



NFDI4
BIOIMAGE

Welcome to Biolmage Town!

Josh Moore, Senior RDM Officer

German BioImaging, e.V. / Open Microscopy Environment

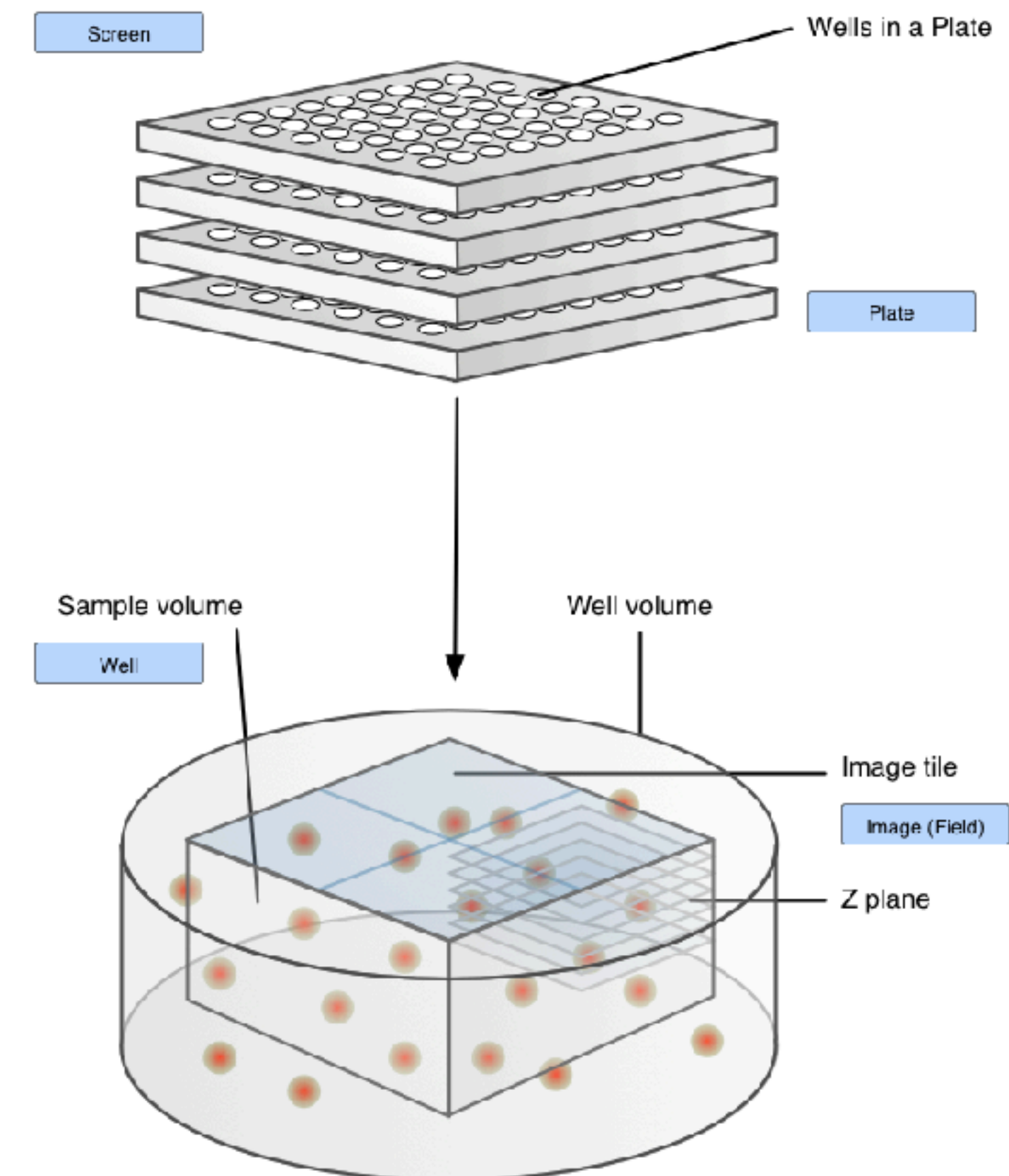
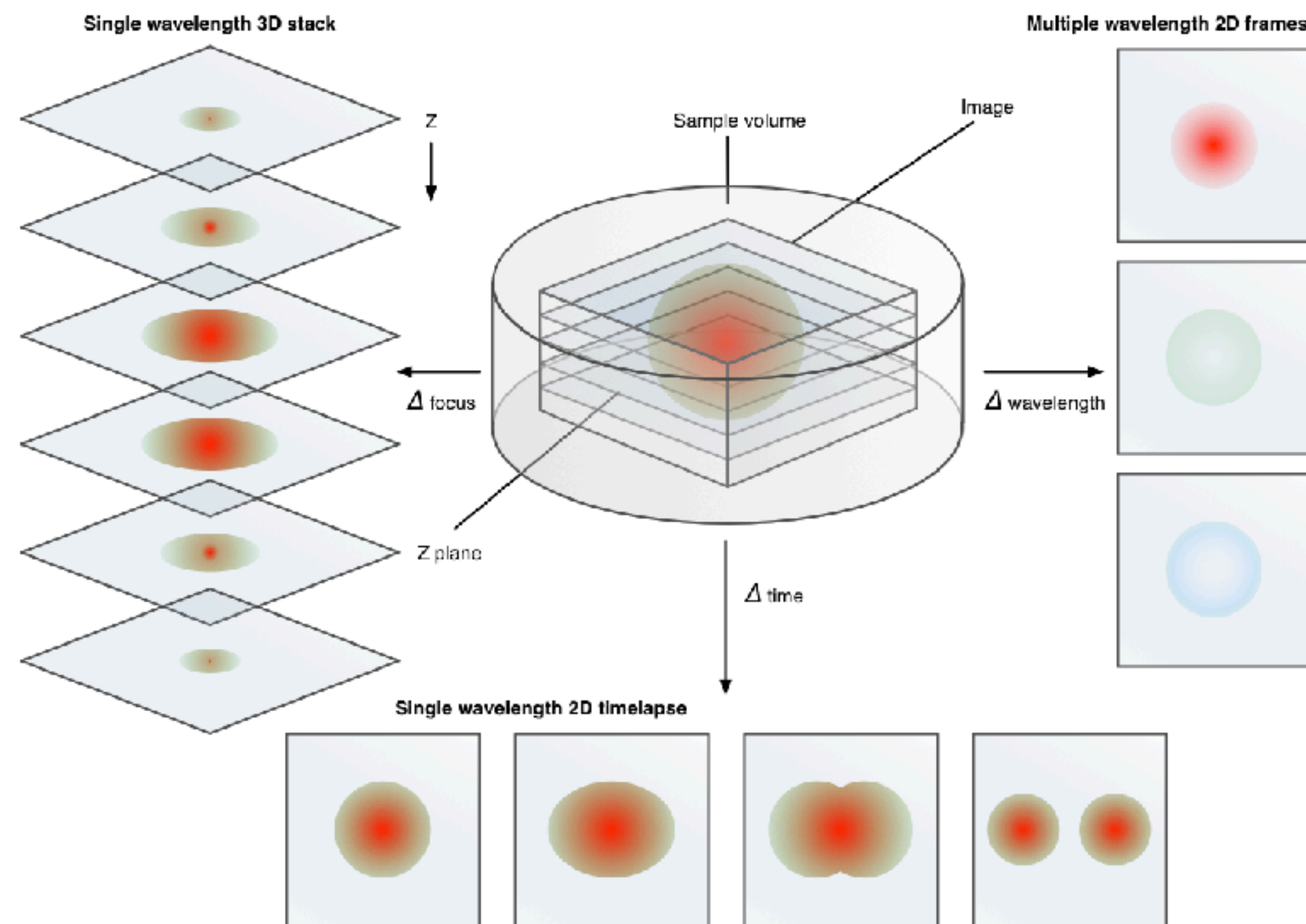


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Special welcome

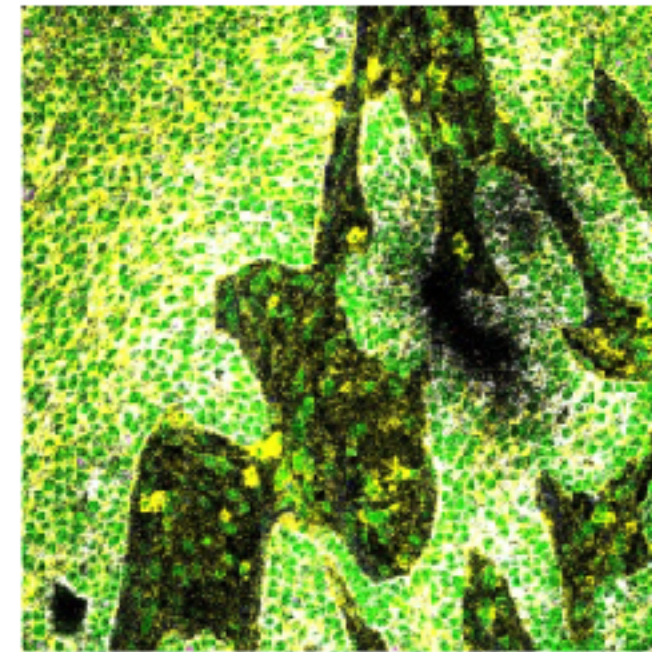


Value of bioimages

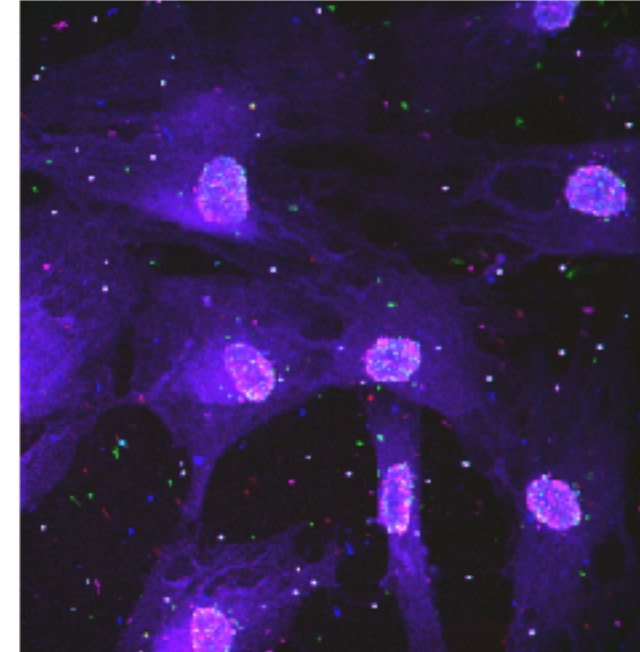


<https://ome-model.readthedocs.io/>

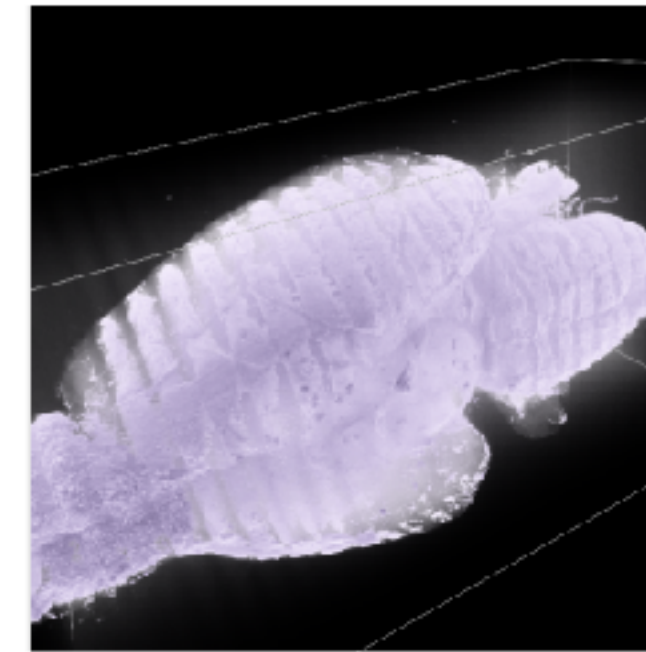
Value of bioimages



Multiplexed



Spatial tx



Light-sheet



Infraread



Scanning EM



Digital pathology

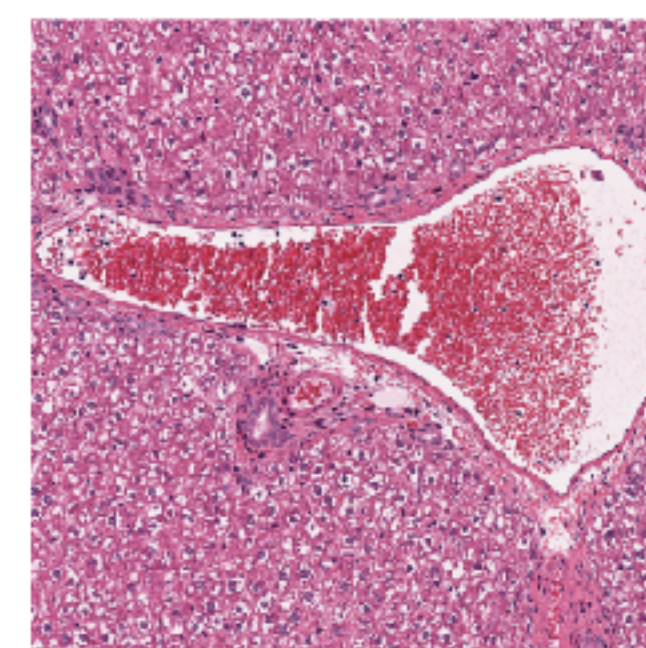
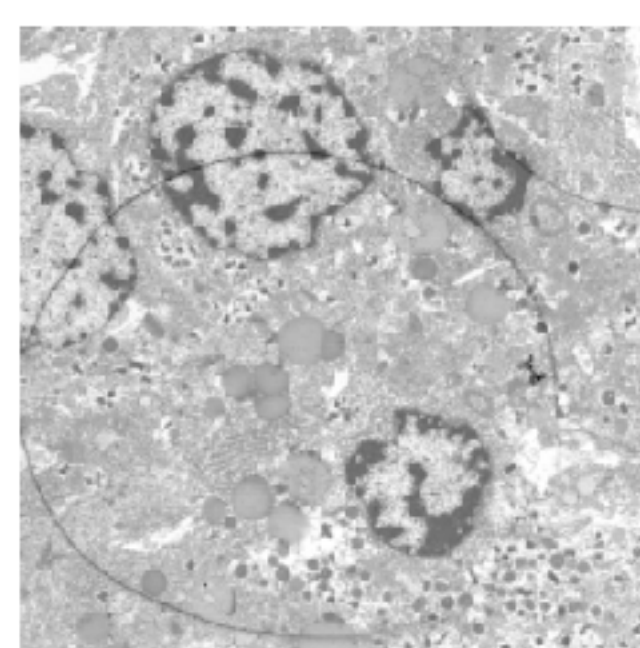


Image Data Management isn't always FAIR

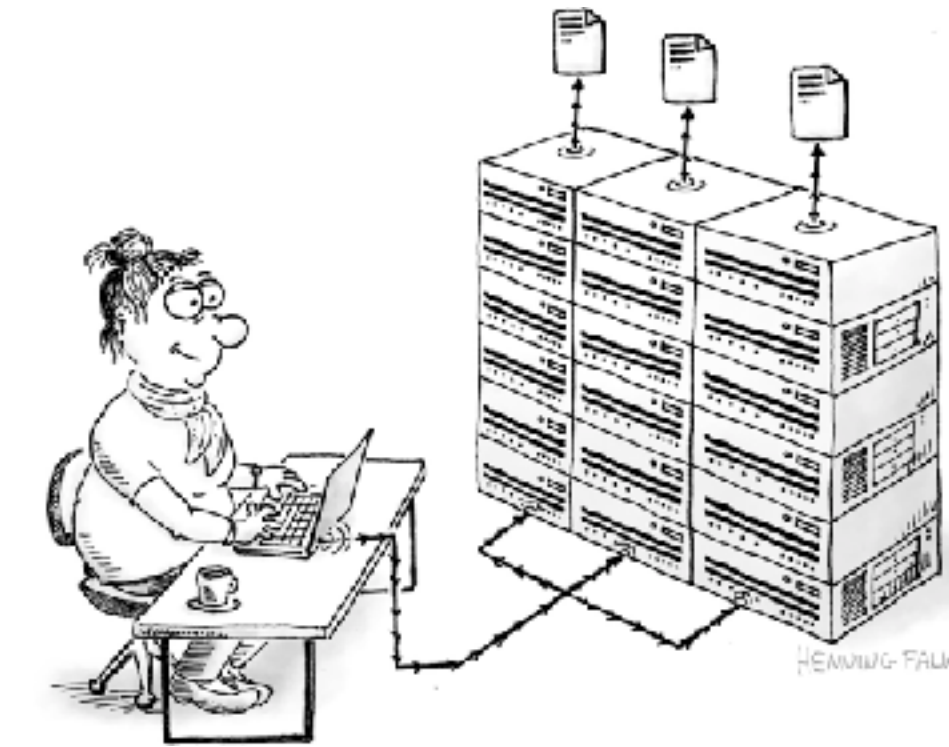


"Clara shares" by Henning Falk, ©2022 NumFOCUS, is used under a CC BY 4.0 license.
<https://github.com/zarr-developers/zarr-illustrations-falk-2022#clara-shares>



Image: Simon Li
<https://twitter.com/penguinoops/status/643812318699225088>

A brief history of making images go



"Bea computes" by Henning Falk, ©2022 NumFOCUS, is used under a CC BY 4.0 license.

<https://github.com/zarr-developers/zarr-illustrations-falk-2022#bea-computes>



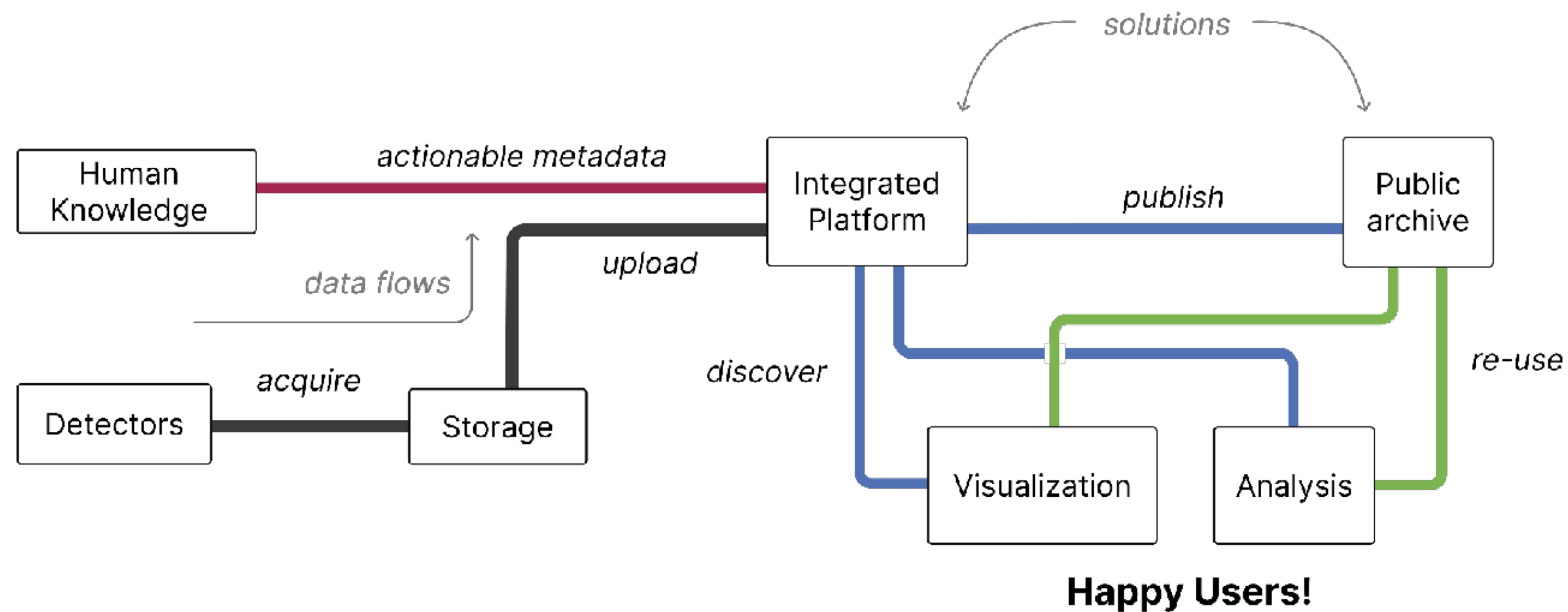
NFDI 4
BIOIMAGE

JSON RFC (2006)

"FAIR" Wilkinson (2016)

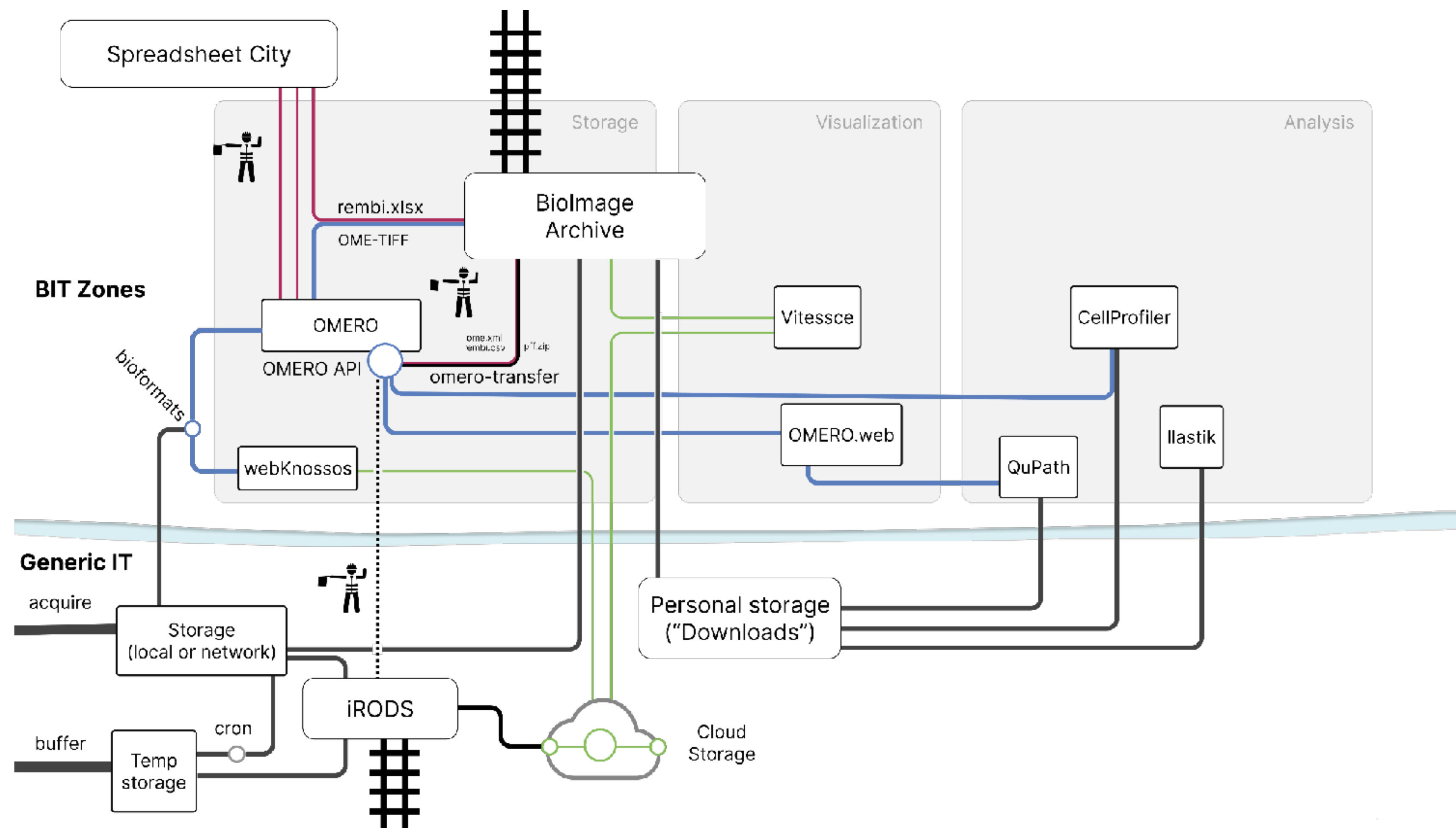
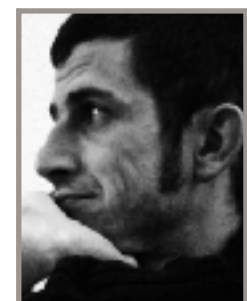
Utopian Biolmage Town (BIT)

