



NFDI4  
BIOIMAGE

# Biolmage Data Handling and Analysis with OMERO

Workshop in 4 Modules

May 13th, 2024

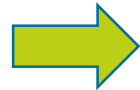
Trainers: Michele Bortolomeazzi, Riccardo Massei, Christian Schmidt

Support: Lena Krämer & Tom Boissonnet



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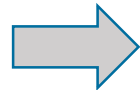
# Programme



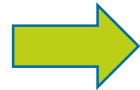
Module 1 (9 am - 10.15 am):  
Basics of OMERO, data structuring and annotation  
(Christian)

Module 2 (10.45 am - 12.45 pm):  
OMERO and Fiji  
(Michele)

Time to go to Lunch



Module 3 (1.45 pm - 3.45 pm):  
OMERO and Jupyter Notebooks  
(Riccardo)



Module 4 (4.15 pm - 6. pm):  
Publication-ready figures and data with OMERO  
(Christian, Riccardo, Michele)

# Who are the trainers?

Dr. Riccardo Massei (Helmholtz-Center for Environmental Research, UFZ, Leipzig) -  
Data Steward for Bioimaging Data in NFDI4BIOIMAGE

Dr. Michele Bortolomeazzi (DKFZ, Single cell Open Lab, bioimage data specialist,  
bioinformatician, staff scientist in the NFDI4BIOIMAGE project)

Dr. Christian Schmidt (Science Manager for Research Data Management in  
Bioimaging, DKFZ, Heidelberg, Project Coordinator of the NFDI4BIOIMAGE  
project)

# Introduction and expectations

- Join your nearest neighbors into groups of 3 – 5 people
- Find two things you have all in common
- Collect your expectations for this workshop (excalidraw)

5 min only!



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# Introduction to OMERO and structured annotations

Workshop: **Bioimage data management and analysis with OMERO**

May 13th, 2024, Module 1

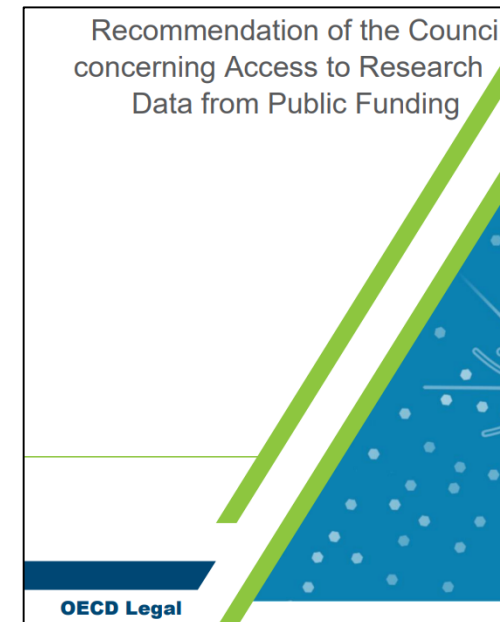
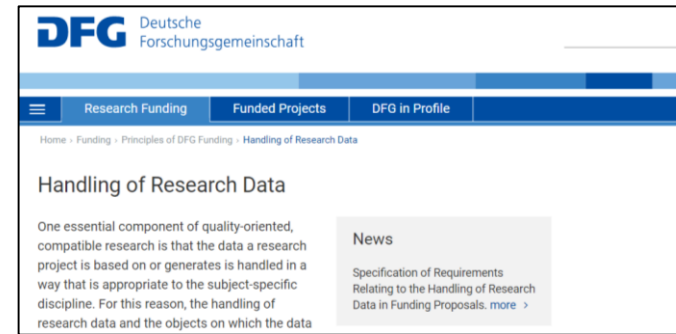
Trainers: Michele Bortolomeazzi, Riccardo Massei, **Christian Schmidt**



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# Significance of research data management

- **Intrinsic motivation**
- Impact and efficiency of my research
- **Extrinsic factors**
- Funding agency demands
- Good Scientific Practice
- **Ethical aspect**
- Make science more sustainable
- Promote *Open Science* and data sharing



