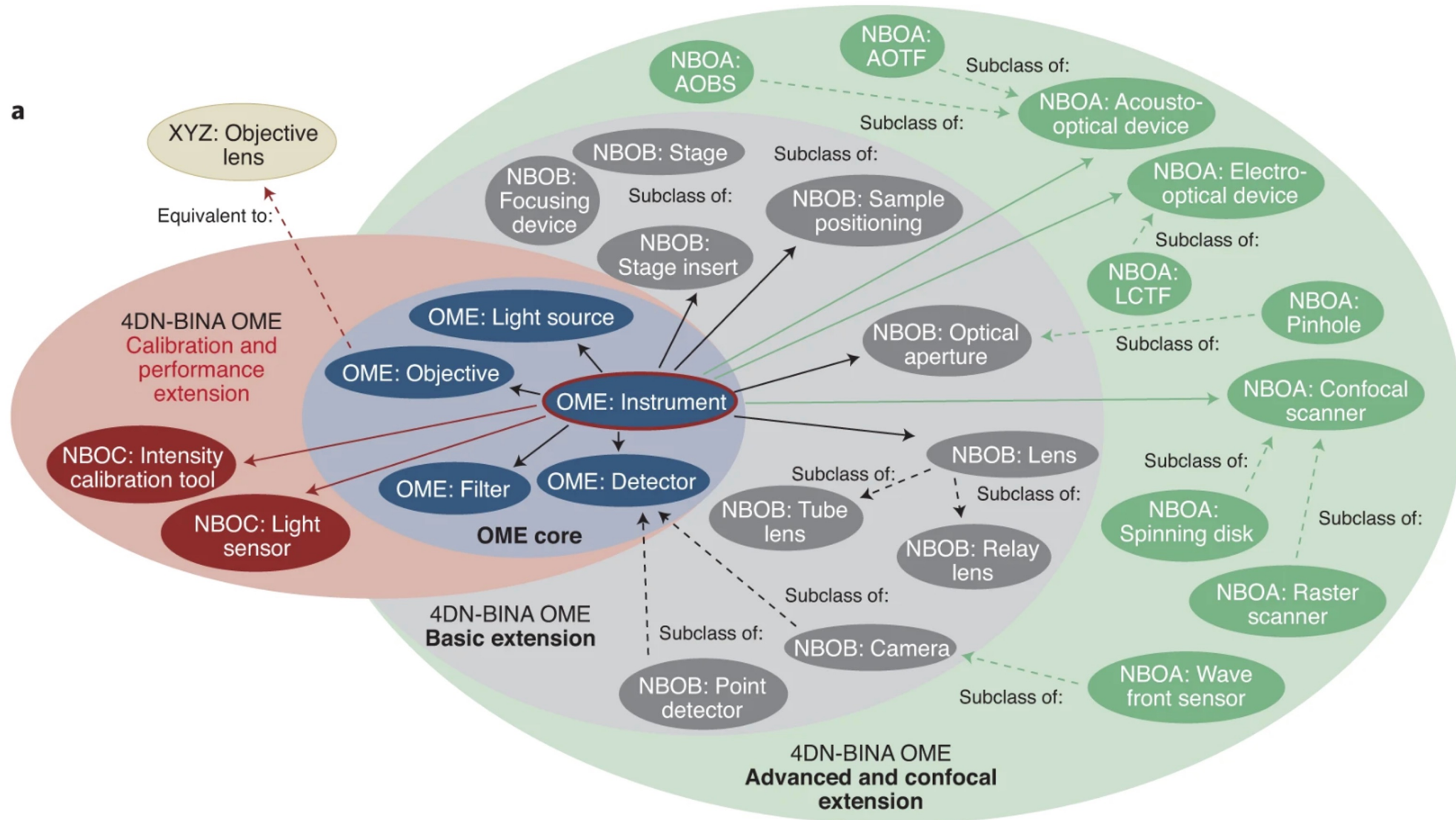


Hammer et al. (2021) *Nat Methods*;  
<https://doi.org/10.1038/s41592-021-01327-9>





# Community standards: Light Microscopy (LiMi) Metadata to expand the OME model





# Community standards: Light Microscopy (LiMi) Metadata to expand the OME model



# Micro-Meta App: an example of a metadata annotation tool to collect light microscopy metadata based on community specifications



Brief Communication

Open Access

3 Dec 2021

[Nature Methods](#)



## Micro-Meta App: an interactive tool for collecting microscopy metadata based on community specifications

Micro-Meta App is an intuitive, highly interoperable, open-source software tool designed to facilitate the extraction and collection of relevant microscopy metadata as specified by recent community guidelines.

Alessandro Rigano, Shannon Ehmsen ... Caterina Strambio-De-Castillia

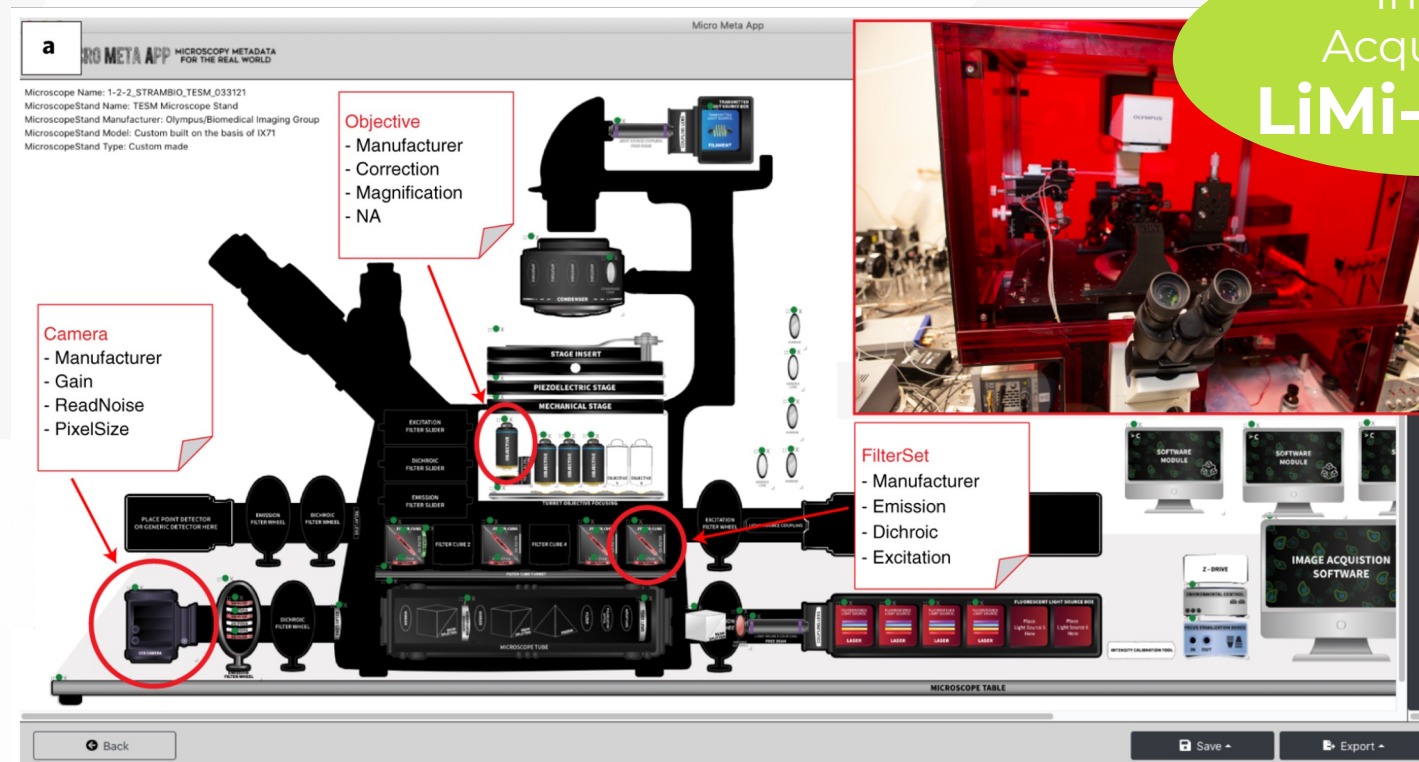
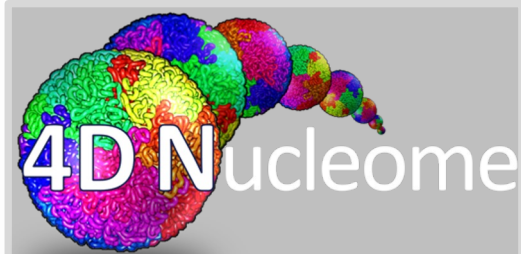
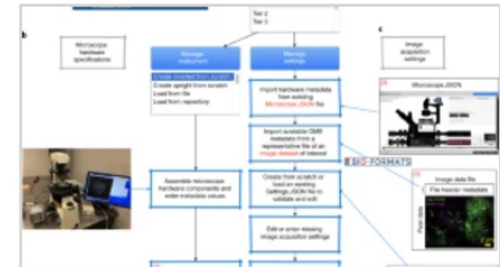
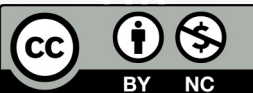


Image Acquisition  
**LiMi-Model**



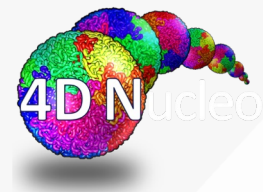
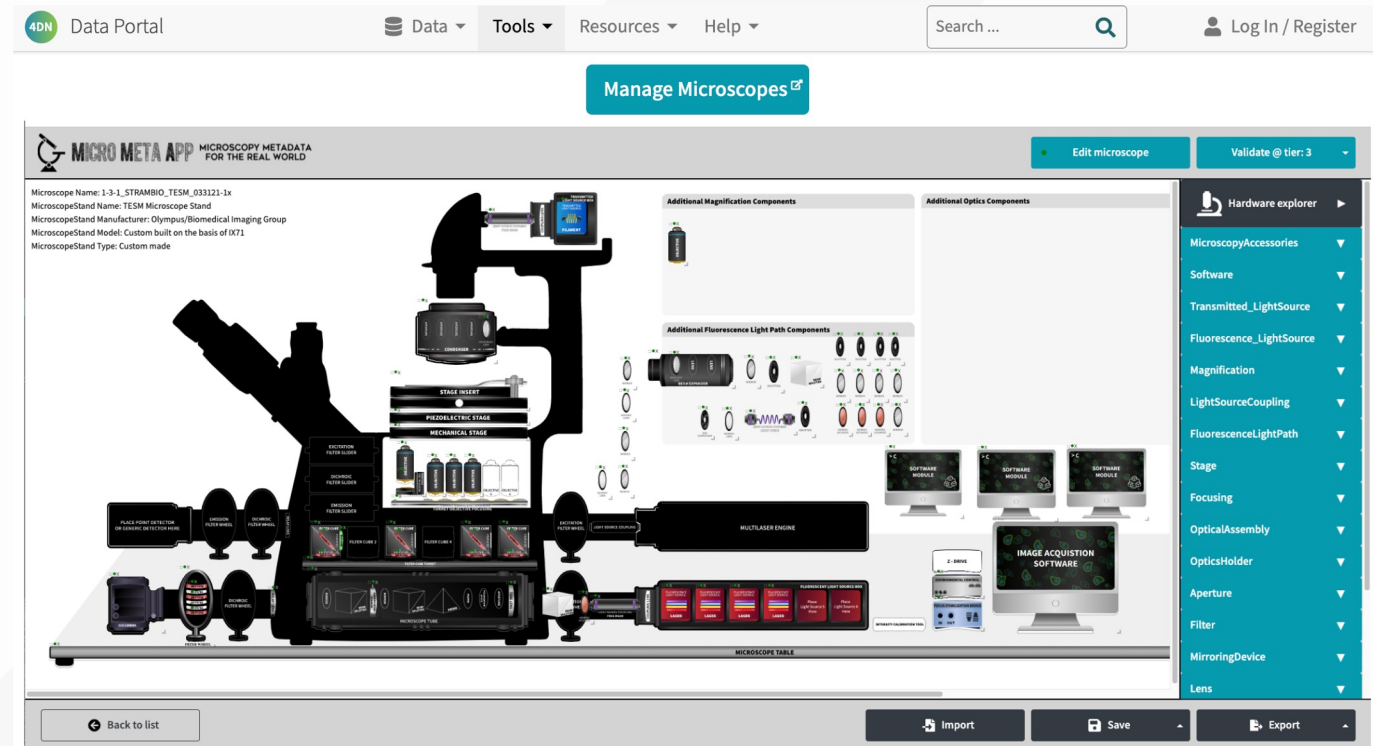
Alex Rigano



# Who is using LiMi-Model and/or Micro-Meta App?



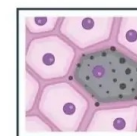
- NIH 4D Nucleome
- BINA
- Canada BioImaging
- NIH HuBMAP & SenNet
- RIKEN
- Inscoper
- Pending: Brain Image Library, others?



**BioImaging  
North America**



**HuBMAP**  
Human BioMolecular Atlas Program



SenNet





# Community standards: Light Microscopy (LiMi) Metadata to expand the OME model



- QUAREP-LiMi in charge of hosting, maintenance and governance
- Covers hardware configuration, image acquisition settings and quality control metadata
- Revision process governed by clear rules
- Large community of imaging scientists, microscopy experts, manufacturers and standards organizations stakeholders

## LiMi-Model

Home / Working Groups / WG 7 – Metadata / LiMi-Model

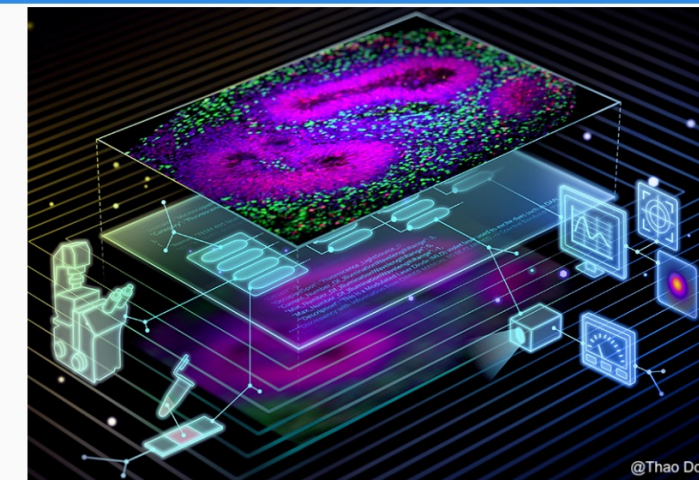
## LiMi-Model

The **Light-Microscopy (LiMi) Model** aims to harmonize the description of light microscopy hardware, acquisition settings, and quality-control metrics to enhance image quality, reproducibility, and to fulfill the **FAIR** (Findable, Accessible, Interoperable, and Reusable) data principles.

Join QUAREP WG7 (Metadata)

### Purpose

- Promote the harmonized generation and pre-publication management of image datasets from the ground up.
- Facilitate the deposition of microscopy datasets to public image data repositories (e.g., [BioImage Archive](#), [OME-Image Data Resource](#), RIKEN [SSBD](#), [Brain Image Library](#), [Imaging Data Commons](#), etc.).
- Facilitate data reuse and the extraction of quantitative information from image data using advanced bioimage analysis techniques, including AI/ML.
- Define the light-microscopy implementation of the Image Acquisition module of the [Recommended Metadata for Biological Images](#) (REMBI) guidelines.



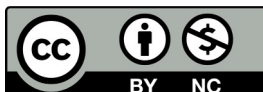
Microscopy metadata is essential for image data QC, interpretation, analysis and sharing.

### Deliverables

- A flexible and adaptable community-agreed vocabulary to describe microscopy hardware, image acquisition settings, and their associated quality control measurements.
- A metadata model to structure the vocabulary and organize the data.
- A set of machine-actionable representations of the metadata model leveraging the latest Linked Data technology.

Join us at our next WG7 (Metadata) meeting!

<https://quarep.org/working-groups/wg-7-metadata/>

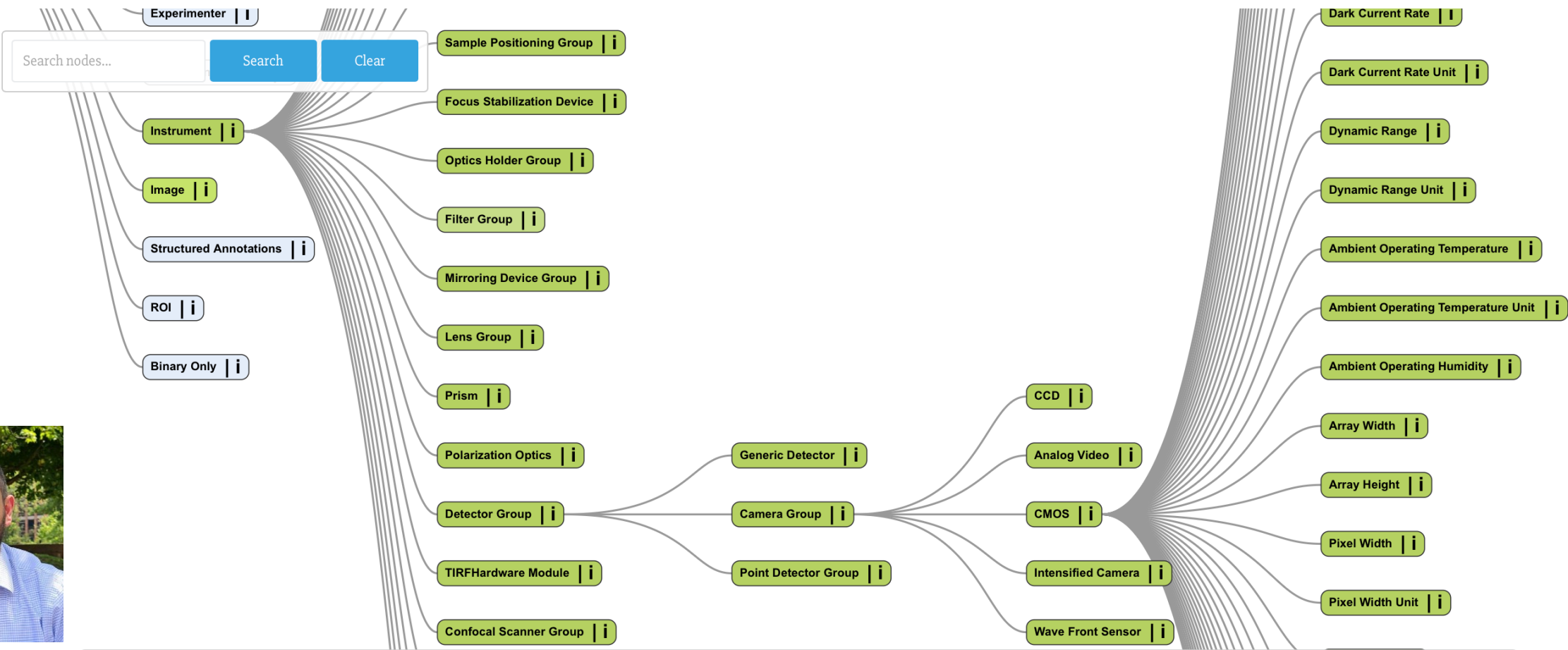


# Light Microscopy (LiMi) Model Viewer: make it easy to understand the model



## LiMi-Model Viewer

Home / Working Groups / WG 7 – Metadata / LiMi-Model / LiMi-Model Viewer



### Details for Detector Group:

This element describes a Detector available for this Instrument. An Instrument may have more than one Detector of different types, such as a Photomultiplier, or a Camera. The Detector ID can be used as a reference within the Channel element values stored in Detector represent the fixed values, variable values modified during the Acquisition go in DetectorSettings.