FAIR Data Metro Map



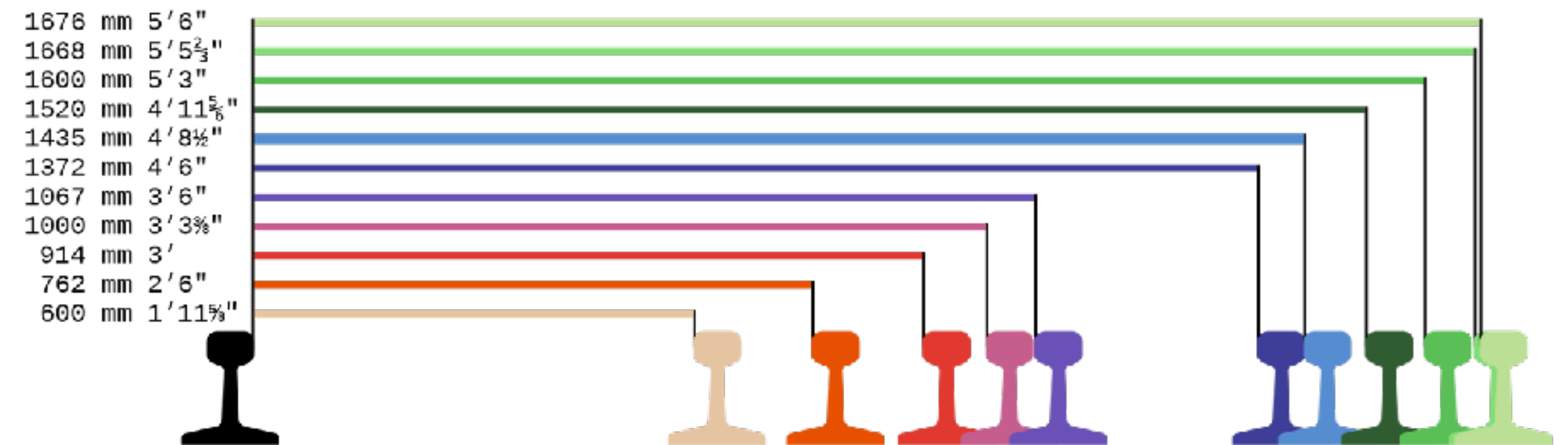
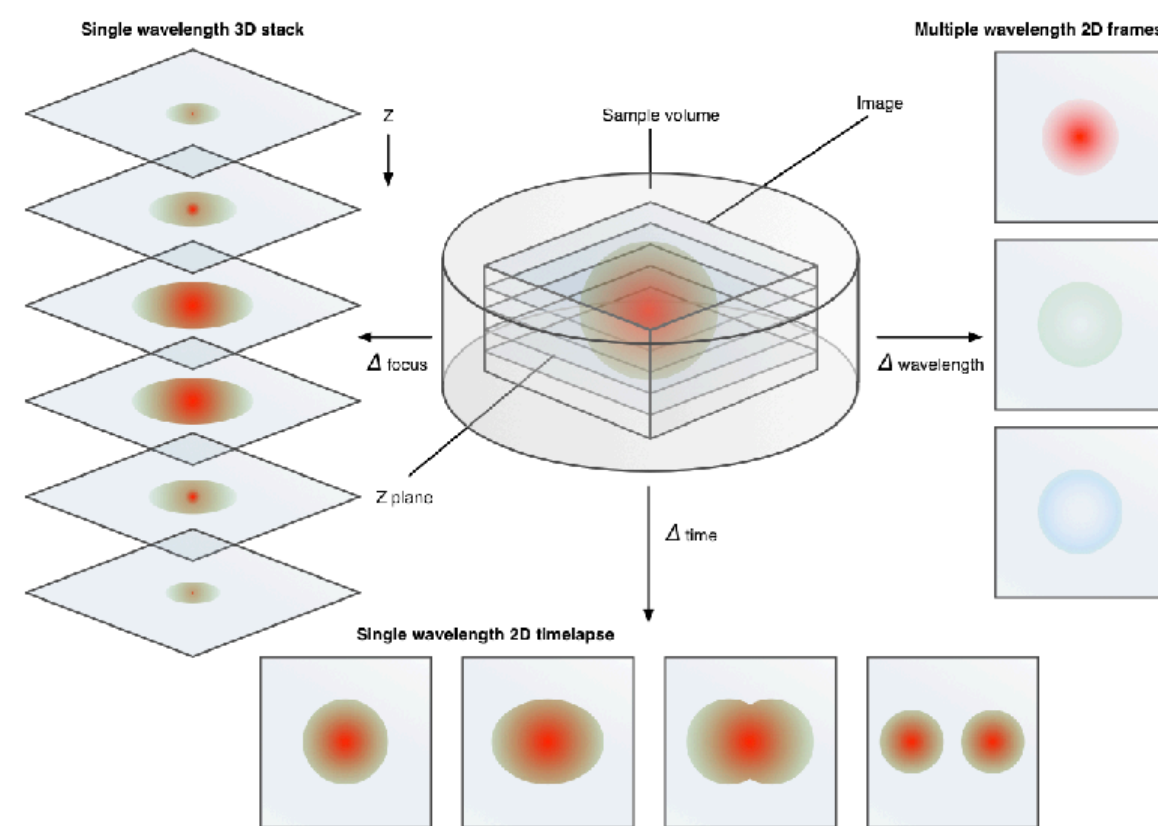
Current (& partial) Biolmage Town (BIT)

FAIR Data Metro Map



<https://doi.org/10.5281/zenodo.8019760>

Moore et al., CC-BY 4.0



https://en.wikipedia.org/wiki/Rapid_transit_track_gauge

“The OME Model is a specification for storing data on biological imaging. The model includes image parameters, such as XYZ dimensions and pixels type, as well as extensive metadata on, for example, image acquisition, annotation, and regions of interest (ROIs). This common specification is essential for the exchange of image data between different software packages.

Swedlow et al. (2003) *Informatics and quantitative analysis in biological imaging*. Science 300(5616), 100-2. Published 4 April 2003

DOI: [10.1126/science.1082602](https://doi.org/10.1126/science.1082602)

<https://bit.ly/citing-ome>

```
<?xml version="1.0" encoding="UTF-8" ?>
<OME xmlns="http://www.openmicroscopy.org/Schemas/OME/2016-06"
      xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
      xsi:schemaLocation="http://www.openmicroscopy.org/Schemas/OME/2016-06
      http://www.openmicroscopy.org/Schemas/OME/2016-06/ome.xsd">
  <Image ID="Image:0" Name="6x6x1x8-swatch.tif">
    <AcquisitionDate>2010-02-23T12:51:30</AcquisitionDate>
    <Pixels DimensionOrder="XYZCT" ID="Pixels:0:0" PhysicalSizeX="10000.0"
      PhysicalSizeY="10000.0" Type="uint8" SizeC="1" SizeT="1" SizeX="6"
      SizeY="4" SizeZ="1">...</Pixels>
    <AnnotationRef ID="Annotation:1"/>
    <AnnotationRef ID="Annotation:2"/>
  </Image>
  <StructuredAnnotations>
    <!-- First Tag -->
    <MapAnnotation ID="Annotation:1">
      <Description>This is the description of the sample map A</Description>
      <Value>
        <M K="SampleKeyA">SampleValueA</M>
      </Value>
    </MapAnnotation>
    <!-- Second Tag -->
    <MapAnnotation ID="Annotation:2">
      <Description>This is the description of the sample map B</Description>
      <Value>
        <M K="SampleKeyB-1">SampleValueB-1</M>
        <M K="SampleKeyB-2">SampleValueB-2</M>
      </Value>
    </MapAnnotation>
  </StructuredAnnotations>
</OME>
```

Goldberg, et al. (2005) *The Open Microscopy Environment (OME) Data Model and XML File: Open Tools for Informatics and Quantitative Analysis in Biological Imaging*. *Genome Biol.* 6:R47.
DOI: [10.1186/gb-2005-6-5-r47](https://doi.org/10.1186/gb-2005-6-5-r47)

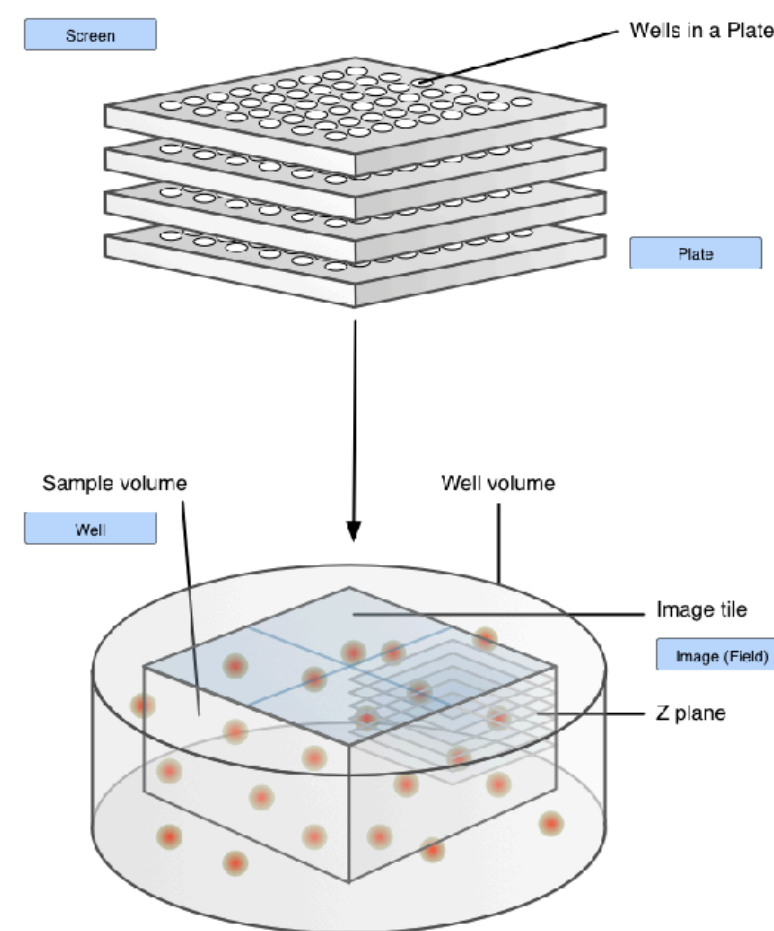
<https://bit.ly/citing-ome>

<div>Image</div> <div>AcquiredDate Description Name</div> <div>ImagingEnvironment</div> <div>ObjectiveSettings</div> <div>CorrectionColor</div> <div>Medium</div> <div>RefractiveIndex</div> <div>Pixels</div> <div>DimensionOrder</div> <div>PhysicalSizeX</div> <div>PhysicalSizeY</div> <div>PhysicalSizeZ</div> <div>SizeC</div> <div>SizeT</div> <div>SizeX</div> <div>SizeY</div> <div>SizeZ</div> <div>TimeIncrement</div> <div>Type</div> <div>BinData</div> <div>TiffData</div> <div>FirstC</div> <div>FirstT</div> <div>FirstZ</div> <div>IFO</div> <div>PlaneCount</div> <div>LUID</div> <div>FileName</div> <div>Channel</div> <div>AcquisitionMode</div> <div>Color</div> <div>ContrastMethod</div> <div>EmissionWavelength</div> <div>ExcitationWavelength</div> <div>Fluor</div> <div>IlluminationType</div> <div>Name</div> <div>NDFilter</div> <div>PinholeSize</div> <div>PocketCellSetting</div> <div>SampleRef</div> <div>DetectorSettings</div> <div>Binning</div> <div>Gain</div> <div>Offset</div> <div>ReadOutRate</div> <div>Voltage</div> <div>LightSourceSettings</div> <div>Attenuation</div> <div>Wavelength</div> <div>Plane</div> <div>DeltaT</div> <div>ExposureTime</div> <div>PositionX</div> <div>PositionY</div> <div>PositionZ</div> <div>StageLabel</div> <div>Name</div> <div>X</div> <div>Y</div> <div>Z</div>	<div>Image</div> <div>AcquiredDate Description Name</div> <div>ImagingEnvironment</div> <div>AirPressure CO2Percent Humidity Temperature</div> <div>ObjectiveSettings</div> <div>CorrectionColor</div> <div>Medium</div> <div>RefractiveIndex</div> <div>Pixels</div> <div>DimensionOrder</div> <div>PhysicalSizeX</div> <div>PhysicalSizeY</div> <div>PhysicalSizeZ</div> <div>SizeC</div> <div>SizeT</div> <div>SizeX</div> <div>SizeY</div> <div>SizeZ</div> <div>TimeIncrement</div> <div>Type</div>	<div>Describes the actual image and its metadata.</div> <div>The acquisition date of the Image.</div> <div>A multi-line description for the image.</div> <div>A short description for the image. This would be used to, for example, select the image from a list.</div> <div>Describes the environment that the biological sample was in during the experiment.</div> <div>AirPressure in millibars[mbar].</div> <div>%CO2 as a percent-fractions from 0.0 to 1.0 [%].</div> <div>Humidity as a percent-fraction from 0.0 to 1.0 [%].</div> <div>Temperature [degrees Celsius].</div> <div>Describes any settings on or around the objective</div> <div>An adjustable ring on the objective that corrects for changes in immersion medium refractive index. Arbitrary scale and unitless.</div> <div>A description of a Medium used for the lens. e.g., Oil, Water, WaterDipping, Air, Multi, Glycerol, Other</div> <div>Refractive index is that of the immersion medium.</div> <div>Defines the location and parameter of the Pixels, the actual binary image data</div> <div>The order in which the individual planes of data are interleaved. e.g., XYZCT, XYZTC, XYCTZ, XYCZT, XYTCZ, XYTCC</div> <div>Physical size in x, y, z of a pixel in microns[um]</div> <div>Dimensional size x, y, z, c, t of pixel data array</div> <div>Used for time series that have a global timing specification instead of per-timepoint timing info, e.g., a video stream. [s].</div> <div>The variable type used to represent each pixel in the image. e.g., int8, int16, int32, uint8, uint16, uint32, float, bit, double, complex, double-complex</div>
--	--	---

2000



2008



Last major modeling effort for **high-content screening**

Study Type	Protein localisation using fluorescence microscopy
Organism	Homo sapiens
Experiment Type	Immunocytochemistry
Imaging Method	Deconvolution widefield fluorescence microscopy
Data Analysis	OMERO.mtools http://help.openmicroscopy.org/workflows-mtools.html
Publication Title	The Ndc80 complex targets Bod1 to human mitotic kinetochores
Publication Authors	Katharina Schleicher, Michael Porter, Sara ten Have, Ramasubramanian Sundaramoorthy, Iain M Porter, Jason R Swedlow
PubMed ID	29142109
PMC ID	tba
Publication DOI	10.1098/rsob.170099
License	Attribution 4.0 International (CC BY 4.0) https://creativecommons.org/licenses/by/4.0/
Data Publisher	University of Dundee
Data DOI	http://dx.doi.org/10.17867/10000109

2013

Add **key-value (K/V)** pair annotation

2010

```
<?xml version="1.0" encoding="UTF-8"?>
<OME xmlns="http://www.openmicroscopy.org/Schemas/OME/2016-06"
xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
xsi:schemaLocation="http://www.openmicroscopy.org/Schemas/OME/2016-06 http://www.openmicroscopy.org/Schemas/OME/2016-06/ome.xsd">
  <Image ID="Image:0" Name="6x6x1x8-swatch.tif">
    <AcquisitionDate>2010-02-23T12:51:30</AcquisitionDate>
    <Pixels DimensionOrder="XYZCT" ID="Pixels:0:0"
PhysicalSizeX="10000.0" PhysicalSizeY="10000.0" Type="uint8"
SizeC="1" SizeT="1" SizeX="6" SizeY="4" SizeZ="1">...</Pixels>
    <AnnotationRef ID="Annotation:1"/>
  </Image>
  <StructuredAnnotations>
    <CommentAnnotation ID="Annotation:1">
      <Value>Fred</Value>
    </CommentAnnotation>
  </StructuredAnnotations>
</OME>
```

Added flexible **structured annotations** for user-extensions

2016

Attributes 8

Cell Lines

Added by: Public data

Cell Line	HeLa
-----------	------

Gene

Added by: Public data

Gene Identifier	9070
Gene Symbol	ASH2L

Phenotype

Added by: Public data

Phenotype	elongated cells
Phenotype Term Name	elongated cell phenotype
Phenotype Term Accession	CMPO_0000077

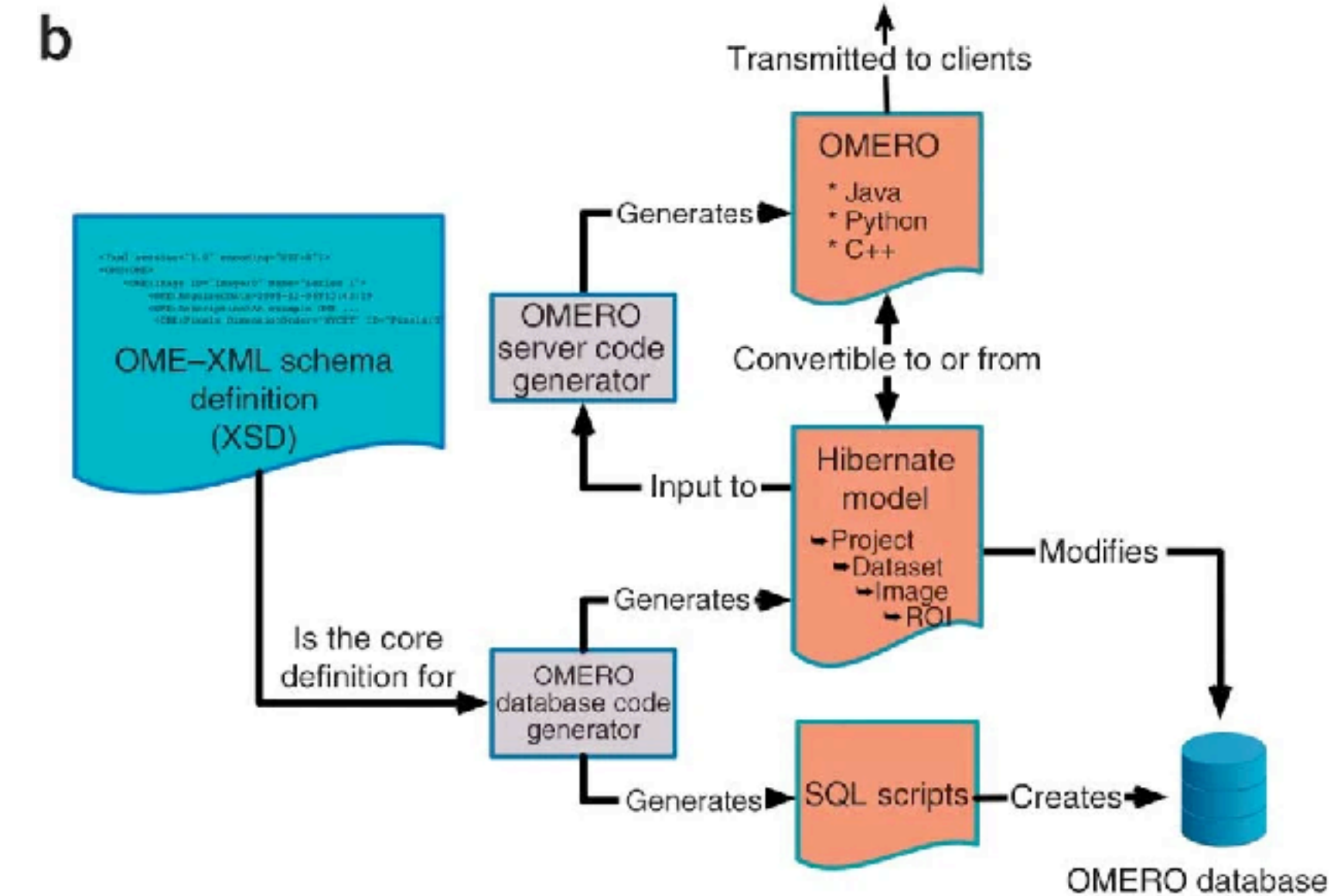
Use k/v for **ontology links**

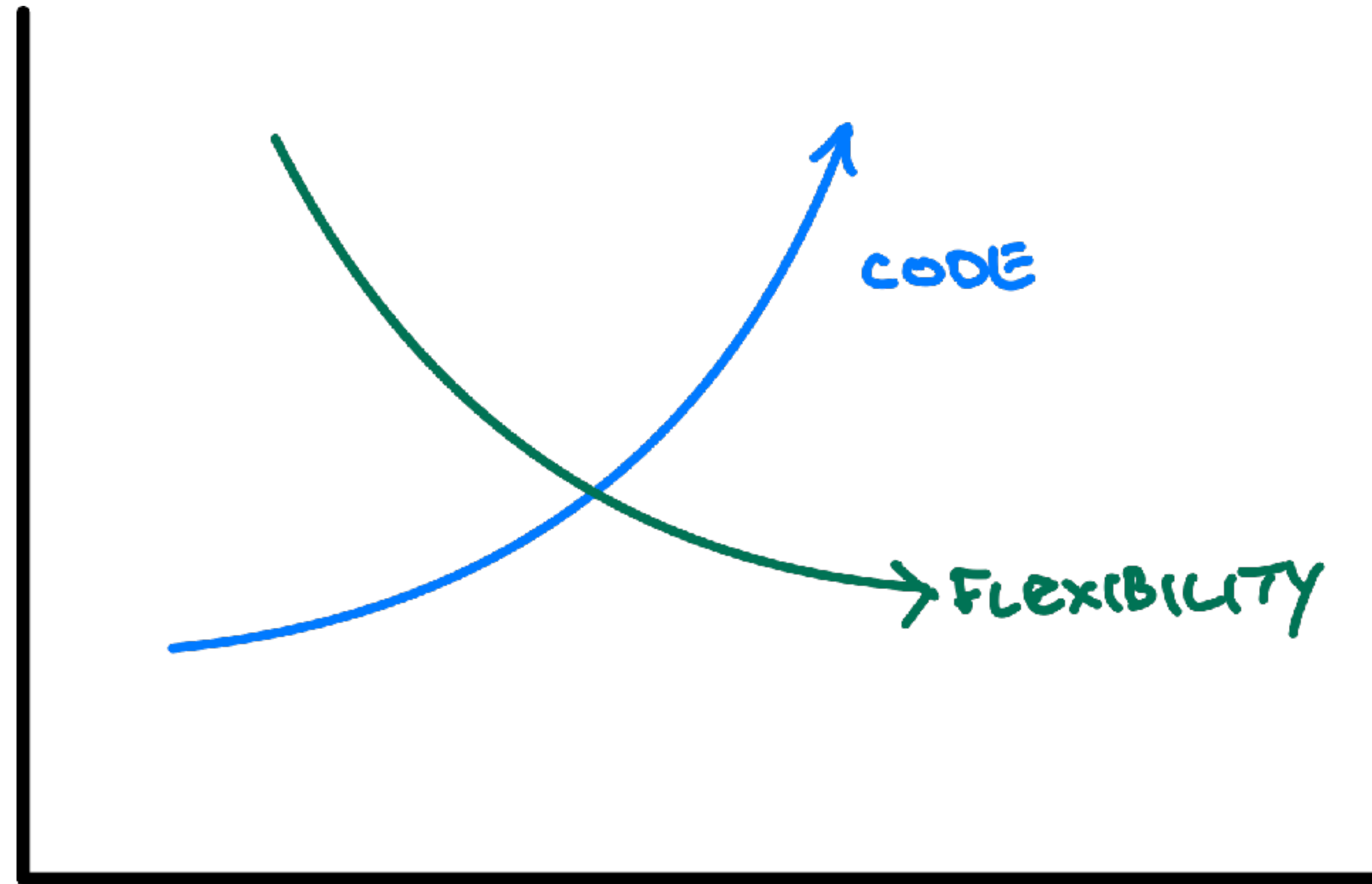
Targets

Source	2016-06	2015-01	2013-06	2012-06	2011-06	2010-06	2010-04	2009-09	2008-09	2008-02	2007-06	2003-FC
2016-06	--	good	good	good	good	good	fair	fair	fair	poor	poor	poor
2015-01		--	good	good	good	good	fair	fair	fair	poor	poor	poor
2013-06			--	good	good	good	fair	fair	fair	poor	poor	poor
2012-06				--	good	good	fair	fair	fair	poor	poor	poor
2011-06					--	good	fair	fair	fair	poor	poor	poor
2010-06						--	fair	fair	poor	poor	poor	poor
2010-04							--	poor	poor	poor	poor	poor
2009-09								--	poor	poor	poor	poor
2008-09									--	poor	poor	poor
2008-02						excellent				--	poor	poor
2007-06											--	poor
2003-FC												--