- [https://www.dfg.de/en/research\\_funding/principles\\_dfg\\_funding/research\\_data/index.html](https://www.dfg.de/en/research_funding/principles_dfg_funding/research_data/index.html)
- [https://erc.europa.eu/sites/default/files/document/file/ERC\\_info\\_document-Open\\_Research\\_Data\\_and\\_Data\\_Management\\_Plans.pdf](https://erc.europa.eu/sites/default/files/document/file/ERC_info_document-Open_Research_Data_and_Data_Management_Plans.pdf)
- [https://twitter.com/BMBF\\_Bund/status/1571801906074337280?s=20&t=krDcwOPMuPwjs-VisYBgVg](https://twitter.com/BMBF_Bund/status/1571801906074337280?s=20&t=krDcwOPMuPwjs-VisYBgVg)
- <https://legalinstruments.oecd.org/en/instruments/OECD-LEGAL-0347>

# The FAIR principles for data and data stewardship



**Findable**

**Accessible**

**Interoperable**

**Reusable**

## Box 2 | The FAIR Guiding Principles

### To be Findable:

- F1. (meta)data are assigned a globally unique and persistent identifier
- F2. data are described with rich metadata (defined by R1 below)
- F3. metadata clearly and explicitly include the identifier of the data it describes
- F4. (meta)data are registered or indexed in a searchable resource

### To be Accessible:

- A1. (meta)data are retrievable by their identifier using a standardized communications protocol
  - A1.1 the protocol is open, free, and universally implementable
  - A1.2 the protocol allows for an authentication and authorization procedure, where necessary
- A2. metadata are accessible, even when the data are no longer available

### To be Interoperable:

- I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
- I2. (meta)data use vocabularies that follow FAIR principles
- I3. (meta)data include qualified references to other (meta)data

### To be Reusable:

- R1. meta(data) are richly described with a plurality of accurate and relevant attributes
  - R1.1. (meta)data are released with a clear and accessible data usage license
  - R1.2. (meta)data are associated with detailed provenance
  - R1.3. (meta)data meet domain-relevant community standards

- Wilkinson et al., 2016, Scientific Data, DOI: 10.1038/sdata.2016.18, CC-BY 4.0 (<http://creativecommons.org/licenses/by/4.0>)
- Jacobsen et al., 2020, FAIR Principles: Interpretations and Implementation Considerations. Data Intelligence, DOI: 10.1162/dint\_r\_00024

