

Harmonizing the Generation and Pre-publication Stewardship of FAIR bioimage data

Contributors

Nikki Bialy [0000-0001-9681-9632](#) (1), Frank Alber [0000-0003-1981-8390](#) (2), Brenda Andrews [0000-0001-6427-6493](#) (3), Michael Angelo (4), Brian Beliveau [0000-0003-1314-3118](#) (5), Lacramioara Bintu [0000-0001-5443-6633](#) (4), Alistair Boettiger [0000-0002-3554-5196](#) (4), Ulrike Boehm [0000-0001-7471-2244](#) (6), Claire M. Brown [0000-0003-1622-663X](#) (7), Mahmoud Bukar Maina [0000-0002-7421-3813](#) (8), James J. Chambers [0000-0003-3883-8215](#) (9), Beth A. Cimini [0000-0001-9640-9318](#) (10), Kevin Eliceiri [0000-0001-8678-670X](#) (1, 11), Rachel Errington (12), Orestis Faklaris [0000-0001-5965-5405](#) (13), Nathalie Gaudreault [0000-0002-9220-5366](#) (14), Ronald N. Germain [0000-0003-1495-9143](#) (15), Wojtek Goscinski [0000-0001-6587-1016](#) (16), David Grunwald [0000-0001-9067-804X](#) (17), Michael Halter [0000-0002-1628-324X](#) (18), Dorit Hanein [0000-0002-6072-4946](#) (19), John W. Hickey [0000-0001-9961-7673](#) (20), Judith Lacoste [0000-0002-8783-8599](#) (21), Alex Laude [0000-0002-3853-1187](#) (22), Emma Lundberg (4, 23), Jian Ma [0000-0002-4202-5834](#) (24), Leonel Malacrida [0000-0001-6253-9229](#) (25), Josh Moore [0000-0003-4028-811X](#) (26), Glyn Nelson [0000-0002-1895-4772](#) (22), Elizabeth Kathleen Neumann [0000-0002-6078-3321](#) (27), Roland Nitschke [0000-0002-9397-8475](#) (28), Shuichi Onami [0000-0002-8255-1724](#) (29), Jaime A. Pimentel [0000-0001-8569-0466](#) (30), Anne L. Plant [0000-0002-8538-401X](#) (18), Andrea J. Radtke [0000-0003-4379-8967](#) (15), Bikash Sabata (31), Denis Schapiro [0000-0002-9391-5722](#) (32), Johannes Schöneberg [0000-0001-7083-1828](#) (33), Jeffrey M. Spraggins [0000-0001-9198-5498](#) (34), Damir Sudar [0000-0002-2510-7272](#) (35), Wouter-Michiel Adrien Maria Vierdag [0000-0003-1666-5421](#) (36), Niels Volkmann [0000-0003-1328-6426](#) (19), Carolina Wählby [0000-0002-4139-7003](#) (37), Siyuan (Steven) Wang [0000-0001-6550-4064](#) (38), Ziv Yaniv [0000-0003-0315-7727](#) (15) and Caterina Strambio-De-Castillia [0000-0002-1069-1816](#) (17)

-
- (1) Morgridge Institute for Research, Madison, USA.
 - (2) University of California Los Angeles, USA
 - (3) University of Toronto, Toronto Canada
 - (4) Stanford University, Palo Alto, USA
 - (5) University of Washington, Seattle, USA
 - (6) Carl Zeiss AG, Oberkochen, Germany
 - (7) McGill University, Montreal, Canada
 - (8) University of Sussex, Sussex, UK and Yobe State University, Nigeria

- (9) University of Massachusetts, Amherst, USA
- (10) Broad Institute of MIT and Harvard, Imaging Platform, Cambridge, USA
- (11) University of Wisconsin-Madison, Madison, USA.
- (12) Cardiff University, Cardiff, UK
- (13) Univ. Montpellier, CNRS, INSERM, Montpellier, France
- (14) Allen Institute for Cell Science, Seattle, USA
- (15) National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, USA
- (16) National Imaging Facility, Brisbane, Australia
- (17) UMass Chan Medical School, Worcester, USA
- (18) National Institute of Standards and Technology, Gaithersburg, USA
- (19) University of California, Santa Barbara, USA
- (20) Duke University, Durham, USA
- (21) MIA Cellavie Inc., Montreal, Canada
- (22) Newcastle University, Newcastle upon Tyne, UK
- (23) SciLifeLab, KTH Royal Institute of Technology, Stockholm, Sweden
- (24) Carnegie Mellon University, Pittsburgh, USA
- (25) Institut Pasteur de Montevideo, & Universidad de la República, Montevideo, Uruguay
- (26) German BioImaging-Gesellschaft für Mikroskopie und Bildanalyse e.V., Constance, Germany
- (27) University of California, Davis, Davis, USA
- (28) University of Freiburg, Freiburg, Germany
- (29) RIKEN Center for Biosystems Dynamics Research, Kobe, Japan
- (30) Universidad Nacional Autónoma de México, Cuernavaca, México
- (31) Altos Labs, Redwood City, USA
- (32) Heidelberg University Hospital, Heidelberg, Germany
- (33) University of California San Diego, San Diego, USA
- (34) Vanderbilt University School of Medicine, Nashville, USA
- (35) Quantitative Imaging Systems LLC, Portland, USA
- (36) European Molecular Biology Laboratory, Heidelberg, Baden-Württemberg, Germany
- (37) Uppsala University, Uppsala, Sweden
- (38) Yale University, New Haven, USA

This manuscript is published with a closely related companion entitled, [Enabling Global Image Data Sharing in the Life Sciences](#), which can be found at the following link, [arXiv:2401.13023 \[q-bio.OT\]](https://arxiv.org/abs/2401.13023).

Abstract

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, quality-assured bioimage data must be shared among labs at a global scale to be compared, pooled, and reanalyzed, thus unleashing untold potential beyond the original purpose for which the data was generated. There are two broad sets of requirements to enable bioimage data sharing in the life sciences. One set of requirements is articulated in the companion White Paper entitled “Enabling Global Image Data Sharing in the Life Sciences,” which is published in parallel and addresses the need to build the cyberinfrastructure for sharing bioimage data (arXiv:2401.13023 [q-bio.OT], <https://doi.org/10.48550/arXiv.2401.13023>). Here, we detail a broad set of requirements, which involves collecting, managing, presenting, and propagating contextual information essential to assess the quality, understand the content, interpret the scientific implications, and reuse bioimage data in the context of the experimental details. We start by providing an overview of the main lessons learned to date through international community activities, which have recently made generating community standard practices for imaging Quality Control (QC) and metadata (Faklaris et al., 2022; Hammer et al., 2021; Huisman et al., 2021; *Microscopy Australia*, 2016; Montero Llopis et al., 2021; Rigano et al., 2021; Sarkans et al., 2021). We then provide a clear set of recommendations for amplifying this work. The driving goal is to address remaining challenges and democratize access to common practices and tools for a spectrum of biomedical researchers, regardless of their expertise, access to resources, and geographical location.

Background and Motivation

Biological image data provides unique temporal and spatial data about biological molecules, which significantly enhances our understanding of complex biological systems. Moreover, sharing the vast amount of information captured in biological image data promises to advance human health and the economy, much the way sharing of genomics data and protein structure data has (i.e., the Human Genome Project, <https://www.genome.gov/human-genome-project>; and the Protein Data Bank - PDB, <https://www.rcsb.org>). Cellular, tissue, and medical imaging, for example, hold the answers to disease

management (i.e., surveillance, prevention, diagnosis, and treatment), newly manufactured products, environmental resilience, and other global issues. Achieving this vision will require the interoperability, integration, and sharing of bioimage data across laboratories and research studies, thus maximizing the value of the billions of dollars invested annually in research around the globe.

Data sharing is globally recognized as highly desirable (UNESCO, 2022; UNESCO & Canadian Commission for UNESCO, 2022), but too often, publicly available imaging data lacks sufficient information to evaluate its validity and reproducibility independently and to assess its reusability (Botvinik-Nezer et al., 2020; Chen et al., 2023; Eriksson & Pukonen, 2018; Linkert et al., 2010; Marqués et al., 2020; Nature Editorial Staff, 2018; Pines, 2020; Sheen et al., 2019; Viana et al., 2023). Funding agencies have been working to improve the situation, for example, by requiring detailed data management and sharing plans (California Digital Library, 2022; European Research Council - Scientific Council, n.d.; *NOT-OD-21-013: Final NIH Policy for Data Management and Sharing*, n.d., *Preparing Your Data Management Plan*, n.d.). To improve reproducibility in research, many publishers now require more detailed materials and methods sections (Heddleston et al., 2021; Lee et al., 2024; Montero Llopis et al., 2021; Nature Editorial Staff, 2018; Schmied et al., 2023). In 2016, stakeholders from academia, industry, funding agencies, and publishing arrived at a set of so-called FAIR Data Principles—“Findable, Accessible, Interoperable and Reusable”—which are expected to expand the utility of data well beyond its original purpose (Wilkinson et al., 2016).