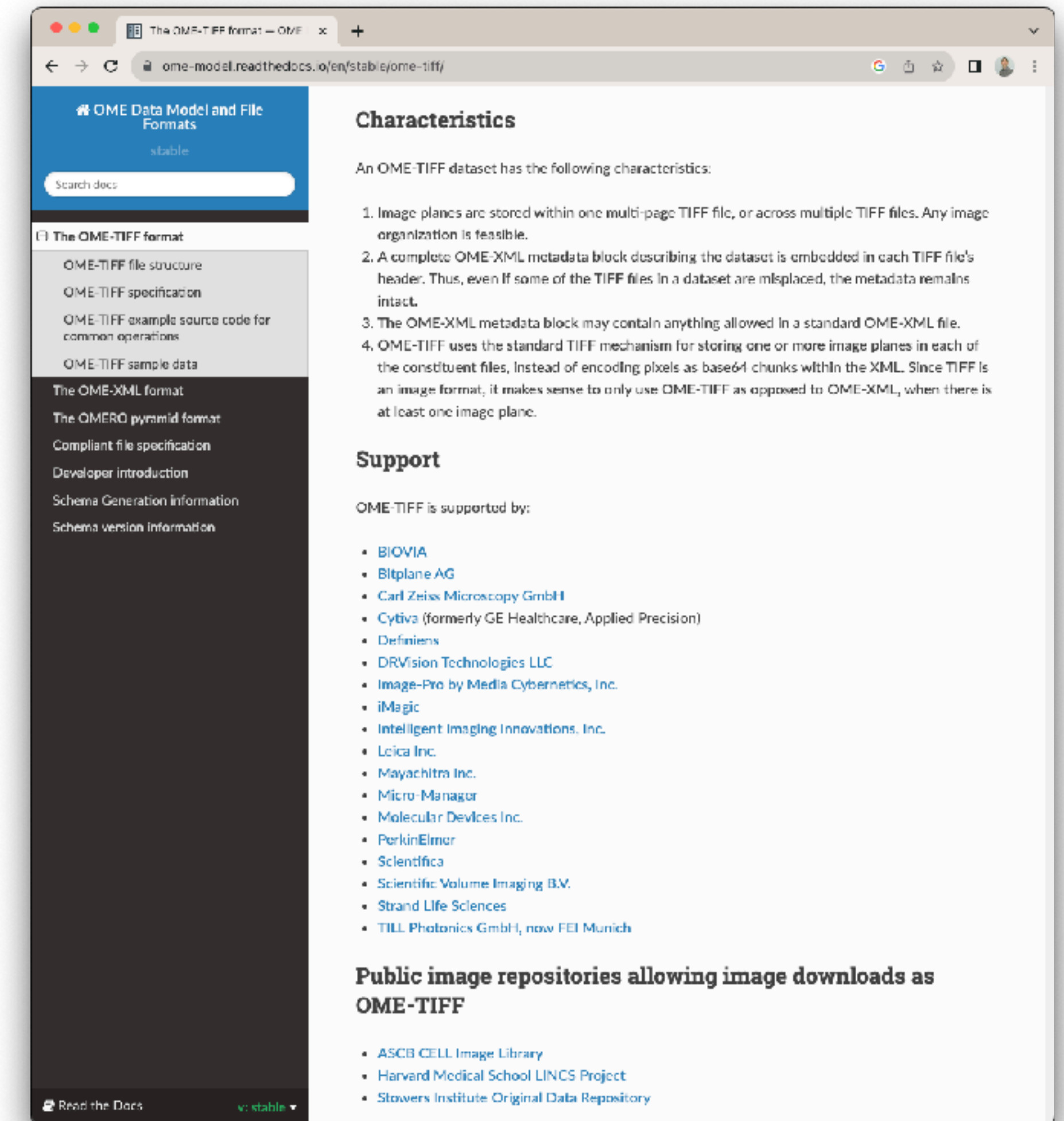
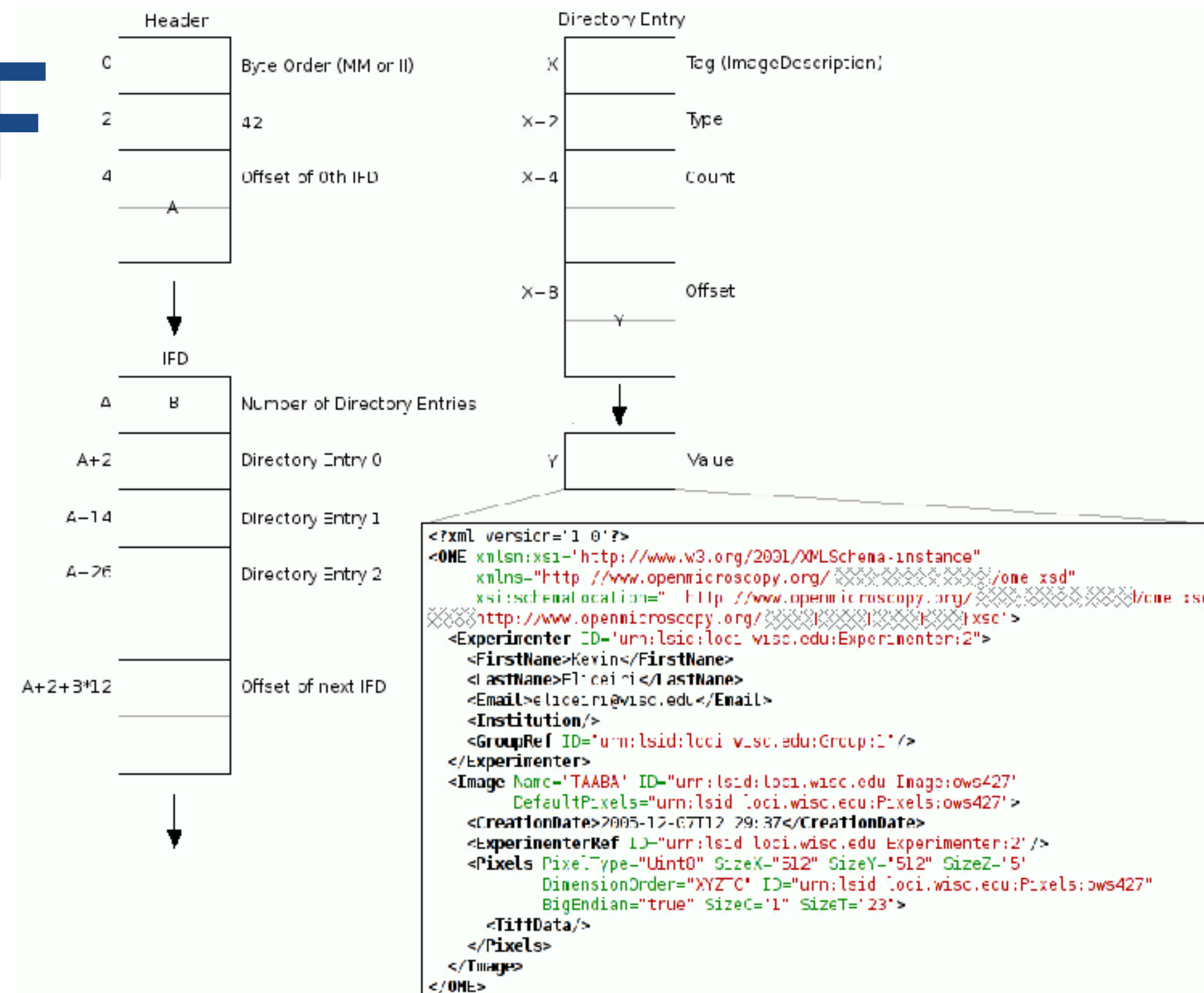
Downgrades (indicated by the right side of the table)

Upgrades (indicated by the bottom of the table)





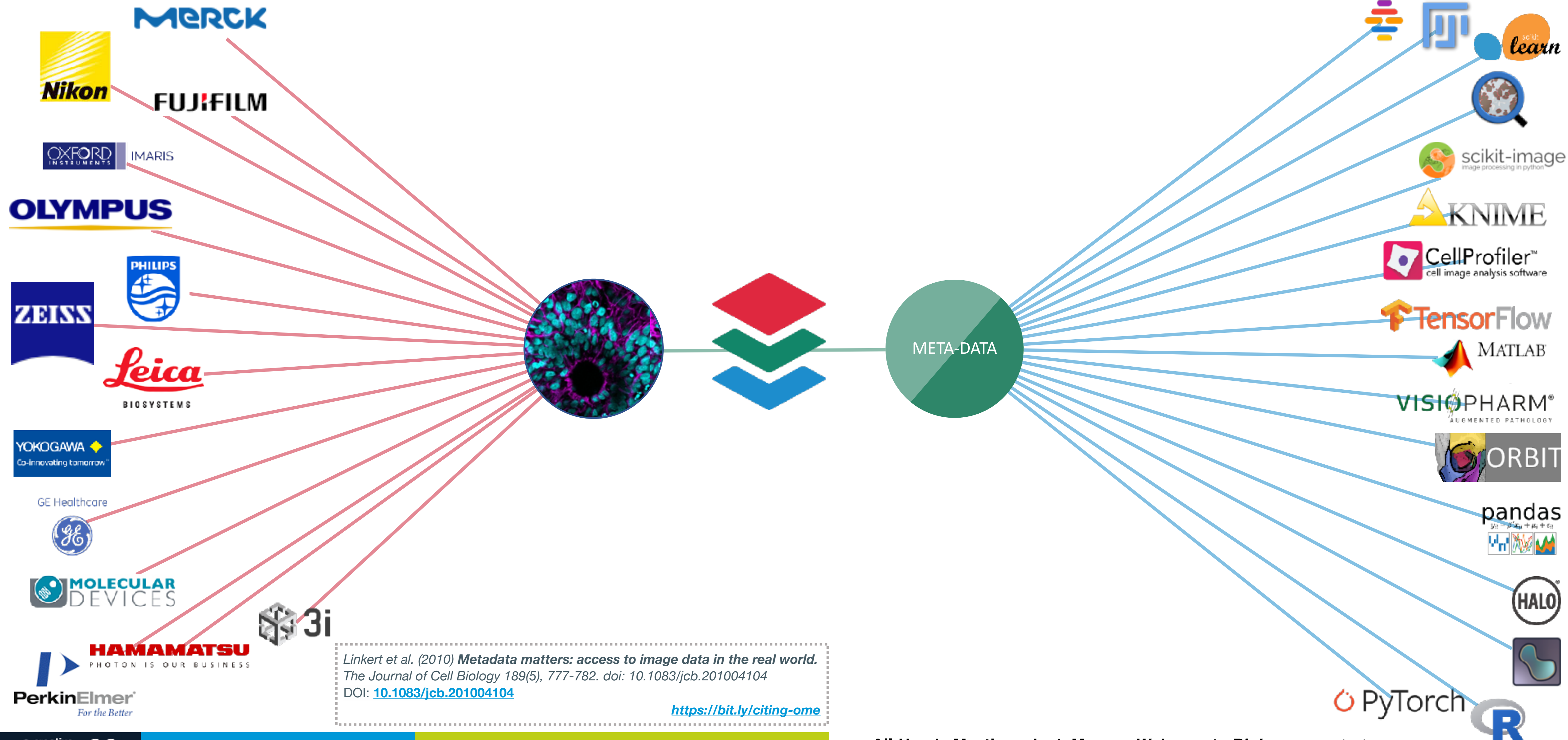
TIFF



<https://ome-model.readthedocs.io/en/stable/ome-tiff/specification.html>

2005

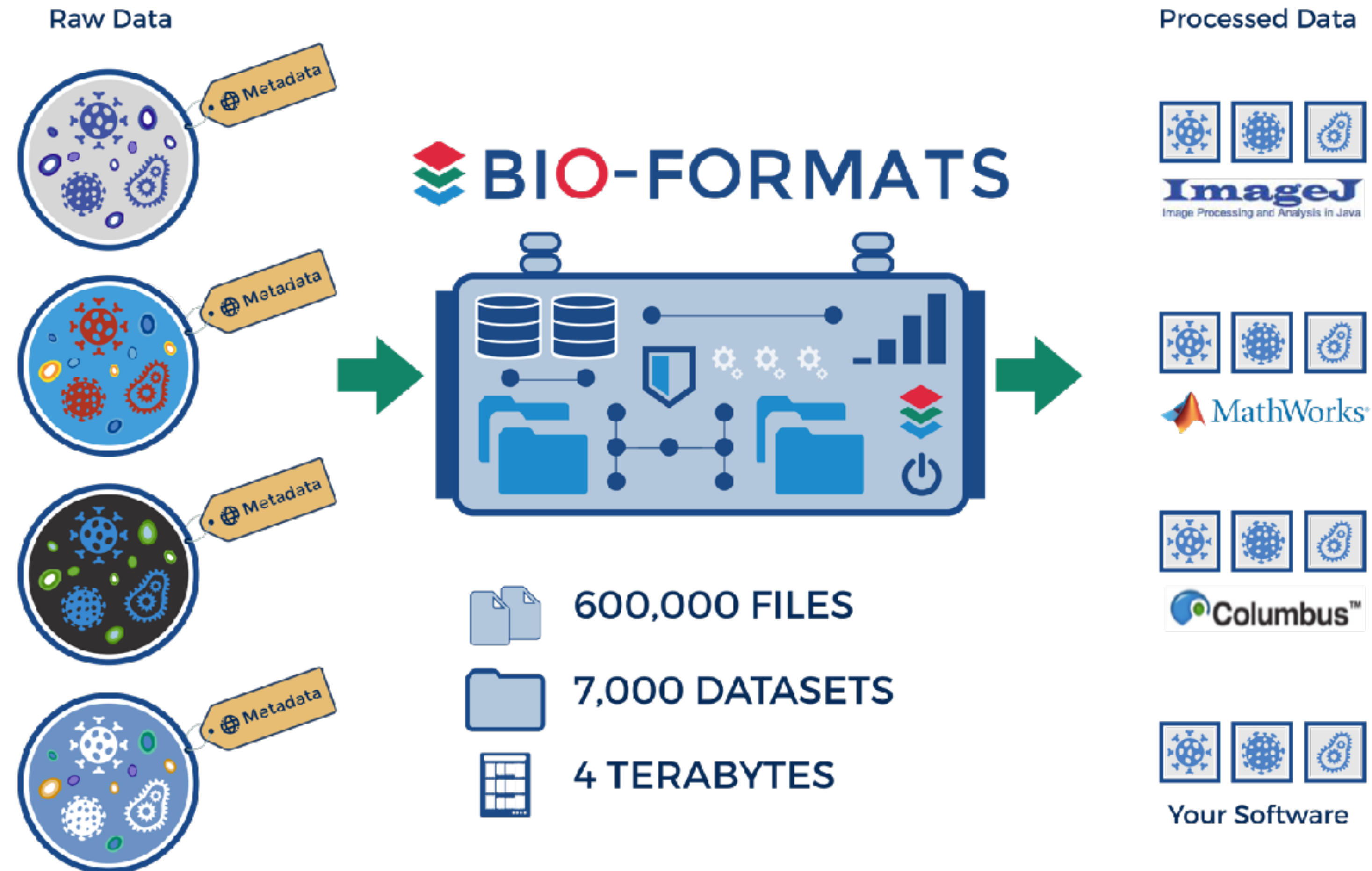
BIO-FORMATS





```
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtFrameHeight #1=512
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtFrameWidth #1=512
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtLinePeriod #1=3.0000000000000001e-005
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtOffsetX #1=0
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtOffsetY #1=0
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtRegionHeight #1=512
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtRegionWidth #1=512
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtSuperSampling #1=1
Experiment|AcquisitionBlock|AcquisitionModeSetup|RtZoom #1=1
Experiment|AcquisitionBlock|AcquisitionModeSetup|ScalingX #1=4.1513291872589499e-007
Experiment|AcquisitionBlock|AcquisitionModeSetup|ScalingY #1=4.1513291872589499e-007
Experiment|AcquisitionBlock|AcquisitionModeSetup|ScalingZ #1=9.999999999999995e-007
Experiment|AcquisitionBlock|AcquisitionModeSetup|SimRotations #1=3
Experiment|AcquisitionBlock|AcquisitionModeSetup|TimeSeries #1=false
Experiment|AcquisitionBlock|AcquisitionModeSetup|TrackMultiplexType #1=ZStack
Experiment|AcquisitionBlock|AcquisitionModeSetup|UseRois #1=false
Experiment|AcquisitionBlock|AcquisitionModeSetup|ZoomX #1=1
Experiment|AcquisitionBlock|AcquisitionModeSetup|ZoomY #1=1
Experiment|AcquisitionBlock|Laser|LaserName #1=HeNe633
Experiment|AcquisitionBlock|Laser|LaserName #2=Diode 405-30
Experiment|AcquisitionBlock|Laser|LaserName #3=Argon
Experiment|AcquisitionBlock|Laser|LaserName #4=HeNe594
Experiment|AcquisitionBlock|Laser|LaserPower #1=0.0050000000000000001
Experiment|AcquisitionBlock|Laser|LaserPower #2=0.029999999999999999
Experiment|AcquisitionBlock|Laser|LaserPower #3=0.025000000000000001
Experiment|AcquisitionBlock|Laser|LaserPower #4=0.002
```

...



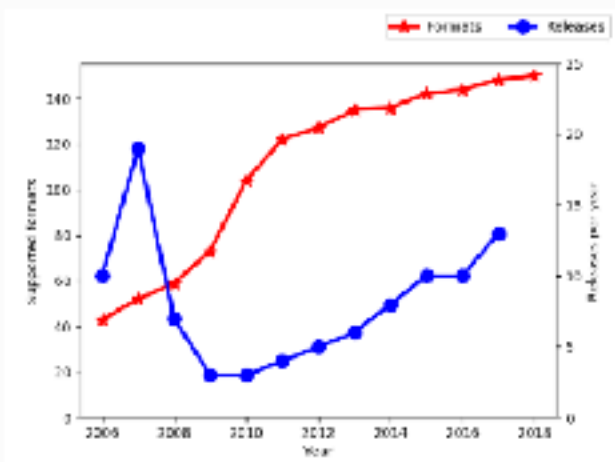
→ Apps using Bio-Formats were started >100,000 times per day in 2015 - 2022. ←

OME's position regarding file formats

[← Back to Blog](#)

Below is a statement delivered November 2018 to the Cure-DiImaging Industry Board regarding the support of proprietary file formats by Bio-Formats. This was discussed during the [From Images to Knowledge with ImageJ & Friends](#) meeting in December and since then, there have been a growing number of conversations about a common format for bioimaging data. We're posting it here to tie the conversations back together and continue an open discussion of this critical issue.

As many of you know, work on Bio-Formats began in 2006, and over the first 10 years of development, support was added for over 140 file formats. If you include the per-format variants that have emerged over the years, that might be as much as 5 or 10 times higher, but precise numbers are difficult at best.



In 2016, we issued a [public statement](#) that OME, or more specifically its funding model, was not going

openmicroscopy.org/2019/06/25/formats.html

Building open collaborations for the sustainable support of proprietary file formats

[← Back to Blog](#)

The challenges and cost associated with the development and maintenance of software for reading images stored in proprietary file formats (PFFs) have been discussed at length in previous blog posts [1](#), [2](#). One approach to help address these issues is the development of community collaborations that provide sustainable solutions to PFF support in Bio-Formats.

In this blog post, we want to describe two successful examples of partnerships established with well-recognized commercial entities: [Carl Zeiss Microscopy GmbH](#) and [Intelligent Imaging Innovations \("3i"\)](#) and how this will result in more open, reusable code and better tools for the imaging community.

ZEISS: Open support for JPEG-XR compression

Some image acquisition systems built by Carl Zeiss Microscopy GmbH store binary image data using [JPEG-XR](#) compression. Open-source efforts to decode data stored using this technology have to date been unsuccessful. As we have noted previously, the complexity of providing a pure Java implementation of this compression scheme was simply too high to be fully assumed by a non-profit, grant-funded organization like OME.

In response, the user community has raised their concerns to ZEISS and a partnership has been established with [Glencoe Software](#) to add a Java-based JPEG-XR decoder to Bio-Formats. Thanks to extensive, fruitful discussions with ZEISS all outputs of this partnership are publicly available and all source code licensed identically to other OME projects. Some public examples of this ongoing work are:

openmicroscopy.org/2016/08/31/bf-partnerships.html

Supporting complex formats - what we will and won't do, and what you can do to help

[← Back to Blog](#)

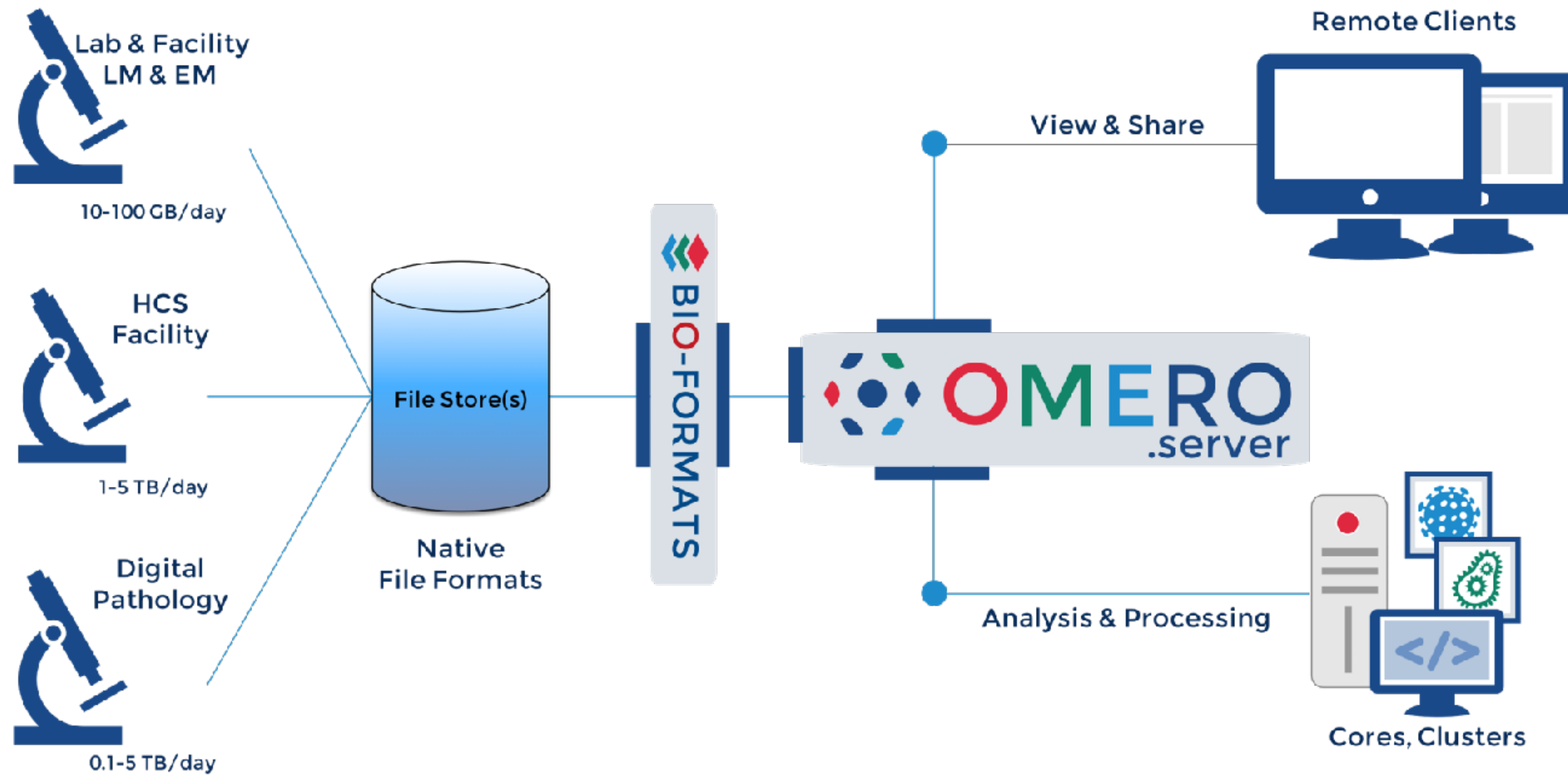
You may have noticed that a few months ago, we received an email asking us about when we expect to support 3D HISTECH .mrxs files. This sort of request isn't particularly unusual and the reply gives an insight into one of the key challenges we face.

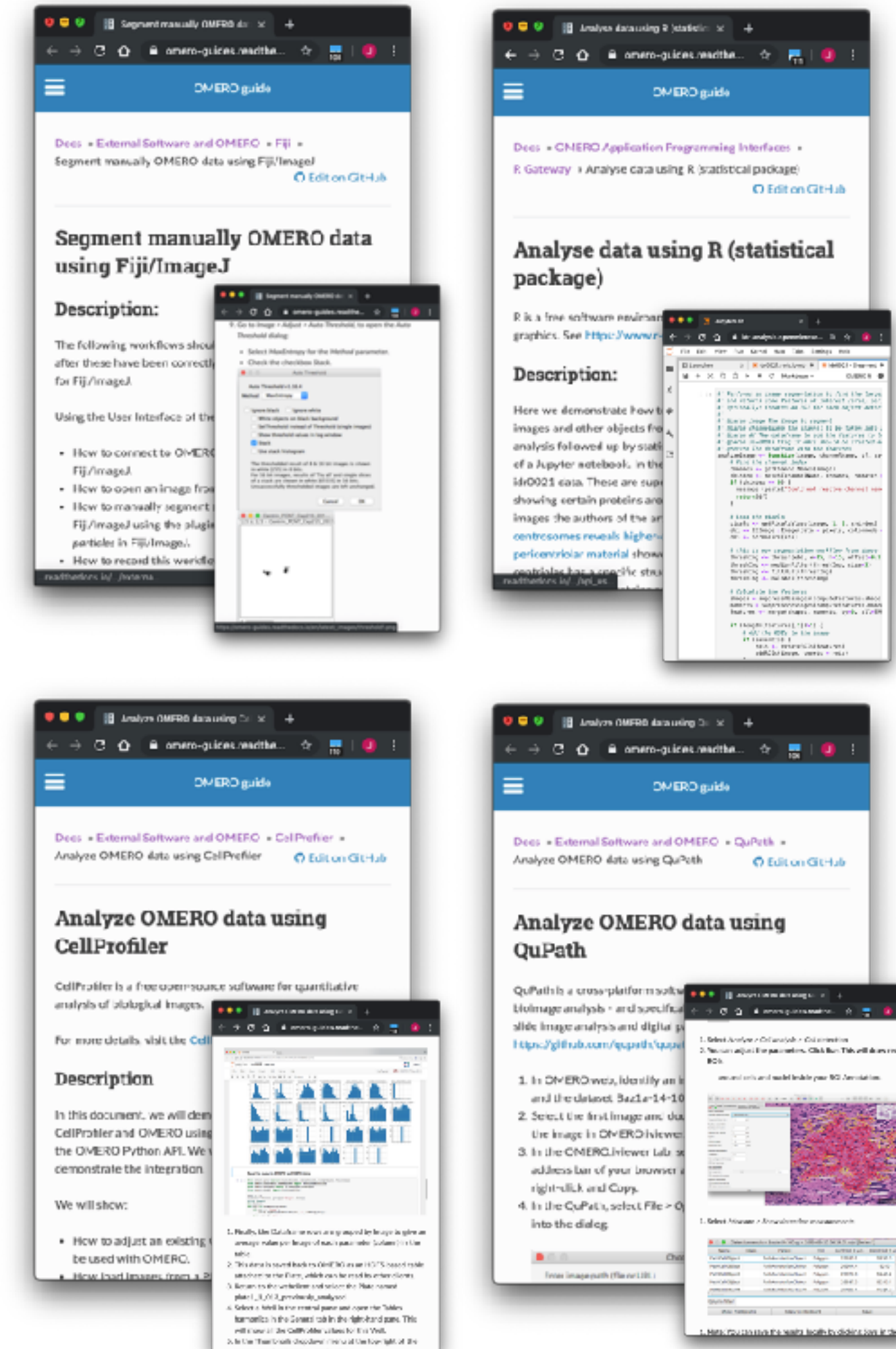
Just because we don't have a reader, doesn't mean we haven't done any work

3D HISTECH .mrxs is an example of a complex format, the design of which does not make our work any easier. In fact, we can say with some confidence that the 3D HISTECH .mrxs file format is the most complex whole slide imaging file format we have ever encountered. We can say this because although we haven't delivered a full reader for .mrxs—and there hasn't been substantial public development—we have spent a great deal of time examining the format and potential solutions, and building test readers. Thanks to the example data the community has generously provided, we have been able to analyse the on-disk layout as well as the compression types, and map out the details of what an implementation would entail.