## **Guiding principles**

*(not a dictation of technical solutions)*

## **Goal is machine-readability**

*(not only human ability to reuse)*

## **Guidelines for data producers and publishers**

## **Applies to data and their provenance**

FAIR is *not*

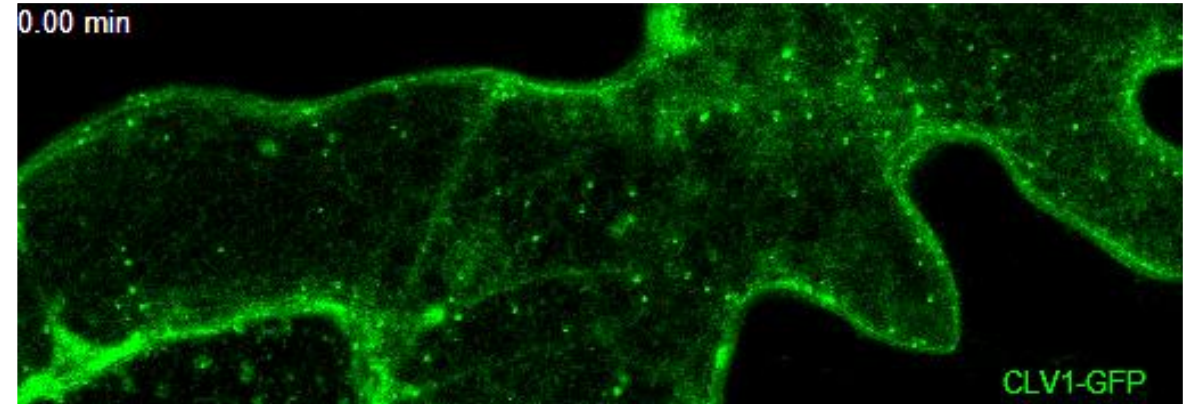
- the same as „open“
- a standard



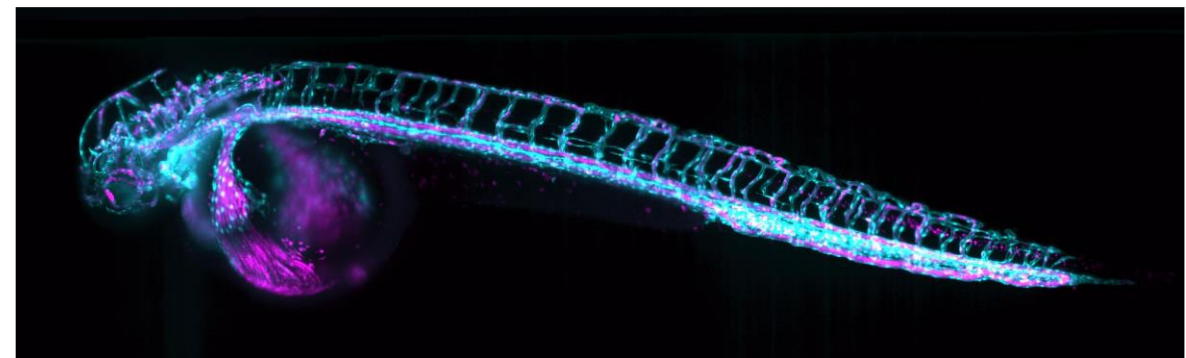
# The bioimage data type

Microscopy data is (often):

- high-dimensional (X, Y, Z, Channel, Time, ...)
- saved in proprietary file formats
- of large file size  
(often in GB-, sometimes in TB-range)
- produced with complex experimental setups
- used for quantitative analysis → derived data
- ... i.e. cumbersome to handle, store, and share?



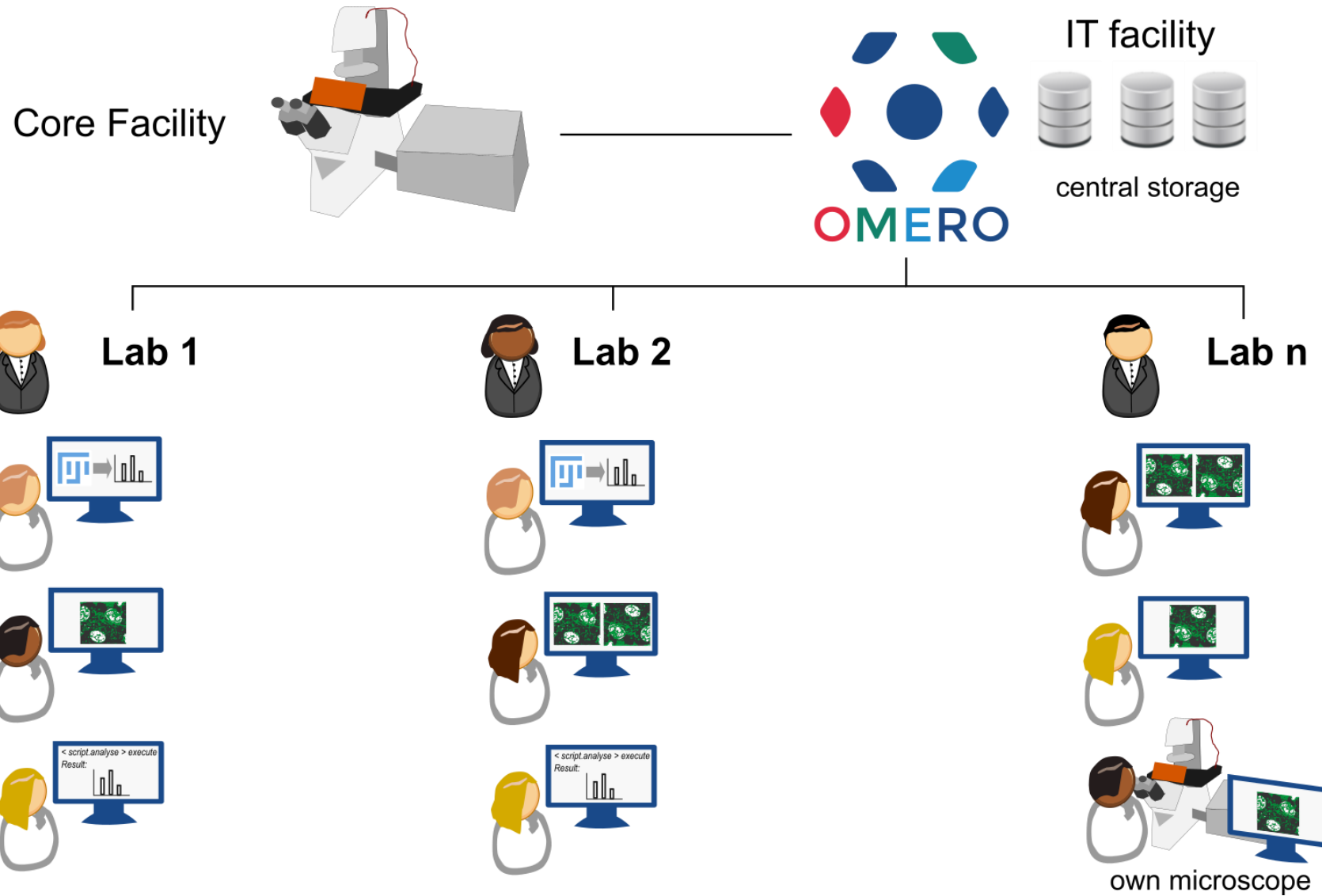
*Courtesy of: Y. Stahl, S. Weidtkamp-Peters, HHU Düsseldorf*