Several international community activities are engaged in addressing the challenges associated with the implementation of FAIR principles during bioimage data generation and post-acquisition processing (Supplemental Table 1). For many years, the Open Microscopy Environment (OME) has encouraged metadata collection and standardization of bioimage data file formats (Allan et al., 2012; Goldberg et al., 2005; Linkert et al., 2010; Moore et al., 2021, 2023; Swedlow et al., 2003, 2006). The global bioimaging community (see Supplemental Table 1) has more recently coalesced around improving standard practices for instrument QC and metadata (Faklaris et al., 2022; Hammer et al., 2021; Huisman et al., 2021; *Microscopy Australia*, 2016; Montero Llopis et al., 2021; Rigano et al., 2021; Sarkans et al., 2021) (Dekker et al., 2017, 2023); (Eriksson & Pukonen, 2018; Global BioImaging, 2015; Swedlow et al., 2021)(Ellenberg et al., 2018); (Strambio-De-Castillia et al., 2019);(Faklaris et al., 2022; Hammer et al., 2021; Huisman et al., 2021; *Microscopy Australia*, 2016; Montero Llopis et al., 2021; Rigano et al., 2021; Sarkans et al., 2021)(Abrams et al., 2020); (Eriksson & Pukonen, 2018; Global BioImaging, 2015; Swedlow et al., 2021); (Boehm et al., 2021; Nelson et al.,

2021); (Faklaris et al., 2022; Hammer et al., 2021; Huisman et al., 2021; *Microscopy Australia*, 2016; Montero Llopis et al., 2021; Rigano et al., 2021; Sarkans et al., 2021)(Kemmer et al., 2023)(Faklaris et al., 2022; Hammer et al., 2021; Huisman et al., 2021; *Microscopy Australia*, 2016; Montero Llopis et al., 2021; Rigano et al., 2021; Sarkans et al., 2021). Through these community efforts, individual imaging laboratories and Shared Research Resources (or “core facilities”) are partnering with instrument manufacturers to define shared metadata frameworks and execute inter-laboratory studies to refine and deploy standard methods for QC (Abrams et al., 2023; Faklaris et al., 2022; Gaudreault et al., 2022; Nelson, 2022). These groups have demonstrated interest and a willingness to commit precious resources voluntarily, and the funding for these efforts has been sufficient to allow limited but significant headway within small pockets of the broader imaging community. Despite several remaining challenges, this progress is the beginning of a path forward for biomedical researchers to generate and manage reliable and well-documented microscopy data that can be trusted and reused. Satisfying FAIR data principles will then help unlock the vast potential of quantitative image-based research.

Most scientists agree with the FAIR data principles and intend to share and reuse bioimage data. Still, key technical hurdles remain, including the need for (i) cyberinfrastructure (Andreev et al., 2021)(Bajcsy et al., 2024);(Andreev et al., 2021)(Nagaraj et al., 2020; *NIH Strategic Plan for Data Science*, n.d.); (Andreev et al., 2021)(Nagaraj et al., 2020; *NIH Strategic Plan for Data Science*, n.d.), and (ii) standard metadata practices for the acquisition, analysis, management, and dissemination of bioimage data. Both are essential elements of good research data management (RDM) and stewardship (Boeckhout et al., 2018; Demchenko & Stoy, 2021; Steeleworthy, 2014).

Here, we summarize recent progress toward standard metadata practices for imaging data and recommend how this work can be extended to address remaining challenges and make best practices and software tools accessible to a wide spectrum of biomedical researchers regardless of their expertise, access to resources, and geographical location.

We start with challenges connected with data generation (i.e., sample preparation and image acquisition). We then describe issues related to the reliability and reproducibility of post-acquisition bioimage data processing, visualization, and quantitative analysis. Finally, we address the importance of data management and stewardship to ensure the link between image data and metadata is maintained across all aspects of the image-data lifecycle. Ensuring that the origin and lineage (i.e., provenance) of data can be tracked and its quality assessed is an essential prerequisite for

guaranteeing FAIR data principles in microscopy. The scientific and sharing value derived from these metadata is the extent to which the associated bioimage data serves its intended scientific purpose and can be shared with other scientists to extract further insights.

Challenges and Recent Progress Associated with Data Generation

The metadata documentation of data generation lies at the very heart of the image data lifecycle, involves considerations made at the planning phase of the research project, is relevant before the sample hits the image acquisition platform, informs all subsequent image processing steps and is essential to ensuring the scientific value of shared image data.

Good practices in data generation and management that ensure that data are “FAIR from the start” are essential for rigorous and reproducible quantitative image-based biomedical research and for producing bioimage data that can be interpreted, trusted, and reused through model-based and data-driven mining, aggregation, reanalysis, and integrative modeling. It is crucial that third-party data users have ready access to all data-related information (i.e., metadata) that allows them to evaluate the suitability of given datasets for answering specific scientific questions before accessing or downloading them. This so-called “bioimage metadata” comprises two types of metadata: (i) *data provenance metadata*, which describes the experimental conditions, sample description and preparation, image acquisition (i.e., hardware description and image acquisition settings), and image processing, visualization, and analysis; and (ii) *QC metadata*, which describes system performance recorded through standardized QC protocols and metrics.

Challenges in Capturing Experimental Conditions and Sample Preparation Metadata

The description and interpretation of the results of any microscopy research project requires an extensive knowledge of the experimental steps preceding image acquisition and sample characteristics. This information should not only be captured in the Methods section of a paper (Larsen et al., 2023; Marqués et al., 2020; Montero Llopis et al., 2021) but it should also be made available as structured machine-readable metadata and include the following information: 1) the experimental procedures preceding image acquisition. 2) The origin of the biological sample and how it was obtained, experimentally treated, and prepared to produce the specimen for image acquisition. 3) The protocols and reagents (e.g., labeling procedures) used to visualize the structure of interest in the specimen. 4) the mounting technique and media used to preserve the integrity of the specimen

during imaging. 5) the receptacle (e.g., slide and coverslip) used to hold the specimen during image acquisition.

Bioimaging communities are beginning to converge on essential metadata guidelines. For example, a 2019 community gathering to address data management and sharing in the light, electron, and X-ray microscopy fields resulted in a Recommended Metadata for Biological Images (REMBI) framework (Sarkans et al., 2021). REMBI provides a high-level map of metadata categories needed to ensure data interpretability and trust and can serve as a point of reference for different communities to converge on shared specifications. Minimum information guidelines for 3D microscopy, highly multiplexed tissue images and cell migration experiments have recently been developed to guide the documentation of experimental procedures and sample preparation (Cell Migration Standardisation Organisation, 2021; Hosseini et al., 2023; Reiff et al., 2022; Ropelewski et al., 2022; Schapiro et al., 2022). Compliance and implementation of metadata guidelines will depend on consistent ontologies for knowledge representation (Herr et al., 2023; Hotchkiss et al., 2019; Jupp, n.d.; Ong et al., 2017; Sickle Cell Disease Ontology Working Group, 2019), and where possible, the automated capture and annotation of metadata (FAIRdom, 2021; Hosseini et al., 2023; Musen et al., 2022; Wolstencroft et al., 2012).

Recent Advances in Capturing Microscopy Acquisition Provenance and QC Metadata

Quality assessment, reproducibility, interpretation, and reuse of image data require sufficient information about the hardware specifications, image acquisition settings, and performance of the instrument at the time of the data acquisition (Hammer et al., 2021; Huisman et al., 2021). A full technical description of the configuration of the imaging system can be used to calculate key information about spatiotemporal resolution, the noise associated with the system, and the physical and temporal dimensions of the image pixel data. An instrument performance assessment plan, including tracking standardized QC metrics at regular intervals, can be used to quantify changes in performance over time (Abrams et al., 2023; Faklaris et al., 2022; Gaudreault et al., 2022; Nelson, 2022). QC metrics allow us to quantify disparities between expected (theoretical) and observed (empirical) values and to compare with values measured at installation (i.e., $t=0$ of the microscope lifetime). Importantly, QC metrics also help to characterize and calibrate derived quantities extracted by image analysis (e.g., co-registration measurements). Ultimately, capturing the overall state (Rigano et al., 2021) and performance of a microscope as part of the metadata at the time of data acquisition is essential to identify potential batch effects in large datasets (Viana et al., 2023). Batch

effects significantly affect the performance of Artificial Intelligence/Machine Learning (AI/ML) algorithms (Arevalo et al., 2023; Cimini et al., 2023; Tromans-Coia et al., 2023), so capturing instrument state and performance is critical for the interpretation of results (Chen et al., 2023; Viana et al., 2023).

Ensuring the Validity and Reproducibility of Image Data Visualization, and Analysis

A detailed workflow must be provided to independently assess the quality and reproducibility and ensure the interpretation of bioimage data analysis, as described in recently developed community guidelines (Aaron and Chew 2021; Miura and Nørrelykke 2021; Schmied et al. 2023). Additionally, the data size, computing hardware characteristics, and networking requirements should be part of the analysis metadata. This is not a trivial request. A data analysis pipeline typically involves a complex dependency chain of multiple software packages (for example, (Ahlers et al., 2023)) that has to be accurately described to ensure the independent assessment and reproducibility of results. As such, analysis metadata must constrain the version of each software component in the chain of dependency to avoid often significant changes. Accurately reporting all dependencies beyond the primary software in a manual fashion is unfeasible and is best performed using automated package managers (e.g., the pip freeze command).

Since image processing pipelines may rely on several tools, care must be taken to ensure that the intermediate and final results of processing and analysis pipelines and the associated metadata are stored in a harmonized and comparable manner across different software tools (Könnecke et al., 2015). To this end, developers have made important strides toward the use of containers (Bajcsy & Hotaling, 2020; González & Evans, 2019; Mitra-Behura et al., 2021; Schapiro et al., 2021), and workflow tools (Berthold, 2023; Di Tommaso & Floden, 2023; KNIME Community & biomi-konstanz, 2023; Stirling et al., 2021; Wollmann et al., 2017, 2023). Future work is needed to make these solutions more robust and to promote their universal adoption.