Manage Co



Anthony Asmar

# Light Microscopy (LiMi) Model Viewer: make it easy to understand the model



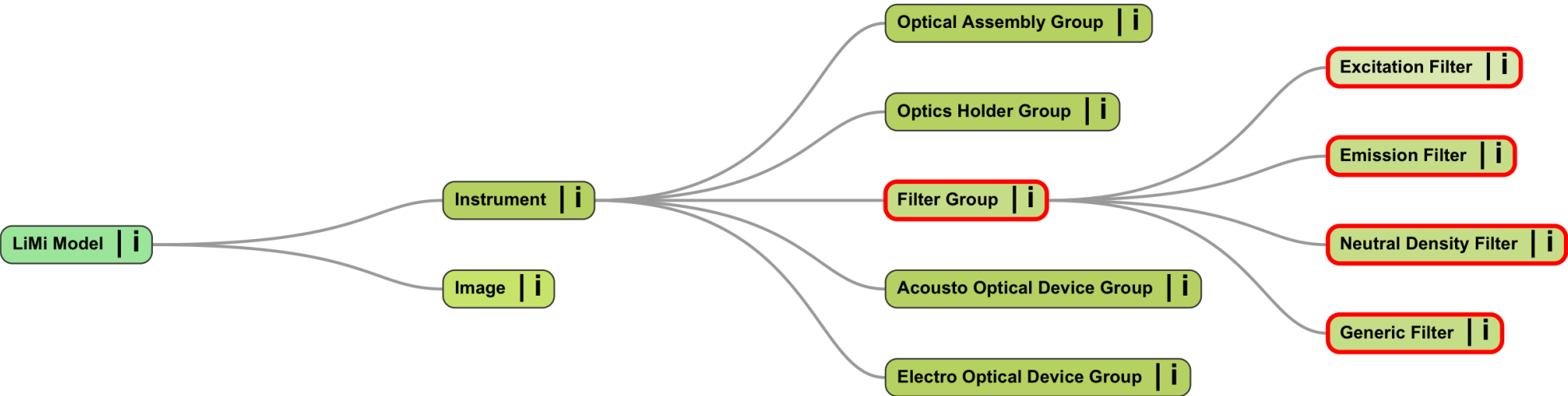
## LiMi-Model Viewer

Home / Working Groups / WG 7 – Metadata / LiMi-Model / LiMi-Model Viewer

Search

Clear

1 of 41



### Details for Filter Group:

This element describes an optical Filter positioned in the Light Path for one or more Channels available for this Instrument. An optical Filter is a device designed to selectively control the Wavelengths, color temperature, vibration direction, and/or intensity of the radiation which it transmits or reflects. An Instrument may have several Filters of different types, such as an Excitation, Emission, Neutral Density or an additional Generic Filter positioned in the Light Path for different purposes. For each fluorescence Image should be at least one Filter element specified per Channel. This element can be associated with an optional Optics Holder, such as a Filter Cube, Filter Turret, Filtr W Filter Slider. Note: Filter Holder is not the same as a Filter Set.

Manage Consent



Anthony Asmar





# A path forward towards LiMi-Model revision in partnership with manufacturers



## The making of microscope camera standards

Cameras are a crucial part of microscopes and are also built into many kinds of instruments. To make their output comparable takes standards.

Vivien Marx

The academics and company scientists in the group Quality Assessment and Reproducibility for Instruments & Images in Light Microscopy (QUAREP-LiMi) are developing standards for microscopy camera output.

As in other areas of standards development, working with companies is crucial; “after all they are the expert of the hardware they are producing,” says Caterina Strambio-de-Castillia, a researcher at the University of Massachusetts Medical School’s Program in Molecular Medicine and a Chan Zuckerberg Imaging Scientist, who spearheads this effort within QUAREP-LiMi. A separate story in this issue of *Nature Methods* about emerging standards in microscopy can be found in this issue.

Part of the work in developing standards for cameras in microscopy and imaging is about creating common definitions as a public resource. “The QUAREP-ers are moving on all that quite well,” says Jason Swedlow of the University of Dundee, who



Cameras are a crucial part of microscopes and imaging systems. Agreeing on standards to provide defined descriptions for aspects such as gain or readout speed is tricky. Credit: W. Bulgar/Science Photo Library

### technology feature

Check for updates

## Imaging standards to ease reproducibility and the everyday

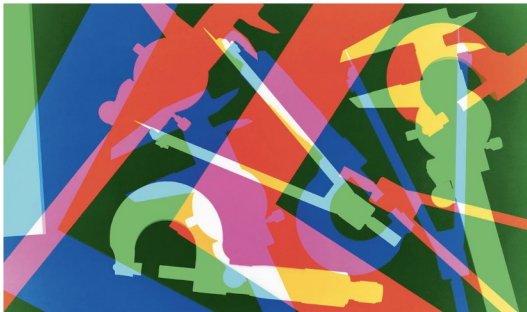
Imaging and microscopy technology advances in leaps and bounds. To address accumulated pain points, academics and companies are making headway on standards.

Vivien Marx

With a view to transparency and reproducibility in microscopy, scientists are hammering out standards to address, for instance, the surprises of fluctuating illumination power, the jungle of file formats, the mysteries of missing metadata and the diversity of camera outputs. A second story in this issue of *Nature Methods* focused on camera standards can be found here.

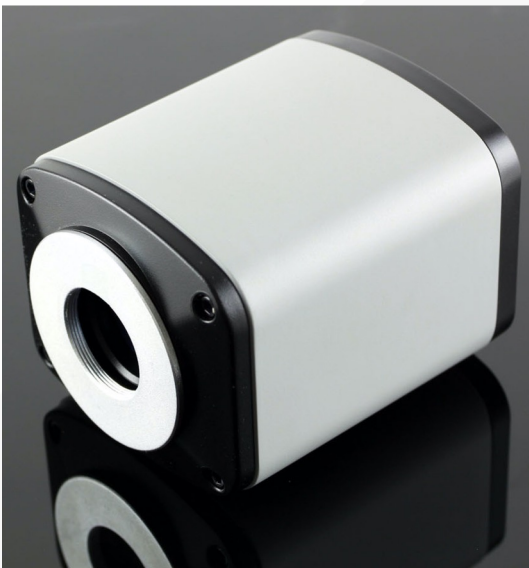
“We need standards,” says Roland Nitschke of the University of Freiburg. Developing standards in imaging is a noble deed that can make some eyes glaze over even beyond the glaze arising from long hours at the microscope. Those who feel they lack the time to pitch in on standards might be glad to hear that some not-so-distant developments stand to help microscopy users pull out their hair a bit less. Here’s a peek at how some emerging standards could address real-world pain points.

Standards development is not a task for



Emerging standards in microscopy are being set up to address many pain points in the field. Credit: TEK Image/Science Photo Library

- 20+ focus groups to build consensus
- **Proposal for Change submitted to QUAREP-LiMi members**
- Coming Soon: Revised Camera section of the LiMi-Model + glossary



### Camera

- Manufacturer: *XYZ*
- Catalog Nr: *0000*
- Mount: *C-mount*
- FrameRate: *20 fps*
- ReadOutRate: *30 MHz*



**EVIDENT**  
**OLYMPUS**

**ZEISS**

**Leica**  
MICROSYSTEMS

**Nikon**

**pco.**

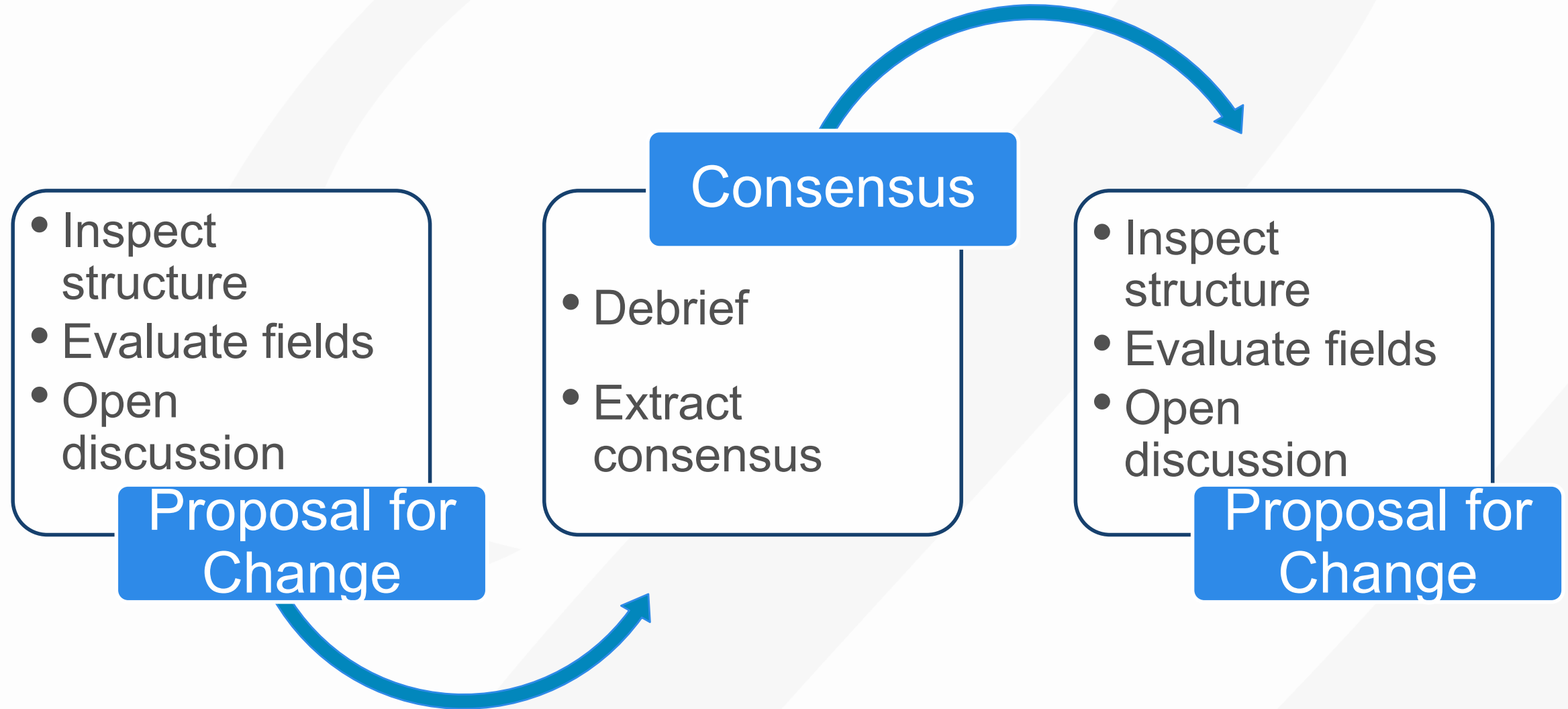
**Ψ Scientifica**

**OXFORD**  
INSTRUMENTS **ANDOR**

**TELEDYNE**  
PHOTOMETRICS

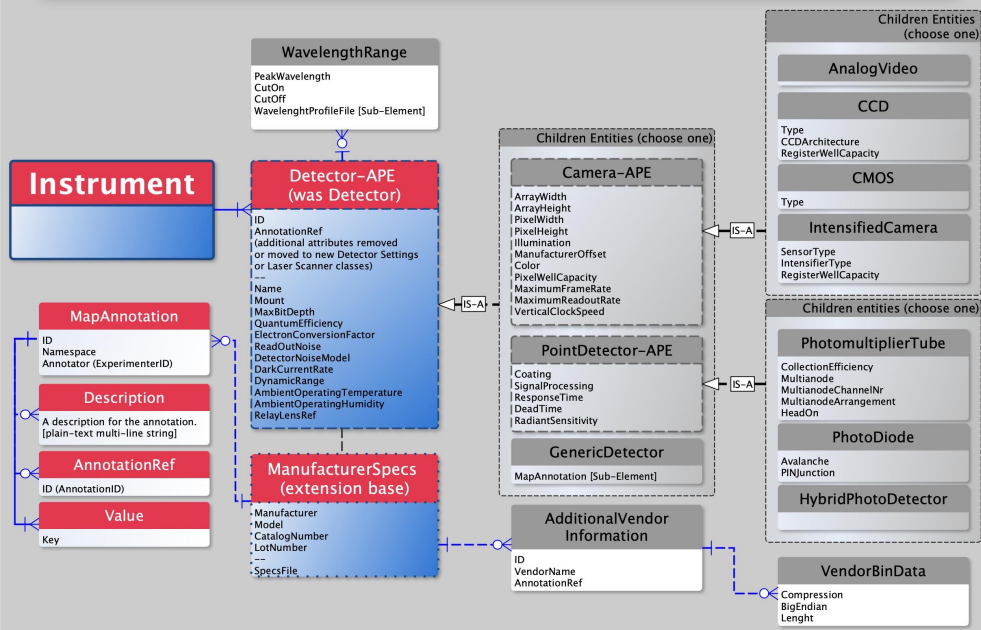
**HAMAMATSU**  
PHOTON IS OUR BUSINESS

# WG2 + WG7 joint endeavor: focus groups to review model elements and definitions

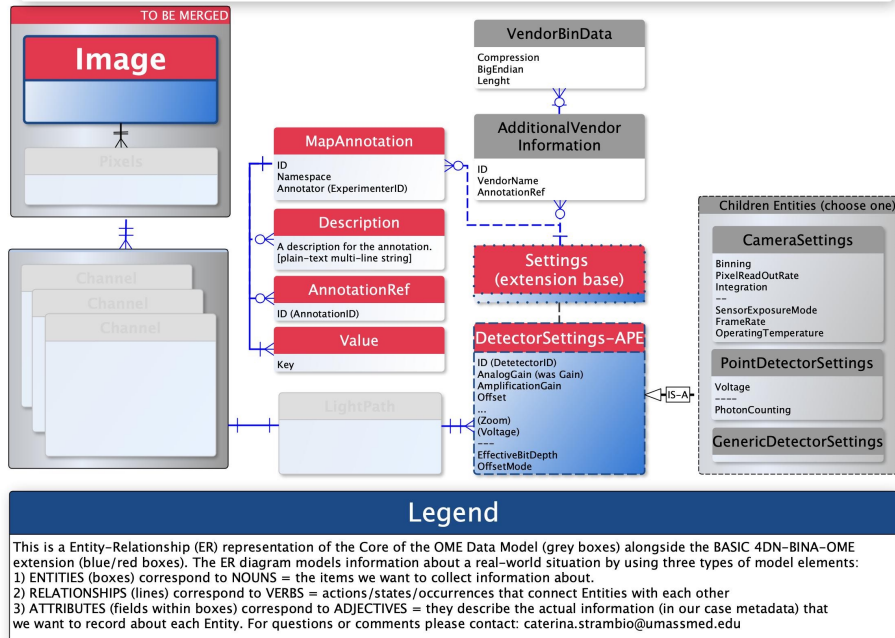


# WG2 + WG7 joint endeavor: revised camera model

## OME Core vs. NBO Basic Extension DETECTOR Hardware Specifications



## OME Core vs. NBO Basic Extension DETECTOR Acquisition Settings



Britta  
Schroth-Diez



Roland  
Nitschke



Mathias  
Hammer



Olaf  
Selchow



David  
Grunwald



Caterina  
Strambio De  
Castillia

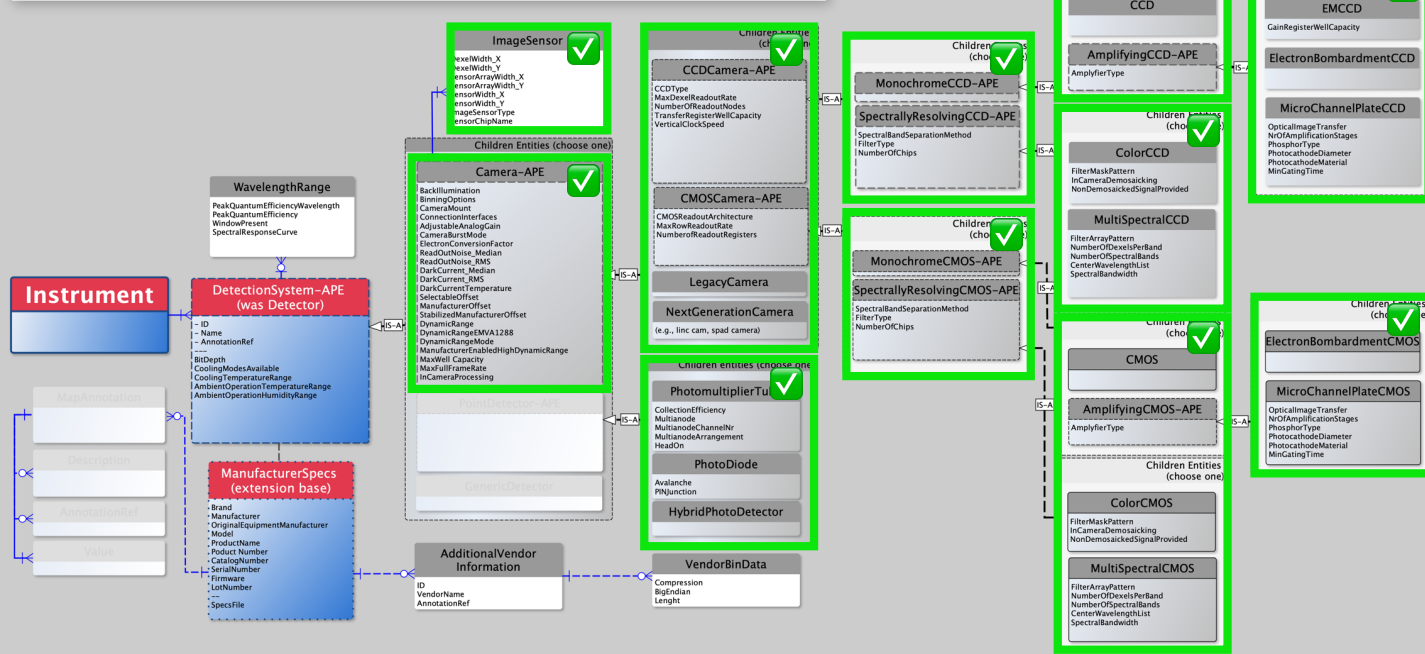
the Camera Model  
revision  
organizing group