*Courtesy of: Jan Huisken, University of Göttingen*



# OMERO – What is it?

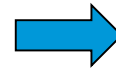


# OMERO – What is it?

## OMERO: An open-source software for image data management

OMERO = „OME Remote Objects“

Created by the **O**pen **M**icroscopy **E**nvironment Consortium (OME)




- User computer
- Microscope computer
- Processing / analysis server



- Installed on an institute or central IT server
- Storage and handling of imaging data
- Accessible from outside via „clients“

# OMERO.web – the main user interface



The screenshot shows the OMERO.web interface with several callouts:

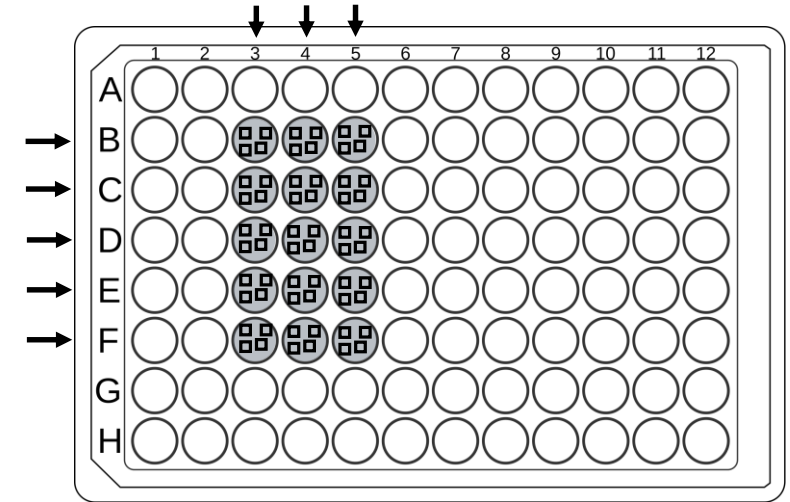
- User-Project-Dataset-Image file:** Points to the file browser on the left side of the interface.
- Figure preparation:** Points to the central area where image thumbnails are displayed.
- Technical metadata:** Points to the right-hand panel showing acquisition parameters like Import Date, Dimensions, and Channels.
- Tags for flexible organization:** Points to the 'Tags' section in the metadata panel.
- Key-Value pairs for metadata annotation:** Points to the 'Key-Value Pairs' section in the metadata panel.
- Preview of the images in the dataset:** Points to a specific image thumbnail in the central view.