Unfortunately, the result of all this work has been the conclusion that we simply do not have the resources to prioritize delivering a complete solution for this format. This is not the only format we have reached this conclusion about. For example, support for [3i Slidebook 6 files](#) was only added to Bio-Formats last May when [3i](#) committed to developing the reader themselves. Obviously, we are very grateful for this, but that doesn't change the fact that we had already spent years working on various versions of this format from initial inquiries in [Slidebook reader](#) was released back in 2006 and

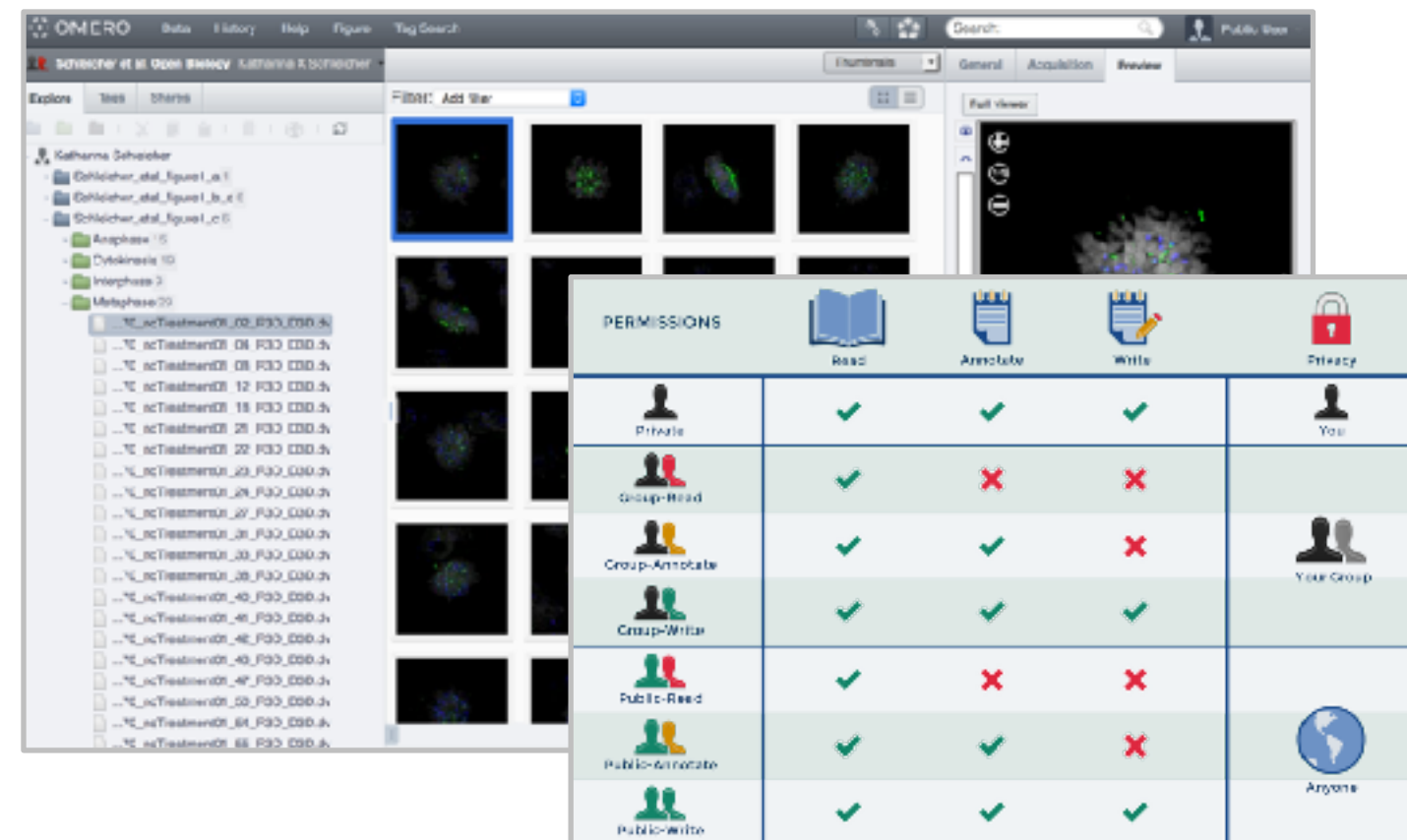
openmicroscopy.org/2016/01/06/format-support.html



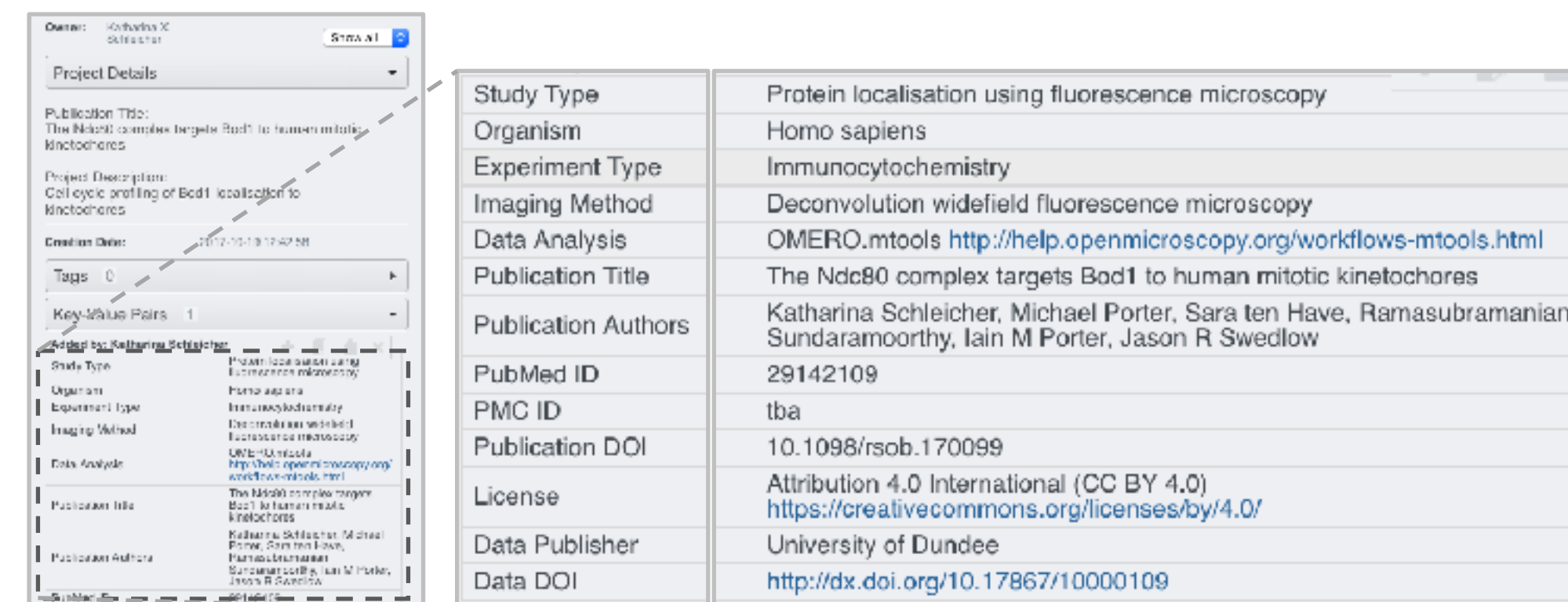


<https://omero-guides.readthedocs.io>

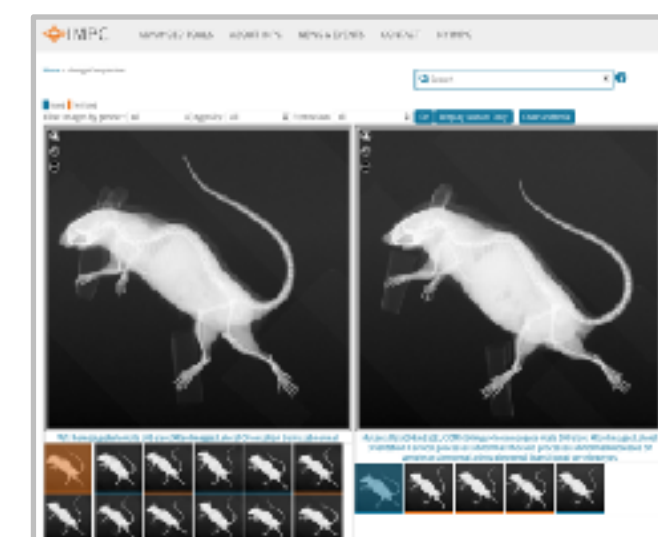
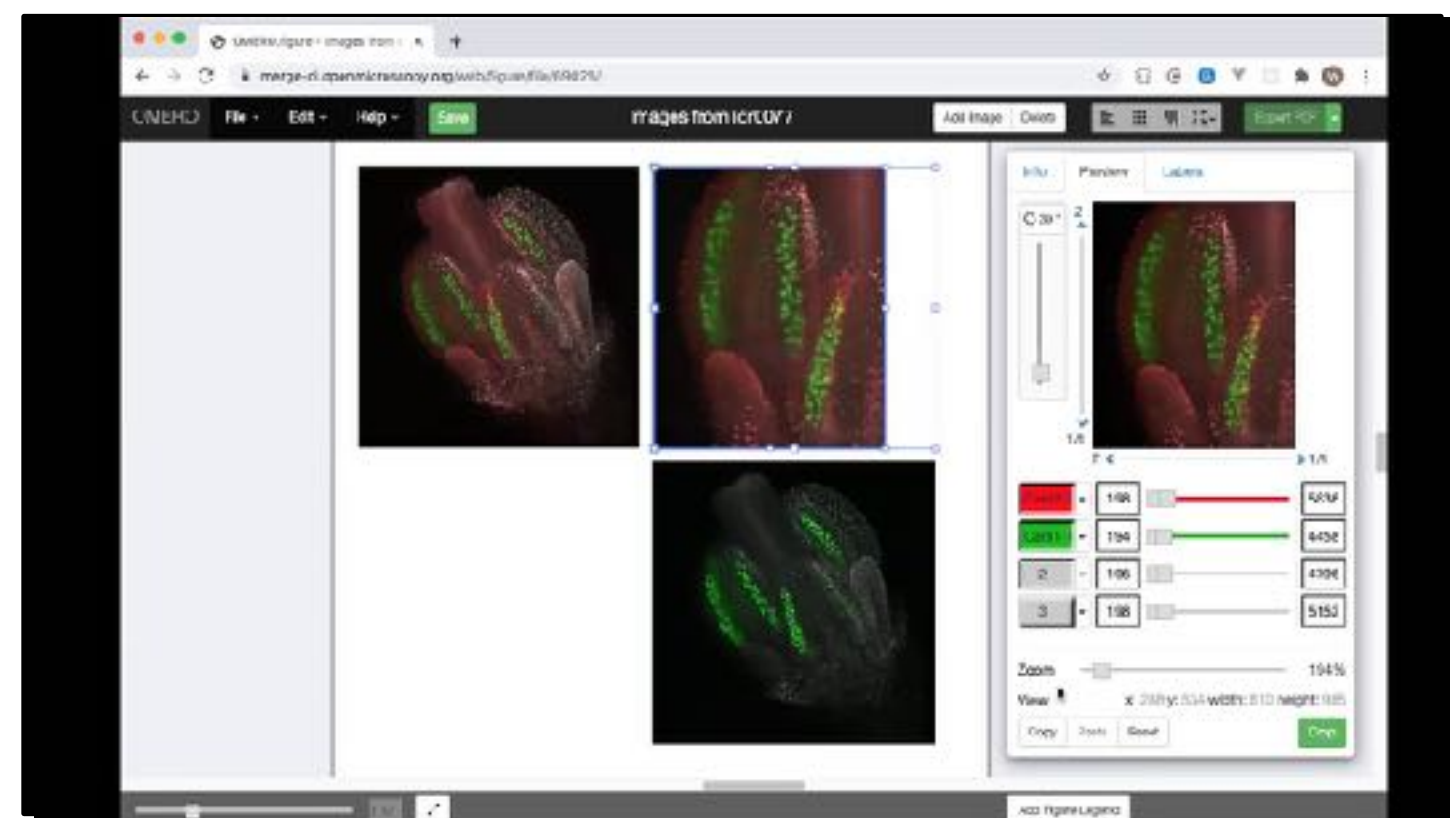
Collaborate on data publication



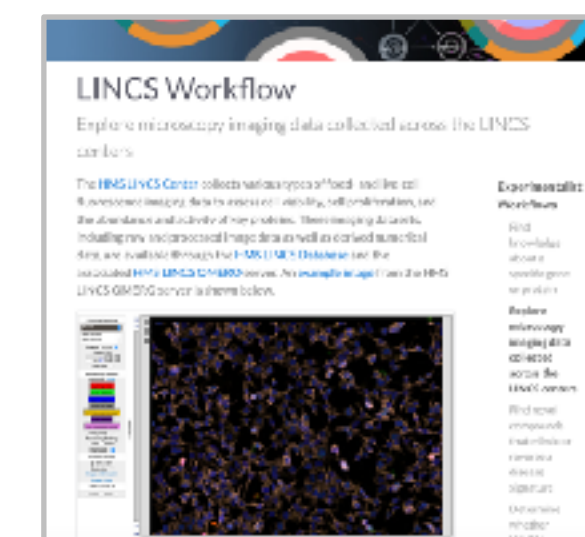
Annotate



Rapidly edit figures



<https://www.mousephenotype.org>




<https://lincs-omero.hms.harvard.edu>



<http://ssbd.qbic.riken.jp/>




 **Image Collections** Nomenclature About Contributors

You are currently viewing **281** out of a possible **281** images
View more about this dataset [here](#).


Dataset: Neonatal Development & Early Life Pancreas (HANDEL-F)

Grid Density: **Sparse** Normal Dense

Filters: [Clear](#)

DISEASE STATUS 

☐ AAB
☐ ND

AGE 

☐ Neonatal
☐ Infancy
☐ Childhood



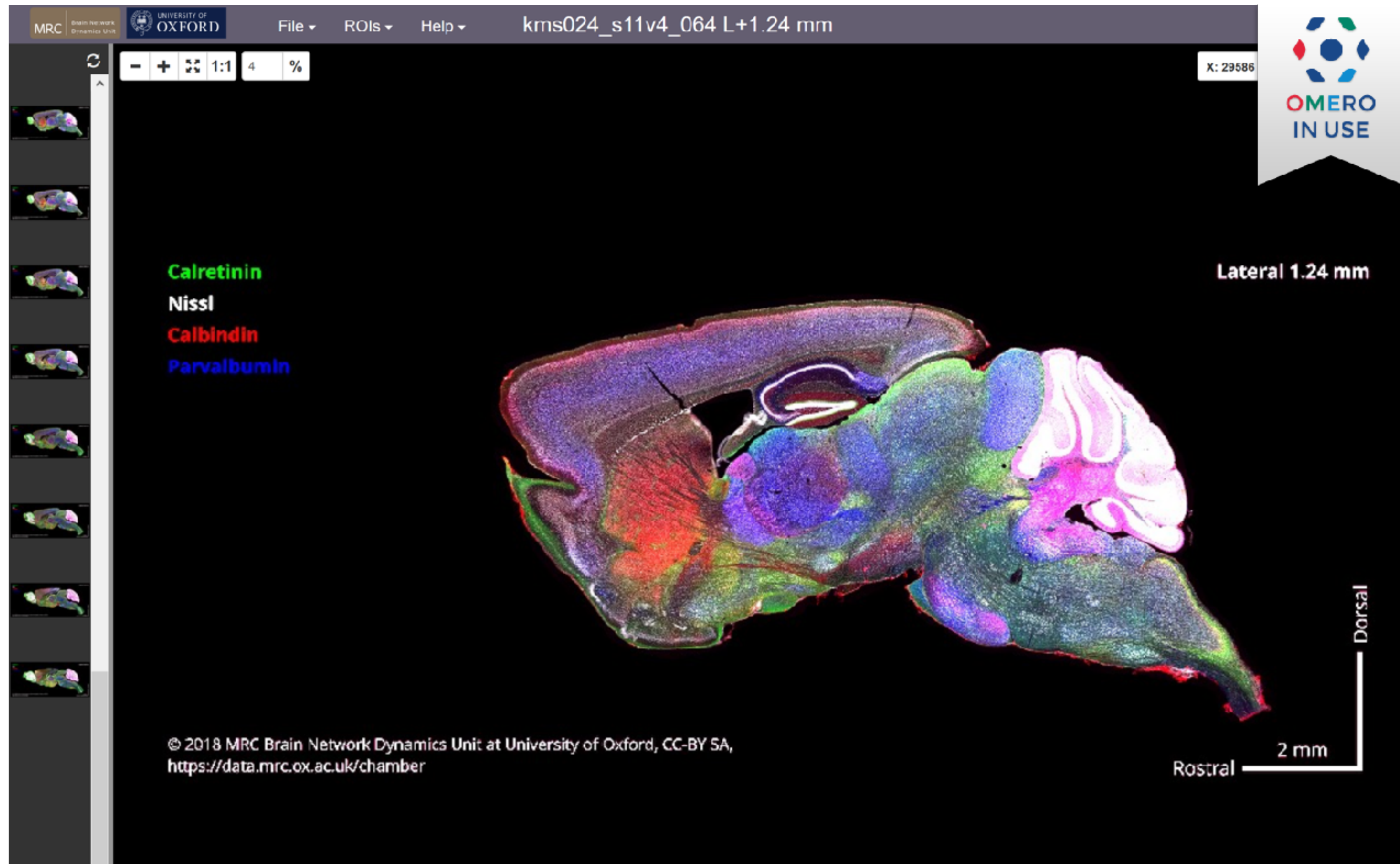
SEX 

Image 1:
Age: 4d
Disease Status: ND
Sex: M
Markers: **INS** **SST** **GCG** **DAPI**
Region: Sagittal, Body
Other Tags: DON22, AFI


Image 2:
Age: 1d
Disease Status: ND
Sex: F
Markers: **SST** **Ki67** **DAPI**
Region: Sagittal, Head
Other Tags: DON66, AFI

Image 3:
Age: 3mo
Disease Status: ND
Sex: M
Markers: **INS** **SST** **GCG** **DAPI**
Region: Sagittal, Body
Other Tags: DON2, AFI





Deep learning for cellular image analysis

Erick Moen, Dylan Bannon, Takamasa Kudo, William Graf, Markus Covert & David Van Valen 

Nature Methods (2019) | [Cite this article](#)

Hypoxia induces rapid changes to histone methylation and reprograms chromatin

Michael Batie^{1,2}, Julianty Frost¹, Mark Frost¹, James W. Wilson¹, Pieta Schofield^{2,*}, Sonia Rocha^{1,2,†}

[+ See all authors and affiliations](#)


Science 15 Mar 2019:
Vol. 363, Issue 6432, pp. 1222-1226
DOI: 10.1126/science.aau5870

The depolymerase activity of MCAK shows a graded response to Aurora B kinase phosphorylation through allosteric regulation

Toni McHugh, Juan Zou, Vladimir A. Volkov, Aurélie Bertin, Sandeep K. Talapatra, Juri Rappsilber, Marileen Dogterom, Julie P. I. Welburn

Journal of Cell Science 2019 132:jcs.228353 doi: 10.1242/jcs.228353 Published 14 January 2019

Pulcherrimin formation controls growth arrest of the *Bacillus subtilis* biofilm




Sofia Arnaoutell, D. A. Matoz-Fernandez,  Michael Porter, Margarita Kalamara,  James Abbott,  Cait E. MacPhee,  Fordyce A. Davidson, and  Nicola R. Stanley-Wall

PNAS July 2, 2019 116 (27) 13553-13562; first published June 19, 2019 <https://doi.org/10.1073/pnas.1903982116>

Edited by Caroline S. Harwood, University of Washington, Seattle, WA, and approved May 13, 2019 (received for review March 7, 2019)



Immuno-SABER enables highly multiplexed and amplified protein imaging in tissues

Sinem K. Saka , Yu Wang , Jocelyn Y. Kishi, Allen Zhu, Yitian Zeng, Wenxin Xie, Koray Kirli, Clarence Yapp, Marcelo Cicconet, Brian J. Beliveau, Sylvain W. Lapan, Siyuan Yin, Millicent Lin, Edward S. Boyden, Pascal S. Kaeser, German Pihan, George M. Church & Peng Yin 

Nature Biotechnology 37, 1080–1090(2019) | [Cite this article](#)

FAM83D directs protein kinase CK1α to the mitotic spindle for proper spindle positioning

Luke J Fulcher, Zhengcheng He , Lin Mei, Thomas J Macartney, Nicola T Wood, Alan R Prescott, Arlene J Whigham, Joby Varghese, Robert Gourlay, Graeme Ball, Rosemary Clarke, David G Campbell, Christopher A Maxwell, Gopal P Sapkota  