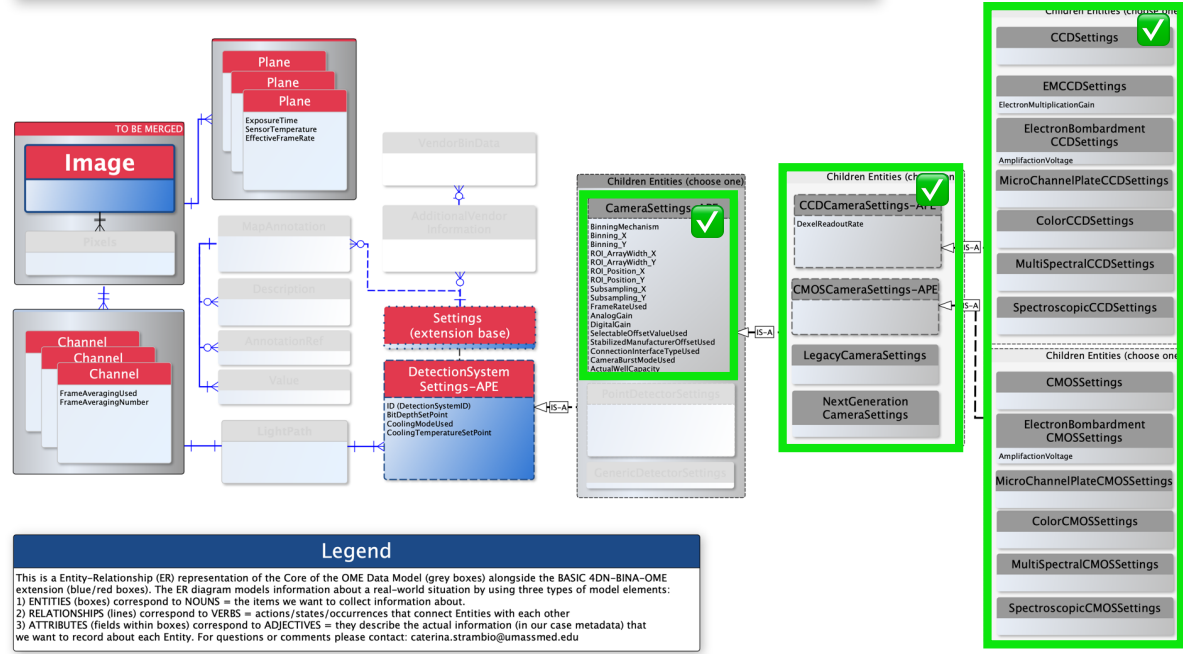
# WG2 + WG7 joint endeavor: revised camera model



## OME Core vs. LiMi-Model DetectionSystem Hardware Specifications



## OME Core vs. LiMi-Model DetectionSystem Image Acquisition Settings



Britta  
Schroth-Diez



Roland  
Nitschke



Mathias  
Hammer



Olaf  
Selchow



David  
Grunwald



Caterina  
Strambio De  
Castillia

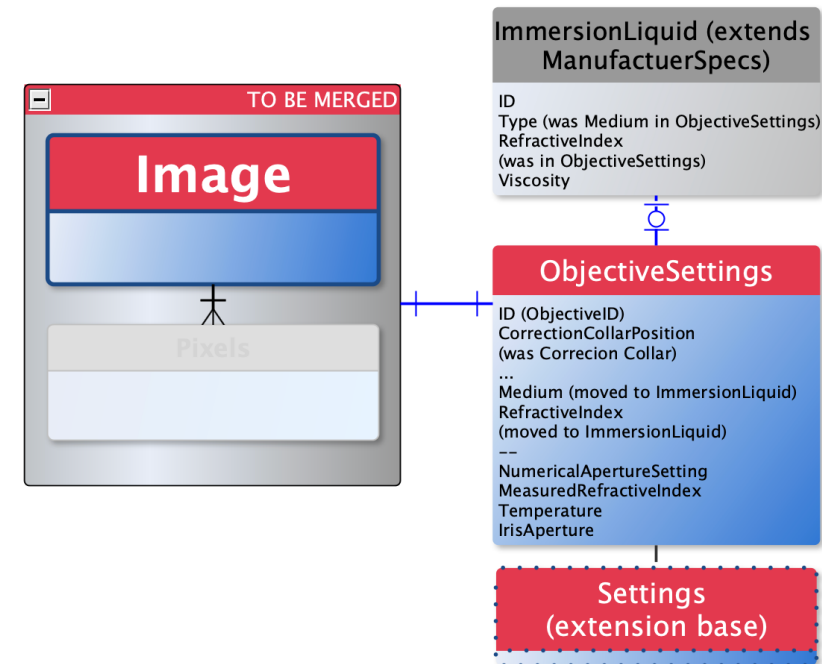
the Camera Model  
revision  
organizing group

# LiMi-Model revision next steps: OBJECTIVES

## LiMi-Model – OBJECTIVE Hardware Specifications

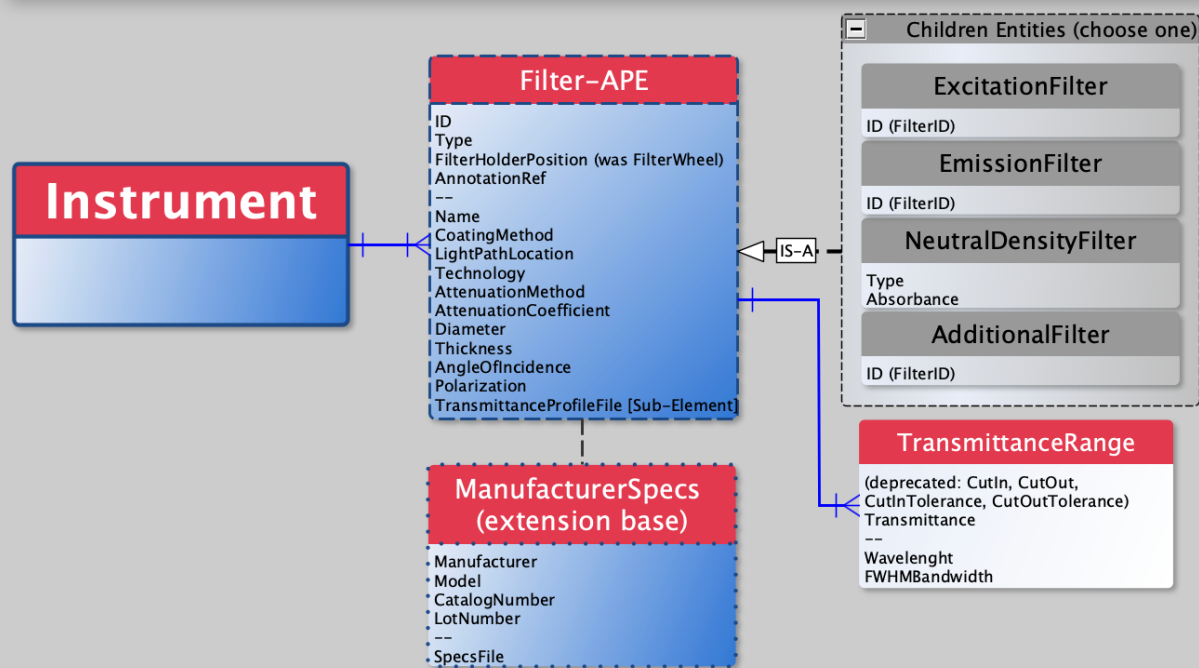


## LiMi-Model – OBJECTIVE Acquisition Settings

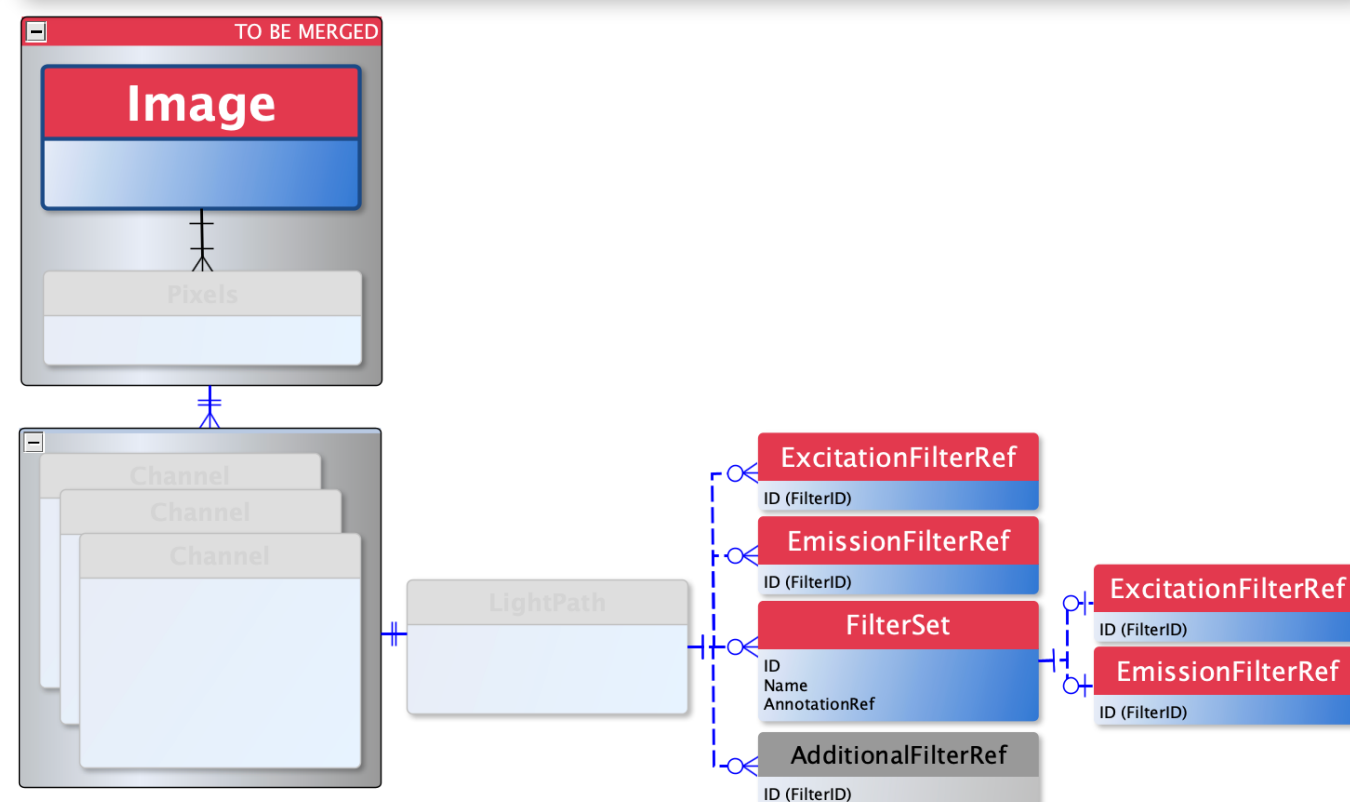


# LiMi-Model revision next steps: FILTERS

## LiMi-Model – FILTER Hardware Specifications



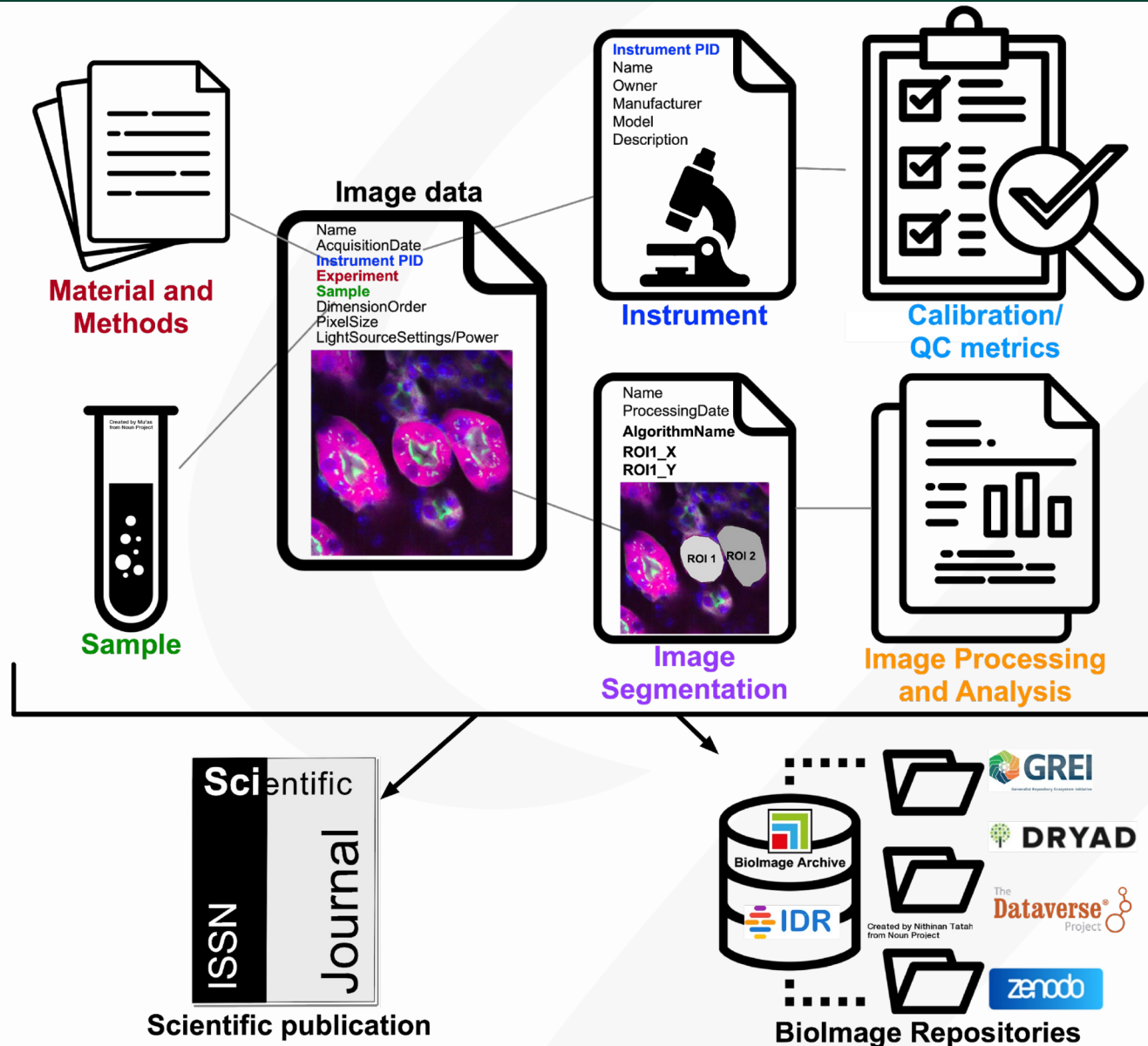
## LiMi-Model – FILTER Image Acquisition Settings



QUAREP-LiMi Working Groups 3,4 and 5

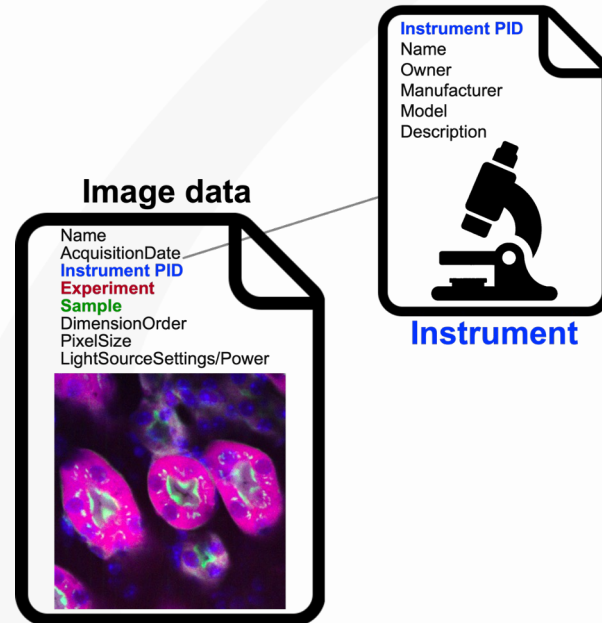


# Where is bioimage metadata?



**PIDs can help maintain links between different essential information**

# Persistent Hardware Descriptors help making data FAIR



## Linked PIDs for

- Instrument instance
- Instrument model
- **Hardware configuration**

# Core Marketplace + RRID: supporting the persistent identification of core-facilities



SEARCH HELP

POSTINGS



Vermont  
Biomedical  
Research  
Network  
An IDeA Network of Biomedical Research Excellence (INBRE)



SEARCH | [ADD/EDIT MY FACILITY](#)

SEARCH THE COREMARKETPLACE



## RESEARCH RESOURCE IDENTIFICATION PORTAL

This is the Resource Identification Portal  
supporting guidelines for Rigor and Transparency  
in scientific publications.