# Demonstration and Exercise

Make yourself familiar with OMERO.web

# Example Data for this workshop

- A plate acquired at week intervals
- One compound per row
  - Compound B, Compound C, ...
- Tested at different concentration (columns):
  - 2  $\mu\text{M}$ , 5  $\mu\text{M}$ , 10  $\mu\text{M}$
- Multiple images are taken from each well for an accurate sampling.
- Two independent samples are tested (with the sample IDs: 18746 and 22123)



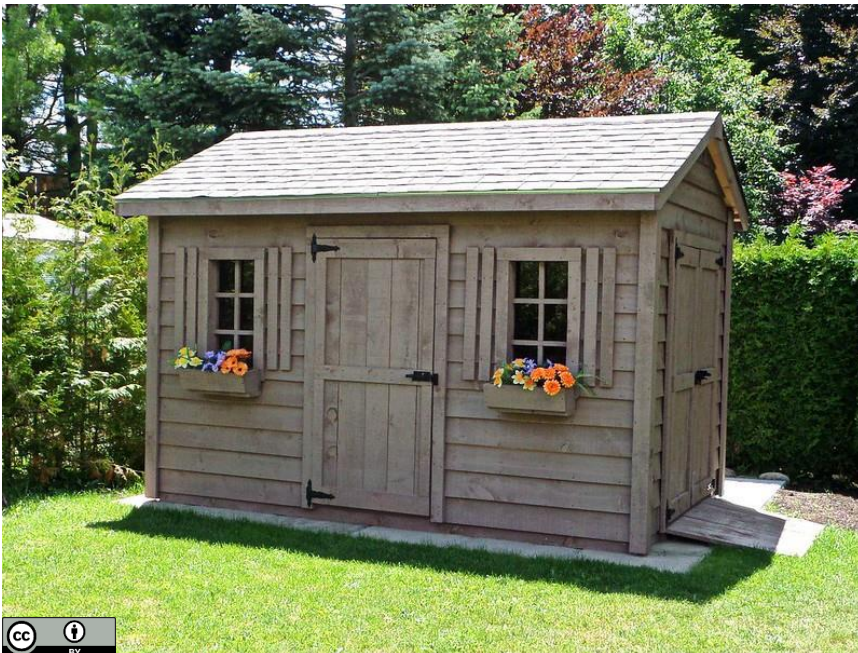
# How is this structured correctly?

- What should our "dataset unit" be ?
  - the whole week, both plates with all images?
  - One whole plate, one dataset per week ?
  - each compound of every week ?
  - each compound of a single week ?
  - ...
- What's a convenient way to describe the data content ?

# A little analogy (not so serious)



annotations



By Tom Rossini,  
CC-BY



By Gordon Jolly,  
<https://flickr.com/photos/loopzilla/8132242517/>,  
CC-BY-SA, <https://creativecommons.org/licenses/by-sa/2.0/>

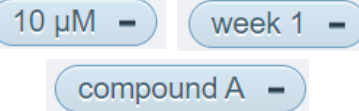


Reused from Tom Boissonnet, available at: Fuchs, V. A. F., Schmidt, C., & Boissonnet, T. (2024, Mai 6). [Workshop] FAIR data handling for microscopy: Structured metadata annotation in OMERO. Zenodo. <https://doi.org/10.5281/zenodo.11109616>, CC-BY 4.0