Suppose one could recreate an analysis environment using the same hardware, operating system, image analysis software, and all parameter settings. In that case, the analysis of the same dataset at two different locations should produce the same result. In practice, however, an image analysis software that uses randomness as part of its computations is unlikely to produce the exact same result; in this context, results within an acceptable margin of error (i.e., similar result) would be considered sufficient (PyTorch Consortium, 2023; *Registration Overview — SimpleITK*, 2024; TensorFlow Development Team, 2023). Finally, algorithms and implementations that utilize

randomness require special care. This entails sharing additional information such as seed values and other software parameters. For example, when using deep learning, replicating results obtained by a retrained or new model requires access to the code and model weights, which should be shared using an interoperable file format across deep learning frameworks (e.g., the Open Neural Network Exchange, ONNX format, <https://onnx.ai/>).

Everyday Stewardship of Image Data and Metadata During Active Data Production

Data stewardship is an intrinsic and essential aspect of generating high-quality image data that is “FAIR from the start.” For this to happen, data stewardship must involve the entire lifecycle of the data, starting with the planning phase and continuing during experimental design and execution, sample preparation, data acquisition, post-processing, visualization, and analysis. In addition, data stewardship must outlive the research project to ensure that well-documented published data remains available for re-use, as detailed in the companion manuscript (Bajcsy et al., 2024). Specifically, correct data stewardship ensures that the conditions used to generate, process, analyze, and validate data are transparent, documented, propagated alongside the data and automatically reported to downstream users in both human-readable forms (i.e., scientific publications) (Heddleston et al., 2021; Larsen et al., 2023; Marqués et al., 2020; Montero Llopis et al., 2021) and structured machine-readable metadata frameworks (Moore & Strambio-De-Castillia, 2021; Soiland-Reyes et al., 2022; Solbrig et al., 2023). Cloud-ready data exchange formats (Moore et al., 2021, 2023; Swedlow et al., 2021) and standardized Application Programming Interfaces (APIs) that allow integration of images and results (Hammer et al., 2021; Moore, 2022; Moore et al., 2021, 2023; Rigano et al., 2021; Sarkans et al., 2021; Schapiro et al., 2022). This, in turn, ensures that data can be trusted, correctly interpreted, reproduced, and reused through data aggregation, mining, integrative modeling, and further analysis (including AI/ML). In addition, proper data stewardship is crucial to organize data, thus avoiding the waste of time and resources needed to re-generate data that has been lost or cannot be interpreted and, as a result, promote efficiency and sustainability (economic, environmental, and societal) (Budtz Pedersen & Hvidtfeldt, 2023; Meyn et al., 2022).

As such, effective data stewardship requires well-maintained, enterprise-grade, scalable, open-source, and democratized cyberinfrastructure (Andreev et al., 2021). This cyberinfrastructure should include the following; 1) Persistent Identifiers (PIDs) for research resources, individuals, publications and data (Brown et al., 2022a, 2022b; Cousijn et al., 2021; McCafferty et al., 2023); 2) shared file formats and associated APIs (Marconato et al., 2023; Moore et al., 2021, 2023); 3) the use

of community-defined ontologies (Côté et al., 2010; Lomax, 2019)(Ciavotta et al., 2022; Khurana et al., 2023); 3) bioimage metadata specifications (Hammer et al., 2021; Sarkans et al., 2021; Schapiro et al., 2022); and 4) community defined Next Generation Metadata frameworks (Moore, 2022). This cyberinfrastructure should interface with Electronic Lab Notebooks (ELN) and Laboratory Information Management Systems (LIMS) and, whenever possible, automatically capture and propagate output metadata from all relevant instrumentation (including but not limited to robotic, microfluidics, and image acquisition hardware) (Marx, 2022a, 2022b). In summary, cyberinfrastructure should cover the following three interconnected aspects:

- **WHAT information should be captured in Bioimage Metadata** (i.e., develop community specifications for Experiment description, Sample preparation, Image acquisition, Image Processing, Visualization, and Analysis metadata; in particular, Image acquisition metadata should include hardware specifications, image acquisition settings, and QC protocols and metrics) (Hammer et al., 2021; Huisman et al., 2021; Sarkans et al., 2021; Schapiro et al., 2022).
- **WHERE Bioimage Metadata should be stored** (i.e., OME-NGFF and Next Generation Metadata with shared APIs) (Moore, 2022)(Moore et al., 2021, 2023)
- **HOW Bioimage Metadata should be captured** to facilitate metadata annotation, data curation, and seamless integration of all aspects of the imaging pipeline (i.e., integration with LIMS, ELNs, and hardware instrumentation; leverage community-specifications and Next Generation Metadata frameworks; ontology-enriched, REMBI-based, modular template spreadsheets; incorporate QC protocols and output metrics as image metadata) (Bukhari et al., 2018; Hammer et al., December, 9-12 2019; Kobayashi et al., 2019/Dec 10-11 2019; Kunis et al., 2021; NFDI4Plants Consortium, 2022; Rigano et al., 2021; Ryan et al., 2021; Sansone et al., 2012; Wolstencroft et al., 2012).

FAIR quality control in Recently Emerging Imaging Modalities

A set of recently developed imaging modalities are emerging as techniques of choice to quantify the spatial distribution of molecules and supramolecular structures at the subcellular, cellular, tissue, and organismal levels as reviewed in (Baysoy et al., 2023; Moffitt et al., 2022; Vandereyken et al., 2023)(Hickey et al., 2022; Kinkhabwala et al., 2022; Rivest et al., 2023). These techniques include spatial RNA profiling methods capable of resolving hundreds of probes at subcellular resolution using light microscopy, *in situ* sequencing (ISS), and capture assay. In addition, several highly multiplexed antibody-based imaging techniques have also been developed and commercialized. Cryogenic

transmission electron microscopy (cryo-EM) provides images of biological matter in a frozen-hydrated, near-native state. The cryo-EM field is recognized as a good example of effectively annotating metadata and stewardship of raw and derived data (Sarkans et al., 2021). The cryo-EM community agrees that detailed metadata must be made publicly available alongside the data and that metadata standards must be reviewed regularly to ensure fitness and relevance to the evolving community needs (Chiu et al., 2021; Sarkans et al., 2021). Data sharing of cryo-EM derived (EMBL-EBI, n.d.-a; Lawson et al., 2011; RCSB Consortium, 2019)) and raw data (EMBL-EBI, n.d.-b; Ludin et al., 2016) - both with associated metadata - has already been established and is enforced by most publishers,

We advocate for a similar approach to be adopted for multiplexed RNA, protein, and multi-omic imaging datasets. The recent introduction of these methods, combined with their complexity and diversity, resulted in various workflows related to sample processing, reagent QC, image acquisition, image processing, and image analysis without agreed-upon community standards (Vierdag & Saka, 2024). The establishment and wide adoption of such standards are essential for cross-lab and cross-platform data interoperability and analysis, which is even more critical to the community since these data are expensive to acquire (Hickey et al., 2022; Quardokus et al., 2023; Vandereyken et al., 2023) and are associated with a number of consortia efforts (Jain et al., 2023; Rozenblatt-Rosen et al., 2020; Snyder & HuBMAP Consortium, 2019). Critical details related to sample preparation, reagent validation, and platform-specific imaging parameters must be recorded and shared using community-defined metadata. Here, we highlight specific challenges around harmonizing multiplexed image processing and reporting that limit current ability towards FAIR data (Wilkinson et al., 2016).

Recommendations Toward Global Image Data Generation and Stewardship Standards

All stakeholders can play a role in all aspects described. Manufacturers could provide automated access to the full community-defined technical descriptions of instruments and QC metrics as part of the metadata (Marx, 2022a, 2022b). Funding agencies could allocate funds to support the development of tools, protocols, and metadata standards by bioimaging communities to be implemented routinely by core facilities and users. Publishers should insist that all aspects of microscopy metadata (i.e., hardware specifications, image acquisition settings, and QC metrics) be a part of the data package. Investigators should adopt the best practices being established by the broader imaging research community, ensuring the data they generate has the necessary human and machine readable metadata to facilitate FAIR requirements for themselves and others. Lastly, if these

practices are to be universally adopted, the development of resources in multiple languages need to be encouraged and supported.

In this section, we recommend steps to promote the production and stewardship of image data that is “FAIR from the start” and ready to be shared and reused. These recommendations are summarized in a to-do list for various stakeholders presented in Text Box 1.