[Learn More](#)

[Find Plasmids](#)

[Find Cells](#)

[Find Organisms](#)



# Core Marketplace + RRID: supporting the persistent identification of core-facilities



SEARCH HELP

POSTINGS



Vermont  
Biomedical  
Research  
Network  
An IDeA Network of Biomedical Research Excellence (INBRE)

## Rigor, Reproducibility, Ruse Use-Case in Light Microscopy

Identification of Instrument Instances +  
Standardized Hardware, Settings and  
Quality Control Description



Learn More

 Find Plasmids

 Find Cells

 Find Organisms

# NSF CSSI #2513921: Imaging-PHD



David Grunwald



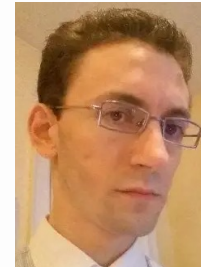
James Chambers



Judith Lacoste



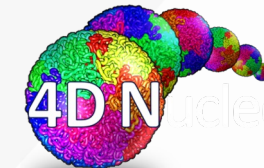
Josh Moore



Damien Goutte-Gattat



**BioImaging  
North America**



Adrian Zai



Koon Wong



Anita Bandrowsky



Nate Herzog



**SciCrunch**



**Vermont  
Biomedical  
Research  
Network**  
An IDeA Network of Biomedical Research Excellence (INBRE)



**UMass Chan  
MEDICAL SCHOOL**



**UMass Chan  
MEDICAL SCHOOL**

RRID

Core Marketplace

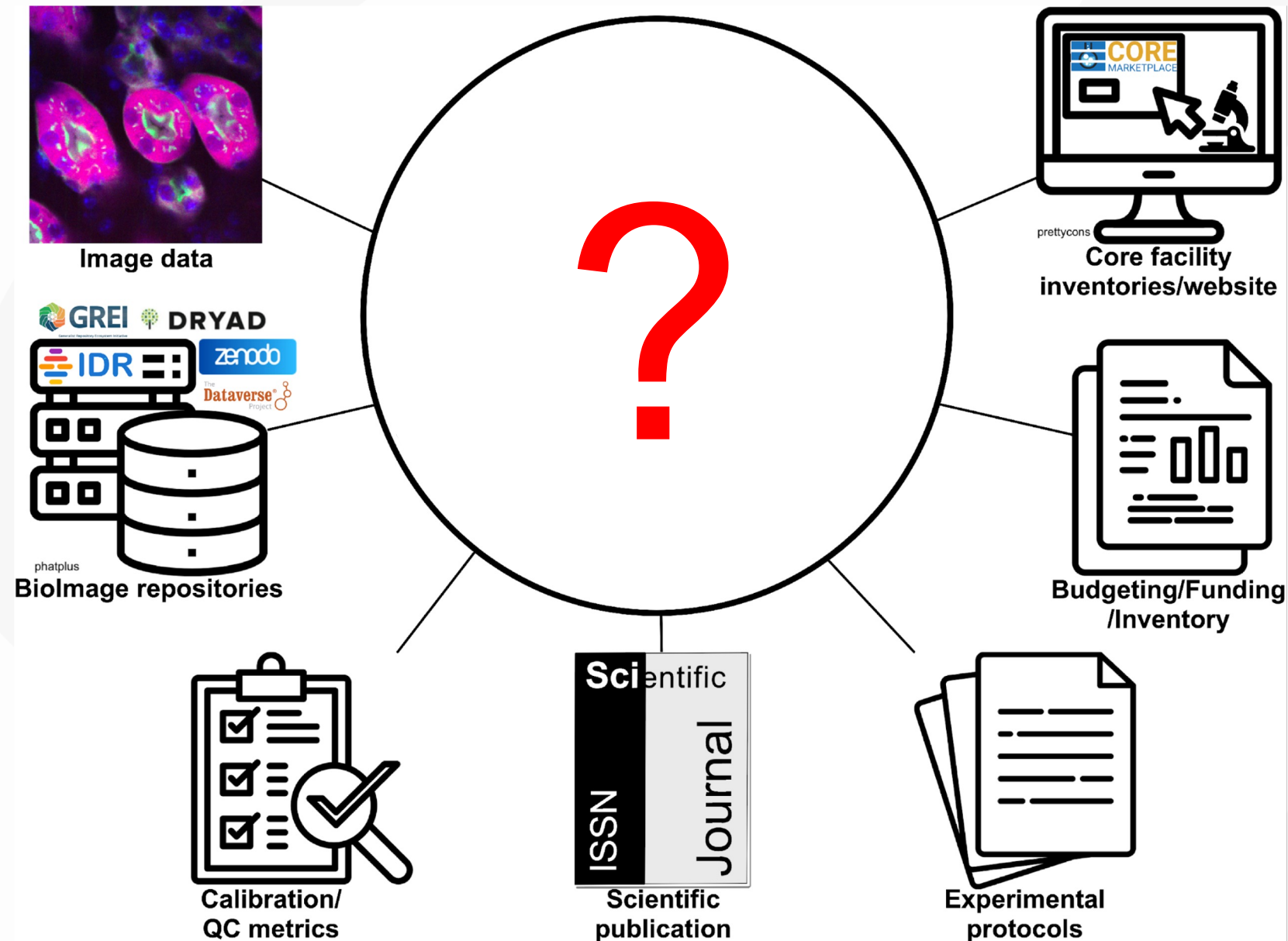
Quality-Control

Next Gen Metadata

Physics and Photonics Core Facility Head

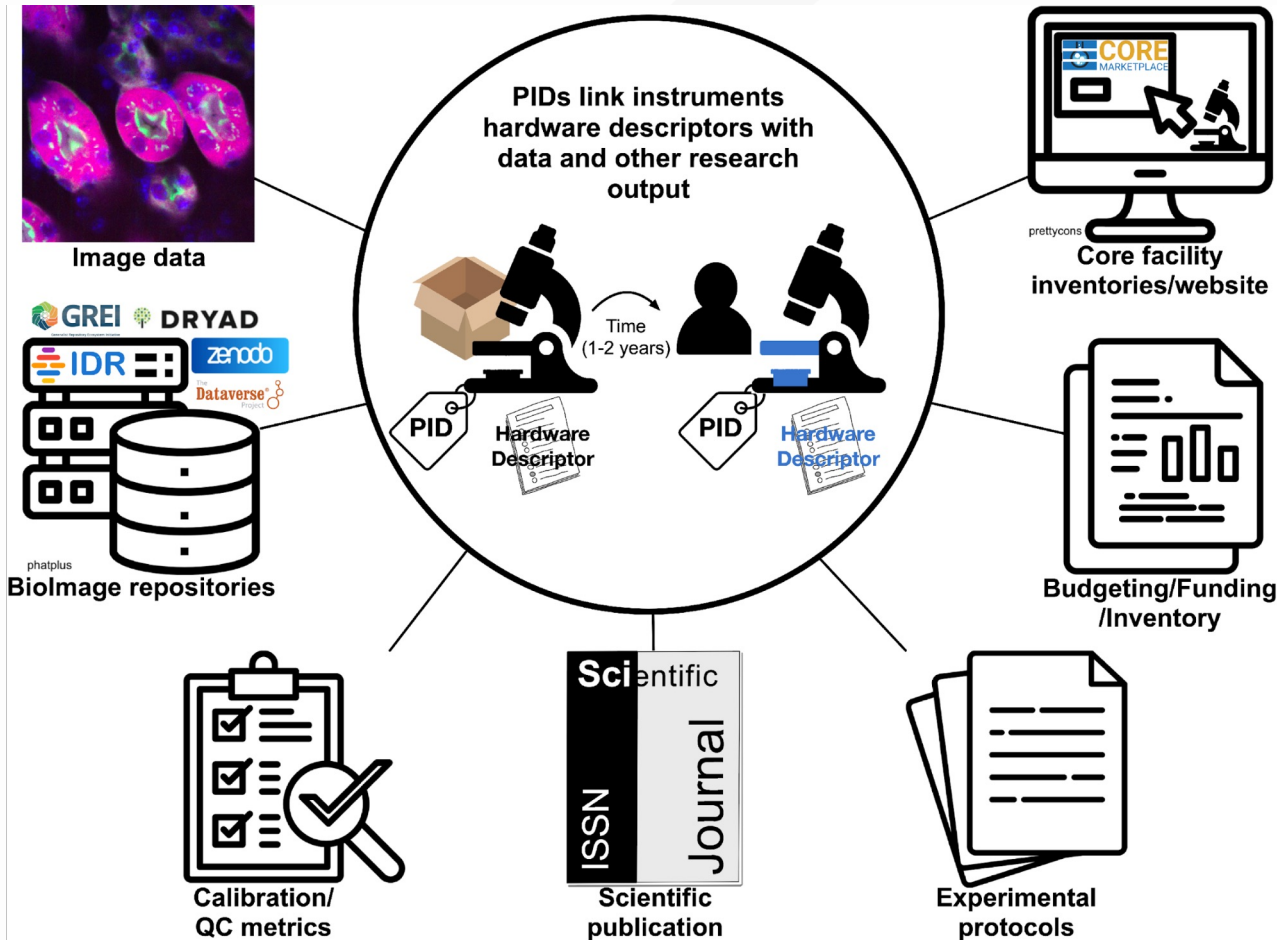
Research Informatics

# Labs and Core Facilities have different overlapping needs for the Instrument Data Management





# PIDs form a cornerstone of research



## Metadata is Scattered

- Critical imaging metadata is stored across disparate locations (files, devices, documents).
- This fragmentation hinders reproducibility, reuse, and proper attribution.

## What Are Persistent Identifiers (PIDs)?

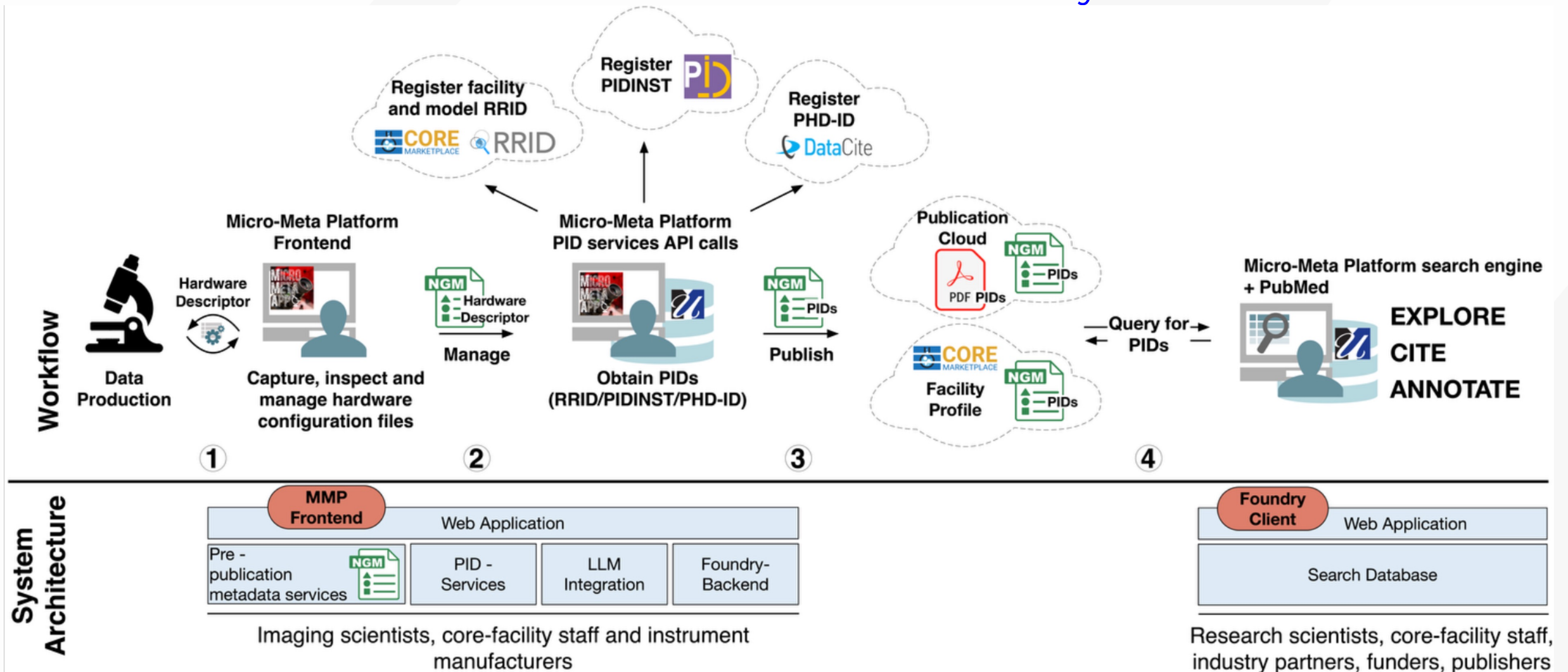
- Unique, long-lasting digital codes assigned to entities like instruments, datasets, and people.
- Maintained by trusted authorities and resolve to stable landing pages with rich metadata.

## Why PIDs Are Essential

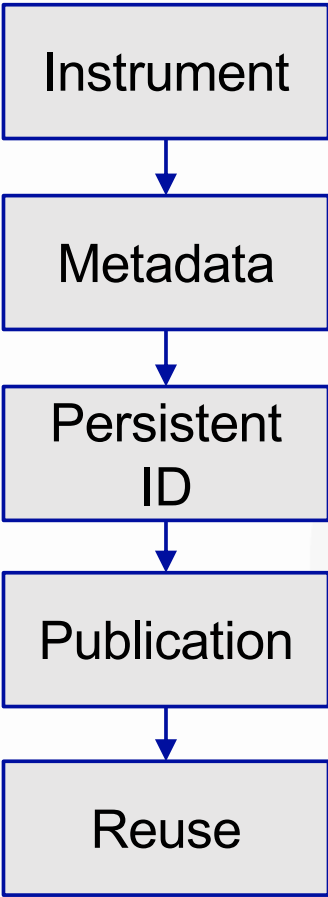
- **Linking:** Connect hardware, datasets, publications, and contributors.
- **Preservation:** Maintain long-term accessibility and integrity of research assets.

# Deliverable - Micro-Meta Platform Workflow and Architecture

Capturing, registering, and reusing persistent hardware metadata across the research lifecycle.



# Intellectual Merits - How this Work Advances Science



Merit Area	Imaging-PHD Contribution
<b>Democratizing Scientific Infrastructure</b>	Makes detailed, standardized instrument metadata openly available via persistent identifiers. Enables smaller labs and under-resourced institutions to build on others' hardware setups.
<b>Ensuring Long-Term Research Quality</b>	PHDs improve instrument lifecycle tracking and quality assurance, supporting replicability and reducing hidden sources of error.
<b>Enabling Workforce Development</b>	Empowers core facility staff and early-career researchers with tools and training for metadata best practices.
<b>Catalyzing New Discovery</b>	Harmonized metadata enables data pooling and cross-study reanalysis, accelerating multi-institutional discoveries.

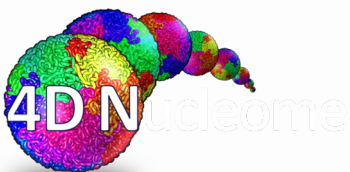
“Our technical design promotes long-term reuse, community adoption, and the scalability of reproducible research.”



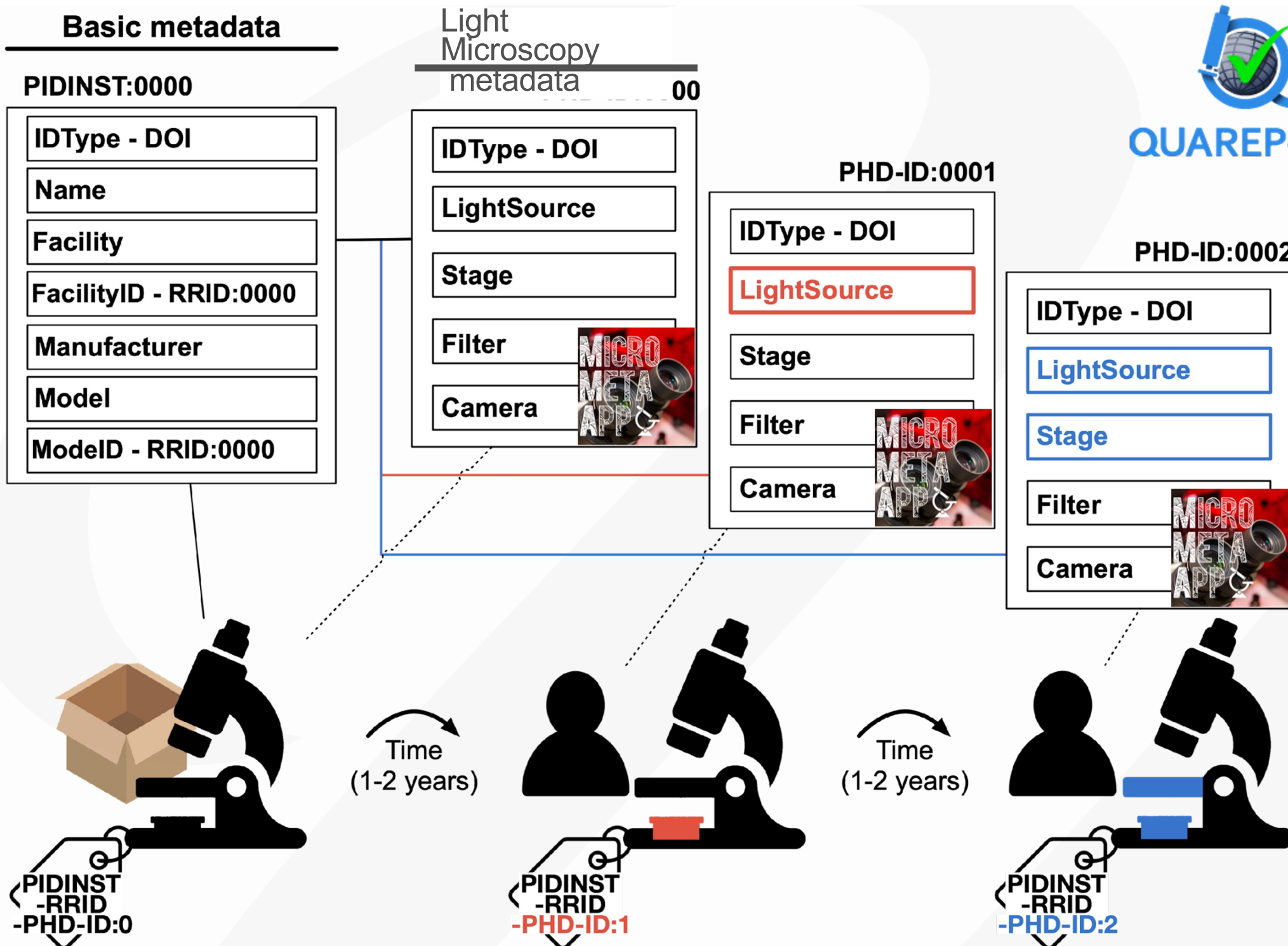
# Broader Impacts - Empowering Researchers, Core Facilities, and Industry Partners

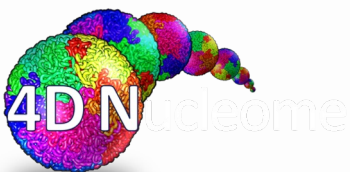
Who Benefits	How Imaging-PHD Helps
Researchers	Gain access to well-documented instrument configurations, improving reproducibility and enabling meta-analyses
Educators & Trainees	Use PHD-linked metadata for real-world training on instrumentation and FAIR practices
Core Facility Staff	Receive credit for their contributions via PID linkage and gain tools for quality tracking
Under-resourced Institutions	Can reuse metadata and design experiments modeled after advanced facilities
Software Developers & Industry Partners	Integrate their tools with standardized APIs, enhancing interoperability and adoption

“Broader impact is embedded in every layer of our platform—tools, people, and community.”