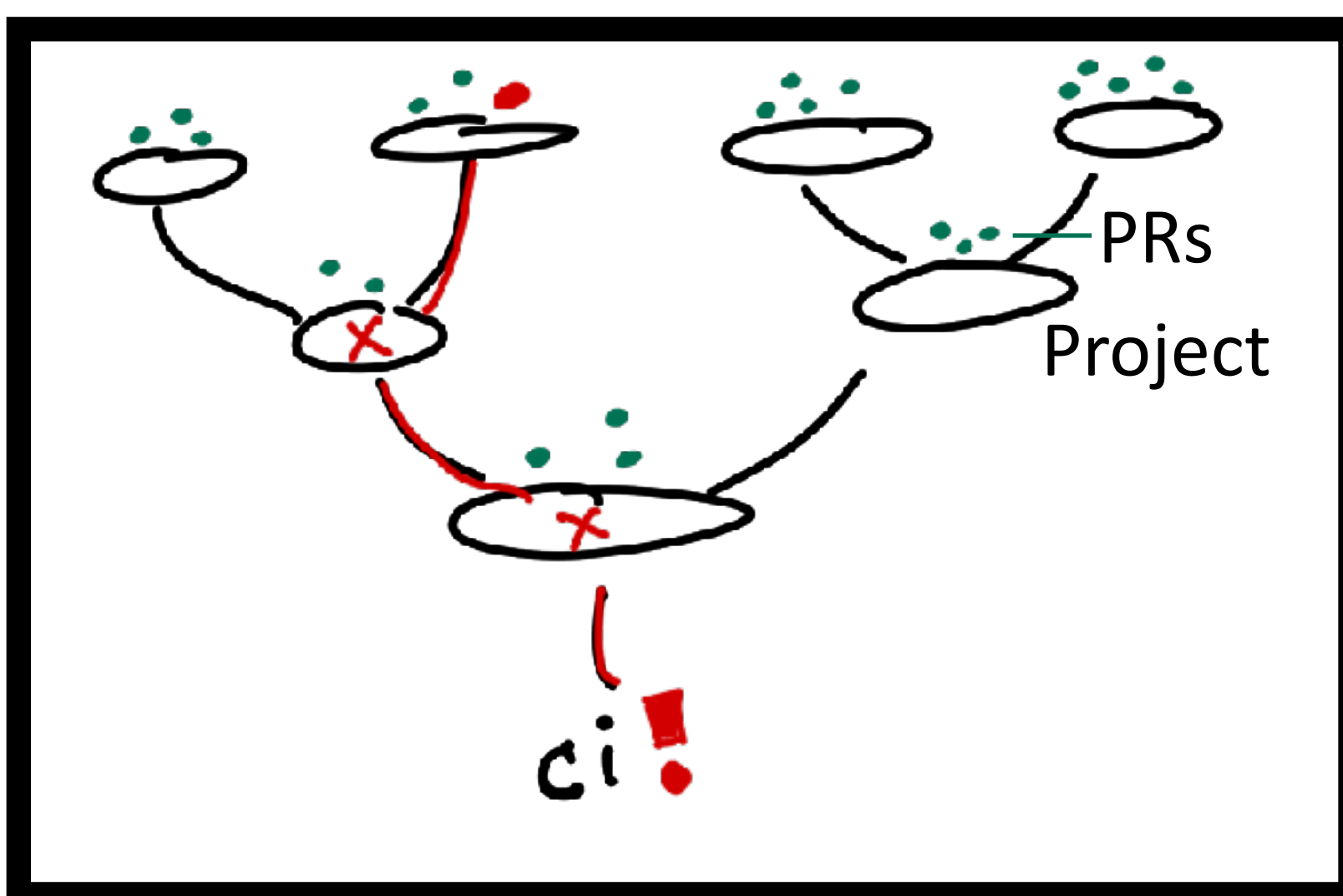
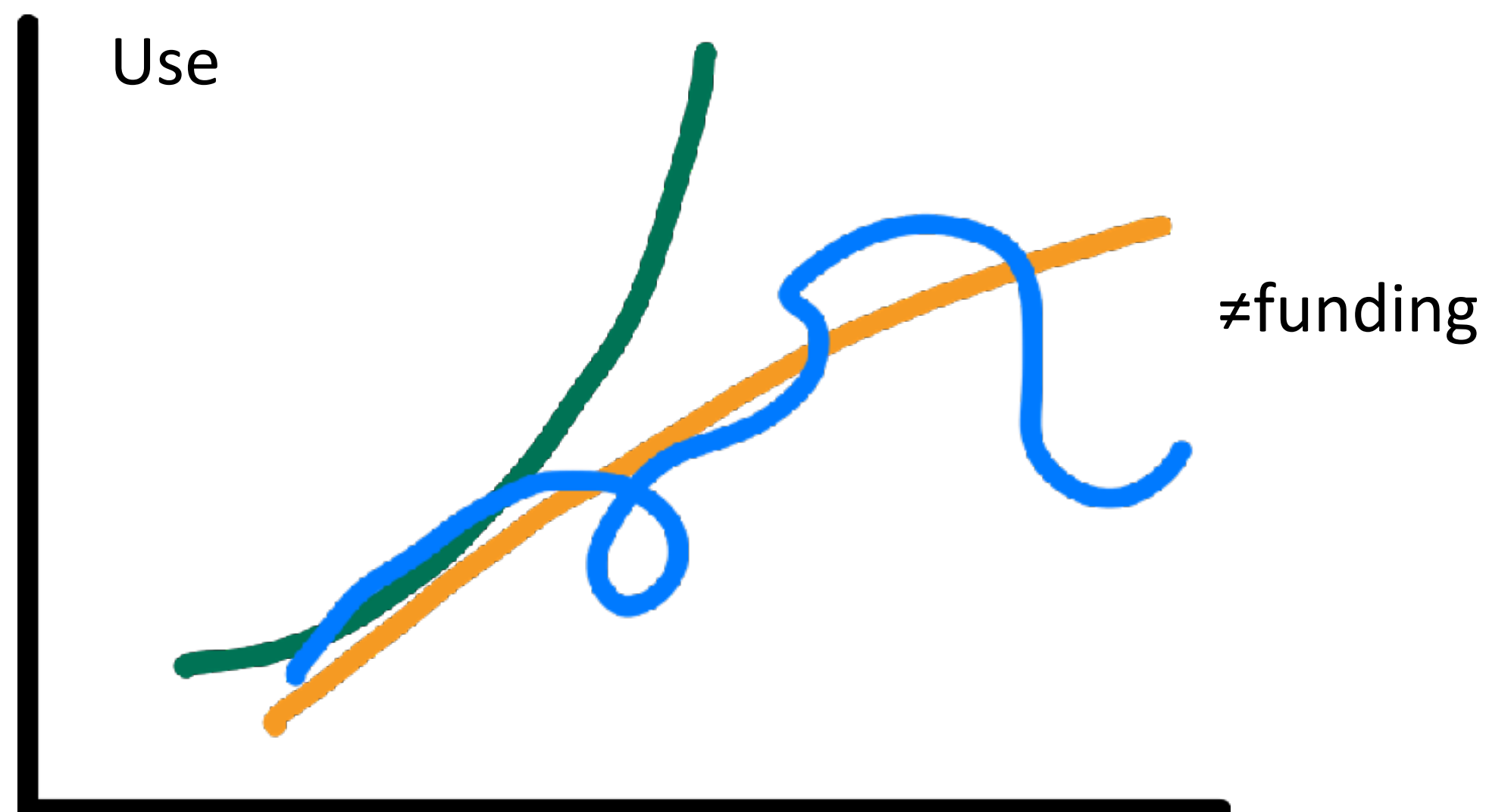
[Author information](#)

EMBO Rep (2019) 20: e47495 | <https://doi.org/10.15252/embr.201847495>

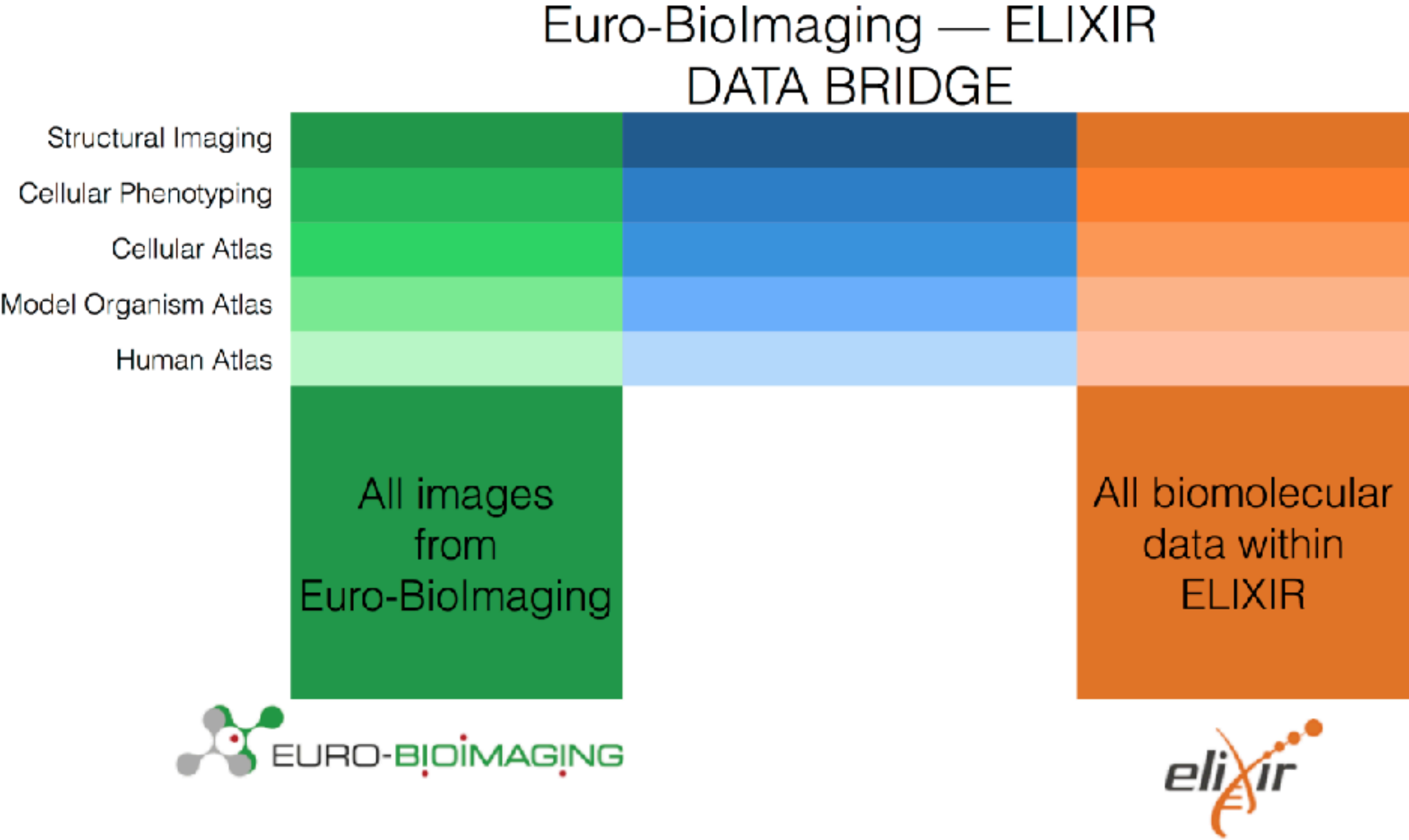
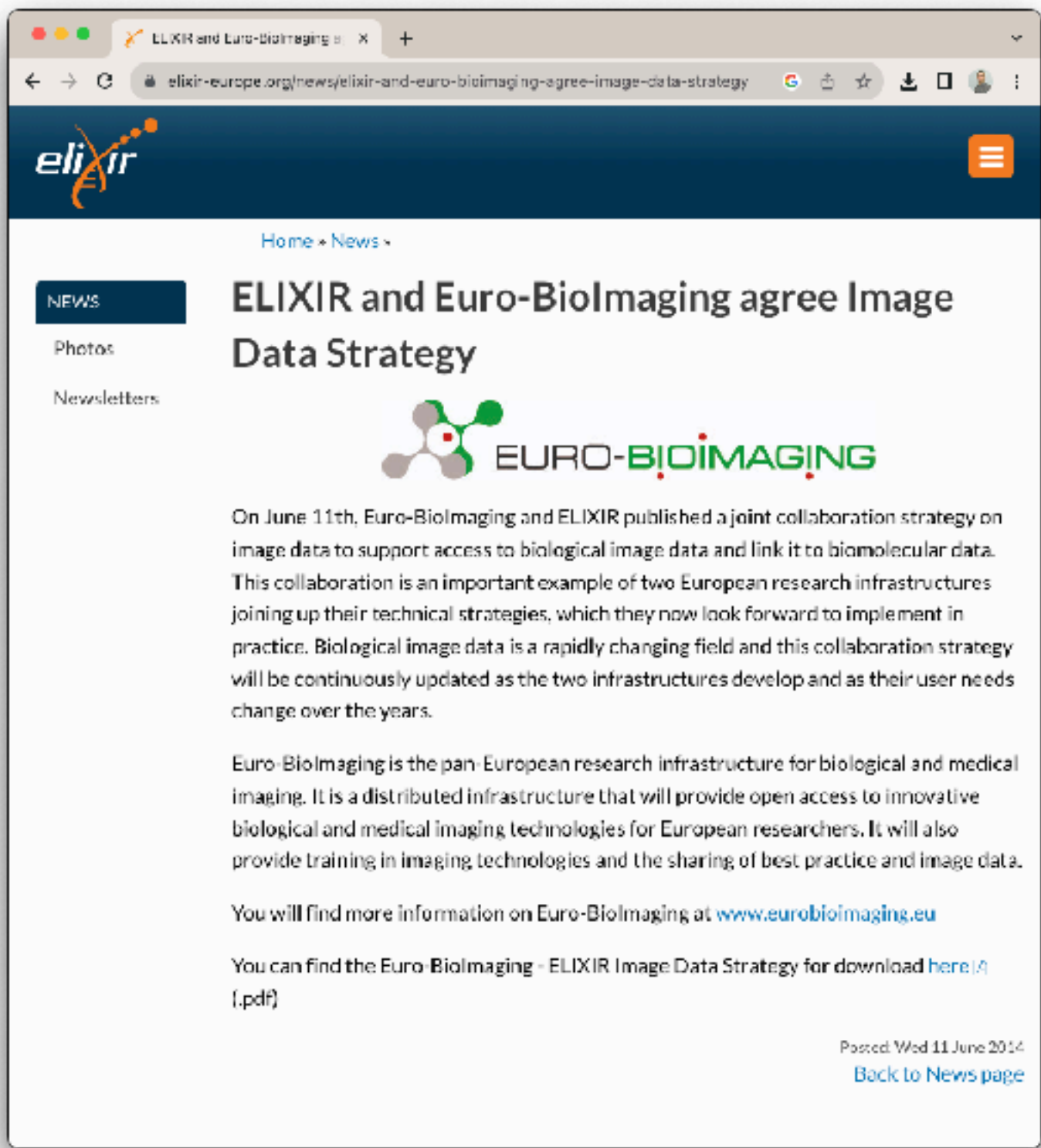
Estimation of Relative and Absolute Risks in a Competing–Risks Setting Using a Nested Case–Control Study Design: Example From the ProMort Study

Renata Zelic , Daniela Zugna, Matteo Bottai, Ove Andrén, Jonna Fridfeldt, Jessica Carlsson, Sabina Davidsson, Valentina Fiano, Michelangelo Fiorentino, Francesca Giunchi, Chiara Grasso, Luca Lianas, Cecilia Mascia, Luca Molinaro, Gianluigi Zanetti, Lorenzo Richiardi, Andreas Pettersson, Olof Akre

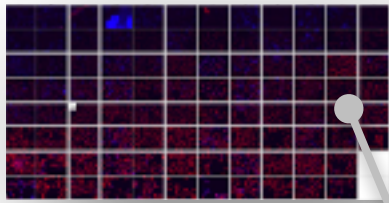
American Journal of Epidemiology, Volume 188, Issue 6, June 2019, Pages 1165–1173, <https://doi.org/10.1093/aje/kwz026>



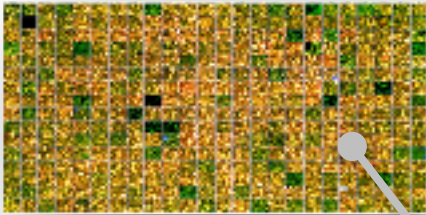
DB



Euro-Biolmaging– ELIXIR Image Data Strategy
https://elixir-europe.org/sites/default/files/documents/euro-bioimaging_elixir_image_data_strategy.pdf



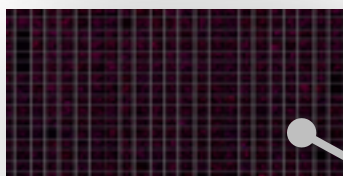
Gene Product Targeting HCS



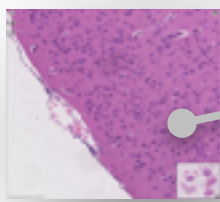
Genetic HCS



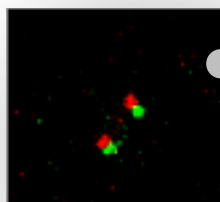
Geographic HCS



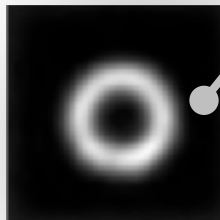
Chemical HCS



Histopathology

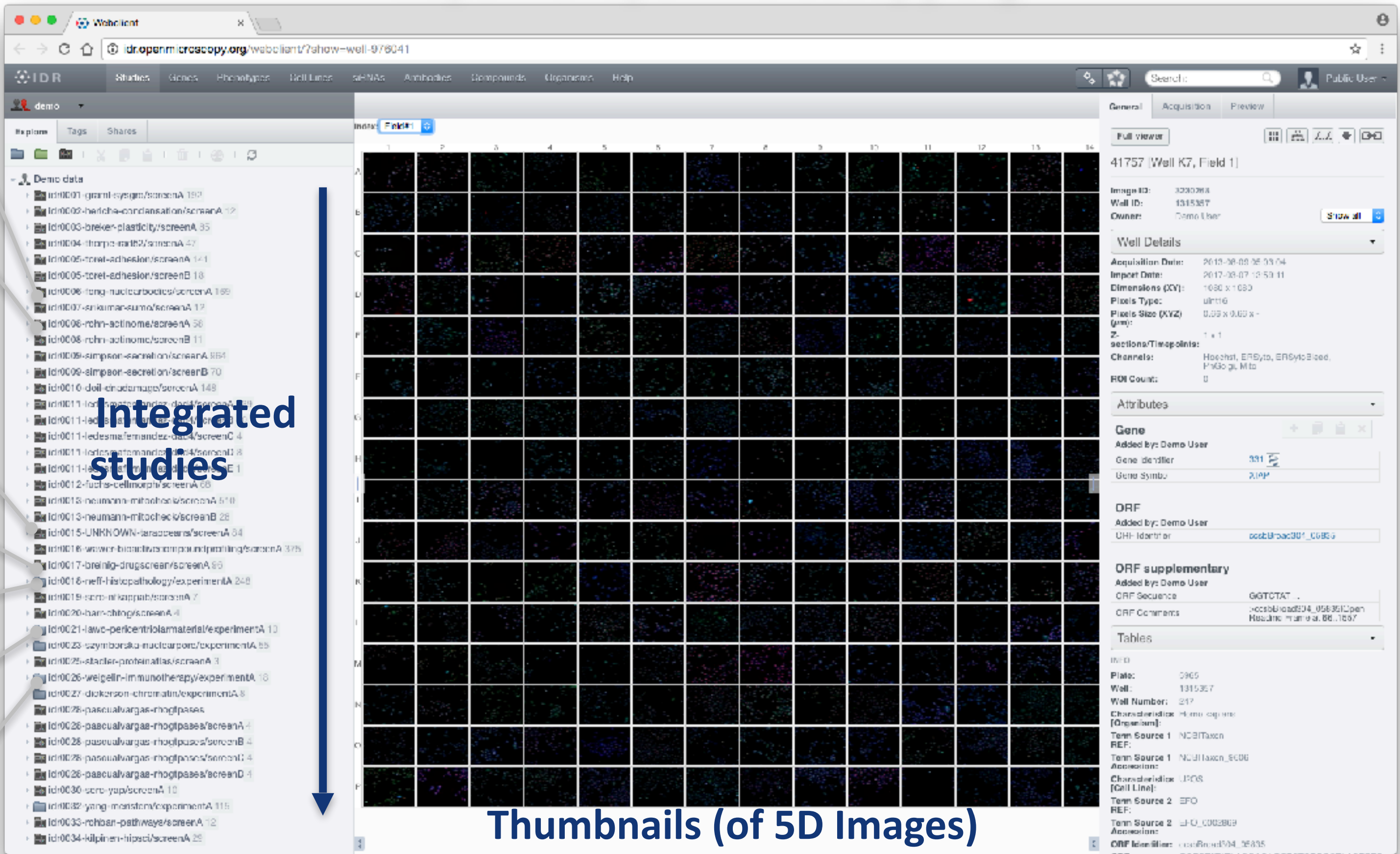


3D-Sim



Super-resolution

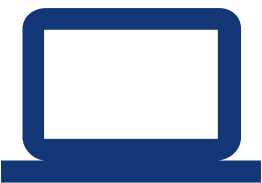
<https://idr.openmicroscopy.org>



The screenshot displays the IDR web application. On the left, a sidebar lists various studies under the heading 'Demo data'. The main area is a large grid of image thumbnails, labeled 'Thumbnails (of 5D Images)'. On the right, a panel shows details for a selected well (Well K7, Field 1), including acquisition date, dimensions, pixel size, and gene information (Gene: RAMP).

Williams et al. (2017) *The Image Data Resource: A Bioimage Data Integration and Publication Platform*. *Nature Methods* 14(8), 775-781. Published 19 June 2017 DOI: [10.1038/nmeth.4326](https://doi.org/10.1038/nmeth.4326)
<https://bit.ly/citing-ome>

Experimental metadata



Cross-data browsing

Biomolecular annotations



Cloud analysis

Analysis results

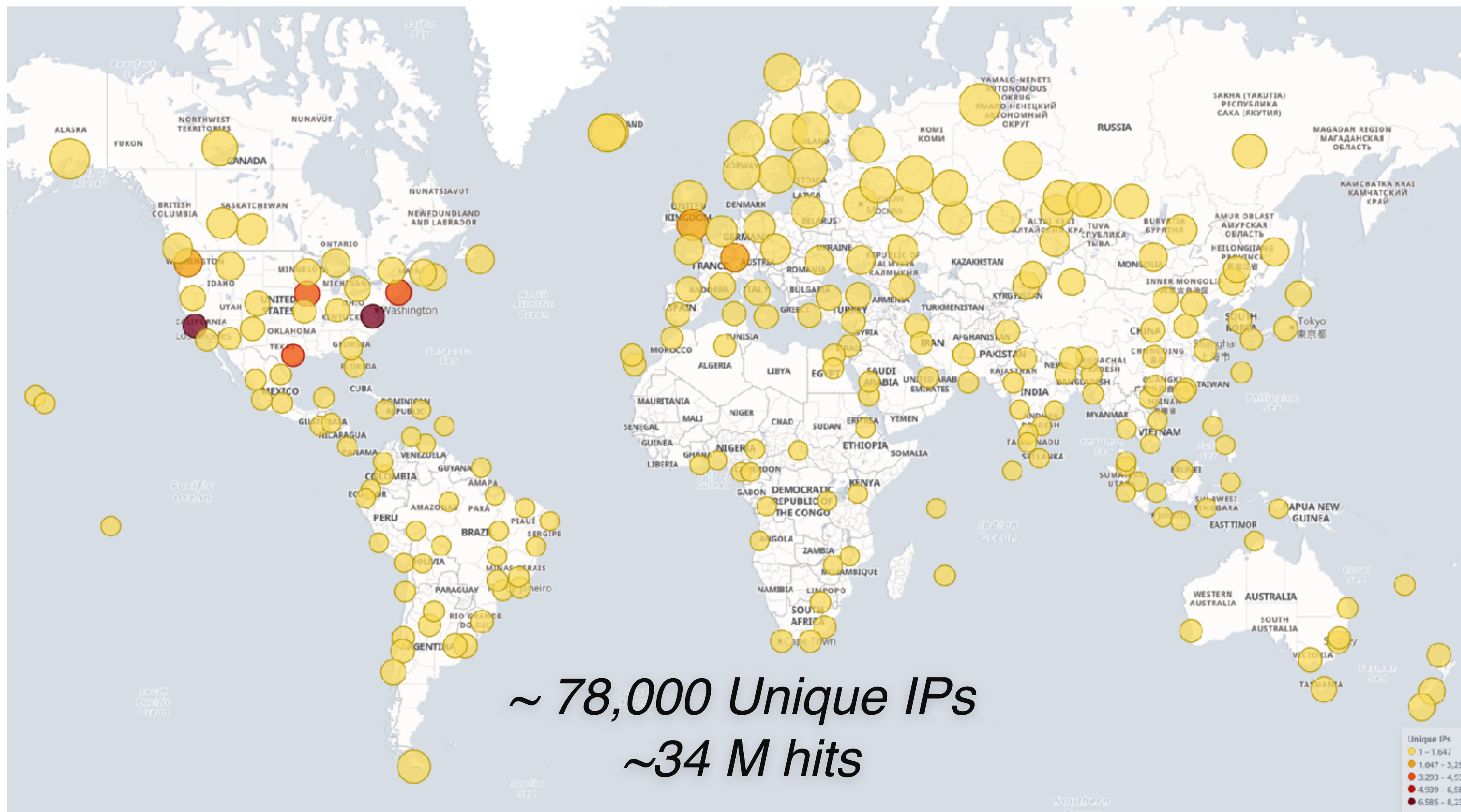


Download (local analysis)

October 2023 Metrics

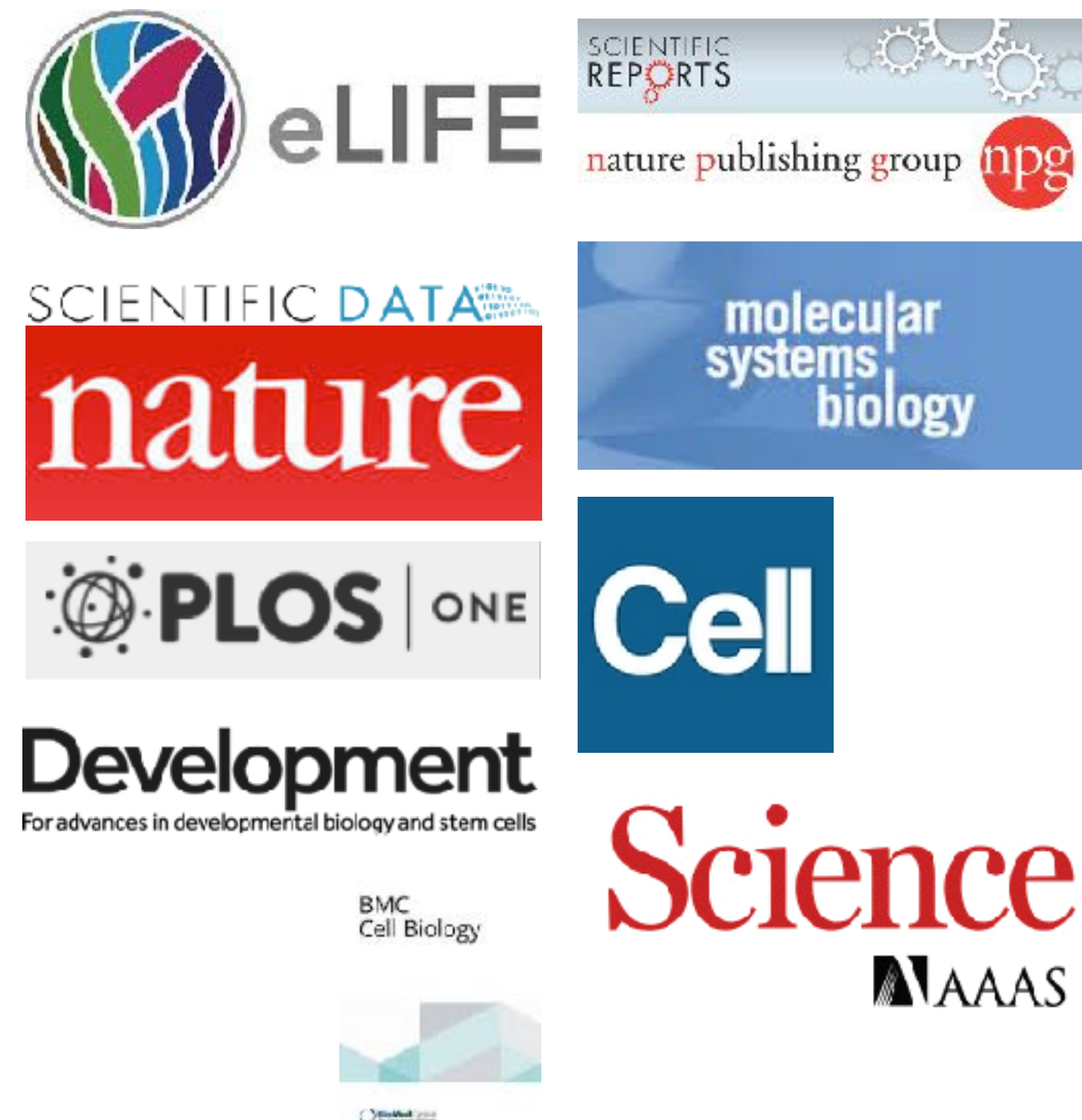
Raw data size	385 TB
Image files	38 M
5D Images	14 M
2D Planes	118 M
Organisms	71
Genes	89 K
Antibodies	12 K
Compounds	40 K

Organism	NCBITaxon https://www.ncbi.nlm.nih.gov/taxonomy
Study Type	Experimental Factor Ontology (EFO) https://www.ebi.ac.uk/efo/
Screen Type (HCS)	Experimental Factor Ontology (EFO) https://www.ebi.ac.uk/efo/
Screen Technology Type (HCS)	Experimental Factor Ontology (EFO) https://www.ebi.ac.uk/efo/
Library Type (HCS)	Experimental Factor Ontology (EFO) https://www.ebi.ac.uk/efo/
Protocol	Experimental Factor Ontology (EFO) https://www.ebi.ac.uk/efo/
Imaging Method	Biological Imaging Methods Ontology (FBbi) https://www.ebi.ac.uk/ols/ontologies/fbbi
Phenotype	Cellular Microscopy Phenotype Ontology (CMPO) https://www.ebi.ac.uk/cmipo/
Clinical/Pathology	SNOMED CT https://bioportal.bioontology.org/ontologies/
Compounds	PubChem https://pubchem.ncbi.nlm.nih.gov/



>100 cross-published studies

**cross-referenced via
accessions and DOIs**



A high-content RNAi screen reveals multiple roles for long noncoding...