Data Generation Recommendations

Overcoming challenges related to the generation of image data that is “FAIR from the start” requires specific solutions that should be planned for and carried out by all interested stakeholders. To guide the development of these solutions, we provide the following specific recommendations:

- **Promote the widespread adoption of persistent identifiers**—institutions (e.g., Research Organization Registry- ROR) (Gould, 2023), core facilities (e.g., ROR and Research Resource Identifier - RRID) (Bandrowski, 2022), personnel (e.g., Open Researcher and Contributor ID - ORCID) (Haak et al., 2012; Shillum et al., 2021), reagents (e.g., RRID) (Bandrowski, 2022), microscope instruments (e.g., PIDINST) (Krahl et al., 2021; McCafferty et al., 2023; Stocker et al., 2020), and datasets (e.g., Digital Object Identifiers - DOI)—to enable the FAIR description of all scientific entities, to facilitate reporting and reproducibility and to recognize the essential roles of imaging scientists and core facilities in the research enterprise (Brown et al., 2022a, 2022b; Cousijn et al., 2021; McCafferty et al., 2023). This recommendation is backed by recent cost-benefit analyses (Brown et al., 2022a, 2022b) that revealed significant financial advantages associated with the adoption of PIDs which would be related to reductions in staff salaries, the time saved from tedious data entry, and in the facilitation of technology advances.
- **Promote the collection of full technical descriptions of microscope hardware specifications, image acquisition settings, and QC protocols and metrics** (aka Microscopy Metadata) that comply 4DN-BINA-OME (NBO-Q) microscopy metadata specifications (Hammer et al., 2021; Huisman et al., 2021) being developed by consensus by imaging scientists and instrument manufacturers (Marx, 2022a, 2022b). Technical descriptions captured in Microscopy Metadata must become obligatory aspects of the production of any image data; in their absence, image data cannot reliably be quantified, reproduced, or reused and ultimately loses scientific value even when it is shared. As such, Microscopy Metadata should be made transparently available to microscope users, automatically collected using

community tools (Kunis et al., 2021; Kunis & Dohle, 2022; Rigano et al., 2021; Ryan et al., 2021), and encoded using shared metadata frameworks (Moore et al., 2021, 2023).

- **Ensure that instrument maintenance and quality assessment are adequately supported to ensure that they become common practice** at all core facilities and individual laboratories utilizing microscopes and regardless of local resource availability. Specific funding mechanisms should be considered to provide the necessary instrumentation, training and personnel or traveling metrology services for under-resourced areas. This will allow for the performance of instruments to be evaluated at regular intervals using community-defined metrology standards and QC procedures that are appropriate for each experimental question (Abrams et al., 2023; Gaudreault et al., 2022; Nelson, 2022). Additional metrics might need to be collected for specific types of experimental approaches and desired outcomes.
- **Emphasize large infrastructure investments in core facilities and regional infrastructural hubs** (Budtz Pedersen & Hvidtfeldt, 2023) who employ trained personnel, including imaging scientists, data stewards, image analysts, and research software engineers. Such shared infrastructure would increase efficiency and reduce costs by maintaining and assessing the performance of instruments; promote the dissemination of technological advances (hardware and software); facilitate user training; provide guidance for experimental procedures, image analysis, and data stewardship; and provide image analysis and RDM services to facilitate the deposition of FAIR data packages containing the appropriate image metadata to specialized bioimage repositories. These infrastructure investments should include providing legal support to review data, identify appropriate Creative Commons (CC) and Open-Source Software (OSS) licensing, and/or carry out Personal Information (PI) redaction (human subject data).
- **Invest in the development of open-hardware devices** (e.g., robotic devices, fluidics systems, environmental control devices, microscopes, etc.) to carry out all aspects of data generation as the most appropriate way to democratize advanced technology and to ensure the efficient use of resources.

Data Processing and Analysis Metadata Recommendations

Once acquired, images often require complex processing, visualization, and analysis steps to extract quantitative information about the signal intensity of a given label, as well as the location, morphological characteristics, association, and movement of biological entities. To ensure that the

results of image processing and analysis pipelines are reproducible and ready for FAIR sharing, community-defined guidelines should be adopted (Bialy et al., 2021; Miura & Nørrelykke, 2021; Schmied et al., 2023). In particular:

- Image processing and analysis workflows should be shared in binary containers such as Docker, Singularity, or Podman, and include the complete software environment to ensure that all aspects of the pipeline remain identical for all users.
- The processing and analysis workflow should specify which aspects of the microscopy acquisition process (e.g., magnification, resolution, and signal intensity) can affect its execution and should, therefore, be encoded in metadata.
- All aspects of the processing and analysis pipeline—including but not limited to data structure and size, rendering and processing steps, algorithm version and input parameters, and computing and networking requirements—must be documented in both human- and machine-readable formats to ensure interpretability, reproducibility, and downstream reuse. Such metadata should be captured either in the image data file (e.g., information about image rendering and processing) or as part of the documentation of the workflow (e.g., algorithm version and input parameters).
- As such, it is imperative that analysis metadata be captured using community-defined metadata specifications and storage frameworks to ensure maximal efficiency with which this information can be extracted and tracked across all steps of the pipeline without the need for repeated time-consuming interactions with the image data itself.

Data Stewardship Recommendations

- The everyday stewardship of data and associated metadata throughout the entire lifecycle of quantitative imaging experiments is essential to ensure rigor, reproducibility, and the production of high-quality image data that can be interpreted and is ready to be reused according to FAIR principles.
- The generation and stewardship of FAIR image data require full transparency, management, and reporting of all information related to the conditions used for data generation (e.g., experimental conditions, sample preparation, and image acquisition), as well as processing and analysis (e.g., image analysis, and visualization).

- RDM cyberinfrastructure supporting the generation and pre-publication stewardship of high-quality FAIR image data should be made available to all biomedical researchers using microscopes as an essential prerequisite for image data sharing and reuse.
- Such imaging RDM cyberinfrastructure must include advanced computing and data repositories that provide integrated data stewardship, metadata annotation, visualization environments, processing pipelines, and analysis routines (including AI/ML). Different components must be connected via high-speed networks to expedite upload and download as needed.
- RDM cyberinfrastructure is best supported by easy-to-use, enterprise grade, robust, and continually maintained and supported open-source software to carry out all steps of the imaging pipeline from experimental procedure (i.e., LIMS or ELN) to image acquisition (i.e., Micro-Manager, Pycro-Manager, Python Microscope, etc.) to image processing, visualization, and analysis and data processing pipeline (i.e., CellProfiler, Fiji, napari, CellPose, etc.).
- When proprietary software and instrumentation must be used, community-defined standards must be used to ensure transparency regarding all relevant algorithms and input parameters as well as instrument configuration and performance.
- Collection and reporting of metadata must be based on community-defined standards, and it must occur at two highly interconnected levels:
 - **Human readable**, which is primarily related to Materials and Methods (Heddleston et al., 2021; Larsen et al., 2023; Marqués et al., 2020; Montero Llopis et al., 2021), and represent a subset of the information captured in Bioimage Metadata, enabling users to understand and describe the imaging experiment.
 - **Machine-readable**, which is captured in Bioimage Metadata (i.e., all information needed to understand the lineage - aka provenance - and quality of image data) and represents the complete technical description to ensure full quality, reproducibility, and reusability (Moore, 2022; Moore et al., 2021, 2023) .
- **To ensure Machine Readability:**
 - **Metadata should be encoded in community-specified frameworks** to be associated with standardized image data file formats (Moore, 2022; Moore et al., 2021, 2023), or workflow documentation, and equipped with readily available software API to facilitate the transfer of information across the different steps of the imaging pipeline. For example, it should be

possible to be put in an SQL database automatically. A potential framework that could fulfill these requirements is LinkML (Solbrig et al.). It allows for easy authoring of metadata schemas in the YAML format, which can be exported into other formats. It is also able to create classes in various programming languages that can serve to validate metadata.

- It is imperative to use **specific annotation tools and automation** at all aspects of the imaging pipeline to ensure that image processing, visualization, and analysis pipelines can leverage metadata. Particular emphasis should be given to (i) automated processes for microscope systems and peripheral components, including community-defined QC procedures to ensure optimal instrument performance (Hammer et al., 2021; Schapiro et al., 2022); (ii) automated metadata annotation at all phases of the image-data life cycle (Kunis et al., 2021; Rigano et al., 2021; Ryan et al., 2021); and (iii) integrated image processing, visualization, and analysis pipelines.
- **Metadata annotations should be backed by ontologies and knowledge graphs.** Ontologies provide descriptions of the hierarchical relationship between concepts and can be used to make metadata machine-readable. Their role in the harmonization of knowledge and data in biomedicine is increasingly recognized, especially in the context of AI, where they can provide valuable constraints that make ML more efficient (Lomax, 2019). Tools such as the Ontology Look Up Service (OLS) (Côté et al., 2010) can be used to locate appropriate ontological terms, although further development is needed to help sort through duplicates and identify which terms should be used in different contexts.
- Quality, transparency, reproducibility, and reusability require standards defined by all imaging community stakeholders.
 - Recent advancements have made it clear that the community, when participating in bioimaging organizations, networks, and initiatives, is willing and ready to take on this challenge.
 - However, deliberate, directed, targeted funding is needed to ensure that ongoing standardization efforts can be expanded to cover all essential aspects of the imaging pipeline.
- In addition to being essential for generating standards, community organizations are ideal ways to promote the broader adoption of standards via education, training, and outreach. As such, novel

funding models should be implemented to ensure the sustainability of these essential endeavors, promoting the advancement of quantitative imaging and science as a whole.

- Cyber infrastructure for RDM is expected to impact the economy beyond the biological research enterprise. Tested and trusted microscope QC protocols and commonly accepted and unambiguous reporting criteria will be beneficial to the many applications of quantitative imaging for cellular analysis, including pathology, cell therapies, and regenerative medicine.

Text Box 1 - A to-do list for various stakeholders

Towards Global Image Data Generation and Stewardship

A to-do list for various stakeholders

More details on the action items below are provided in Supplemental Material.