# A little analogy (not so serious)



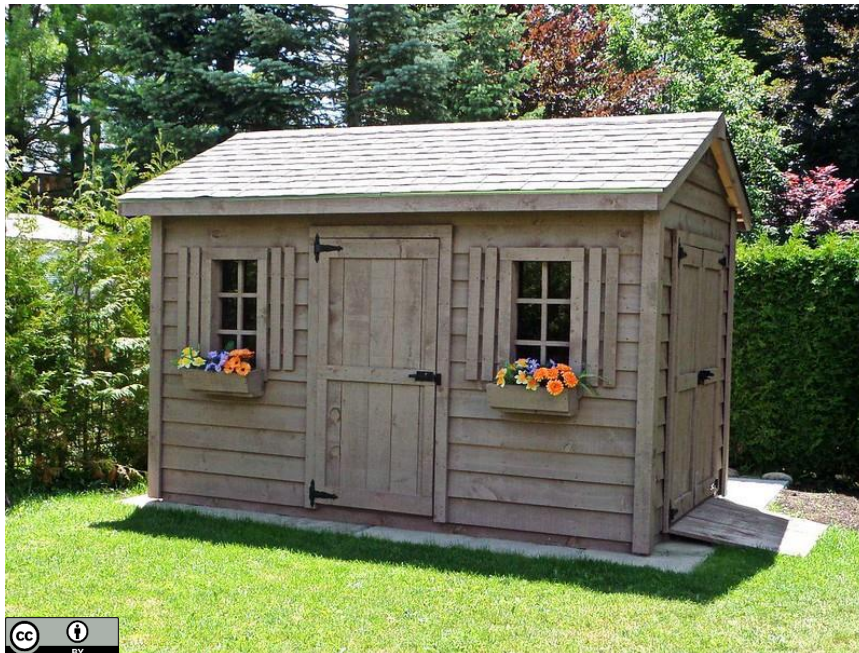
Tags



Key-value

|               |       |
|---------------|-------|
| compound      | A     |
| concentration | 10 µM |
| week          | 1     |

Week1\_150607\_B02\_s1\_c1-DAPI\_compoundA\_10µM.tif



By Tom Rossini,  
CC-BY



By Gordon Jolly,  
<https://flickr.com/photos/loopzilla/8132242517/>,  
CC-BY-SA, <https://creativecommons.org/licenses/by-sa/2.0/>