Data availability


A reporting summary for this article is available as a [Supplementary Information file](#). Sequencing data are available in the ArrayExpress database (<http://www.ebi.ac.uk/arrayexpress>) with the accession codes [E-MTAB-7432](#) (RNA-seq), [E-MTAB-7418](#) (CHART-seq) and [E-MTAB-7419](#) (CUT&RUN). The imaging data have been submitted to the Image Data Resource (<https://idr.openmicroscopy.org>) under IDR accession number [idr0056](#). The source data

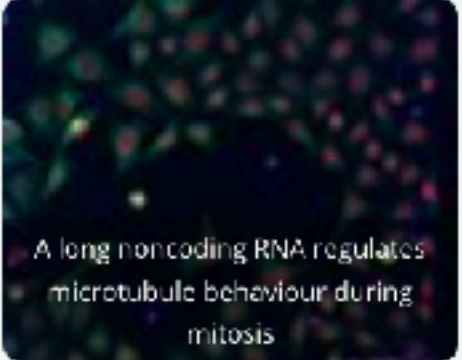
IDR CELL - IDR ISSUE - IDR ABOUT SUBMISSIONS

Search by: Name (IDR number)

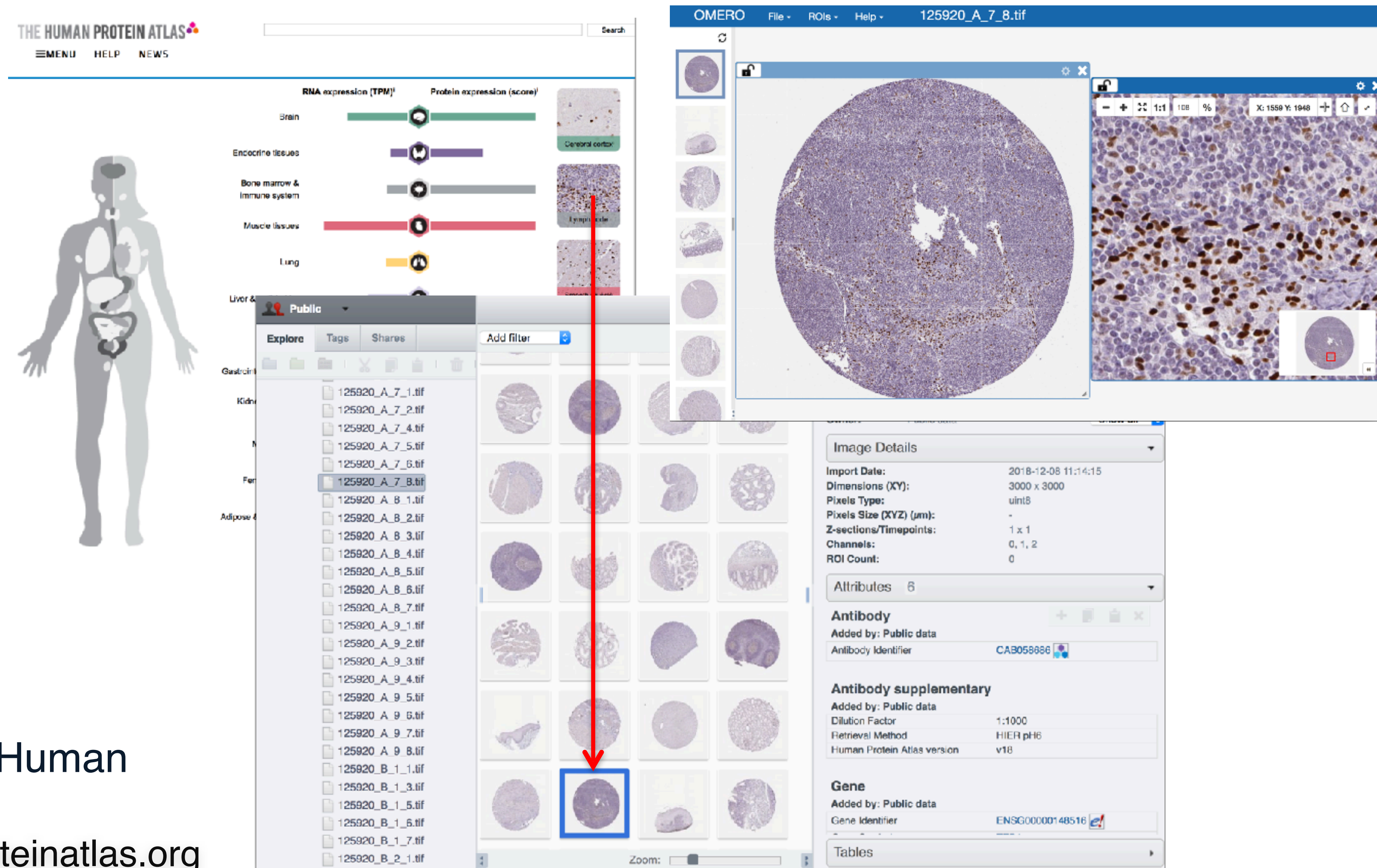
Found 3 studies with Name: **idr0056**

idr0056C Stojic L et al.  A long noncoding RNA regulates microtubule behaviour during mitosis

idr0056B Stojic L et al.  A long noncoding RNA regulates microtubule behaviour during mitosis

idr0056A Stojic L et al.  A long noncoding RNA regulates microtubule behaviour during mitosis

<https://idr.openmicroscopy.org/about/studies.html>



The screenshot displays two main interfaces: The Human Protein Atlas and OMERO.

The Human Protein Atlas: The top section shows RNA expression (TPM) and Protein expression (score) for various tissues. A human silhouette on the left highlights the location of the selected tissue. The bottom section shows a list of files, with '125920_A_7_8.tif' selected. A red arrow points from this file to the OMERO interface.

OMERO: The main window shows a large circular image of a tissue section. A zoomed-in view of a specific region is shown on the right. The bottom right panel displays 'Image Details' and 'Antibody' information.

Image Details:

- Import Date: 2018-12-08 11:14:15
- Dimensions (XY): 3000 x 3000
- Pixels Type: uint8
- Pixels Size (XYZ) (µm): -
- Z-sections/Timepoints: 1 x 1
- Channels: 0, 1, 2
- ROI Count: 0

Antibody:

- Added by: Public data
- Antibody Identifier: CAB058886

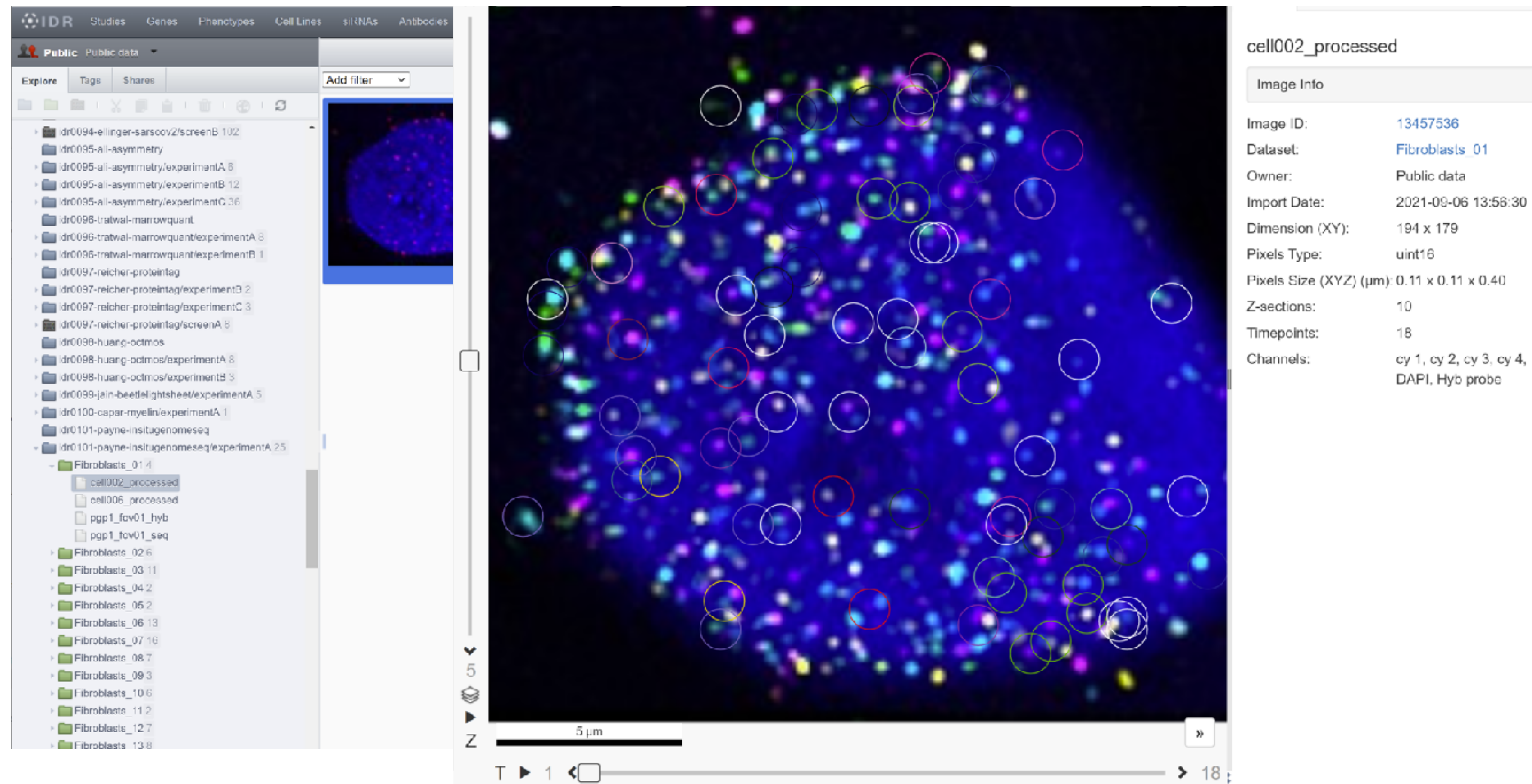
Antibody supplementary:

- Added by: Public data
- Dilution Factor: 1:1000
- Retrieval Method: HIER pH6
- Human Protein Atlas version: v18

Gene:

- Added by: Public data
- Gene Identifier: ENSG00000148516

Tissue Data: Human
Protein Atlas
<https://www.proteinatlas.org>



In Situ Sequencing - Linking Multimodal Metadata
 idr0101, Payne et al *Science* DOI:10.17867/10000169

bulk_annotations

Download as CSV: [Whole Table](#)

Show current page as: [CSV](#) | [JSON](#)

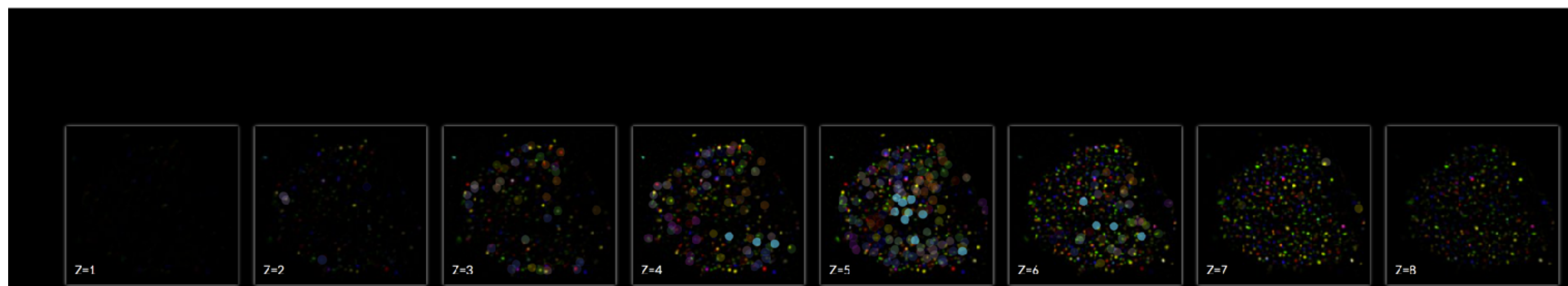
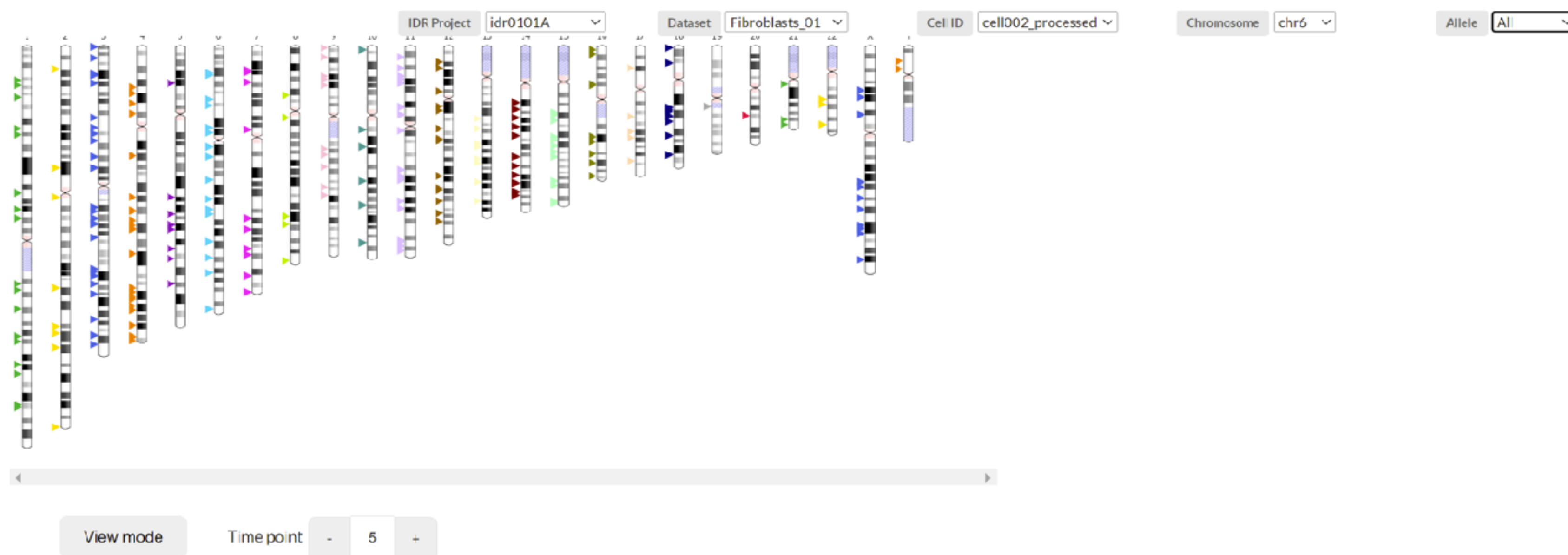
To filter rows you can use a query based on named columns. For example, to filter for rows where **shape** is greater than **6609251** add [?query=shape>6609251](#) to the URL.

For a more complex example, try [?query=\(shape>6609251\)&\(shape<6609254\)](#)

Table rows: 301.

Roi	shape	cell_id	fov	fov_cell	amp_ind	x_um	y_um	z_um	region_size	hg38_chr	hg38_pos	umi_ro	purity_score	umi_seq	
2363501	6609251	1	1	2	6	15.2752294921875	19.9336328125	1.5	6	1	194631781	133144213232111000	0.619711344073634	TTGTATTAGTTTATGAATGCTGCCA	1331
2363501	6609252	1	1	2	11	13.7585400390625	17.2252587890625	2.1	2	1	150295182	131323132424211000	0.833464665274033	AGGTAACAGCCGCCGGTGAAGCCCT	1313
2363501	6609253	1	1	2	31	14.950224609375	17.116923828125	1.5	3	1	225100477	121224444112341000	1.41730804431887	CATTGAGAATGCTAGTTCGTATTCA	1214
2363501	6609254	1	1	2	53	4.550068359375	12.133515625	1.8	3	1	159490134	134342412243342000	1.9908484714265902	AAGGTTGCATAGAGAAAGGTTACCT	1243
2363501	6609255	1	1	2	78	5.3084130859375	12.56685546875	1.8	3	1	23787304	132213213124423000	1.1026393293151202	GTATTAGTTTTGGTGTAGTATGCCA	1322
2363501	6609256	1	1	2	232	13.650205078125	15.816904296875	1.5	4	1	153996406	241442114442434000	2.32473562719153	CTACGGATTATATGTCTTCTTTCCT	2414
2363501	6609257	1	1	2	389	13.3252001953125	18.63361328125	2.4	4	1	173788354	224242441214242000	2.04123888148904	ATAGTTGAGGATCGAGCGGGGGTAT	2113
2363501	6609258	1	1	2	440	2.2750341796875	14.083544921875	1.5	2	1	201029547	233331413324421000	1.45461949740511	TGGACGATCGAGGGTACTGGTGCCA	2313
2363501	6609259	1	1	2	478	4.116728515625	13.3252001953125	1.8	1	1	35436829	243342432343222000	2.10121851879784	CGTGCGTGTTTGATTAGGTTTTCT	2433
2363501	6609260	1	1	2	673	4.3333984375	13.650205078125	1.5	4	1	27082504	333423423413433000	2.12571952800988	TTAGGGTTGATGGTACTGTTGCCA	3334
2363501	6609261	1	1	2	705	4.4417333984375	15.816904296875	2.1	2	1	92374532	312144232424141000	1.74120631396678	GTGTATACTATTTTCATCTGTGTCA	3121
2363501	6609262	1	1	2	780	5.3084130859375	13.866875	1.2	5	1	104368084	324221333321412000	2.53998829881878	TTGAGTAAAGTATCCGTCGTTGCCA	3244
2363501	6609263	1	1	2	785	5.7417529296875	14.083544921875	1.8	6	1	52747838	333343312121144000	2.47414362805048	ATTTCGTGCTTGTAGGTGCGGTCCT	3333
2363501	6609264	1	1	2	857	5.5250830078125	15.383564453125	1.8	2	1	178366318	333341322341142000	1.27093181216116	TAAGTAGGCCGTGAGACGTAGTCCT	3334
2363501	6609265	1	1	2	993	5.0917431640625	13.216865234375	1.5	2	1	112059828	433212413342332000	1.05738785313283	TGCAATTTTGAGTTGGTGGATGCCA	4332
2363501	6609266	1	1	2	1081	3.3583837890625	11.916845703125	1.2	5	1	57737183	414422212422322000	0.958035105708203	AGCCATGCCCTTTTATTCATCCCT	4143
2363501	6609267	1	1	2	1083	3.03337890625	14.950224609375	1.8	2	1	226248521	414234421211223000	1.33164034014242	GTTGGAAAGTAGATTCGAAAAGTAT	4142
2363502	6609268	1	1	2	35	13.7585400390625	6.6084326171875	1.8	2	2	11330392	124244422331142000	2.9277222459427406	ATTGTTTTAAAAGTCGAGTATTCCT	2422
2363502	6609269	1	1	2	351	17.6585986328125	10.83349609375	1.2	4	2	154125297	214132314424122000	1.5961370210682602	GCTCAATACCAGTGCGGATGGTCA	2141
2363502	6609270	1	1	2	613	10.183486328125	14.950224609375	1.8	1	2	79069289	222223234132422000	1.82441769480011	CTTGAACCCAAATTTTACTTTCA	2222
2363502	6609271	1	1	2	722	11.050224609375	17.6585986328125	1.8	2	2	210055247	214142413231142000	2.50048835734024	CTTACTCCCTTTATTTCCCGCTCCT	2222

Nucleome Browser - IDR Interaction Demo

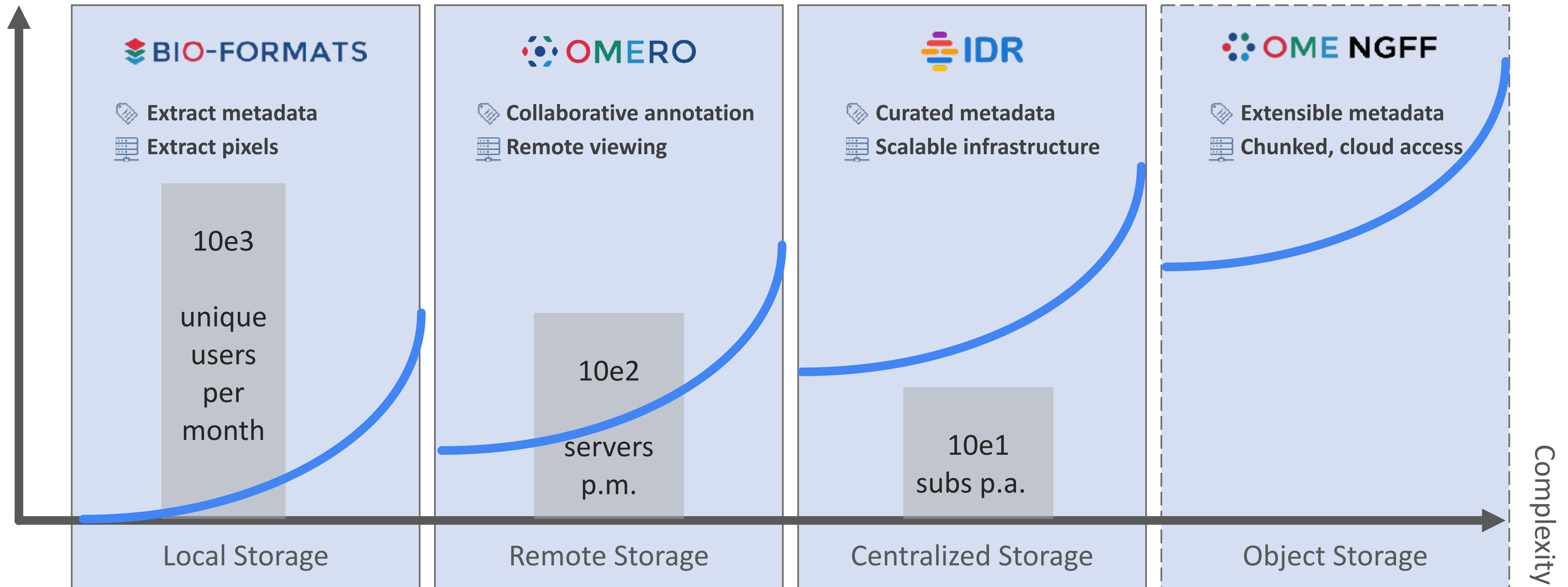


DEVOPS ++
CURATION ++



BioImage Archive

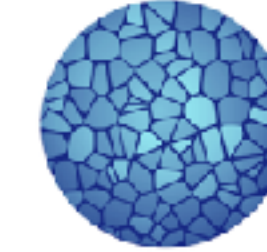
Cost



Imaging repositories



BioImage Archive

EMPIAR
Electron Microscopy Public Image ArchiveHUMAN
CELL
ATLAS

Upload

Download

OME-FILES
BIO-FORMATS
OMERO

Proprietary File Formats (PFF)