1. Ensure the **long-term sustainability of national and international bioimaging communities** (e.g., ABIC, ABRF, BINA, CBI, GBI, LABI, and QUAREP-LiMi; see also [Table 1 in supplemental materials](#)), with the specific purpose of enabling recurring gatherings to coordinate (i.e., discuss, recommend, update) the development of:
 - a. **Consensus guidelines for quality control procedures and standards** to encourage the implementation and reporting of QC protocols and performance benchmarks, including for imaging instrumentation.
 - b. **Shared metadata specifications, exchange frameworks, and tools** to minimize barriers to adopting metadata guidelines for academic, government, and industry stakeholders.
 - c. **Shared computational cyberinfrastructure is needed to generate and manage image data before publication.** This infrastructure should include well-documented and high-speed software tools, frameworks, computing and storage equipment, and networks. It will support all stages of the imaging process, from data annotation to image acquisition and analysis. Community-defined standards are essential to ensure transparency about the instruments and algorithms used.
2. **Invest in core facilities (aka Shared Research Resources) and their Personnel from all backgrounds and regions** to:
 - a. **Provide expertise** in sample preparation, validation of staining protocols, image acquisition, and image analysis.
 - b. **Democratize access** through shared resources and promote collaborations to facilitate access to advanced technology.
 - c. Serve as **pivotal hubs for disseminating expertise and user training** on all topics essential for preparing FAIR image data for sharing and engendering maximum reuse value across resourced and under-resourced regions and communities.
 - d. **Develop strong connections with software development centers** to ensure cyberinfrastructure's usability, customization, and democratization for imaging pipeline automation.
3. Support the **career and recognition of imaging scientists** specializing in generating and stewardship of FAIR image data. These include core facility personnel, image data curators, bio-image analysis experts, and research software engineers.
4. In collaboration with vendors, **develop and deploy automated methods to capture harmonized and consistent metadata documenting all steps of the imaging pipeline**, from reagents used to generate image data to microscopy instruments and peripherals.
5. **Promote the use of Persistent Identifiers (PID) for the FAIR description of research resources** (e.g., reagents, instruments, core facilities) and outputs (e.g., datasets) to facilitate reproducibility and reuse and ensure that the personnel involved in the research enterprise are appropriately acknowledged.
6. **Develop metrics that describe the qualities of resultant image data.**

References

- Abrams, B., Brown, C., Callahan, L., Cole, R., Pengo, T., & Wee, T.-L. (2020). ABRF light microscopy research group study 3: The development and implementation of new tools for microscope quality assurance testing. *Journal of Biomolecular Techniques: JBT*, 31(Suppl), S33.
<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7646864/>
- Abrams, B., Pengo, T., Wee, T.-L., Deagle, R. C., Vuillemin, N., Callahan, L. M., Smith, M. A., Kubow, K. E., Girard, A.-M., Rappoport, J. Z., Bayles, C. J., Cameron, L. A., Cole, R., & Brown, C. M. (2023). Tissue-like 3D standard and protocols for microscope quality management. *Microscopy and Microanalysis: The Official Journal of Microscopy Society of America, Microbeam Analysis Society, Microscopical Society of Canada*, 29(2), 616–634. <https://doi.org/10.1093/micmic/ozad014>
- Ahlers, J., Althviz Moré, D., Amsalem, O., Anderson, A., Bokota, G., Boone, P., Bragantini, J., Buckley, G., Burt, A., Bussonnier, M., Can Solak, A., Caporal, C., Doncila Pop, D., Evans, K., Freeman, J., Gaifas, L., Gohlke, C., Gunalan, K., Har-Gil, H., ... Yamauchi, K. (2023). *napari: a multi-dimensional image viewer for Python*. <https://doi.org/10.5281/zenodo.8115575>
- Allan, C., Burel, J.-M., Moore, J., Blackburn, C., Linkert, M., Loynton, S., MacDonald, D., Moore, W. J., Neves, C., Patterson, A., Porter, M., Tarkowska, A., Loranger, B., Avondo, J., Lagerstedt, I., Lianas, L., Leo, S., Hands, K., Hay, R. T., ... Swedlow, J. R. (2012). OMERO: flexible, model-driven data management for experimental biology. *Nature Methods*, 9(3), 245–253.
<http://www.nature.com/doifinder/10.1038/nmeth.1896>
- Allen, L., O'Connell, A., & Kiermer, V. (2019). How can we ensure visibility and diversity in research contributions? How the Contributor Role Taxonomy (CRediT) is helping the shift from authorship to contributorship. *Learned Publishing: Journal of the Association of Learned and Professional Society Publishers*, 32(1), 71–74. <https://doi.org/10.1002/leap.1210>
- Andreev, A., Morrell, T., Briney, K., Gesing, S., & Manor, U. (2021). Biologists need modern data infrastructure on campus. In *arXiv [q-bio.OT]*. <http://arxiv.org/abs/2108.07631>
- Arevalo, J., van Dijk, R., Carpenter, A. E., & Singh, S. (2023). Evaluating batch correction methods for image-based cell profiling. *bioRxiv : The Preprint Server for Biology*.

<https://doi.org/10.1101/2023.09.15.558001>

- Bajcsy, P., Bhattiprolu, S., Borner, K., Cimini, B., Collinson, L., Ellenberg, J., Fiolka, R., Giger, M., Goscinski, W., Hartley, M., Hotaling, N., Horwitz, R., Jug, F., Kreshuk, A., Lundberg, E., Mathur, A., Narayan, K., Onami, S., Plant, A. L., ... Keppler, A. (2024). Enabling Global Image Data Sharing in the Life Sciences. In *ArXiv*. <https://doi.org/10.48550/arXiv.2401.13023>
- Bajcsy, P., & Hotaling, N. (2020). Interoperability of Web Computational Plugins for Large Microscopy Image Analyses. *NISTIR 8297*. <https://doi.org/10.6028/NIST.IR.8297>
- Bandrowski, A. (2022). A decade of GigaScience: What can be learned from half a million RRIDs in the scientific literature? *GigaScience*, *11*. <https://doi.org/10.1093/gigascience/giac058>
- Baysoy, A., Bai, Z., Satija, R., & Fan, R. (2023). The technological landscape and applications of single-cell multi-omics. *Nature Reviews. Molecular Cell Biology*, *24*(10), 695–713. <https://doi.org/10.1038/s41580-023-00615-w>
- Berthold, M. R. (2023). *KNIME: open for innovation*. <http://knime.org/>
- Bialy, N., Alber, F., Andrews, B., Angelo, M., Beliveau, B., Bintu, L., Boettiger, A., Boehm, U., Brown, C. M., Maina, M. B., Chambers, J. J., Cimini, B. A., Eliceiri, K., Errington, R., Faklaris, O., Gaudreault, N., Germain, R. N., Goscinski, W., Grunwald, D., ... Strambio-De-Castillia, C. (2021). A guide to accurate reporting in digital image processing - can anyone reproduce your quantitative analysis? *Journal of Cell Science*, *134*(6). <https://doi.org/10.1242/jcs.254151>
- Boeckhout, M., Zielhuis, G. A., & Bredenoord, A. L. (2018). The FAIR guiding principles for data stewardship: fair enough? *European Journal of Human Genetics: EJHG*, *26*(7), 931–936. <https://doi.org/10.1038/s41431-018-0160-0>
- Boehm, U., Nelson, G., Brown, C. M., Bagley, S., Bajcsy, P., Bischof, J., Dauphin, A., Dobbie, I. M., Eriksson, J. E., Faklaris, O., Fernandez-Rodriguez, J., Ferrand, A., Gelman, L., Gheisari, A., Hartmann, H., Kukat, C., Laude, A., Mitkovski, M., Munck, S., ... Nitschke, R. (2021). QUAREP-LiMi: a community endeavor to advance quality assessment and reproducibility in light microscopy. *Nature Methods* (<https://doi.org/10.1038/s41592-021-01162-Y>), *18*, 1423–1426. <https://doi.org/10.1038/s41592-021-01162-y>

- Botvinik-Nezer, R., Holzmeister, F., Camerer, C. F., Dreber, A., Huber, J., Johannesson, M., Kirchler, M., Iwanir, R., Mumford, J. A., Adcock, R. A., Avesani, P., Baczkowski, B. M., Bajracharya, A., Bakst, L., Ball, S., Barilari, M., Bault, N., Beaton, D., Beitner, J., ... Schonberg, T. (2020). Variability in the analysis of a single neuroimaging dataset by many teams. *Nature*, *582*(7810), 84–88.
<https://doi.org/10.1038/s41586-020-2314-9>
- Brown, J., Jones, P., Meadows, A., & Murphy, F. (2022a). Incentives to invest in identifiers: A cost-benefit analysis of persistent identifiers in Australian research systems. In *Zenodo*.
<https://doi.org/10.5281/zenodo.7100578>
- Brown, J., Jones, P., Meadows, A., & Murphy, F. (2022b). Revised cost-benefit analysis for the UK PID Support Network. In *Zenodo*. Zenodo. <https://doi.org/10.5281/zenodo.7356219>
- Budtz Pedersen, D., & Hvidtfeldt, R. (2023). The missing links of research impact. *Research Evaluation*, *rvad011*. <https://doi.org/10.1093/reseval/rvad011>
- Bukhari, S. A. C., Martínez-Romero, M., O' Connor, M. J., Egyedi, A. L., Willrett, D., Graybeal, J., Musen, M. A., Cheung, K.-H., & Kleinstein, S. H. (2018). CEDAR OnDemand: a browser extension to generate ontology-based scientific metadata. *BMC Bioinformatics*, *19*(1), 268.
<https://doi.org/10.1186/s12859-018-2247-6>
- California Digital Library. (2022). *DMPTool* (v4.1.6 © 2023). The Regents of the University of California.
<https://dmptool.org/>
- Cell Migration Standardisation Organisation. (2021). *Minimum Information About Cell Migration Experiments (MIACME 0.2)*. Cell Migration Standardisation Organisation. <https://cmso.science/MIACME/v0.2/>
- Chen, J., Viana, M. P., & Rafelski, S. M. (2023). When seeing is not believing: application-appropriate validation matters for quantitative bioimage analysis. *Nature Methods*, *20*(7), 968–970.
<https://doi.org/10.1038/s41592-023-01881-4>
- Chiu, W., Schmid, M. F., Pintilie, G. D., & Lawson, C. L. (2021). Evolution of standardization and dissemination of cryo-EM structures and data jointly by the community, PDB, and EMDB. *The Journal of Biological Chemistry*, *296*, 100560. <https://doi.org/10.1016/j.jbc.2021.100560>
- Ciavotta, M., Cutrona, V., De Paoli, F., Nikolov, N., Palmonari, M., & Roman, D. (2022). Supporting Semantic