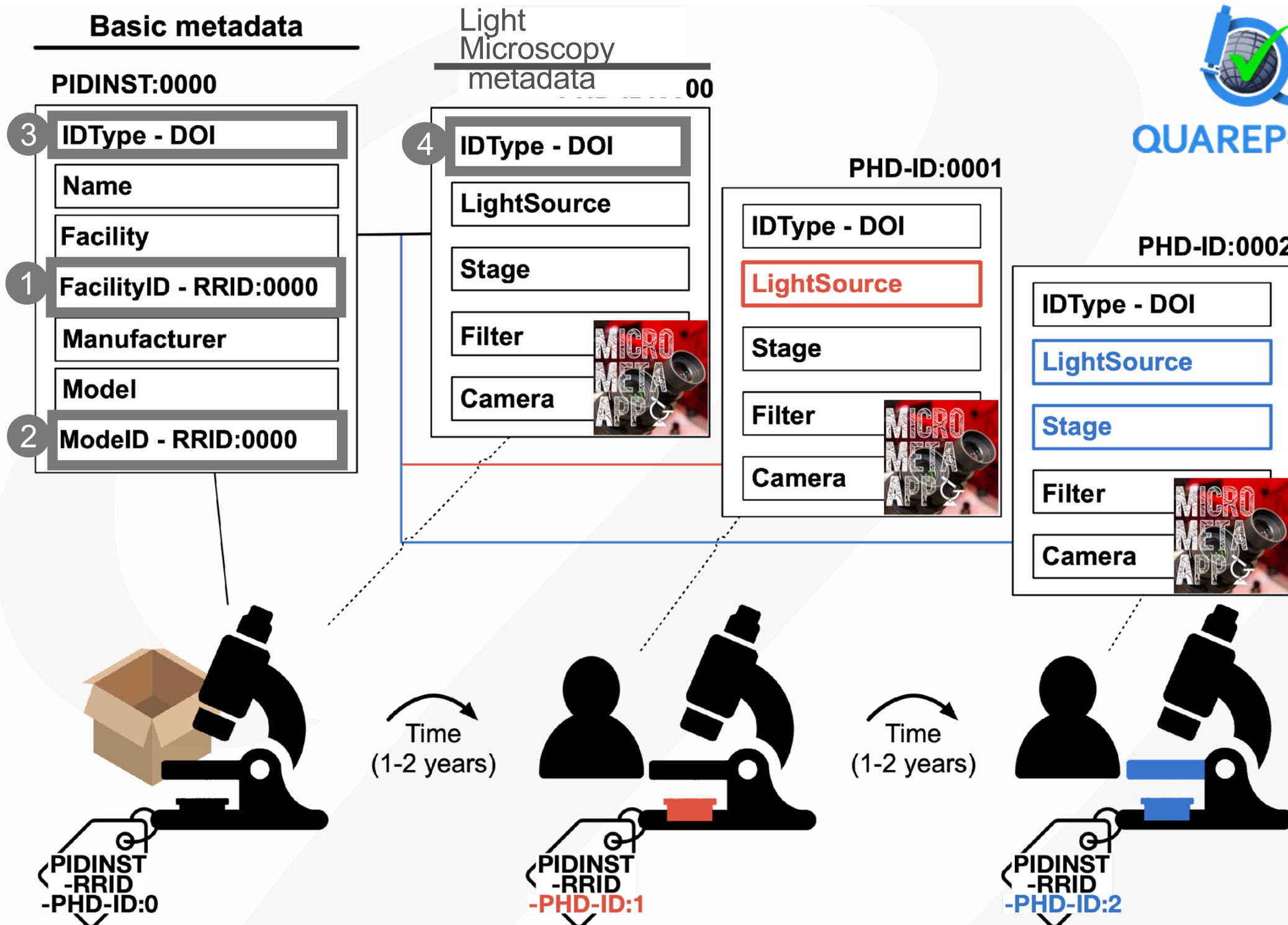


QUAREP-LiMi

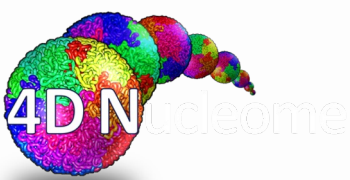




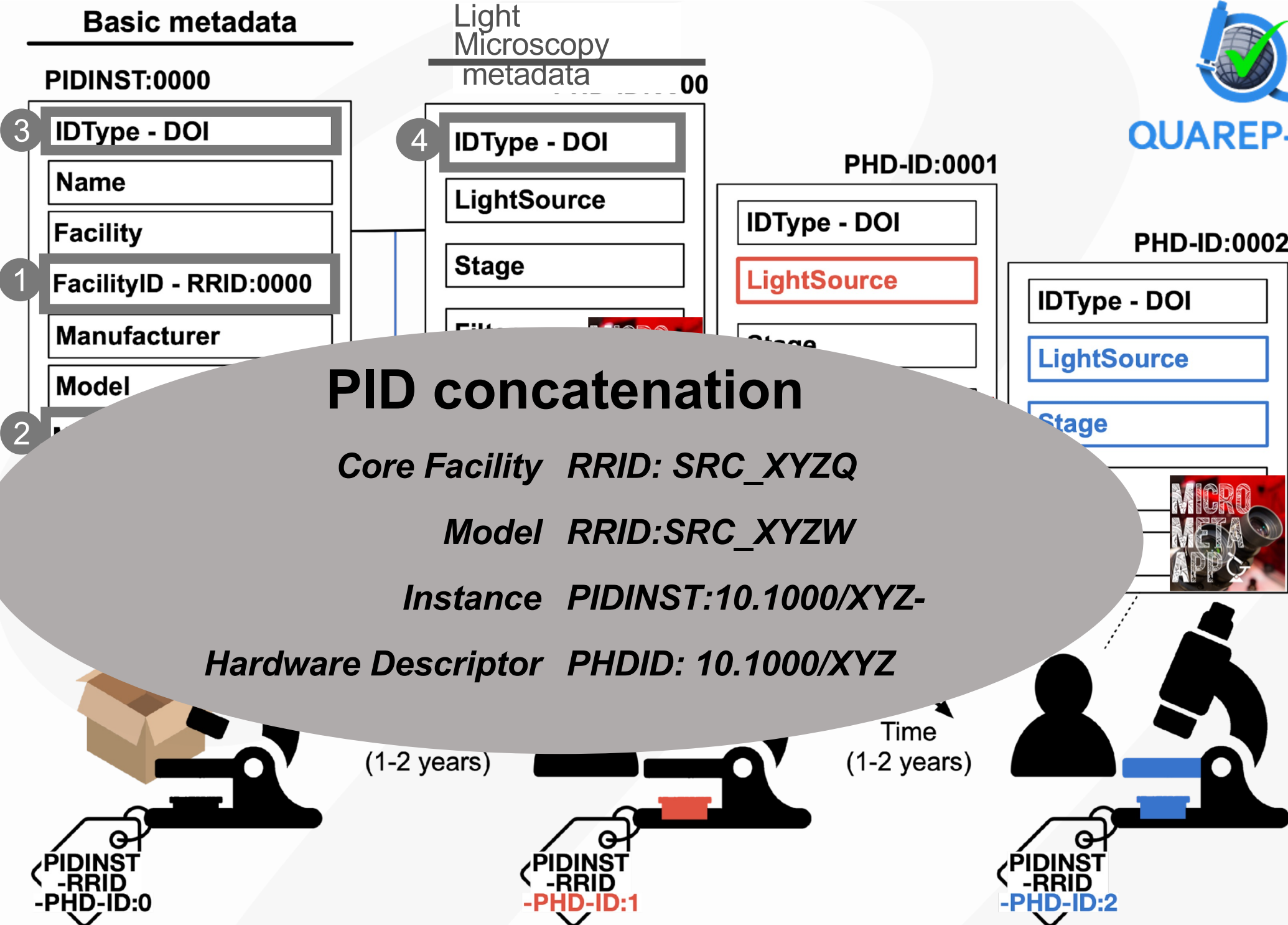
QUAREP-LiMi



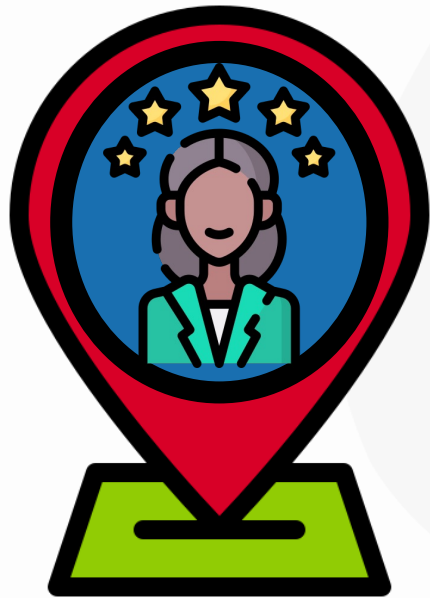




QUAREP-LiMi

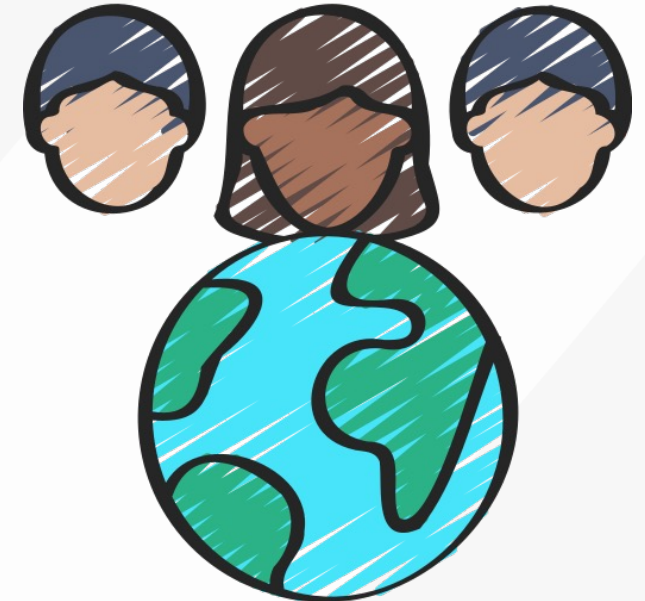


# Bringing it all back home!



Local  
expertise

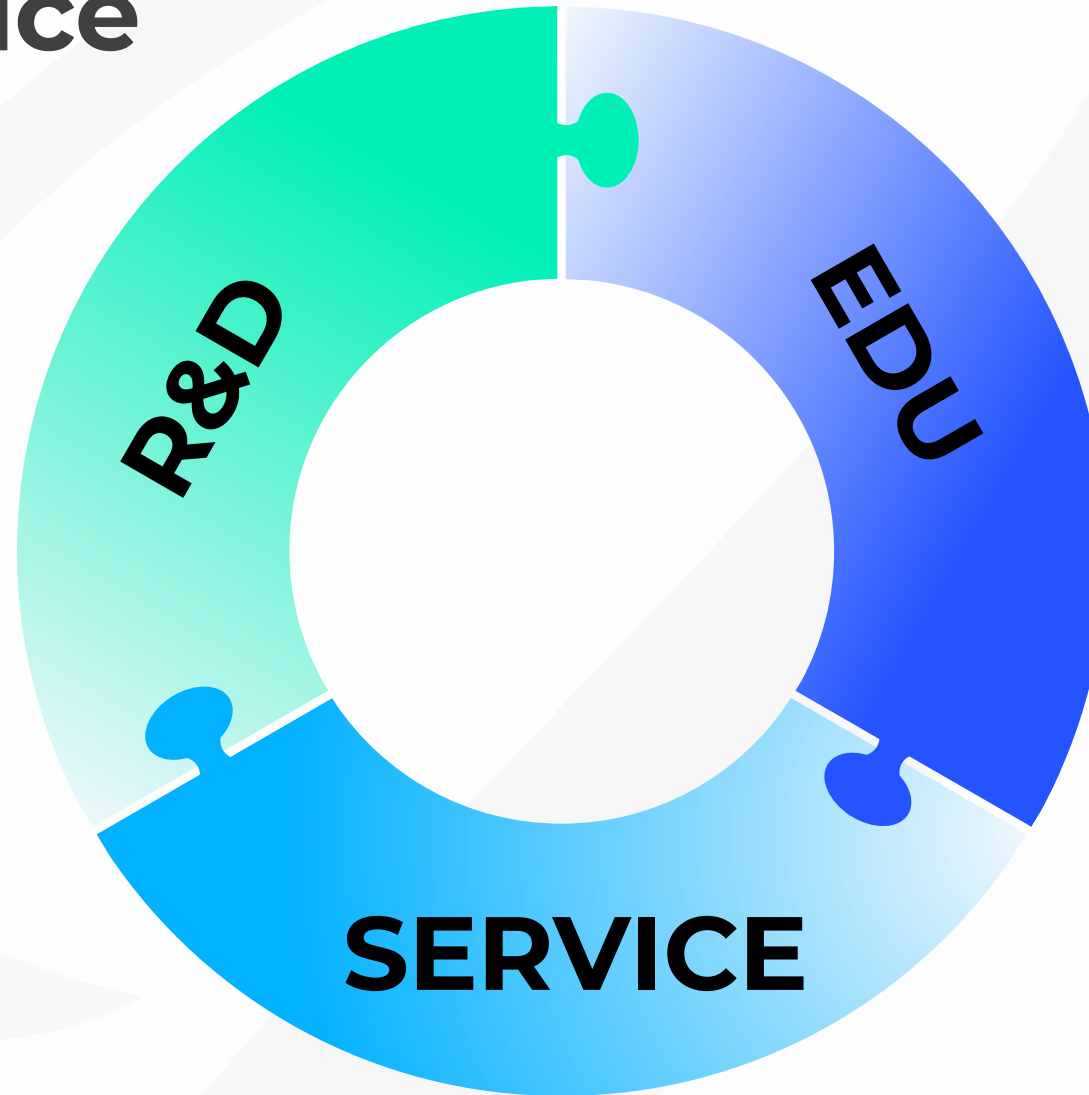
Community  
Guidelines,  
Specifications  
and Tools



# Vision: BioImage DMS as a service



Develop **FAIR**  
**metadata**  
**specifications,**  
**software tools, and**  
**cyberinfrastructure**



Increase  
**awareness and**  
**expertise** among  
research  
scientists

Make state-of-the-art Bioimage  
DMS **accessible to all at scale**



# Mission: BioImage DMS as a service



## Research & Innovation:

Open-source platform  
incorporating state-of-  
the-art methods



**Education & Training:**  
Scientists at all  
career stages

## Service provision:

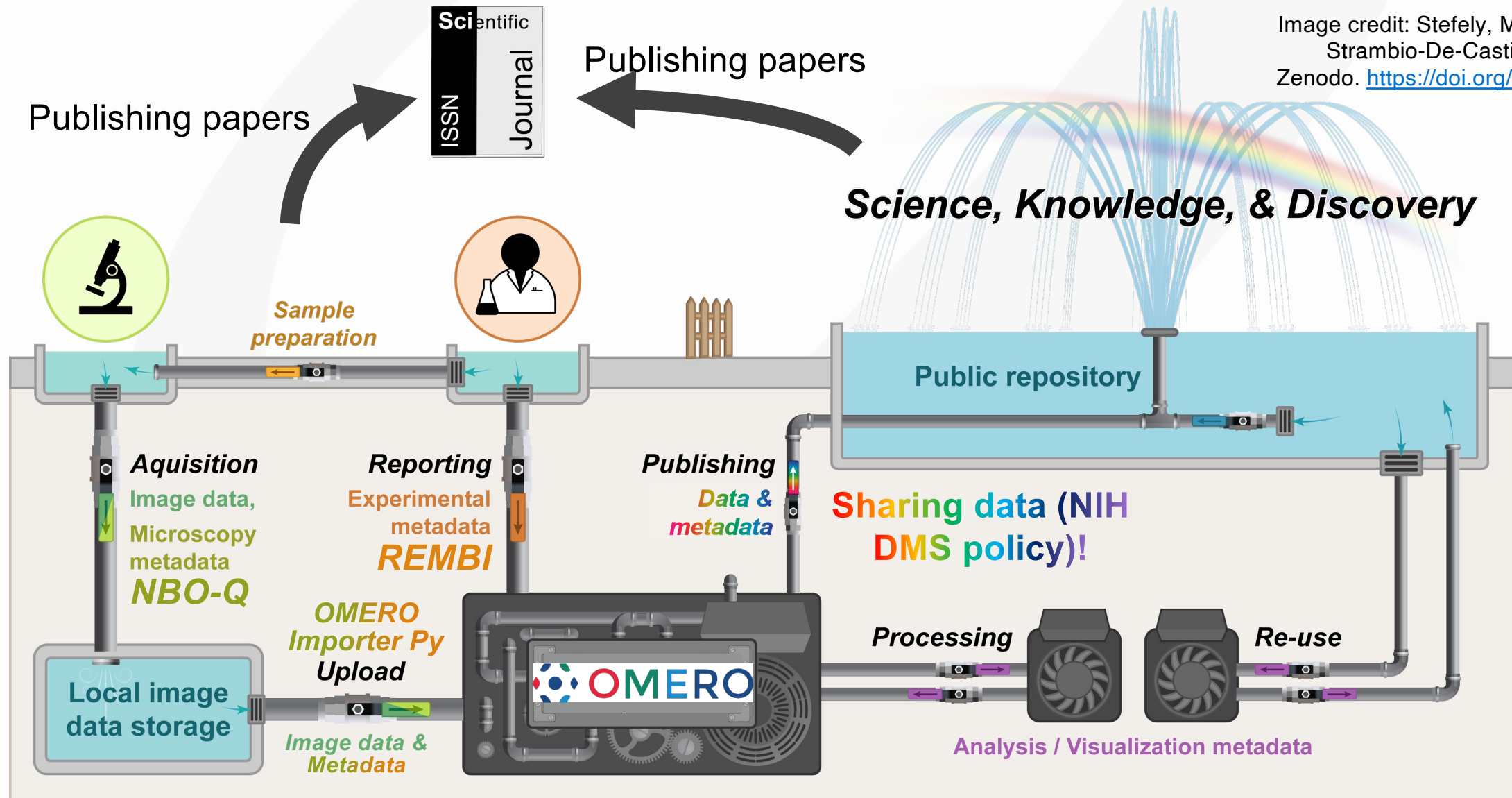
Platform deployment and user support



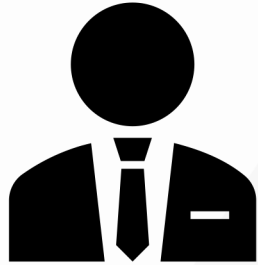
# OMERO-based pipes at UMass Chan and Canada Biolmaging



Image credit: Stefely, M., Bialy, N., & Strambio-De-Castillia, C. (2024)  
Zenodo. <https://doi.org/10.5281/zenodo.14020675>

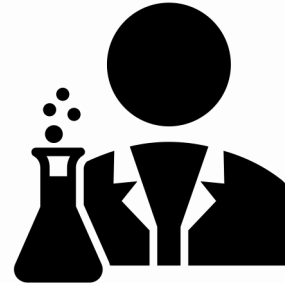


# Vision: Provide widespread solutions for BioImage DMS at the site of data production



## ■ Group leaders

- Strategy
- Project overview
- Visualize image data and monitor progress
- Long term preservation and accessibility of image data