On-the-fly
translation

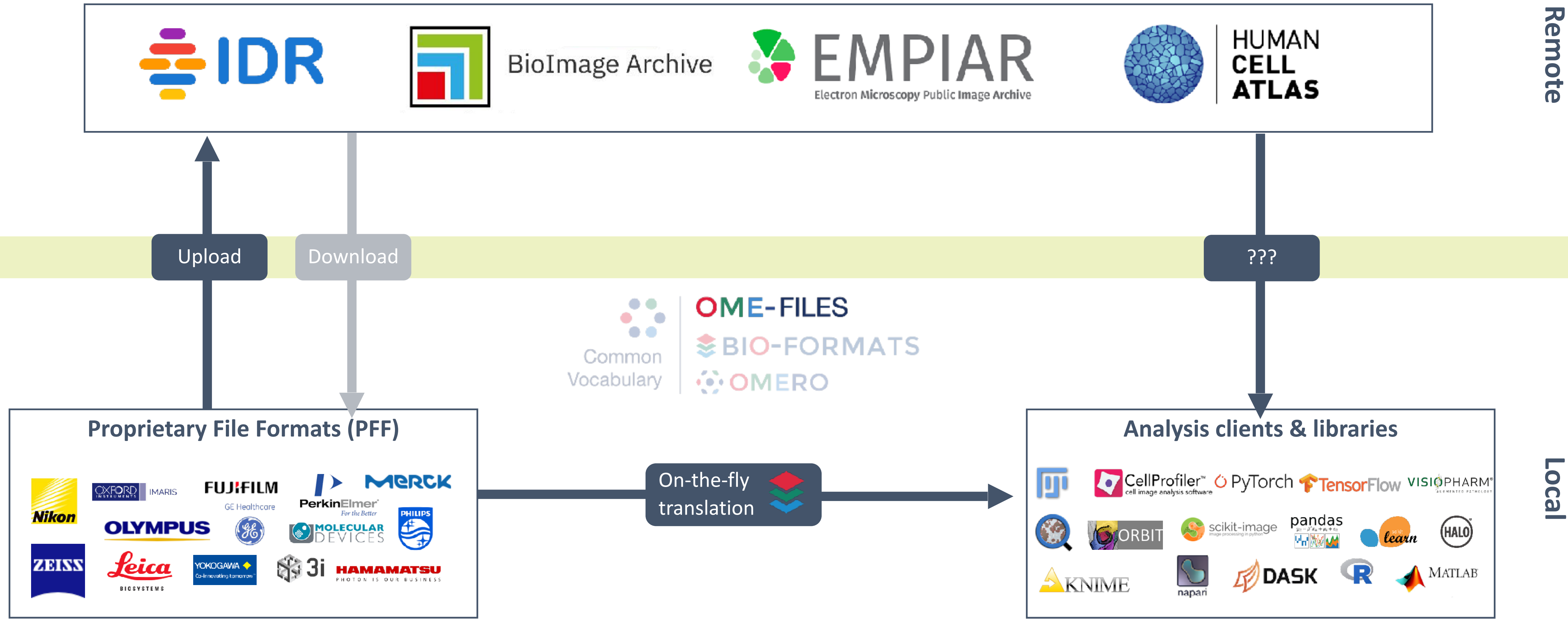
Analysis clients & libraries

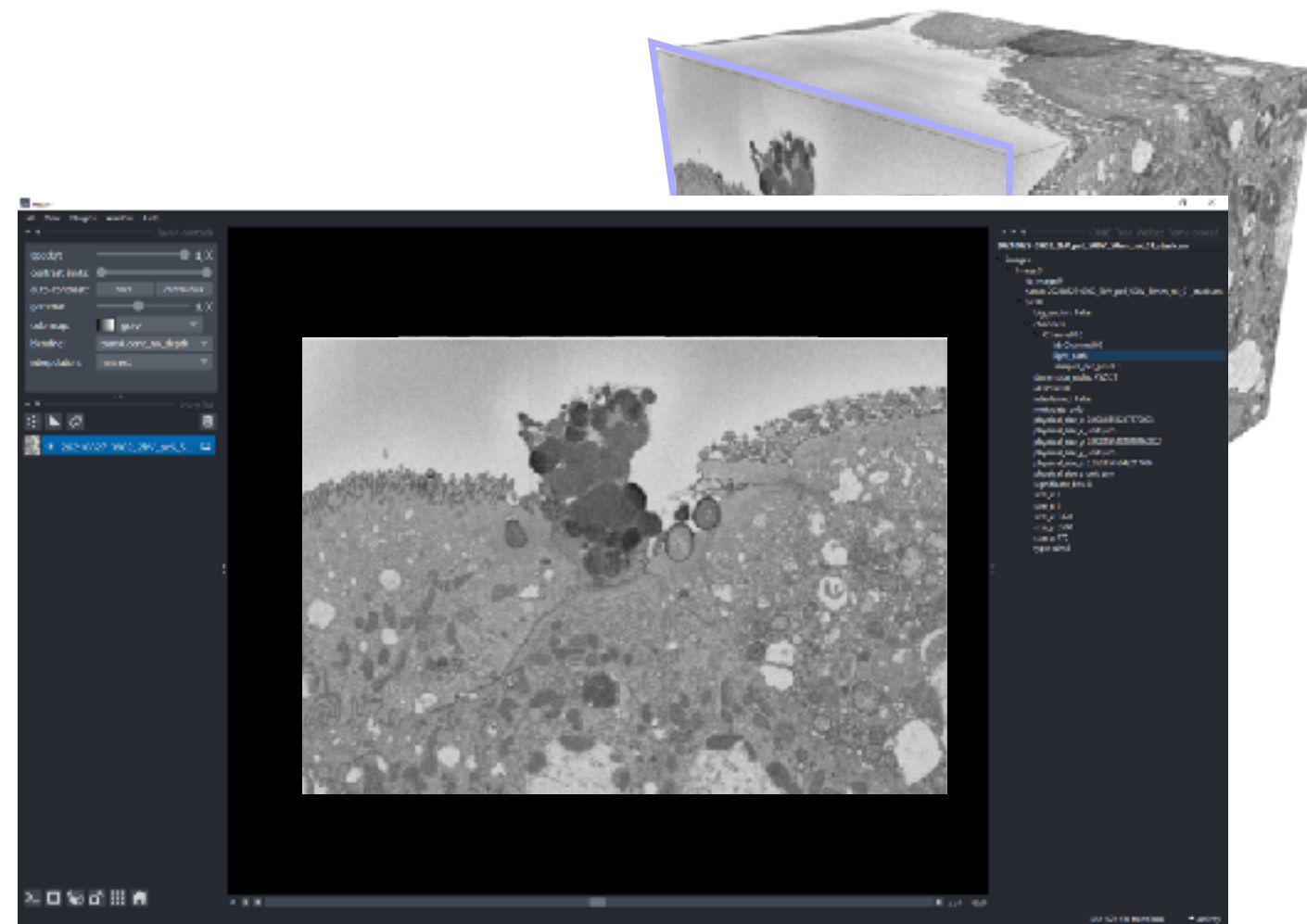


Remote

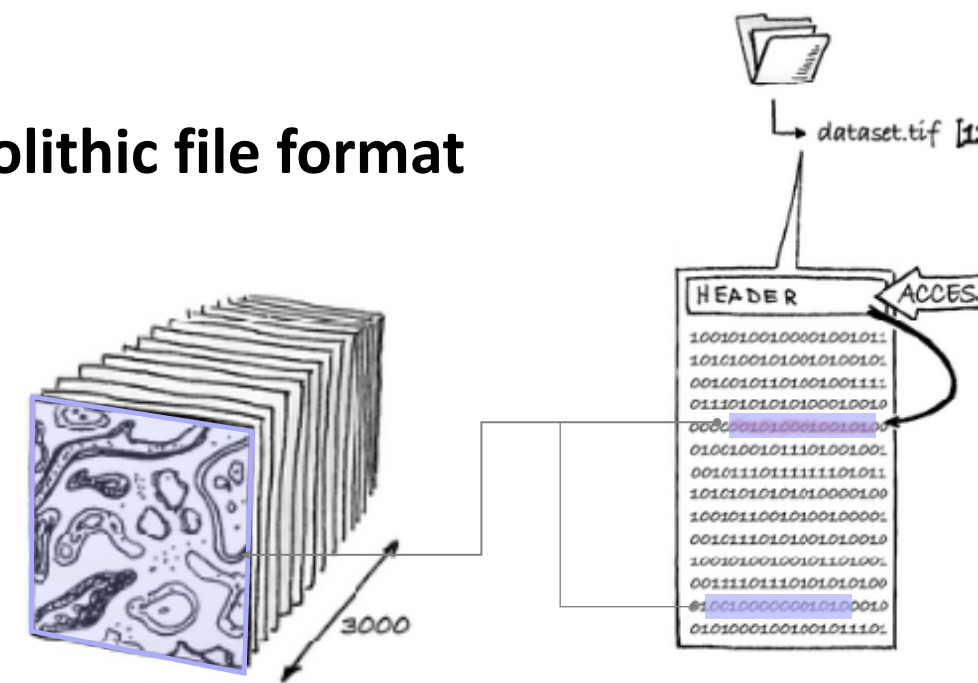
Local

Imaging repositories

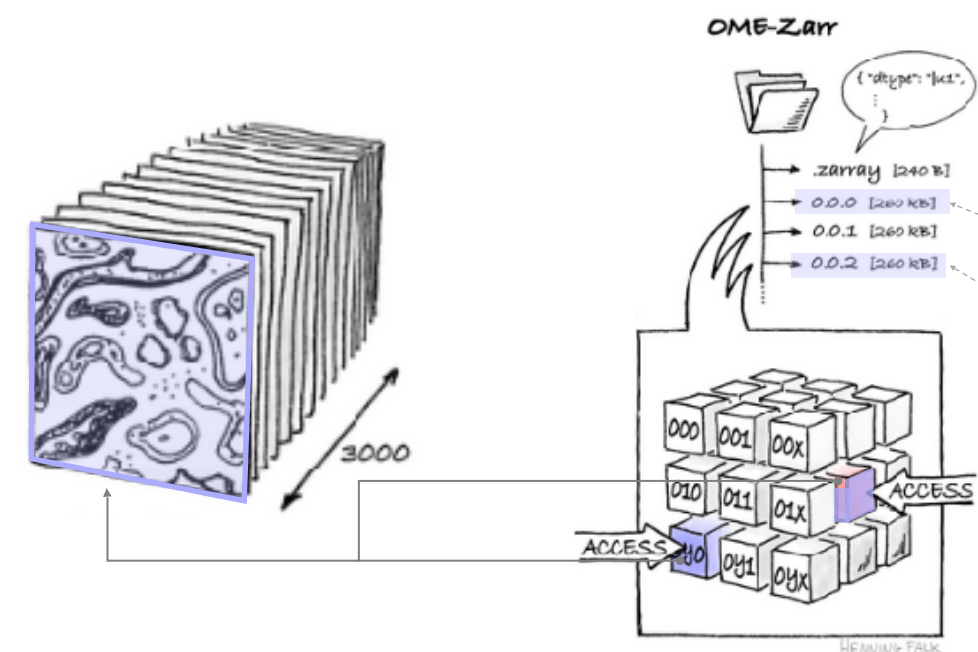




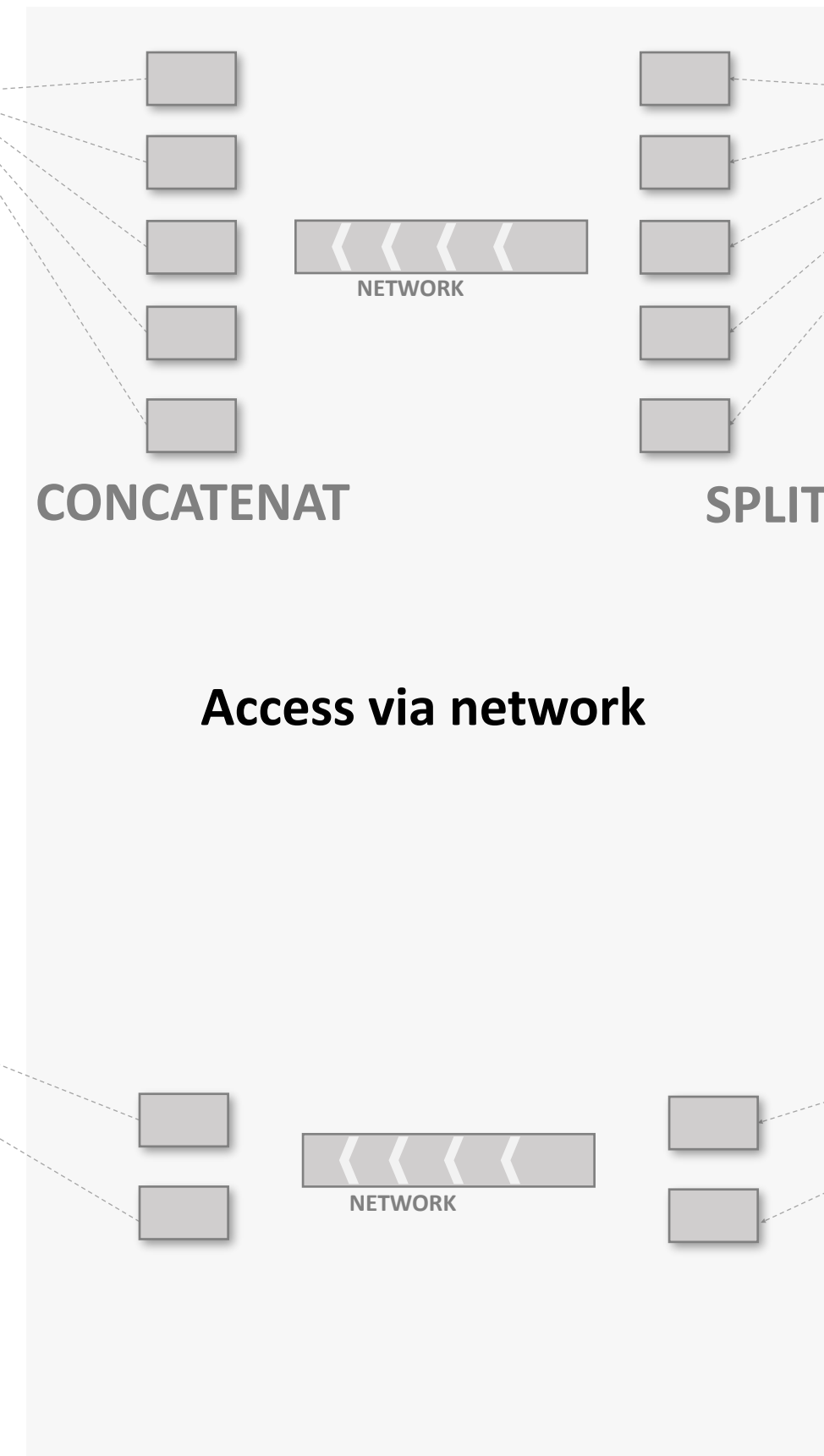
Monolithic file format



Local computer

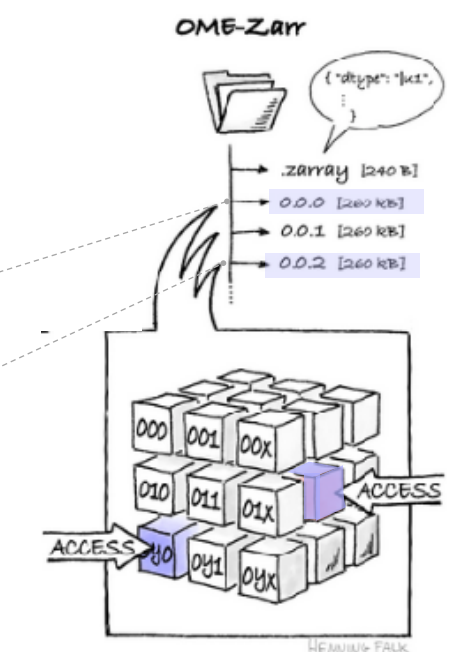


Chunkable file format



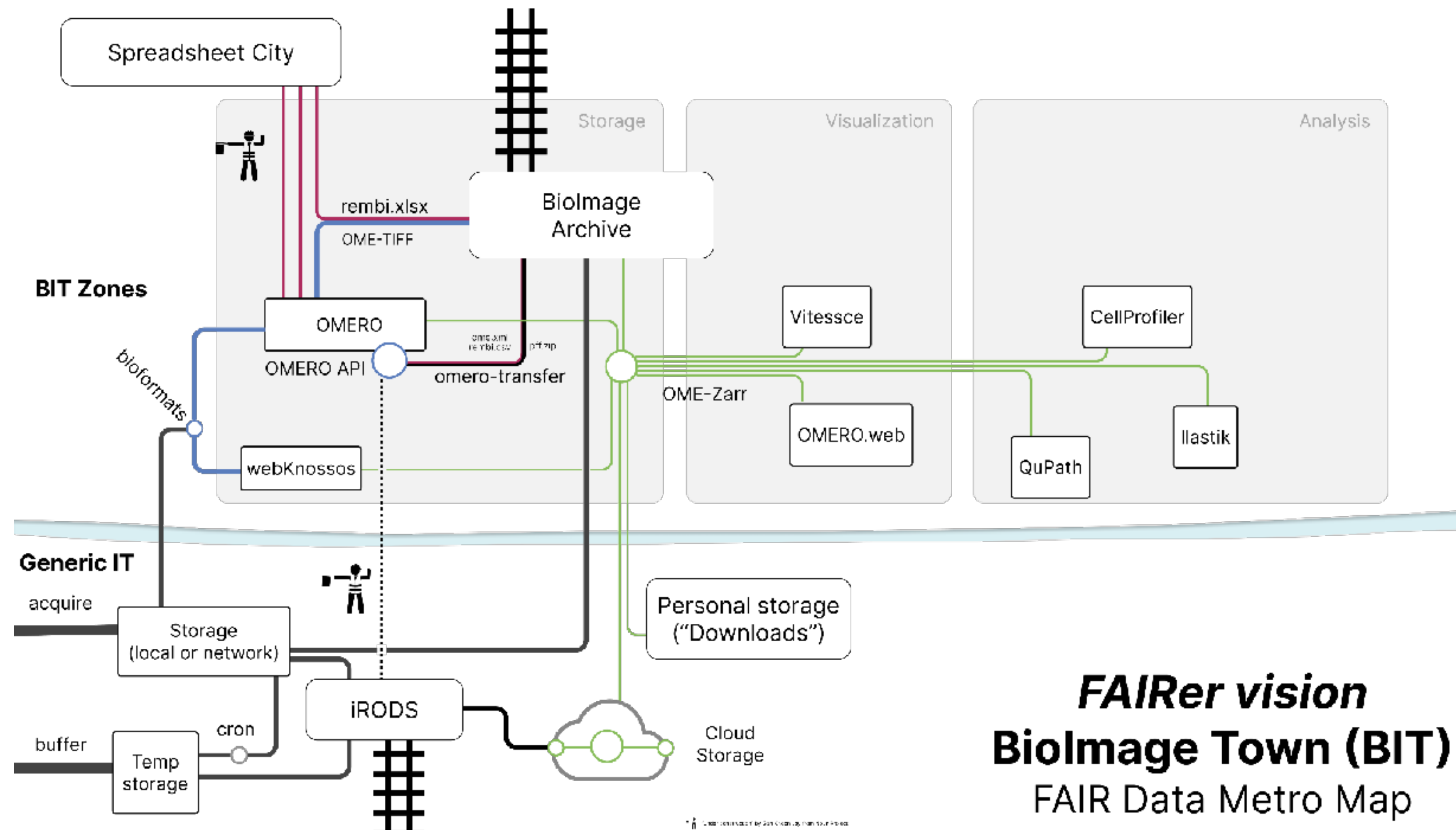
Access via network

External data storage



Moore et al. (2021). **OME-NGFF: a next-generation file format for expanding bioimaging data-access strategies.** *Nature methods* (2021). Published: 29 November 2021 DOI: [10.1038/s41592-021-01326-w](https://doi.org/10.1038/s41592-021-01326-w)

<https://bit.ly/citing-ome>



FAIRer vision
Biolmage Town (BIT)
 FAIR Data Metro Map



TECHNOLOGY FEATURE | 02 October 2023

How open-source software could finally get the world's microscopes speaking the same language

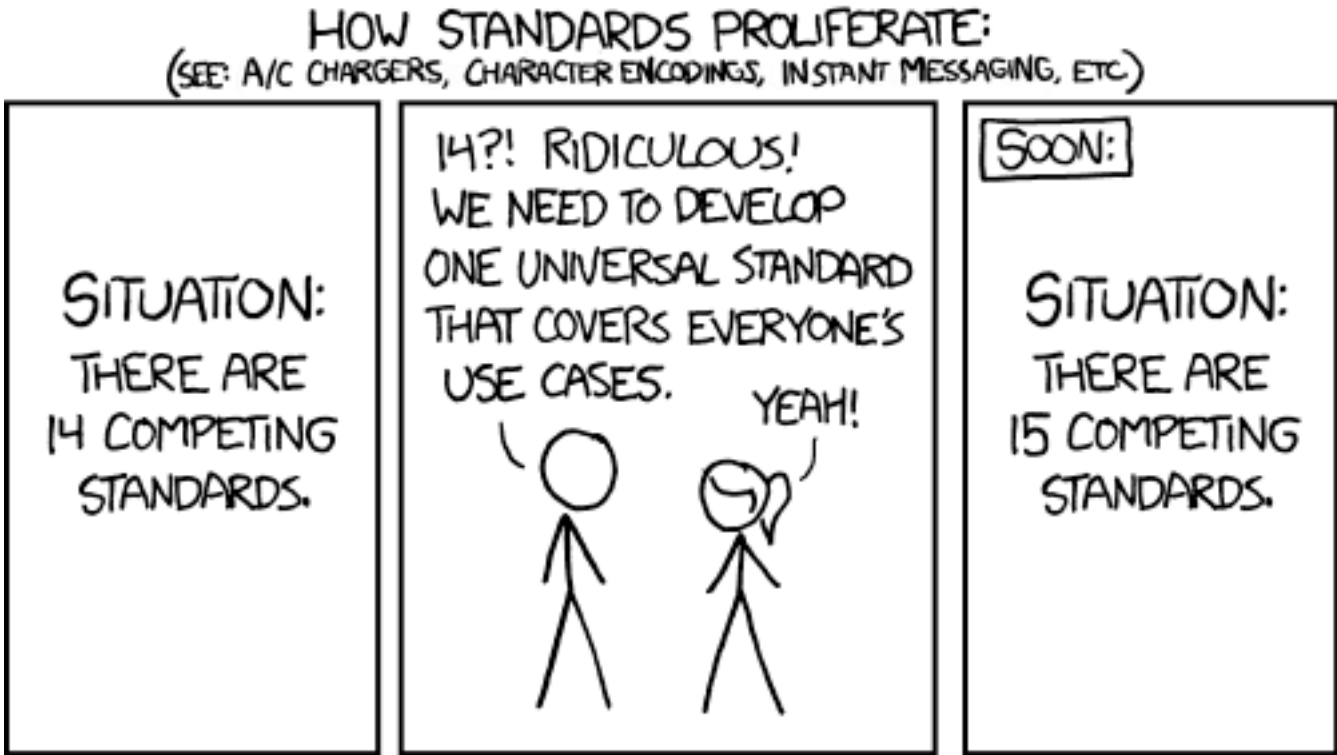
A plethora of standards mean shareable and verifiable microscopy data often get lost in translation. Biologists are working on a solution.