- Data Enrichment at Scale. In E. Curry, S. Auer, A. J. Berre, A. Metzger, M. S. Perez, & S. Zillner (Eds.), *Technologies and Applications for Big Data Value* (pp. 19–39). Springer International Publishing.
https://doi.org/10.1007/978-3-030-78307-5_2
- Cimini, B. A., Chandrasekaran, S. N., Kost-Alimova, M., Miller, L., Goodale, A., Fritchman, B., Byrne, P., Garg, S., Jamali, N., Logan, D. J., Concannon, J. B., Lardeau, C.-H., Mouchet, E., Singh, S., Shafqat Abbasi, H., Aspesi, P., Jr, Boyd, J. D., Gilbert, T., Gnutt, D., ... Carpenter, A. E. (2023). Optimizing the Cell Painting assay for image-based profiling. *Nature Protocols*, *18*(7), 1981–2013.
<https://doi.org/10.1038/s41596-023-00840-9>
- Côté, R., Reisinger, F., Martens, L., Barsnes, H., Vizcaino, J. A., & Hermjakob, H. (2010). The Ontology Lookup Service: bigger and better. *Nucleic Acids Research*, *38*(Web Server issue), W155–W160.
<https://doi.org/10.1093/nar/gkq331>
- Cousijn, H., Braukmann, R., Fenner, M., Ferguson, C., van Horik, R., Lammey, R., Meadows, A., & Lambert, S. (2021). Connected Research: The Potential of the PID Graph. *Patterns (New York, N.Y.)*, *2*(1), 100180.
<https://doi.org/10.1016/j.patter.2020.100180>
- Dekker, J., Alber, F., Aufmkolk, S., Beliveau, B. J., Bruneau, B. G., Belmont, A. S., Bintu, L., Boettiger, A., Calandrelli, R., Disteche, C. M., Gilbert, D. M., Gregor, T., Hansen, A. S., Huang, B., Huangfu, D., Kalhor, R., Leslie, C. S., Li, W., Li, Y., ... Zhong, S. (2023). Spatial and temporal organization of the genome: Current state and future aims of the 4D nucleome project. *Molecular Cell*.
<https://doi.org/10.1016/j.molcel.2023.06.018>
- Dekker, J., Belmont, A. S., Guttman, M., Leshyk, V. O., Lis, J. T., Lomvardas, S., Mirny, L. A., O'Shea, C. C., Park, P. J., Ren, B., Politz, J. C. R., Shendure, J., Zhong, S., & 4D Nucleome Network. (2017). The 4D nucleome project. *Nature*, *549*(7671), 219–226. <https://doi.org/10.1038/nature23884>
- Demchenko, Y., & Stoy, L. (2021, April 21). Research data management and data stewardship competences in university curriculum. *2021 IEEE Global Engineering Education Conference (EDUCON)*. 2021 IEEE Global Engineering Education Conference (EDUCON), Vienna, Austria.
<https://doi.org/10.1109/educon46332.2021.9453956>
- Di Tommaso, P., & Floden, E. (2023). *A DSL for parallel and scalable computational pipelines*.

<https://www.nextflow.io/index.html>

Ellenberg, J., Swedlow, J. R., Barlow, M., Cook, C. E., Sarkans, U., Patwardhan, A., Brazma, A., & Birney, E. (2018). A call for public archives for biological image data. *Nature Methods*, 15(11), 849–854.

<https://doi.org/10.1038/s41592-018-0195-8>

EMBL-EBI. (n.d.-a). *Electron Microscopy Data Bank (EMDB)*. EMBL European Bioinformatics Institute (EMBL-EBI) - Electron Microscopy Data Bank. Retrieved October 30, 2023, from

<https://www.ebi.ac.uk/emdb/>

EMBL-EBI. (n.d.-b). *EMPIAR - Electron Microscopy Public Image Archive*. EMBL European Bioinformatics Institute (EMBL-EBI) - Electron Microscopy Public Image Archive. Retrieved October 30, 2023, from

<https://www.ebi.ac.uk/empiar/>

Eriksson, J., & Pukonen, I. (2018). *D2.3 Common international recommendation for quality assurance and management in open access imaging infrastructures*. Global BioImaging Project.

https://www.globalbioimaging.org/user/pages/05.documents/D2.3_Publication%20of%20common%20recommendation_quality%20assurance%20and%20management%20in%20open%20access%20imaging%20infrastructures.pdf

European Research Council - Scientific Council. (n.d.). *Open Research Data and Data Management Plans*.

FAIRdom. (2021). *RightField* (Version 0.26.1). <https://rightfield.org.uk/>

Faklaris, O., Bancel-Vallée, L., Dauphin, A., Monterroso, B., Frère, P., Geny, D., Manoliu, T., de Rossi, S., Cordelières, F. P., Schapman, D., Nitschke, R., Cau, J., & Guilbert, T. (2022). Quality assessment in light microscopy for routine use through simple tools and robust metrics. *The Journal of Cell Biology*, 221(11).

<https://doi.org/10.1083/jcb.202107093>

Gaudreault, N., Nelson, G., Alexopoulos, I., Azevedo, M., Barachati, F., Belyaev, Y., Carvalho, M. T., Cesbron, Y., Dauphin, A., Corbett, A. D., Gelman Laurent, D. I., Halidi, N., Hao, X., Hartmann, H., Heintzmann, R., Hemmerich, P., Kirchner, M., Lacoste, J., Liu, P., ... Faklaris, O. (2022). *Illumination power, stability, and linearity measurements for confocal and Widefield microscopes v2*. Protocols.io.

<https://doi.org/10.17504/protocols.io.5jyl853ndl2w/v2>

Global BioImaging. (2015). *Global BioImaging*. Global BioImaging. <https://globalbioimaging.org/>

- Goldberg, I. G., Allan, C., Burel, J.-M., Creager, D., Falconi, A., Hochheiser, H., Johnston, J., Mellen, J., Sorger, P. K., & Swedlow, J. R. (2005). The Open Microscopy Environment (OME) Data Model and XML file: open tools for informatics and quantitative analysis in biological imaging. *Genome Biology*, 6(5), R47. <http://genomebiology.com/2005/6/5/R47>
- González, G., & Evans, C. L. (2019). Biomedical Image Processing with Containers and Deep Learning: An Automated Analysis Pipeline: Data architecture, artificial intelligence, automated processing, containerization, and clusters orchestration ease the transition from data acquisition to insights in medium-to-large datasets. *BioEssays: News and Reviews in Molecular, Cellular and Developmental Biology*, 41(6), e1900004. <https://doi.org/10.1002/bies.201900004>
- Gould, M. (2023, May 31). ROR and organizational identifier interoperability in publishing systems. *ROR and Organizational Identifier Interoperability in Publishing Systems*. 45th SSP Annual Meeting. <https://doi.org/10.14293/s2199-ssp-am23-01030>
- Haak, L. L., Fenner, M., Paglione, L., Pentz, E., & Ratner, H. (2012). ORCID: a system to uniquely identify researchers. *Learned Publishing: Journal of the Association of Learned and Professional Society Publishers*, 25(4), 259–264. <https://doi.org/10.1087/20120404>
- Hammer, M., Huisman, M., Rigano, A., Boehm, U., Chambers, J. J., Gaudreault, N., Pimentel, J. A., Sudar, D., Bajcsy, P., Brown, C. M., Corbett, A. D., Faklaris, O., Lacoste, J., Laude, A., Nelson, G., Nitschke, R., North, A. J., Gopinathan, R., Farzam, F., ... Strambio-De-Castillia, C. (2021). Towards community-driven metadata standards for light microscopy: tiered specifications extending the OME model. *Nature Methods* (<https://doi.org/10.1038/s41592-021-01327-9>), 18, 1427–1440. <https://doi.org/10.1038/s41592-021-01327-9>
- Hammer, M., Rigano, A., Farzam, F., Huisman, M., Grünwald, D., & Strambio-De-Castillia, C. (December, 9-12 2019). The 4DN-OME ontology: an OME-OWL extension with emphasis on usability, minimum information guidelines, and quality control for super-resolution fluorescence microscopy - Poster. *12th Annual 2019 SWAT4(HC)LS (Semantic Web Applications and Tools for Healthcare and Life Sciences) Conference*. The 12th International SWAT4HCLS Conference, Edinburgh, UK. <https://doi.org/10.6084/m9.figshare.12758957.v1>