## ■ Experimenters

- Records all the details of a project, which experiment worked, which had an issue
- Organize and annotate the data with relevant metadata
- Prepare figures for publication



## ■ Bioimage analyst

- Needs metadata for processing
- Share results back
- Reproducibility and traceability of analysis

Image credit: modified from Tom Boissonnet



# OMERO: glue supporting the full bioimage data life cycle

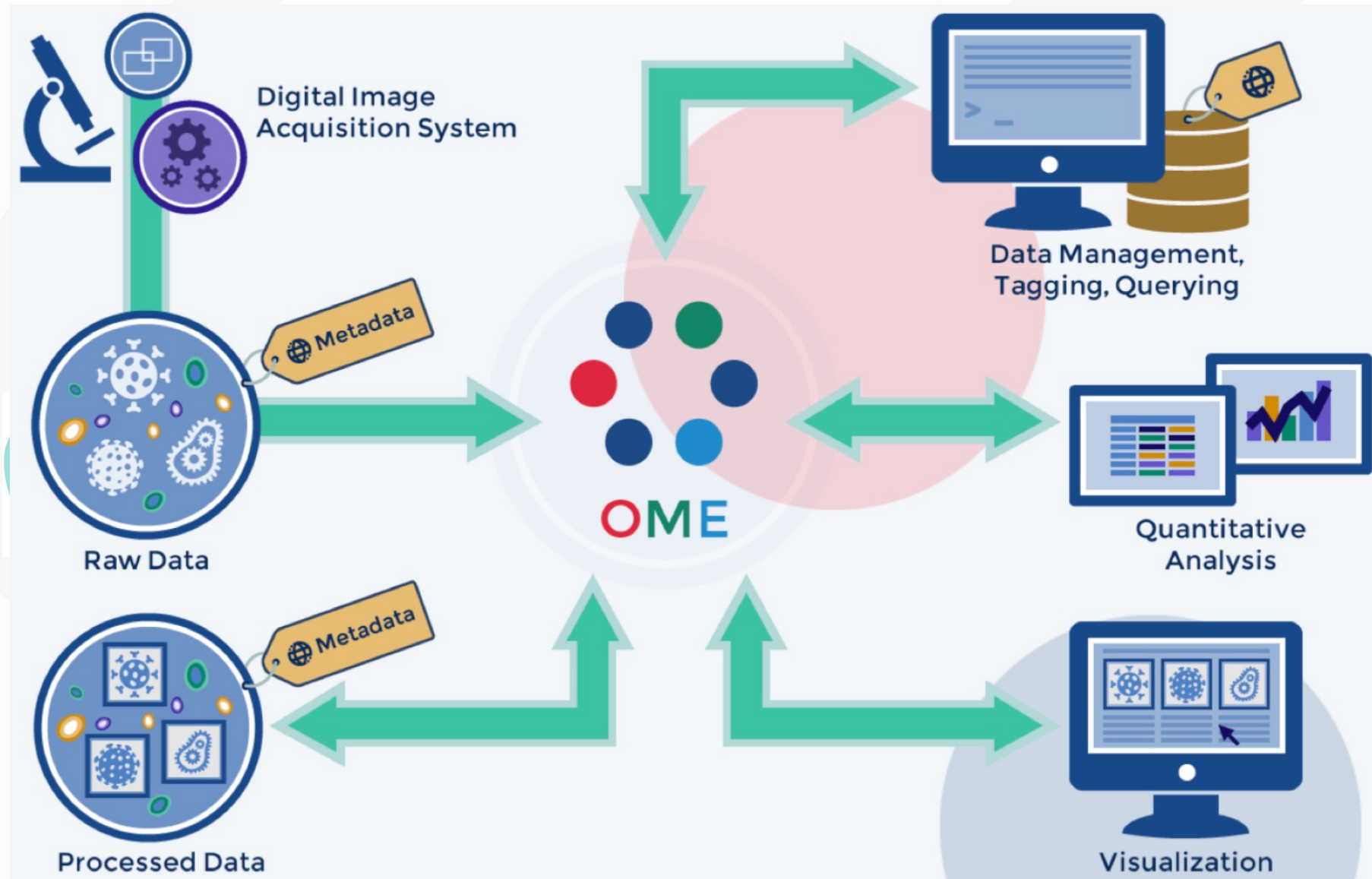


Image credit:  
openmicroscopy.org



# OMERO: supports 160 different bioimage file formats (including DICOM)

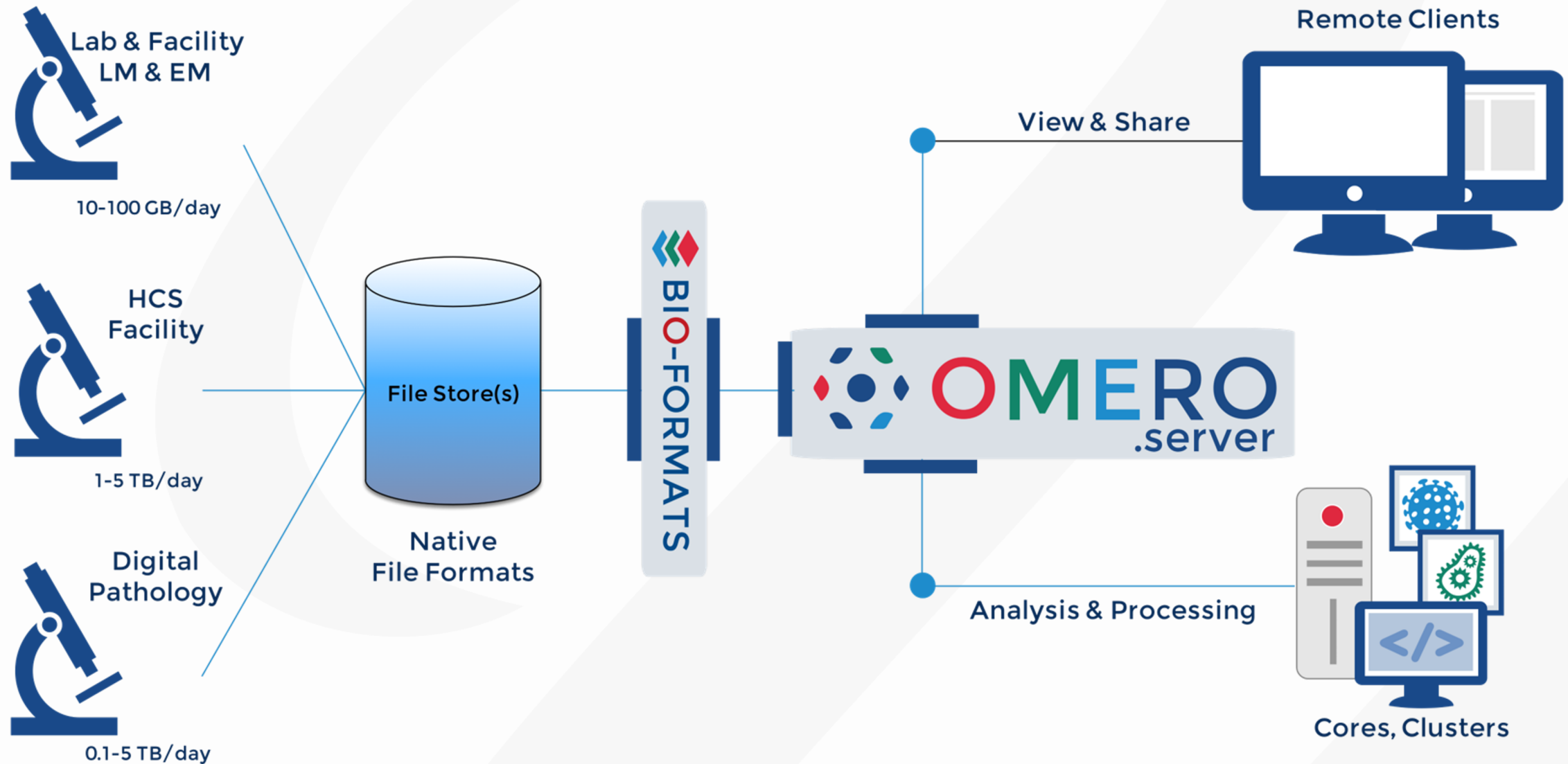
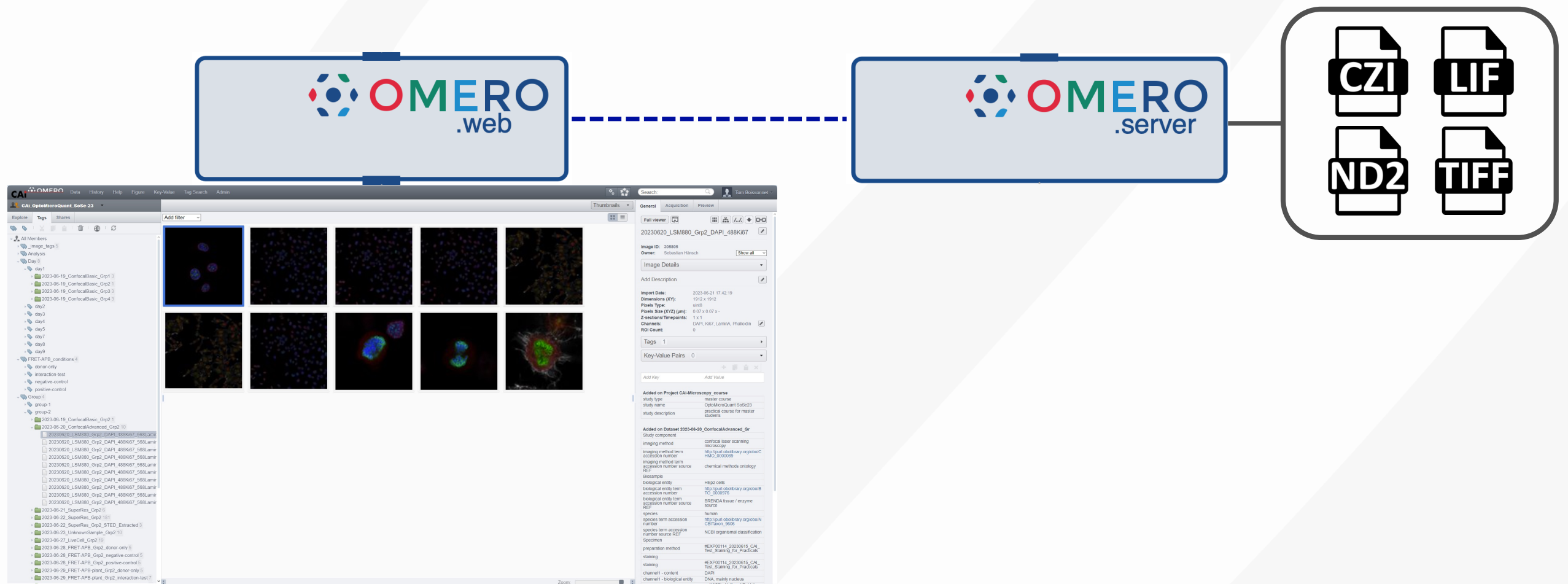


Image credit: Josh Moore

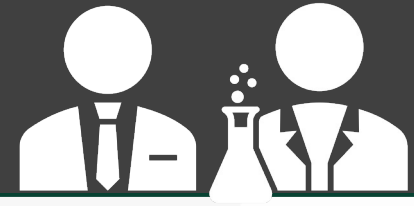
# OMERO for Biolmage DMS

- OMERO.web is one of the ways to access data in OMERO.server





# Data overview, exploration



OMERO Data History Help Figure Key-Value Tag Search

Search:  Tom Boissonnet

Pazour Laboratory Abigail Smith

ES clock All Members

Greer Laboratory Owners

Grunwald laboratory Gregory Pazour

Hedtrich laboratory Members

HMS-Nikon Imaging Center Lyu Bo

Kiepas et al.\_2020\_10.1242/jcs.242834 Paurav Desai

Lawrence Laboratory Mohona Gupta

Luban laboratory Kenley Preval

Abigail Smith

Caterina Strambio De Castillia

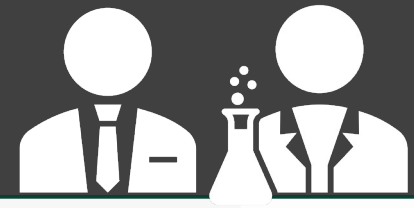
Michael Stuck

PI

users/lab members

General Acquisition Preview

# Data overview, exploration



OMERO Data History Help Figure Key-Value Tag Search

Pazour Laboratory Mohona Gupta

Explore Tags Shares

Mohona Gupta

- e626x rho 2
- Final Figures 2
- inpp5e 12 dpi rho 1
- Inpp5e 7 dpi rho 2
- Inpp5e icre P15 phalloidin 1
- Inpp5e icre P21 phalloidin 2
- Inpp5e iCre75 march 3 1
- Inpp5e iCre75 P15 3
- Inpp5e icre75 P21 1
- Inpp5e icre75 P21
- Inpp5e Pde6g ko rhodopsin 1
- Inpp5e phalloidin 12 dpi 1
- Inpp5e phalloidin 7 dpi 3
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  - phalloidin 9
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    - ...594 (500) wga 488 (20 slices).czi
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    - ...594 (500) wga 488 (20 slices).czi

image data repository

General Acquisition Preview

Full viewer

2. (max 2 slices) zoom in 28986 tam Inpp5e ko 7 dpi ph 594 (500) wga 488 (20 slices).czi

Image ID: 68034  
Owner: Mohona Gupta

Image Details

Add Description

Acquisition Date: 2023-04-18 15:28:43  
Import Date: 2023-04-28 15:27:23  
Dimensions (XY): 1102 x 1102  
Pixels Type: uint16  
Pixels Size (XYZ) (µm): 0.04 x 0.04 x -  
Z-sections/Timepoints: 1 x 4  
Channels: AF594-T1, AF594#-T1, AF488-T2, AF488#-T2, DAPI-T3, DAPI#-T3  
ROI Count: 0

Tags 0

Key-Value Pairs 0

Add Key Add Value

Tables

Attachments 0

Comments 0

Ratings 0

Others 1

# Data overview, exploration and collaboration



OMERO Data History Help Figure Key-Value Tag Search

Pazour Laboratory Mohona Gupta

Explore Tags Shares

Mohona Gupta

- e626x rho 2
- Final Figures 2
- inpp5e 12 dpi rho 1
- Inpp5e 7 dpi rho 2
- Inpp5e icre P15 phalloidin 1
- Inpp5e icre P21 phalloidin 2
- Inpp5e iCre75 march 3 1
- Inpp5e iCre75 P15 3
- Inpp5e icre75 P21 1
- Inpp5e icre75 P21
- Inpp5e Pde6g ko rhodopsin 1
- Inpp5e phalloidin 12 dpi 1
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    - ...594 (500) wga 488 (20 slices).czi

2. (max 2 slices) [edu:4080/webclient/?show=image-68034](https://4080.webclient/?show=image-68034)

Image ID: 68034  
Owner: Mohona Gupta

Image Details

Add Description

Acquisition Date: 2023-04-18 15:28:43  
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Channels: AF594-T1, AF594#-T1, AF488-T2, AF488#-T2, DAPI-T3, DAPI#-T3  
ROI Count: 0

Tags 0

Key-Value Pairs 0

Add Key Add Value

Tables

Attachments 0

Comments 0

Ratings 0

Others 1



# Automated metadata annotation



OMERO Data History Help Figure Tag Search Any Value Forms Designer **Micro-Meta-App** Search: Caterina Strambio De Castillia

Strambio laboratory Caterina Strambio De Castillia

Explore Tags Shares Add filter

Caterina Strambio De Castillia

- 2017-06-30\_Mu\_Zeiss acquisition test 3
- 2017-07-06\_Dan\_Mu\_IL-6\_enhancers 1
- 2022 Pazour import test 2
- 2022 Pazour Import Test Project 2
  - Dataset 1 6
    - Image-415.czi
    - Image-416.czi
    - Image-417.czi
    - Image-418.czi
    - Image-419.czi
    - Image-420.czi
  - Dataset 2 4
- Fiji analysis\_examples 2
- HIV\_entry\_2006-2008\_OpenLab 24
- HIV\_entry\_2007-2008\_LeicaSP5 16
- Hunter lab images 7
- KNIME demo 1
- Melikian lab images 1
- MLP\_resubmission\_2011\_FRAP 5
- MLP\_resubmission\_2012\_IF 2
- MMA\_Microscopes
- OMEGA\_benchmarking 6
- OMEGA\_demo 5
- OMERO training 2

Thumbnails

General Acquisition Preview

Dataset 1

Dataset ID: 2841  
Owner: Caterina Strambio De Castillia

Dataset Details

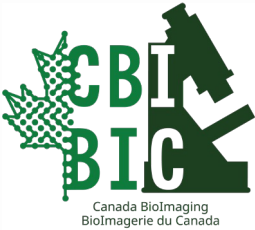
Key-Value Pairs 1

Cell_Sample_Type	cell line			
Cell_Sample_Type_accession_number	<a href="http://purl.obolibrary.org/obo/CLO_0000019">http://purl.obolibrary.org/obo/CLO_0000019</a>			
Tissue_Source_accession_number	not available			
Fixation_condition	2% PFA 15 min			
Embedding_Condition	not applicable			
Section_Thickness	not applicable			
Antigen_Retrieval	0.05% SDS 5 minutes			
Number_of_Channels	3			
Counterstaining_Channel	1			
DNA_counterstain	DAPI			

Attachments 2

- umms-pmm\_pazour\_lab\_lscm\_zeiss\_lsm-900-airyscan2.json (101.73 KB)
- image-415.czi\_#1\_as.json (17.82 KB)

Zoom:



Digital Research  
Alliance of Canada

Alliance de recherche  
numérique du Canada

Sample  
Preparation  
Metadata

Microscopy  
Metadata



# OMERO: key functions



Experimenter

OMERO.figure

OMERO.iviewer

OMERO.tagsearch

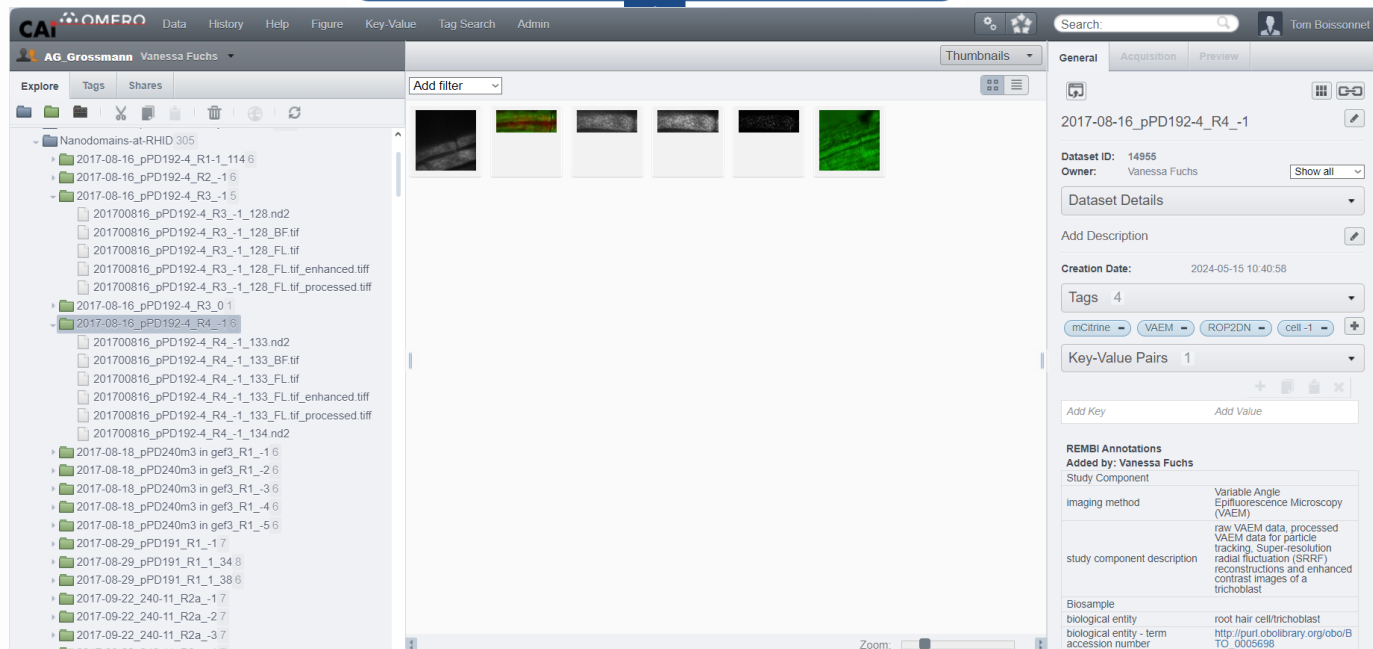
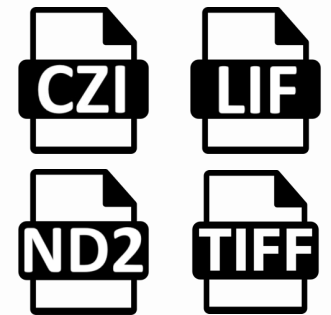
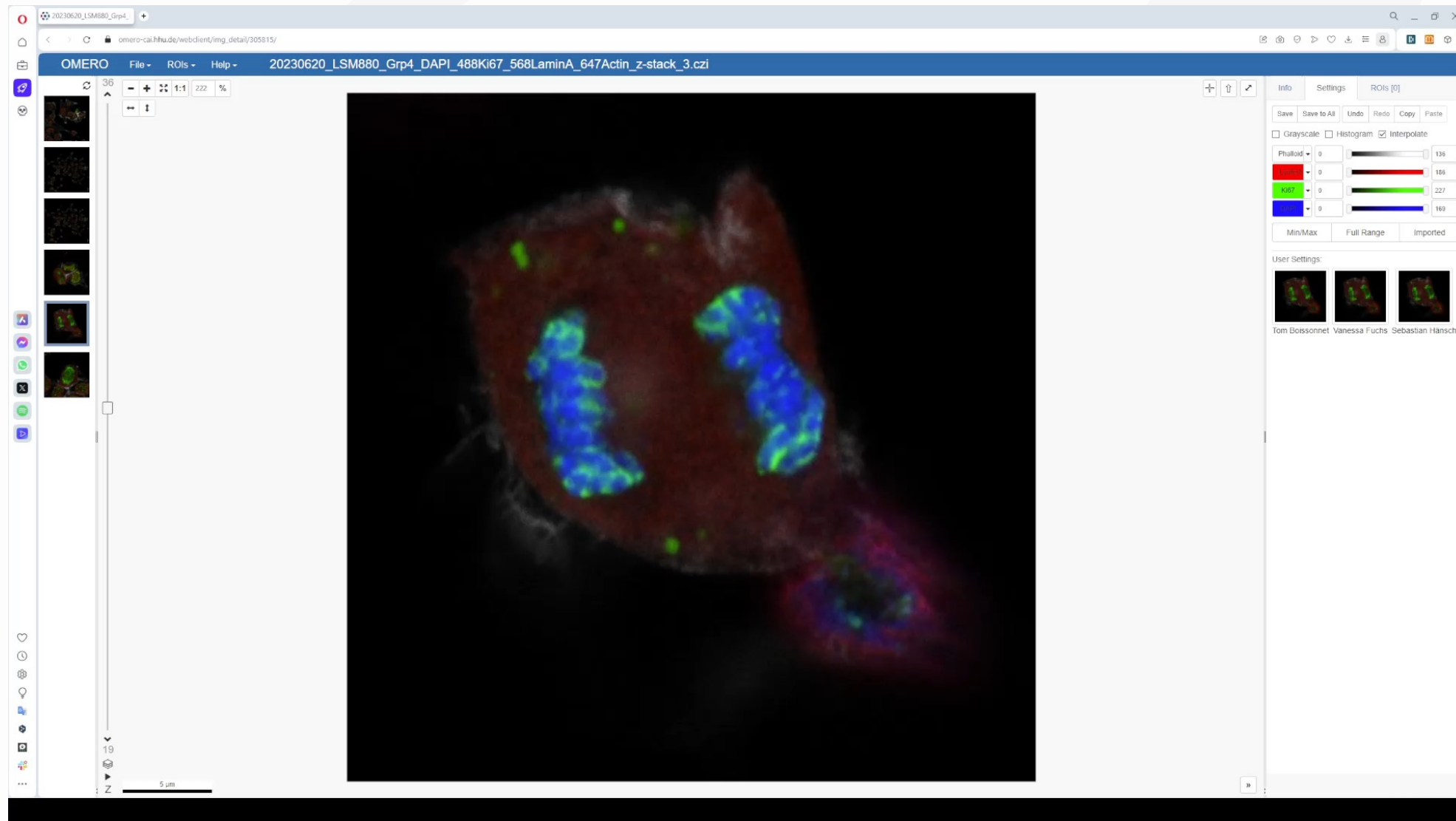


Image credit: modified from Tom Boissonnet

# OMERO.iviewer



Experimenter







omero-training.gerbi-gmb.de/figure/file/798

OMERO File Edit Help Save figure\_kv-pairs Add Image Delete Export PDF

added from key-value pairs

compound: C  
concentration: 2  $\mu$ M  
sample ID: 18746

compound: D  
concentration: 10  $\mu$ M  
sample ID: 22123

week: 1

week: 2

100  $\mu$ m

100  $\mu$ m

100  $\mu$ m

100  $\mu$ m

Info Preview Labels

0° Z

1/1 T 1/1

DAPI 112 6437

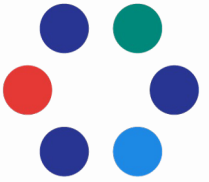
Zoom % 100

View x: 0 y: 0 width: 1280 height: 1024

Copy Paste Reset Crop

109 Add Figure Legend

# OMERO: searching and retrieving on the basis of metadata



OMERO Data History Help Figure Admin

Shared-ExpathCore-fc-01 Valeria Mezzano Robinson

Filter Results 77 results

**Search** Advanced [Show search hints ?](#)

Search:















**Restrict by Field:** ?  
☐ Name ☐ Description ☐ Annotations ?

**Search for:**  
☒ Images ☒ Datasets ☒ Projects  
☒ Wells ☒ Plates ☒ Screens

**Scope:**  
In group:   
Data owned by:

Date:  ?  
 -  ?

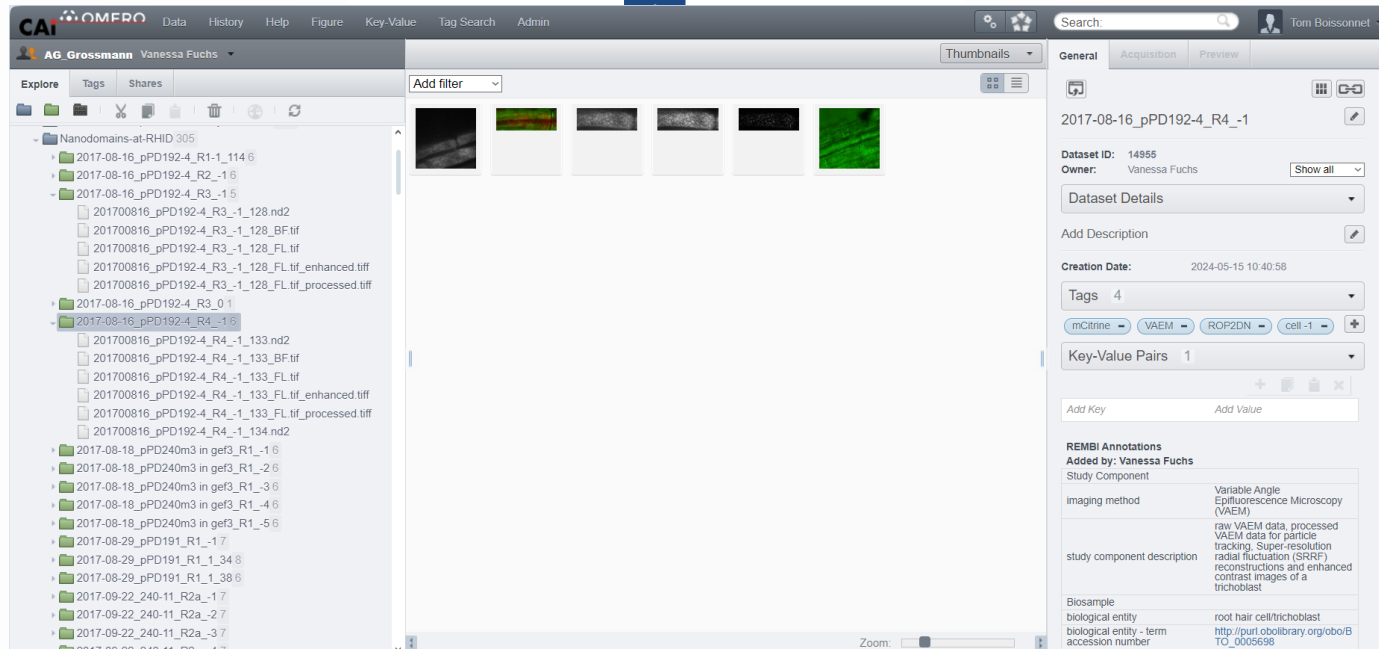
**Search**

Type	Name	Acquired	Imported	Group	Link
	Annotated		2020-05-08 15:12:04	ReadAnnotate_group	<a href="#">Browse</a>
	examples		2020-05-07 22:39:13	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061384_2020-04-14 17_06_54.scn [1]	2020-04-14 22:01:37	2020-05-07 22:39:20	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061385_2020-04-14 17_17_13.scn [macro]	2020-04-14 21:56:04	2020-05-08 13:40:30	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061385_2020-04-14 17_17_13.scn [1]	2020-04-14 22:12:02	2020-05-08 13:40:30	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061386_2020-04-14 17_26_47.scn [macro]	2020-04-14 21:56:06	2020-05-08 13:40:41	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061386_2020-04-14 17_26_47.scn [1]	2020-04-14 22:21:49	2020-05-08 13:40:41	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061386_2020-04-14 17_26_47.scn [2]	2020-04-14 22:26:45	2020-05-08 13:40:41	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061387_2020-04-14 17_38_00.scn [macro]	2020-04-14 21:56:08	2020-05-08 13:40:52	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061387_2020-04-14 17_38_00.scn [1]	2020-04-14 22:32:36	2020-05-08 13:40:52	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061387_2020-04-14 17_38_00.scn [2]	2020-04-14 22:37:59	2020-05-08 13:40:52	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061388_2020-04-14 17_47_30.scn [macro]	2020-04-14 22:39:23	2020-05-08 13:41:02	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061388_2020-04-14 17_47_30.scn [1]	2020-04-14 22:44:10	2020-05-08 13:41:02	Shared-ExpathCore-fc-01	<a href="#">Browse</a>
	collection_0000061388_2020-04-14 17_47_30.scn [2]	2020-04-14 22:44:53	2020-05-08 13:41:02	Shared-ExpathCore-fc-01	<a href="#">Browse</a>

# OMERO analysis

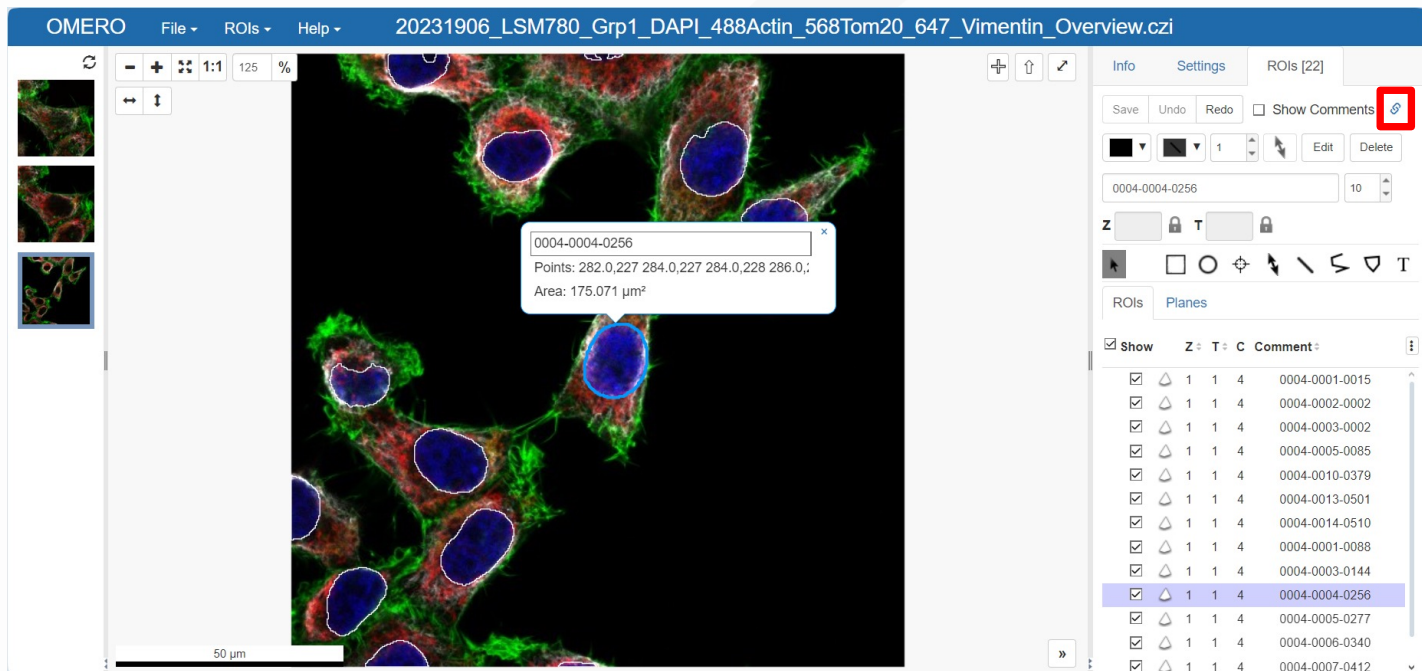


BioImage  
Analyst





# Storing results – ROI & Tables



dataset	image	roi	shape	cell_index	temperature	roi_area	roi_mean
12409	381487	69002	501669	1	T32	0.21474598181052906	81.41065830721003
12409	381487	69003	501670	1	T32	0.19387725003583817	97.52083333333333
12409	381487	69004	501671	1	T32	0.06933804428365045	77.90291262135922
12409	381487	69005	501672	1	T32	0.1837794765964716	94.41025641025641
12409	381487	69006	501673	1	T32	0.24369293233671324	114.26519337016575
12409	381487	69007	501674	1	T32	0.09289951564217244	79.01449275362319
12409	381487	69008	501675	1	T32	0.11376824741686337	80.03550295857988
12409	381487	69009	501676	1	T32	0.16358392971773844	88.90946502057614
12409	381487	69010	501677	1	T32	0.13127105471176542	71.82051282051282
12409	381487	69011	501678	1	T32	0.061933010428114964	90.40217391304348
12409	381487	69012	501679	1	T32	0.08347492709876365	105.70161290322581

# OMERO: high throughput screening



OMERO Data History Help

Study B (ra)

Explore Tags Shares

All Members

- Earth Science 2
  - MicroCT 3
    - Bentheimer\_1000c\_3p0035um.nhdr
    - Berea.ome.tif
    - Estallades\_1000c\_3p31136um.nhdr
  - MicroCT 3
  - Fluorescence Microscopy 2
  - Fluorescent Pathology 2
    - Study 1 5
    - Study 2 4
  - For Review 1
  - H&E Pathology 1
  - Medical 1
    - CIVM Data 3
      - civm\_rhesus\_v1\_b0.nii
      - civm\_rhesus\_v2\_b0.tif
      - CT5D.ome.tif
  - Multiplexed Pathology 1
  - Multispectral imaging 2
  - Paper Submission 1
  - Plate 1
  - TCGA 2
  - BBBC013 1
    - ...lasm-nucleus translocation [BBBC013]
  - BBBC022 10
  - Other Screen A 5
  - Other Screen B 10
  - Other Screen C 20
  - Test Screen 2
  - Orphaned Images 2

Thumbnails

General Acquisition Preview

Full viewer

D5

Well ID: 36991  
Owner: Emil Rozbicki

Tags 0

Key-Value Pairs 1

Tables

INFO

ImageNumber:	74
PlateName:	Human U2OS cells cytoplasm nucleus translocation [BBBC013]
Well:	36991
Drug:	Wortmannin
Dose:	3.91
log(Dose):	0.59
Control:	0
Count_Cells:	196
Count_Cytoplasm:	196
Count_Nuclei:	196
Mean_Cells_AreaShape_Area:	1103.71
Mean_Cells_AreaShape_Center_X:	292.12
Mean_Cells_AreaShape_Center_Y:	305.78
Mean_Cells_AreaShape_Compactness:	1.31
Mean_Cells_AreaShape_Eccentricity:	0.76
Mean_Cells_AreaShape_Orientation:	3.36
Mean_Cells_Intensity_IntegratedIntensity_GFP:	163.79
Mean_Cells_Intensity_MaxIntensity_GFP:	0.38
Mean_Cells_Intensity_MeanIntensity_GFP:	0.15
Mean_Cells_Intensity_MinIntensity_GFP:	0.03
Mean_Cells_Location_CenterMassIntensity_X_GFP:	292.15
Mean_Cells_Location_CenterMassIntensity_Y_GFP:	306.44
Mean_Cells_Location_Center_X:	292.51
Mean_Cells_Location_Center_Y:	306.38
Mean_Cells_Location_MaxIntensity_X_GFP:	292.14
Mean_Cells_Location_MaxIntensity_Y_GFP:	305.1
Mean_Cytoplasm_Location_Center_X:	292.51
Mean_Cytoplasm_Location_Center_Y:	306.36
Mean_Nuclei_AreaShape_Area:	231.58
Mean_Nuclei_AreaShape_Center_X:	292.26
Mean_Nuclei_AreaShape_Center_Y:	306.52
Mean_Nuclei_AreaShape_Compactness:	1.16
Mean_Nuclei_AreaShape_Eccentricity:	0.75
Mean_Nuclei_AreaShape_Orientation:	-0.27
Mean_Nuclei_Intensity_IntegratedIntensity_DNA:	70.26
Mean_Nuclei_Intensity_MaxIntensity_DNA:	0.48
Mean_Nuclei_Intensity_MeanIntensity_DNA:	0.3
Mean_Nuclei_Intensity_MinIntensity_DNA:	0.09

Zoom:

Image credit:  
openmicroscopy.org





# OMERO: histology



OMERO

DataHistoryHelp

Study B (ra)

ExploreTagsShares

All Members

Earth Science 2

Fluorescence Microscopy 2

Fluorescent Pathology 2

For Review 1

H&E Pathology 1

Medical 1

Multiplexed Pathology 1

Multispectral imaging 2

Paper Submission 1

Plate 1

TCGA 2

ACC 231

...231-4880-83AB-D17520D1AC95.svs

...B-D17520D1AC95.svs [label image]

...-D17520D1AC95.svs [macro image]

...1C7-4296-BECF-53E1440AB353.svs

...F-53E1440AB353.svs [label image]

...-53E1440AB353.svs [macro image]

...9D6-49EF-A4A2-C5803E3D2234.svs

...2-C5803E3D2234.svs [label image]

...-C5803E3D2234.svs [macro image]

...428-4BFD-85CE-628FBC4180F8.svs

...E-628FBC4180F8.svs [label image]

...-628FBC4180F8.svs [macro image]

...93A-43DB-8F7A-30A55534FA04.svs

...A-30A55534FA04.svs [label image]

Parade

Add filter...