[Michael Brooks](#)

<https://www.nature.com/articles/d41586-023-03064-9>

<https://news.ycombinator.com/item?id=37737318>

Volume EM



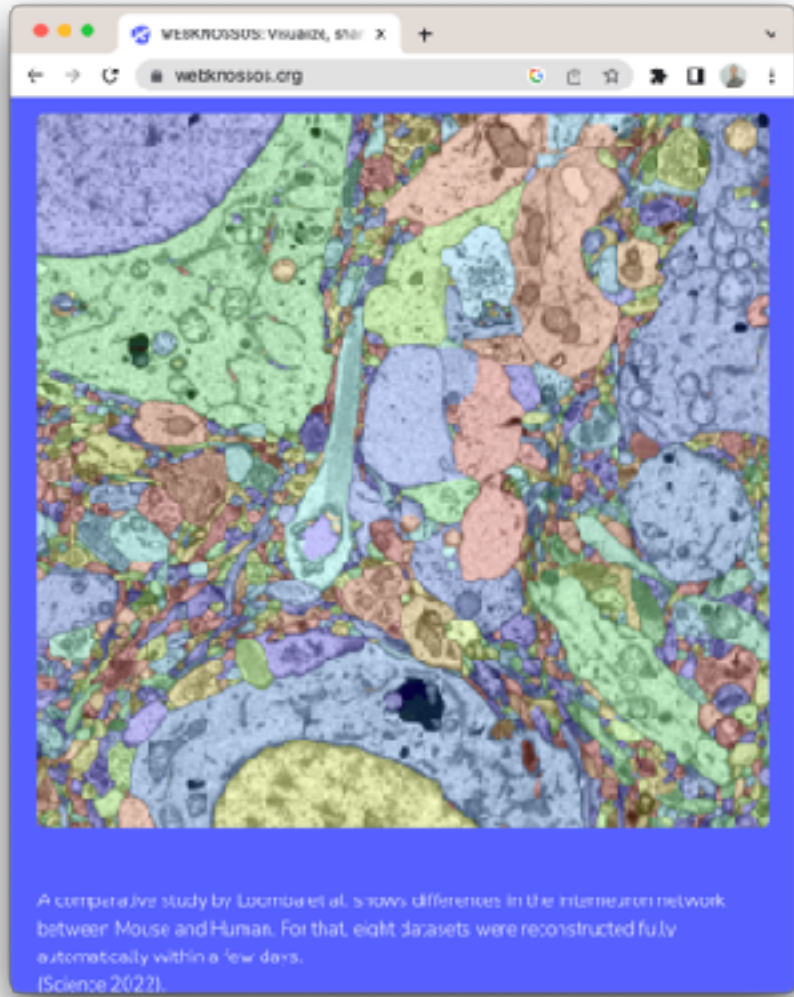
<https://xkcd.com/927/>

N5



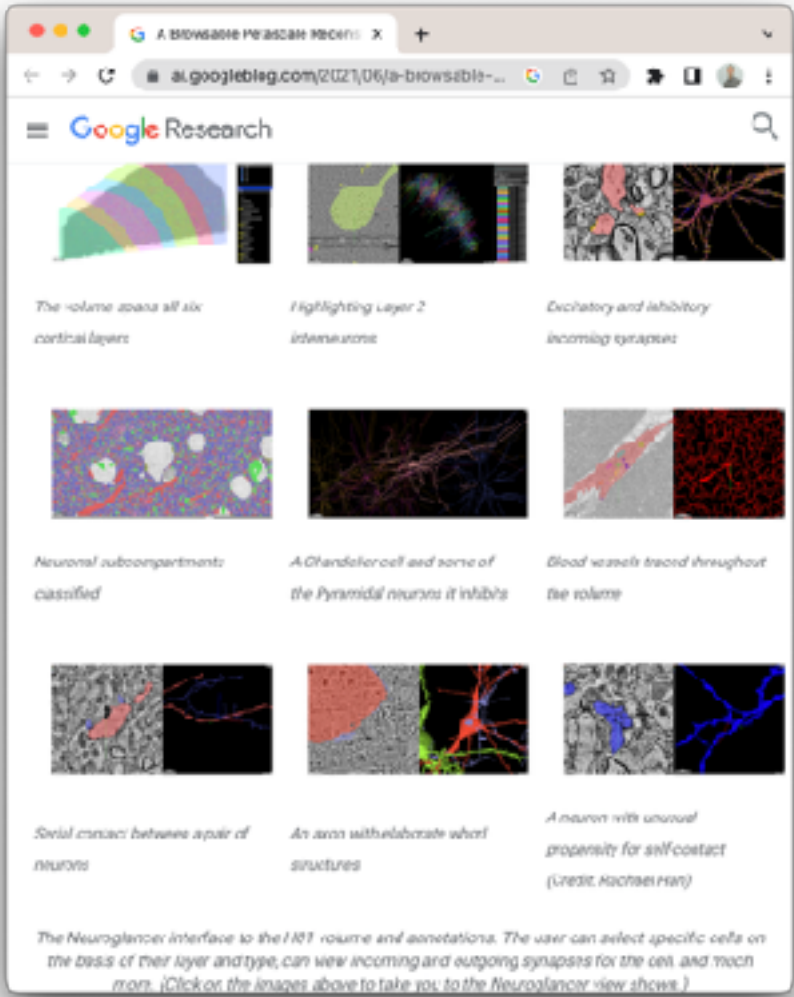
<https://openorganelle.janelia.org/datasets>

WKW



<https://webknossos.org/>

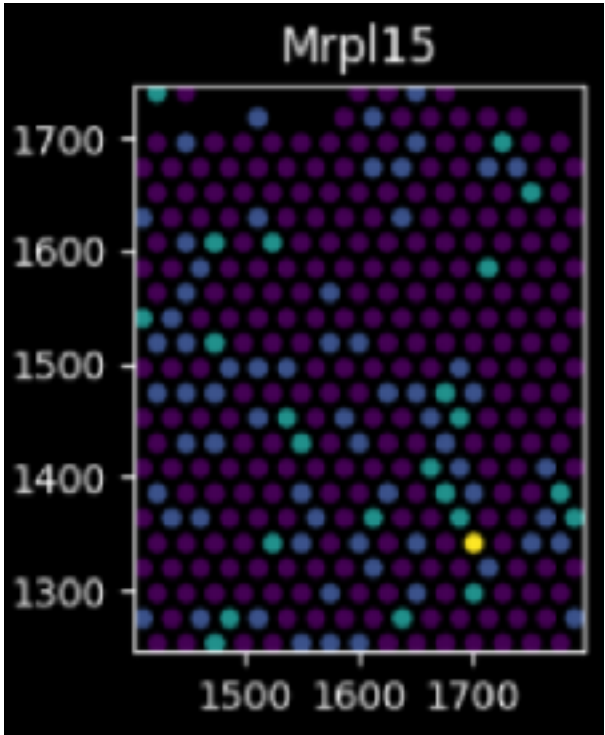
Precomputed



<https://github.com/google/neuroglancer>


```
-- 152811
|-- 152811_manual_analysis_clustering_graphclust_clusters.csv
|-- 152811_manual_analysis_diffexp_graphclust_differential_expression.csv
152811_manual_analysis_diffexp_kmeans_10_clusters_differential_expression.csv
|-- 152811_manual_analysis_pca_10_components_components.csv
|-- 152811_manual_analysis_pca_10_components_dispersion.csv
|-- 152811_manual_analysis_pca_10_components_features_selected.csv
|-- 152811_manual_analysis_pca_10_components_projection.csv
|-- 152811_manual_analysis_pca_10_components_variance.csv
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|-- 152811_manual_analysis_umap_2_components_projection.csv
|-- 152811_manual.cloupe
|-- 152811_manual_filtered_feature_bc_matrix_barcode.tsv.gz
|-- 152811_manual_filtered_feature_bc_matrix_features.tsv.gz
|-- 152811_manual_filtered_feature_bc_matrix_matrix.mtx.gz
|-- 152811_manual_metric_summary.csv
|-- 152811_manual_molecule_info.h5
|-- 152811_manual_raw_feature_bc_matrix_barcodes.tsv.gz
|-- 152811_manual_raw_feature_bc_matrix_features.tsv.gz
|-- 152811_manual_raw_feature_bc_matrix.h5
|-- 152811_manual_raw_feature_bc_matrix_matrix.mtx.gz
152811_manual_web_summary.html
filtered_feature_bc_matrix.h5
spatial
|-- aligned_fiducials.jpg
|-- detected_tissue_image.jpg
|-- scalefactors_json.json
|-- tissue_hires_image.png
|-- tissue_lowres_image.png
|-- tissue_positions_list.csv
hires_images
152806_20x_highest_res_image.jpg
20201207_LocationModelLinearDependentWMultiExperiment_19clusters_20952locations_
19980genes
|-- adata_visium_joint_obs_table.csv
|-- adata_visium_joint_obs_table.xlsx
|-- sp.h5ad
|-- W_cell_density.csv
|-- W_cell_density_q05.csv
|-- W_mRNA_count.csv
|-- W_mRNA_count_q05.csv
```

Spatial Transcriptomics



```
(base) -bash-4.2$ h5ls filtered_feature_bc_matrix.h5/matrix
barcodes      Dataset {3871}
data          Dataset {4665604/Inf}
features      Group
indices       Dataset {4665604/Inf}
indptr        Dataset {3872/Inf}
shape         Dataset {2/Inf}
```

```
{
  "spot_diameter_fullres": 71.15992000000001,
  "tissue_hires_scalef": 0.13528138,
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  "tissue_lowres_scalef": 0.040584415
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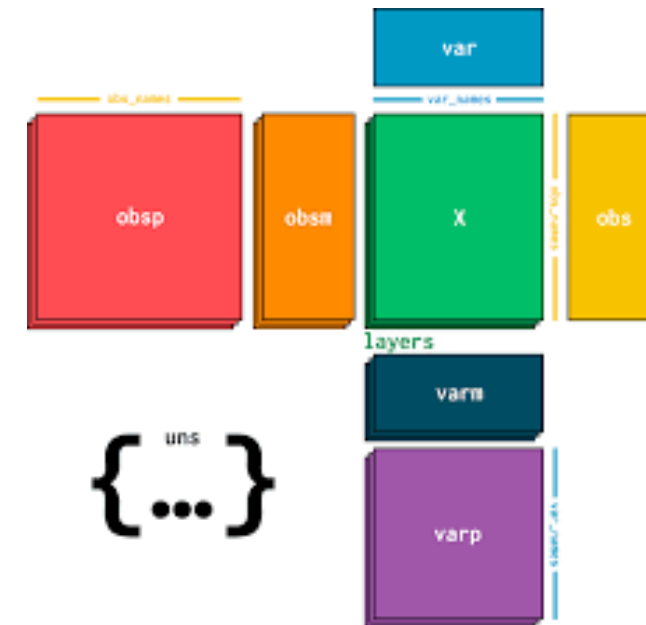
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ATTAAAGCGGACGAGC-1,0,0,2,4044,1338
GATAAGGGACGATTAG-1,0,1,3,4139,1393
GTGCAAATCACCAATA-1,0,0,4,4044,1448
TGTTGGCTGGCGGAAG-1,0,1,5,4140,1502
GCATCCTCTCCTATTA-1,0,0,6,4045,1557
GCGAGGGACTGCTAGA-1,0,1,7,4140,1612
TGGTACCGGCACAGCC-1,0,0,8,4045,1667
GCGCGTTTAAATCGTA-1,0,1,9,4140,1721
```

■ "raw" data ■ processed data

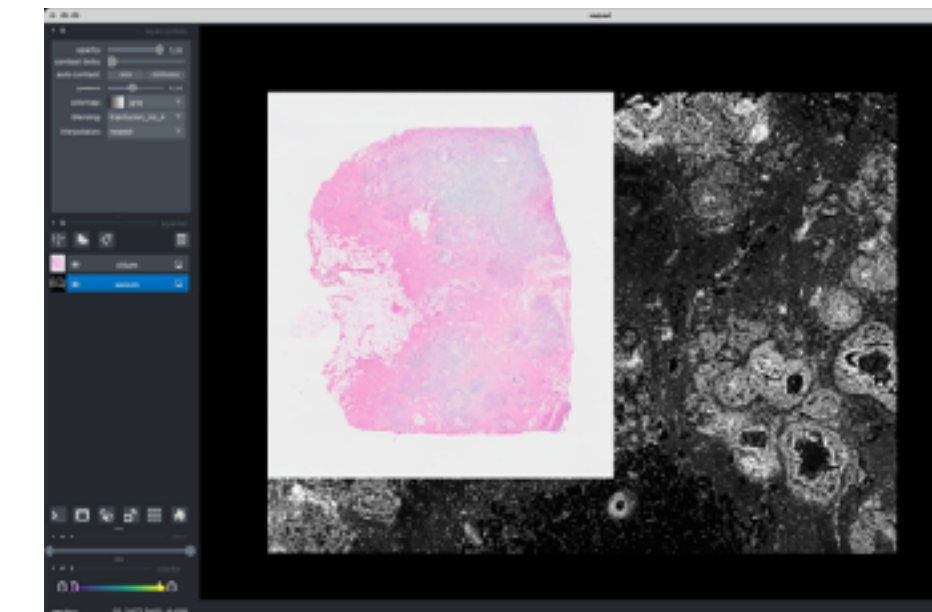
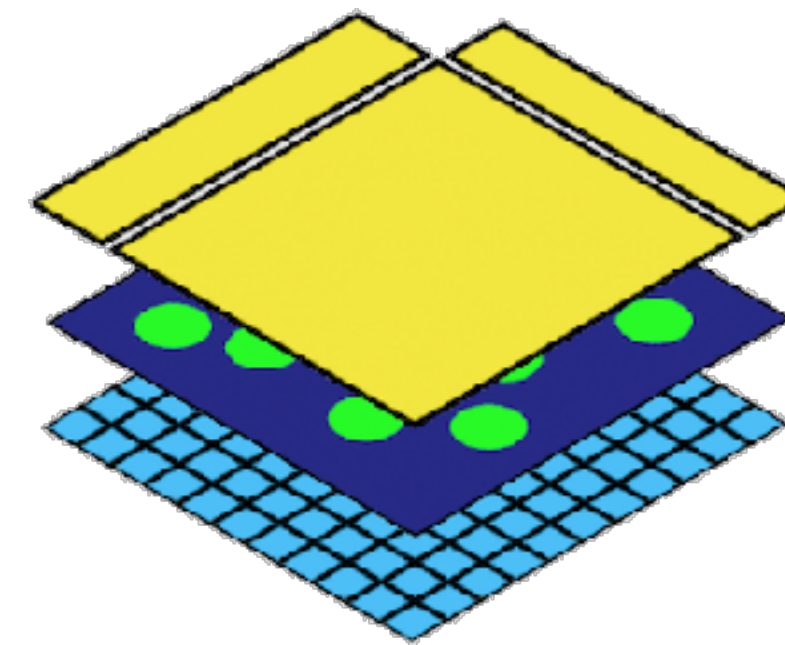
Slide courtesy: Luca Marconato (EMBL)

Single cell and
spatial omics data analysis

AnnData



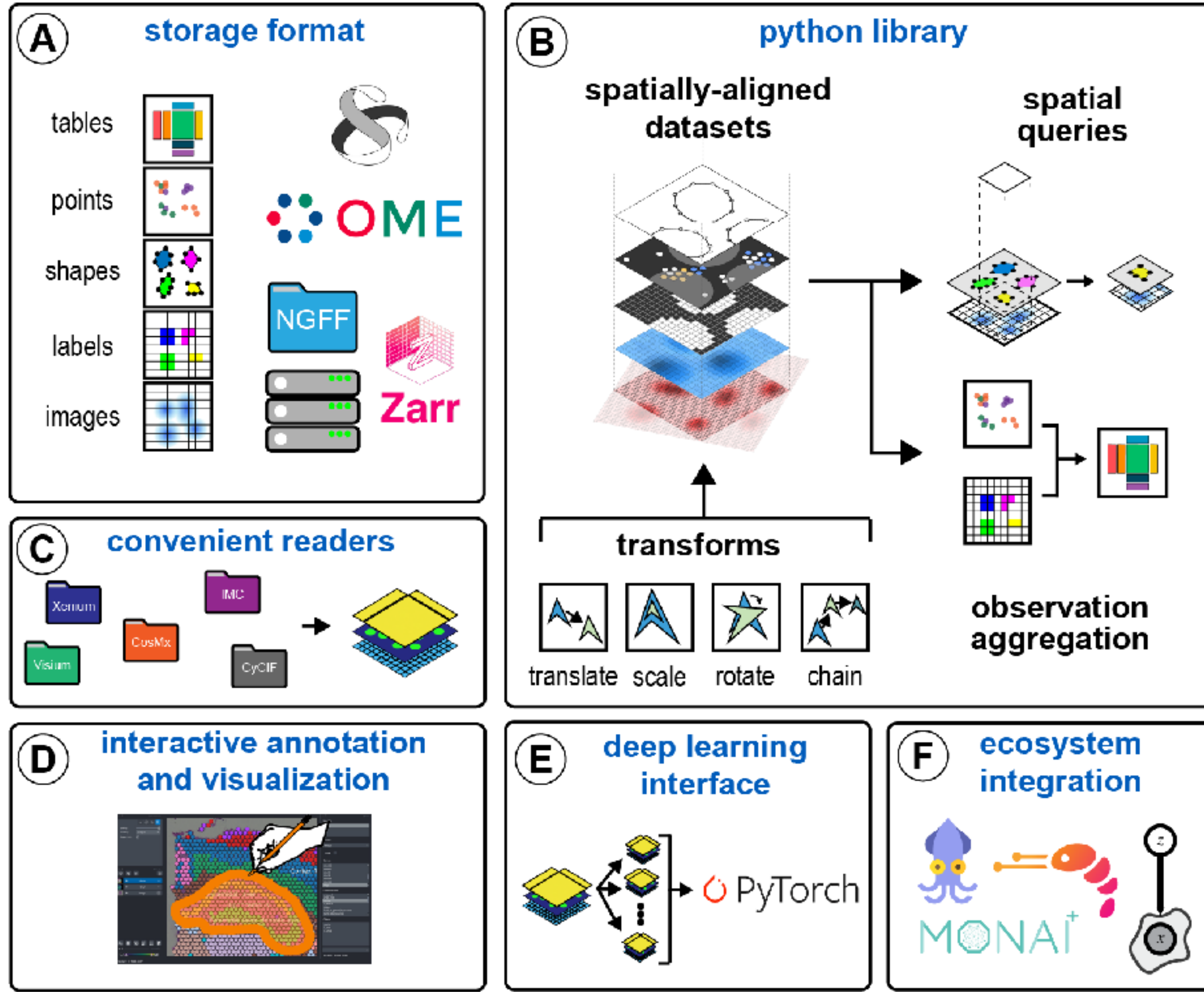
SpatialData



Interactive visualization
and annotation

Very large images, standard
cloud-native formats





```
import spatialdata as sd
from napari_spatialdata import Interactive

sdata = sd.SpatialData.read("spatialdata-sandbox/merfish/data.zarr")
print(sdata)

interactive = Interactive(sdata=sdata)
```



Slide courtesy: Luca Marconato (EMBL)

Consumers

Napari
CZI Core Funding



WebAtlas
HCA WSSS Extension through 2023

BIA
EBI Core Funding

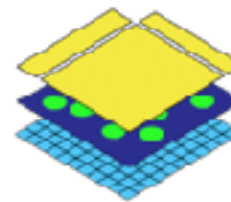


IDR
Wellcome into 2024




Formats Stack

SpatialData
CZI Single Cell - Data Insights 2023-2025




Languages: Javascript, Python, R

NGFF
*NFDI4BIOIMAGE 2023-2028
CZI EOSS5 2022-2024*



Languages: Java, Javascript, Python

Zarr
CZI EOSS4 2021-2024



Languages: C/C++, Java, Javascript, Julia, Python, R, Rust

Development



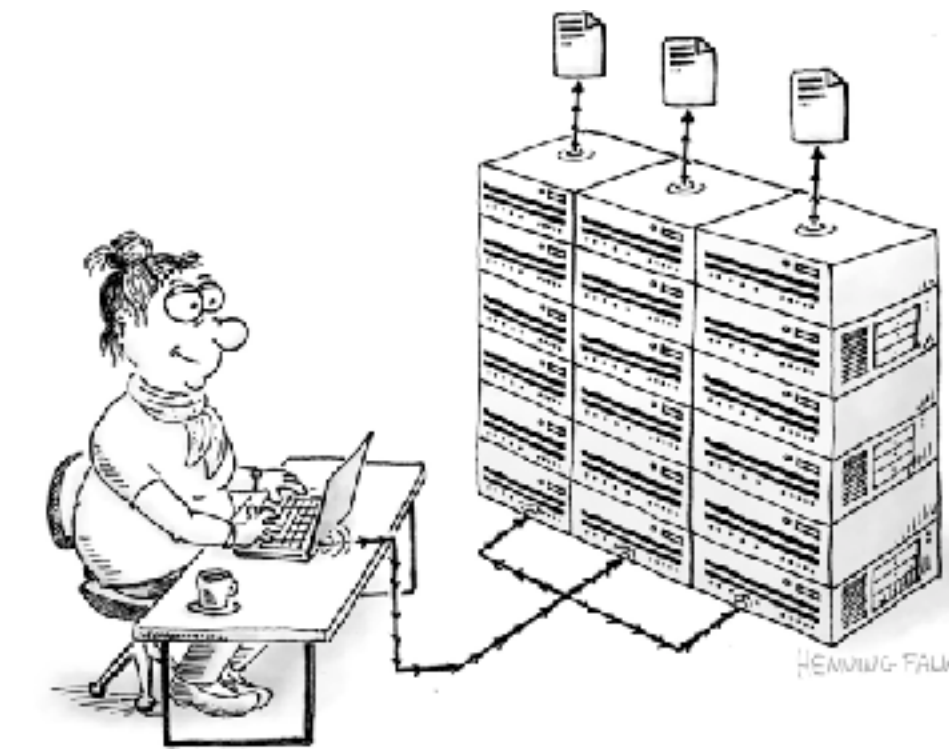








A brief history



"Bea computes" by Henning Falk, ©2022 NumFOCUS, is used under a CC BY 4.0 license.

<https://github.com/zarr-developers/zarr-illustrations-falk-2022#bea-computes>



NFDI 4
BIOIMAGE



- * OME.Perl
- * OMERO3
- * OMERO4
- * OMERO5



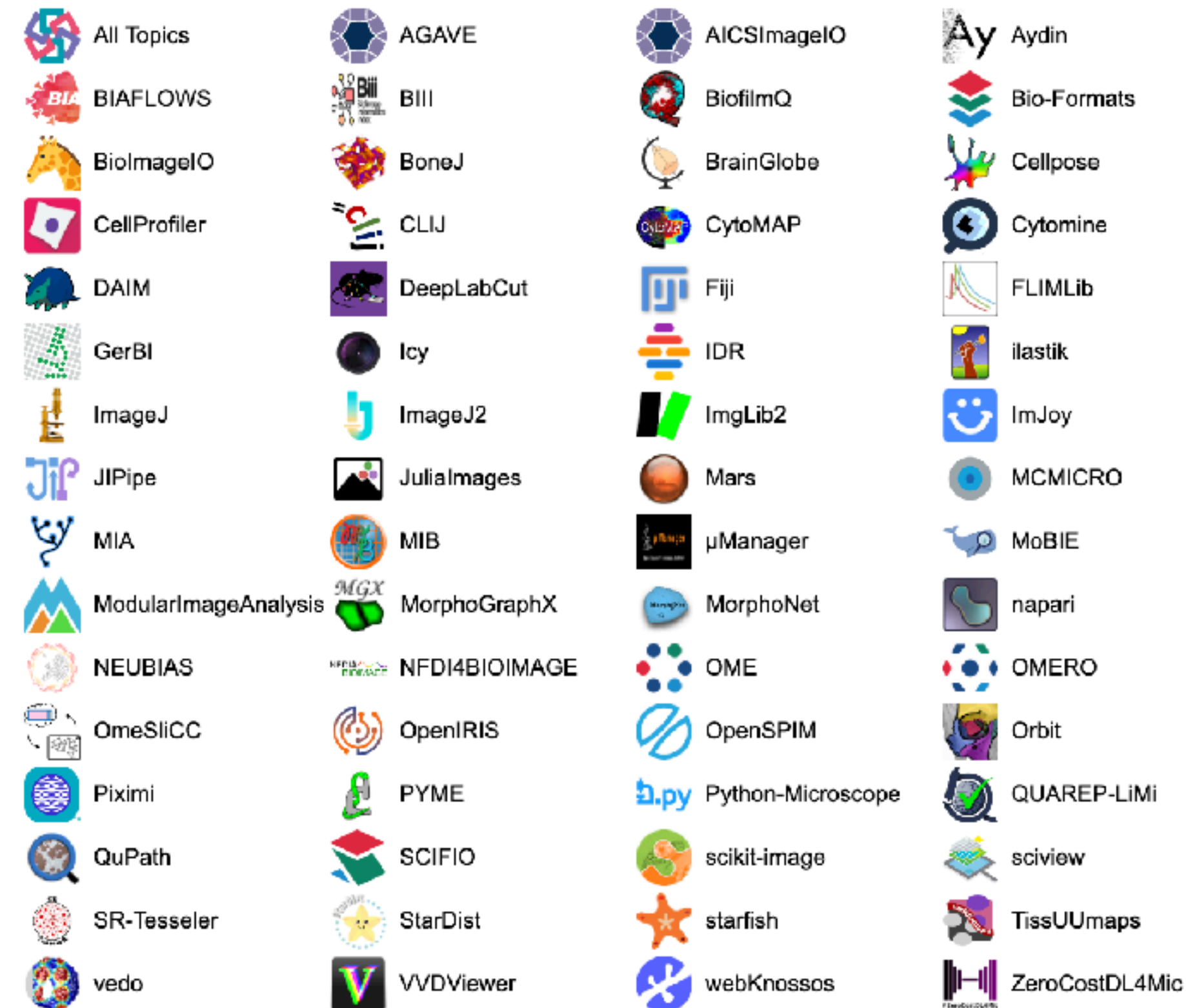
- * XML
- * TIFF
- * Zarr



- * ImageJ Macros
- * Library



Acknowledgments



openmicroscopy.org/about/#consortium

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In cooperation with



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