- Heddleston, J. M., Aaron, J. S., Khuon, S., & Chew, T.-L. (2021). A guide to accurate reporting in digital image acquisition - can anyone replicate your microscopy data? *Journal of Cell Science*, 134(6).
<https://doi.org/10.1242/jcs.254144>
- Herr, B. W., 2nd, Hardi, J., Quardokus, E. M., Bueckle, A., Chen, L., Wang, F., Caron, A. R., Osumi-Sutherland, D., Musen, M. A., & Börner, K. (2023). Specimen, biological structure, and spatial ontologies in support of a Human Reference Atlas. *Scientific Data*, 10(1), 171. <https://doi.org/10.1038/s41597-023-01993-8>
- Hickey, J. W., Neumann, E. K., Radtke, A. J., Camarillo, J. M., Beuschel, R. T., Albanese, A., McDonough, E., Hatler, J., Wiblin, A. E., Fisher, J., Croteau, J., Small, E. C., Sood, A., Caprioli, R. M., Angelo, R. M., Nolan, G. P., Chung, K., Hewitt, S. M., Germain, R. N., ... Saka, S. K. (2022). Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. *Nature Methods*, 19(3), 284–295. <https://doi.org/10.1038/s41592-021-01316-y>
- Hosseini, R., Vlasveld, M., Willemse, J., van de Water, B., Le Dévédec, S. E., & Wolstencroft, K. J. (2023). FAIR High Content Screening in Bioimaging. *Scientific Data*, 10(1), 462.
<https://doi.org/10.1038/s41597-023-02367-w>
- Hotchkiss, J., Manyisa, N., Adadey, S. M., Oluwole, O. G., Wonkam, E., Mnika, K., Yalcouye, A., Nembaware, V., Haendel, M., Vasilevsky, N., Mulder, N. J., Jupp, S., Wonkam, A., & Mazandu, G. K. (2019). The Hearing Impairment Ontology: A Tool for Unifying Hearing Impairment Knowledge to Enhance Collaborative Research. *Genes*, 10(12). <https://doi.org/10.3390/genes10120960>
- Huisman, M., Hammer, M., Rigano, A., Boehm, U., Chambers, J. J., Gaudreault, N., Pimentel, J. A., Sudar, D., Bajcsy, P., Brown, C. M., Corbett, A. D., Faklaris, O., Lacoste, J., Laude, A., Nelson, G., Nitschke, R., North, A. J., Grunwald, D., & Strambio-De-Castillia, C. (2021). A perspective on Microscopy Metadata: data provenance and quality control. *arXiv [q-bio.QM]*: <https://arxiv.org/abs/1910.11370>.
<https://arxiv.org/abs/1910.11370>
- Jain, S., Pei, L., Spraggins, J. M., Angelo, M., Carson, J. P., Gehlenborg, N., Ginty, F., Gonçalves, J. P., Hagood, J. S., Hickey, J. W., Kelleher, N. L., Laurent, L. C., Lin, S., Lin, Y., Liu, H., Naba, A., Nakayasu, E. S., Qian, W.-J., Radtke, A., ... Snyder, M. P. (2023). Advances and prospects for the Human BioMolecular Atlas Program (HuBMAP). *Nature Cell Biology*, 25(8), 1089–1100.

<https://doi.org/10.1038/s41556-023-01194-w>

- Jupp, S. (n.d.). A new Ontology Lookup Service at EMBL-EBI. In J. Malone (Ed.), *Proceedings of SWAT4LS International Conference 2015*.
- Kemmer, I., Keppler, A., Serrano-Solano, B., Rybina, A., Özdemir, B., Bischof, J., El Ghadraoui, A., Eriksson, J. E., & Mathur, A. (2023). Building a FAIR image data ecosystem for microscopy communities. *Histochemistry and Cell Biology*, 160(3), 199–209. <https://doi.org/10.1007/s00418-023-02203-7>
- Khurana, U., Srinivas, K., Galhotra, S., & Samulowitz, H. (2023). A Vision for Semantically Enriched Data Science. In *arXiv [cs.AI]*. <http://arxiv.org/abs/2303.01378>
- Kinkhabwala, A., Herbel, C., Pankratz, J., Yushchenko, D. A., Rüberg, S., Praveen, P., Reiß, S., Rodriguez, F. C., Schäfer, D., Kollet, J., Dittmer, V., Martinez-Osuna, M., Minnerup, L., Reinhard, C., Dzionek, A., Rockel, T. D., Borbe, S., Büscher, M., Krieg, J., ... Bosio, A. (2022). MACSima imaging cyclic staining (MICS) technology reveals combinatorial target pairs for CAR T cell treatment of solid tumors. *Scientific Reports*, 12(1), 1911. <https://doi.org/10.1038/s41598-022-05841-4>
- KNIME Community, & biomi-konstanz. (2023). *KNIME image processing* (Version v 1.8.3). <https://hub.knime.com/biomi-konstanz/extensions/org.knime.knip.feature/latest>
- Kobayashi, N., Moore, J., Onami, S., & Swedlow, J. R. (Dec 10-11 2019). OME Core Ontology: An OWL-based Life Science Imaging Data Model. In R. Cornet & A. Waagmeester (Eds.), *Proceedings of the 12th SWAT4(HC)LS (Semantic Web Applications and Tools for Healthcare and Life Sciences) Conference* (No. 25; Vol. 2849, pp. 149–150). <http://ceur-ws.org/Vol-2849/paper-25.pdf>. <http://ceur-ws.org/Vol-2849/paper-25.pdf> (Original work published 2019)
- Könnecke, M., Akeroyd, F. A., Bernstein, H. J., Brewster, A. S., Campbell, S. I., Clausen, B., Cottrell, S., Hoffmann, J. U., Jemian, P. R., Männicke, D., Osborn, R., Peterson, P. F., Richter, T., Suzuki, J., Watts, B., Wintersberger, E., & Wuttke, J. (2015). The NeXus data format. *Journal of Applied Crystallography*, 48(Pt 1), 301–305. <https://doi.org/10.1107/S1600576714027575>
- Krahl, R., Darroch, L., Huber, R., Devaraju, A., Klump, J., Habermann, T., Stocker, M., & The Research Data Alliance Persistent Identification of Instruments Working Group members. (2021). *Metadata schema for the persistent identification of instruments*. Research Data Alliance. <https://doi.org/10.15497/RDA00070>

- Kunis, S., & Dohle, J. (2022). *Structuring of Data and Metadata in Bioimaging: Concepts and technical Solutions in the Context of Linked Data*. <https://doi.org/10.5281/zenodo.7018750>
- Kunis, S., Hänsch, S., Schmidt, C., Wong, F., Strambio-De-Castillia, C., & Weidtkamp-Peters, S. (2021). MDEmic: a metadata annotation tool to facilitate FAIR image data management in the bioimaging community. *Nature Methods*, *18*, 1415–1416. <https://doi.org/10.1038/s41592-021-01288-z>
- Larsen, D. D., Gaudreault, N., & Gibbs, H. C. (2023). Reporting reproducible imaging protocols. *STAR Protocols*, *4*(1), 102040. <https://doi.org/10.1016/j.xpro.2022.102040>
- Lawson, C. L., Baker, M. L., Best, C., Bi, C., Dougherty, M., Feng, P., van Ginkel, G., Devkota, B., Lagerstedt, I., Ludtke, S. J., Newman, R. H., Oldfield, T. J., Rees, I., Sahni, G., Sala, R., Velankar, S., Warren, J., Westbrook, J. D., Henrick, K., ... Chiu, W. (2011). EMDatabank.org: unified data resource for CryoEM. *Nucleic Acids Research*, *39*(Database issue), D456–D464. <https://doi.org/10.1093/nar/gkq880>
- Lee, R. M., Eisenman, L. R., Khuon, S., Aaron, J. S., & Chew, T.-L. (2024). Believing is seeing - the deceptive influence of bias in quantitative microscopy. *Journal of Cell Science*, *137*(1). <https://doi.org/10.1242/jcs.261567>
- Linkert, M., Rueden, C. T., Allan, C., Burel, J.-M., Moore, W., Patterson, A., Lorange, B., Moore, J., Neves, C., MacDonald, D., Tarkowska, A., Sticco, C., Hill, E., Rossner, M., Eliceiri, K. W., & Swedlow, J. R. (2010). Metadata matters: access to image data in the real world. *The Journal of Cell Biology*, *189*(5), 777–782. <http://jcb-dataviewer.rupress.org/jcb/doi/10.1083/jcb.201004104>
- Lomax, J. (2019, June 11). *Using ontologies to unlock the full potential of your scientific data - Part 1*. SciBite. <https://scibite.com/news/using-ontologies-to-unlock-the-your-scientific-data-1/>
- Ludin, A., Korir, P. K., Salavert-Torres, J., Kleywegt, G. J., & Patwardhan, A. (2016). EMPIAR: a public archive for raw electron microscopy image data. *Nature Methods*, *13*(5), 387–388. <https://doi.org/10.1038/nmeth.3806>
- Marconato, L., Palla, G., Yamauchi, K. A., Virshup, I., Heidari, E., Treis, T., Toth, M., Shrestha, R. B., Vöhringer, H., Huber, W., Gerstung, M., Moore, J., Theis, F. J., & Stegle, O. (2023). SpatialData: an open and universal data framework for spatial omics. In *bioRxiv*. <https://doi.org/10.1101/2023.05.05.539647>
- Marqués, G., Pengo, T., & Sanders, M. A. (2020). Imaging methods are vastly underreported in biomedical