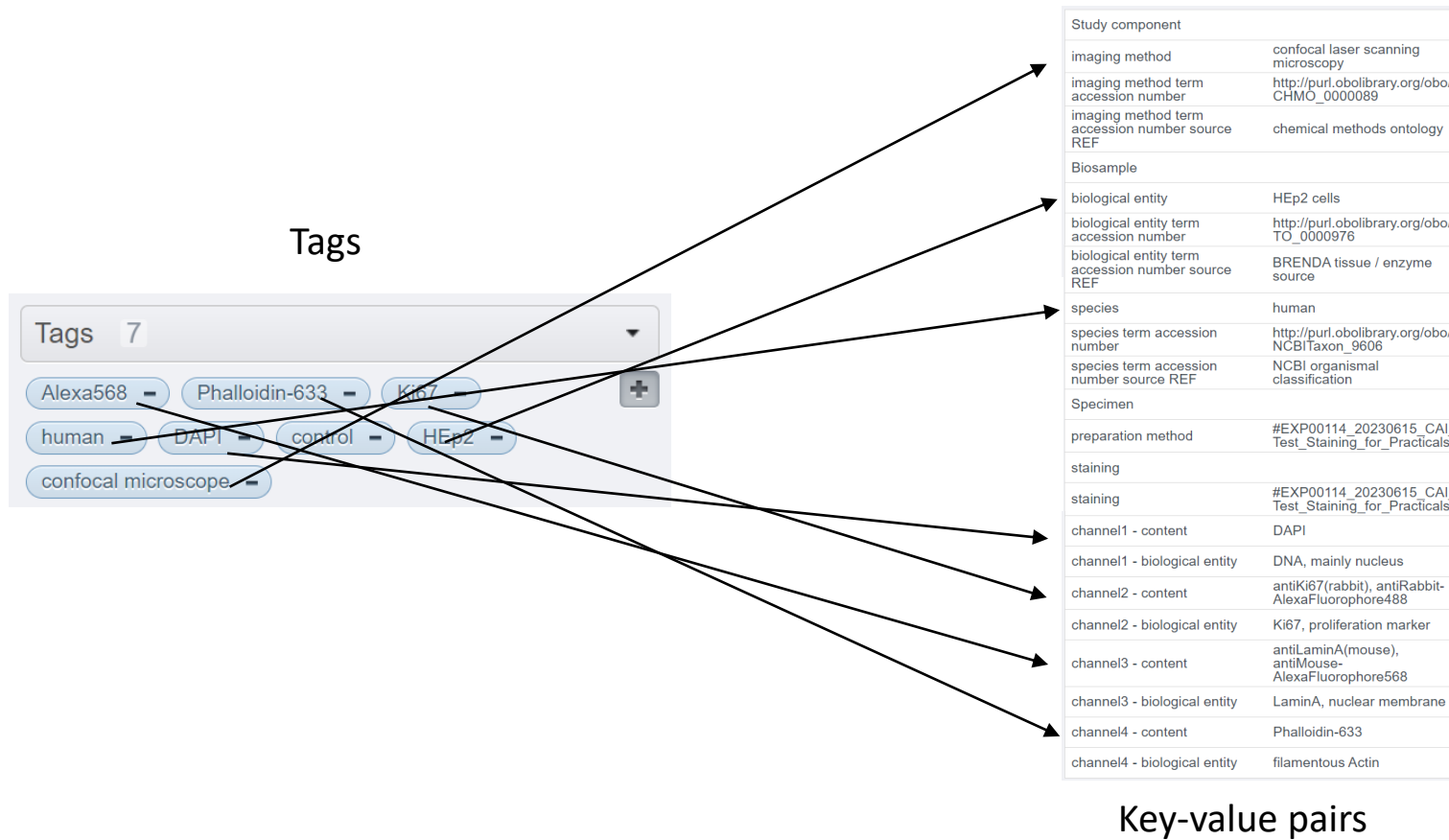


Reused from Tom Boissonnet, available at: Fuchs, V. A. F., Schmidt, C., & Boissonnet, T. (2024, Mai 6). [Workshop] FAIR data handling for microscopy: Structured metadata annotation in OMERO. Zenodo. <https://doi.org/10.5281/zenodo.11109616>, CC-BY 4.0



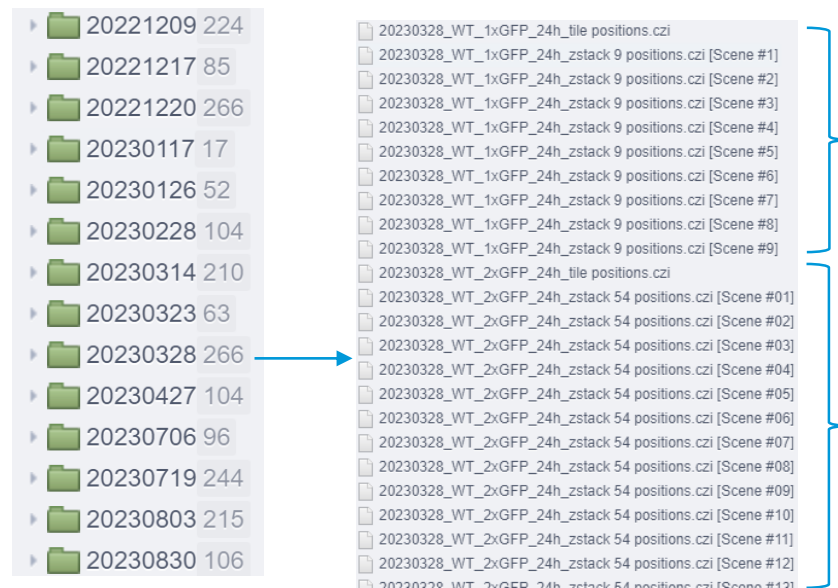
# Redundant concepts?

(REMBI checklist)  
→ Module 4



# Folder hierarchies are what we are used to

- Folder habits are intuitively matched to projects and datasets
- Thinking dataset as folders leads to a confusing structure in OMERO:



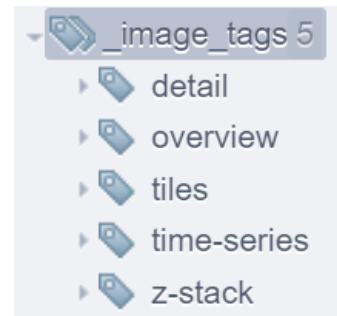
- How should I annotate this?
  - Annotate dataset: unclear to know which images it applies to
  - Annotate first image of every set: other images need reference to the annotated image
  - Annotate every image: tedious and annotation duplication
- What if someone wants to look at the data differently?