Tag Slide Image

Add data...

SETTINGS

ACC

GeneralAcquisitionPreview

Image Details

Aperio Image Library vFS90 a asd

Acquisition Date:2013-01-22 02:23:31

Import Date:2015-11-24 05:40:14

Dimensions (XY):113287 x 40455

Pixels Type:uint8

Pixels Size (XYZ) (µm):0.25 x 0.25 x -

Z-sections/Timepoints:1 x 1

Channels:Channel1, Channel2, Channel3

ROI Count:0

Tags 3

Key-Value Pairs 0

Tables

INFO

Dataset:2601

Image:156028

Nuclear Count:214782

Stromal Count:118372

Epithelial Count:96410

Stromal Area:0.55

Epithelial Area:0.45

Image Name:TCGA-OR-A5J2-01A-01-TS1.F951E65D-4231-4880-83AB-D17520D1AC95.svs

Attachments 0

Comments 0





# OMERO: DICOM



OMERO Data History Help Figure Tag Search Genes Key-Value Admin

Search:  trainer-1 trainer-1

Lab1 trainer-1 trainer-1

Explore Tags Shares

trainer-1 trainer-1

- idr0021 10
- CellProfiler images 3
- condensation 32
- DICOM 15
  - MR000000 [Series 0]
  - MR000000 [Series 1]
  - MR000000 [Series 2]
  - MR000001 [Series 0]
  - MR000001 [Series 1]
  - MR000001 [Series 2]
  - MR000002 [Series 0]
  - MR000002 [Series 1]
  - MR000002 [Series 2]
  - MR000003 [Series 0]
  - MR000003 [Series 1]
  - MR000003 [Series 2]
  - MR000004 [Series 0]
  - MR000004 [Series 1]**
  - MR000004 [Series 2]
- dv-alexia-BoxIt 15
- dv-iain-multiTZ 2
- PTRE 5
- siRNAi-HeLa 33
- svs 6
- western-blots 7
- INMAC384-DAPI-CM-eGFP\_59223\_1 1

Add filter

Thumbnails

General Acquisition Preview

Original Metadata

Download

Series Metadata

0008,1010 Station Name #1 PMSN-X6FNOVG0RR

0008,1030 Study Description #1 MRI Head

0008,103e Series Description #1 T2W\_TSE

0008,1040 Institutional Department Name #1 MRI

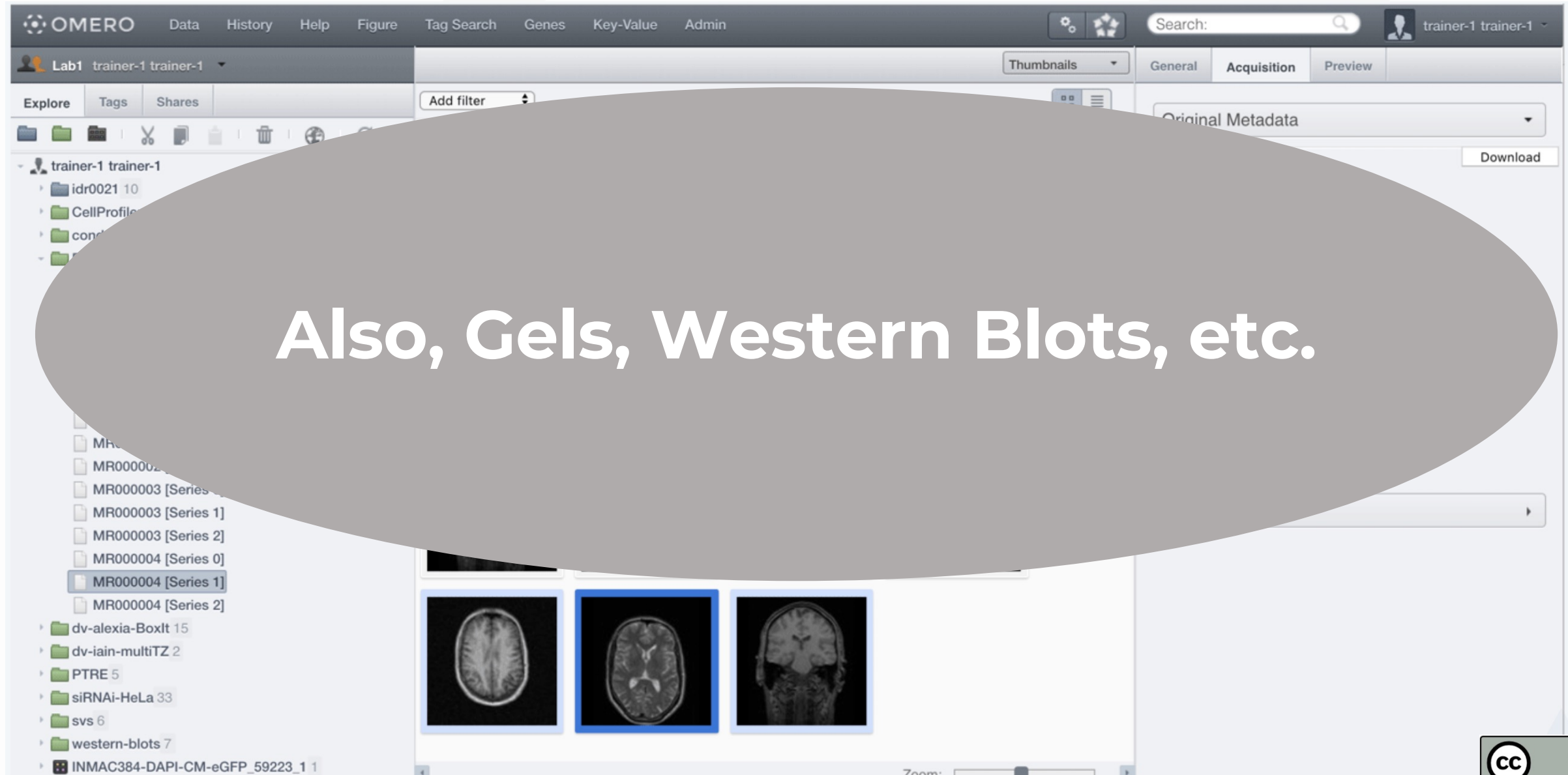
0008,1090 Manufacturer's Model Name #1 Achieva

0008,1150 Referenced SOP Class UID #1 1.2.840.10008.3.1.2.3.3

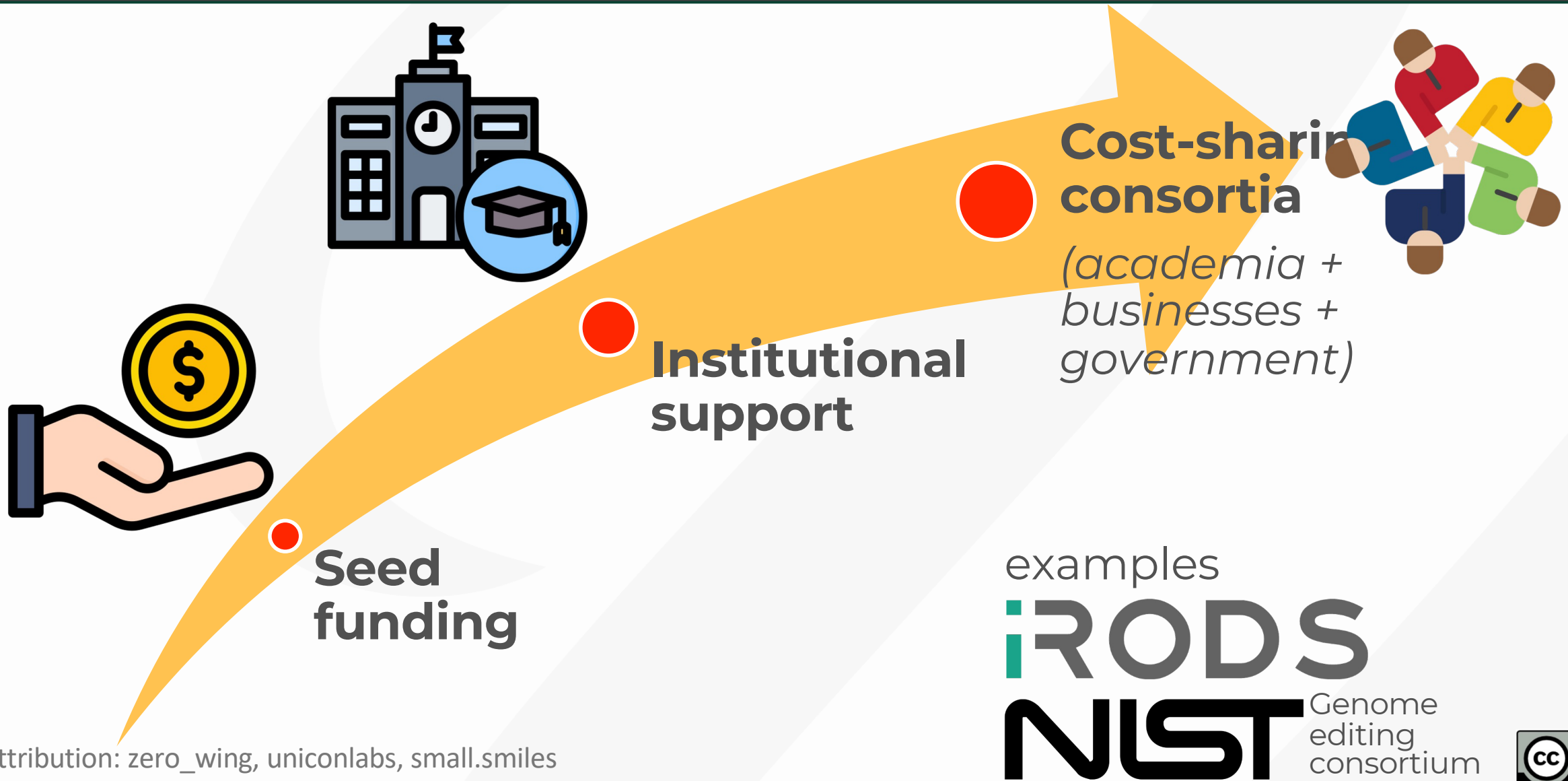
0008,1150 Referenced 1.2.840.10008.5.1.4.1.1.4

0

# OMERO: DICOM



# Sustainability: from seed funding to cost-sharing consortia



Icon attribution: zero\_wing, uniconlabs, small.smiles

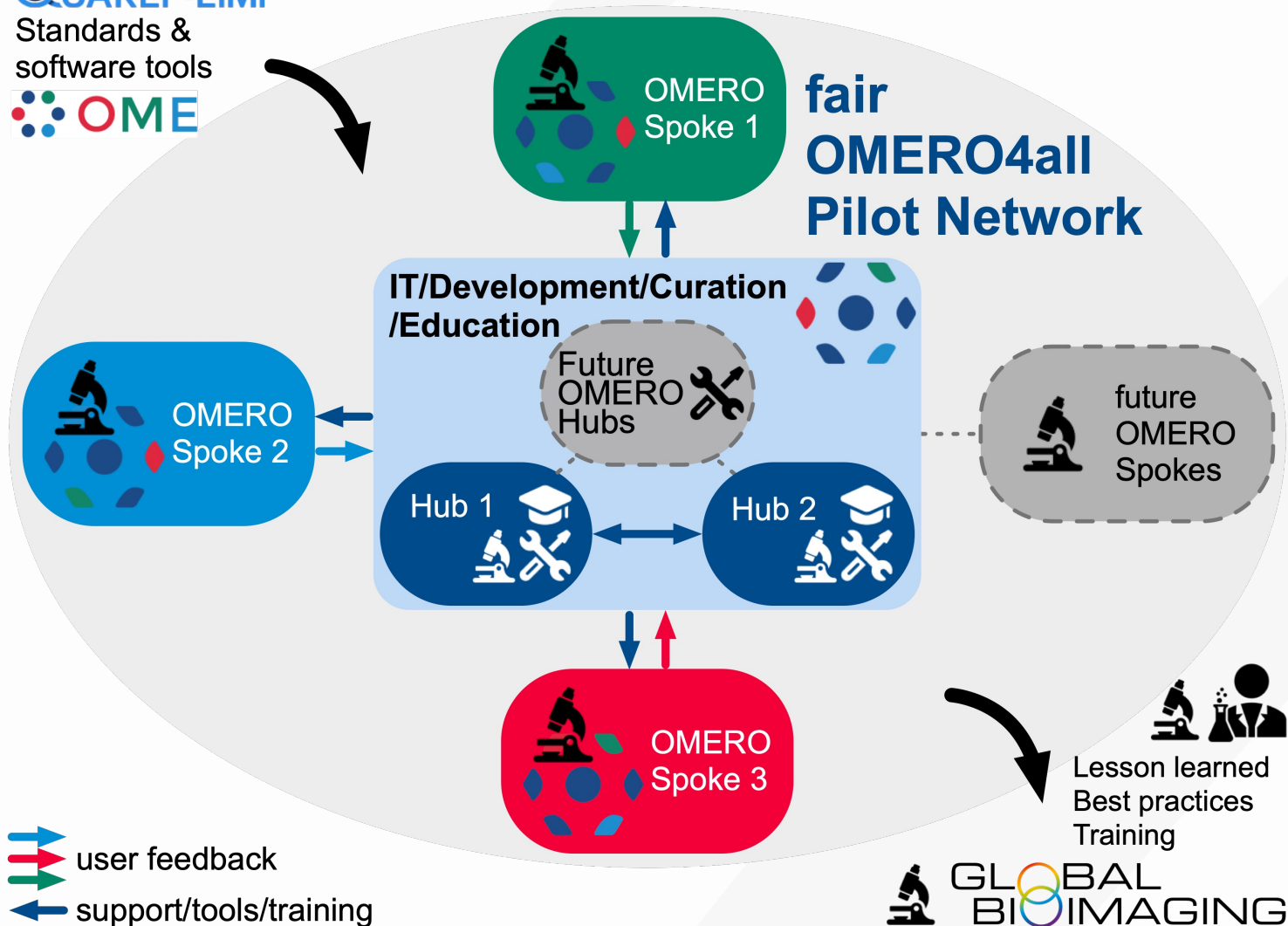




# Sustainability: fairOMERO4all



**QUAREP-LiMi**  
Standards &  
software tools  
**OME**



**FAIR  
Metadata  
Governance  
&  
Benchmarking  
Dashboard  
+  
ConTeXT**

**OBJ. 1**  **INSTALLATION  
PACKAGE**

OMERO INSTALLATION

**OBJ. 2**  **AUTOMATED  
IMPORT**

IMAGE & METADATA  
INGESTION

**OBJ. 3**  **INTEGRATED  
ANALYSIS**

READY FOR FAIR SHARING

**OBJ. 4**  **FAIR SHARING**



# THANK YOU!

## UMass Med + Canada Bioimaging



Judith  
Lacoste



Thomas  
Stroh



Claire  
Brown



Pina  
Colarusso



Alex  
Rigano



Alice  
Kang



Gabriel  
Pelletier



Joel  
Ryan



Stephen  
Ogg



Alex  
Kiepas

### BINA+QUAREP-LiMi

- Alison North, The Rockefeller University
- Roland Nitschke, Uni Freiburg
- Britta Schroth-Diez, Max Plank, Dresden
- Damir Sudar, Uni Oregon, QIS
- Caroline Miller
- Nikki Bilay + Vanessa Orr, BINA
- [BINA Quality Control and Data Management WC](#)
- [QUAREP-LiMi WG7 – Metadata](#)



### Grunwald lab – UMMS-RTI

- David Grunwald
- Mathias Hammer
- Max Huisman
- Farzin Farzam



### 4DN Community

- 4DN IWG: Sarah Aufmkolk, Laca Bintu, Alistair Boettinger, Steve Wang, Ting Wu
- DCIC: Burak Alver, Andrea Cosolo, Shannon Ehmsen, Koray Kirli, Ravi Navelkar, Peter Park, Andrew Schroder, Serkan Utku Ozturk



### HuBMAP Community and Pittsburgh Supercomputing Center (PSC)

- Katy Borner, Phil Blood, Chris Csonka, Stephen Fisher, Brendan Honick, Ajay Pillai, Alex Ropelewski



### Imaging Scientists Community

- Lisa Cameron, Duke
- Michelle Itano, CZI, UNC
- Paula Montero-Llopis, HMS
- Jennifer Waters, CZI, HMS



### OME community

- Jason Swedlow, OME
- Josh Moore, OME
- Shuichi Onami, RIKEN