# Tags are like folders, but better

- We can use tags like folders (not possible with datasets)
- Don't overdo it: less tag categories -> less work  
(and less oversight)
- Tags are flexible and should be used for individual preferences



Need to group images across datasets?  
Tags can do that



# Are datasets even needed?

- KV-pairs takes care of describing the data, so no need to redo it with tags
- Tags are like folders, but better (multiple tags per object, descriptions)
- Tags can be categorized with Tagsets
- > Good for organizing and filtering
- Tags could emulate my datasets (don't try)



- So why should we even bother with datasets ?

# Advantage of metadata annotation

- Datasets can be annotated and used as structure in analysis!
    - Tags
    - Key-value pairs
    - Attachements
    - Ratings
    - Comments
- }
- These will be captured in the Structured Annotation metadata in the OME.XML header of an OME-TIFF
- By annotating a dataset, I can implicitly annotate the images it contains
    - group images of a same experiment in the dataset
    - > less duplication of annotations
    - images can be annotated to give more details

# Structured metadata

```
<StructuredAnnotations>
  <TagAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_47706:2998580">
    <Description>tim of 5 µg/ml anti-CD3/anti-CD28 stimulation before staining (in h)</Description>
    <Value>0 h anti-CD3/CD38</Value>
  </TagAnnotation>

  <TagAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_19802:622773">
    <Description>Experiments with staining for phosphorylated ERK protein</Description>
    <Value>phospho-ERK</Value>
  </TagAnnotation>

  <TagAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_19545:561233">
    <Value>DMSO control</Value>
  </TagAnnotation>

  <MapAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_46089:1280547"
  Namespace="openmicroscopy.org/omero/client/mapAnnotation">
    <Value>
      <M K="Organism">Mus musculus</M>
      <M K="Strain">C57BL/6</M>
      <M K="Organ">Spleen</M>
      <M K="Cell Type">CD4-positive, alpha-beta T cell</M>
      <M K="Manipulation 1">unstimulated</M>
      <M K="Treatment 1">0.3% DMSO (control)</M>
      <M K="Treatment 1 time">0 h</M>
      <M K="Target 1">phospho-ERK</M>
      <M K="Staining Method">immunofluorescence indirect</M>
      <M K="Imaging Method">CLSM</M>
      <M K="Lab Notebook Ref">CSchm#4 page 112</M>
    </Value>
  </MapAnnotation>
</StructuredAnnotations></OME>
```



Tag



Key



Value

# Visualizing the OME.XML metadata in Fiji

```
<StructuredAnnotations>
  <TagAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_47706:2998580">
    <Description>tim of 5 µg/ml anti-CD3/anti-CD28 stimulation before staining (in h)</Description>
    <Value>0 h anti-CD3/CD38</Value>
  <TagAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_19802:622773">
    <Description>Experiments with staining for phosphorylated ERK protein</Description>
    <Value>phospho-ERK</Value>
  <TagAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_19545:561233">
    <Value>DMSO control</Value>
  <MapAnnotation ID="urn:lsid:export.openmicroscopy.org:Annotation:a99ddfbd-769b-474a-8e7b-93bcd175df65_46089:1280547" Namespace="openmicroscopy.org/omero/client/mapAnnotation">
    <Value>
      <M K="Organism">Mus musculus</M>
      <M K="Strain">C57BL/6</M>
      <M K="Organ">Spleen</M>
      <M K="Cell Type">CD4-positive, alpha-beta T cell</M>
      <M K="Manipulation 1">unstimulated</M>
      <M K="Treatment 1">0.3% DMSO (control)</M>
      <M K="Treatment 1 time">0 h</M>
      <M K="Target 1">phospho-ERK</M>
      <M K="Staining Method">immunofluorescence indirect</M>
      <M K="Imaging Method">CLSM</M>
      <M K="Lab Notebook Ref">CSchm#4 page 112</M>
    </Value>
  </MapAnnotation>
</StructuredAnnotations>
```

# Exercise – Bring structure to the data

Enrich the training dataset (structured according to your preference) with Tags (and KV pairs)



# Acknowledgments

In cooperation with  
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<https://www.i3dbio.de/>



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