- research. *eLife*, 9. <https://doi.org/10.7554/eLife.55133>
- Marx, V. (2022a). Imaging standards to ease reproducibility and the everyday. *Nature Methods*, 19(7), 784–788. <https://doi.org/10.1038/s41592-022-01544-w>
- Marx, V. (2022b). The making of microscope camera standards. *Nature Methods*, 19(7), 788–791. <https://doi.org/10.1038/s41592-022-01545-9>
- McCafferty, S., Poger, D., Yvette, W., Seal, C., Burgess, R., & Kenna, E. (2023). Best Practices: PIDs for Instruments. In *Zenodo*. Zenodo. <https://doi.org/10.5281/zenodo.7759201>
- Meyn, S. M., Ramirez-Aguilar, K. A., Gregory, C. W., Mische, S., Ott, A. W., Sol-Church, K., Sturges, M., & Taatjes, D. J. (2022). Addressing the Environmental Impact of Science Through a More Rigorous, Reproducible, and Sustainable Conduct of Research. *Journal of Biomolecular Techniques: JBT*, 33(4). <https://doi.org/10.7171/3fc1f5fe.d085ce95>
- Microscopy Australia*. (2016, June 14). Microscopy Australia. <https://micro.org.au>
- Mitra-Behura, S., Fiolka, R. P., & Daetwyler, S. (2021). Singularity Containers Improve Reproducibility and Ease of Use in Computational Image Analysis Workflows. *Frontiers in Bioinformatics*, 1, 757291. <https://doi.org/10.3389/fbinf.2021.757291>
- Miura, K., & Nørrelykke, S. F. (2021). Reproducible image handling and analysis. *The EMBO Journal*, 40(3), e105889. <https://doi.org/10.15252/embj.2020105889>
- Moffitt, J. R., Lundberg, E., & Heyn, H. (2022). The emerging landscape of spatial profiling technologies. *Nature Reviews. Genetics*, 23(12), 741–759. <https://doi.org/10.1038/s41576-022-00515-3>
- Montero Llopis, P., Senft, R. A., Ross-Elliott, T. J., Stephansky, R., Keeley, D. P., Koshar, P., Marqués, G., Gao, Y.-S., Carlson, B. R., Pengo, T., & Others. (2021). Best practices and tools for reporting reproducible fluorescence microscopy methods. *Nature Methods*, 18(12), 1463–1476. https://idp.nature.com/authorize/casa?redirect_uri=https://www.nature.com/articles/s41592-021-01156-w&casa_token=PACh9_Q1bXIAAAAA:Q_-qCzfAZ2uUL0fpWS9u9ctY-jiNHseLcwwQztqPlqmj0-ybbccjPe2POB0gv8JinC4PiAlLnahijjsE9Q
- Moore, J. (2022, November 29). *The Case for Next-Generation Metadata - Presentation at the OME2022 - Day 3*. 2022 OME Community Meeting , Zoom. <https://doi.org/10.6084/m9.figshare.21556998.v1>

- Moore, J., Allan, C., Besson, S., Burel, J.-M., Diel, E., Gault, D., Kozłowski, K., Lindner, D., Linkert, M., Manz, T., Moore, W., Pape, C., Tischer, C., & Swedlow, J. R. (2021). OME-NGFF: a next-generation file format for expanding bioimaging data-access strategies. *Nature Methods*, *18*(12), 1496–1498.
<https://doi.org/10.1038/s41592-021-01326-w>
- Moore, J., Basurto-Lozada, D., Besson, S., Bogovic, J., Bragantini, J., Brown, E. M., Burel, J.-M., Casas Moreno, X., de Medeiros, G., Diel, E. E., Gault, D., Ghosh, S. S., Gold, I., Halchenko, Y. O., Hartley, M., Horsfall, D., Keller, M. S., Kittisopikul, M., Kovacs, G., ... Swedlow, J. R. (2023). OME-Zarr: a cloud-optimized bioimaging file format with international community support. *Histochemistry and Cell Biology*. <https://doi.org/10.1007/s00418-023-02209-1>
- Moore, J., & Strambio-De-Castillia, C. (2021). *Proposal for a Next-Generation Metadata framework* [Figure]. Zenodo. <https://doi.org/10.5281/zenodo.11265017>
- Musen, M. A., O'Connor, M. J., Schultes, E., Martínez-Romero, M., Hardi, J., & Graybeal, J. (2022). Modeling community standards for metadata as templates makes data FAIR. *Scientific Data*, *9*(1), 696.
<https://doi.org/10.1038/s41597-022-01815-3>
- Nagaraj, A., Shears, E., & de Vaan, M. (2020). Improving data access democratizes and diversifies science. *Proceedings of the National Academy of Sciences of the United States of America*, *117*(38), 23490–23498. <https://doi.org/10.1073/pnas.2001682117>
- Nature Editorial Staff. (2018). Better research through metrology. *Nature Methods*, *15*(6), 395.
<https://doi.org/10.1038/s41592-018-0035-x>
- Nelson, G. (2022). *Monitoring the point spread function for quality control of confocal microscopes v1*. Protocols.io. <https://doi.org/10.17504/protocols.io.bp2l61ww1vqe/v1>
- Nelson, G., Boehm, U., Bagley, S., Bajcsy, P., Bischof, J., Brown, C. M., Dauphin, A., Dobbie, I. M., Eriksson, J. E., Faklaris, O., Fernandez-Rodriguez, J., Ferrand, A., Gelman, L., Gheisari, A., Hartmann, H., Kukat, C., Laude, A., Mitkovski, M., Munck, S., ... Nitschke, R. (2021). QUAREP-LiMi: A community-driven initiative to establish guidelines for quality assessment and reproducibility for instruments and images in light microscopy. *Journal of Microscopy*, *284*(1), 56–73. <https://doi.org/10.1111/jmi.13041>
- NFDI4Plants Consortium. (2022). *Swate: Excel Add-In for annotation of experimental data and computational*

workflows (Version v0.6.2). Github. <https://github.com/nfdi4plants/Swate>

NIH Strategic Plan for Data Science. (n.d.). Retrieved October 27, 2023, from <https://datascience.nih.gov/nih-strategic-plan-data-science>

NOT-OD-21-013: Final NIH Policy for Data Management and Sharing. (n.d.). Retrieved October 24, 2023, from <https://grants.nih.gov/grants/guide/notice-files/NOT-OD-21-013.html>

Ong, E., Sarntivijai, S., Jupp, S., Parkinson, H., & He, Y. (2017). Comparison, alignment, and synchronization of cell line information between CLO and EFO. *BMC Bioinformatics*, 18(Suppl 17), 557. <https://doi.org/10.1186/s12859-017-1979-z>

Pines, J. (2020). Image integrity and standards. *Open Biology*, 10(6), 200165. <https://doi.org/10.1098/rsob.200165>

Preparing your data management plan. (n.d.). NSF - National Science Foundation. Retrieved October 24, 2023, from <https://new.nsf.gov/funding/data-management-plan>

PyTorch Consortium. (2023). *Reproducibility — PyTorch 2.1 documentation*. PyTorch. <https://pytorch.org/docs/stable/notes/randomness.html>

Quardokus, E. M., Saunders, D. C., McDonough, E., Hickey, J. W., Werlein, C., Surrette, C., Rajbhandari, P., Casals, A. M., Tian, H., Lowery, L., Neumann, E. K., Björklund, F., Neelakantan, T. V., Croteau, J., Wiblin, A. E., Fisher, J., Livengood, A. J., Dowell, K. G., Silverstein, J. C., ... Radtke, A. J. (2023). Organ Mapping Antibody Panels: a community resource for standardized multiplexed tissue imaging. *Nature Methods*, 20(8), 1174–1178. <https://doi.org/10.1038/s41592-023-01846-7>

RCSB Consortium. (2019). *Protein Data Bank (PDB)*. Research Collaboratory for Structural Bioinformatics PDB. <https://www.rcsb.org>

Registration overview — SimpleITK. (2024). <https://simpleitk.readthedocs.io/en/master/registrationOverview.html>

Reiff, S. B., Schroeder, A. J., Kırılı, K., Cosolo, A., Bakker, C., Lee, S., Veit, A. D., Balashov, A. K., Vitzthum, C., Ronchetti, W., Pitman, K. M., Johnson, J., Ehmsen, S. R., Kerpedjiev, P., Abdennur, N., Imakaev, M., Öztürk, S. U., Çamoğlu, U., Mirny, L. A., ... Park, P. J. (2022). The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. *Nature Communications*, 13(1), 2365.

<https://doi.org/10.1038/s41467-022-29697-4>

- Rigano, A., Ehmsen, S., Öztürk, S. U., Ryan, J., Balashov, A., Hammer, M., Kirli, K., Boehm, U., Brown, C. M., Bellve, K., Chambers, J. J., Cosolo, A., Coleman, R. A., Faklaris, O., Fogarty, K. E., Guilbert, T., Hamacher, A. B., Itano, M. S., Keeley, D. P., ... Strambio-De-Castillia, C. (2021). Micro-Meta App: an interactive tool for collecting microscopy metadata based on community specifications. *Nature Methods*, *18*(12), 1489–1495. <https://doi.org/10.1038/s41592-021-01315-z>
- Rivest, F., Eroglu, D., Pelz, B., Kowal, J., Kehren, A., Procopio, M. G., Bordignon, P., Pérès, E., Ammann, M., Dorel, E., Scalmazzi, S., Bruno, L., Ruegg, M., Campargue, G., Casqueiro, G., Arn, L., Fischer, J., Brajkovic, S., Joris, P., ... Dupouy, D. (2023). Fully Automated Sequential Immunofluorescence (seqIF) for Hyperplex Spatial Proteomics. In *bioRxiv* (p. 2023.07.07.548135). <https://doi.org/10.1101/2023.07.07.548135>
- Ropelewski, A. J., Rizzo, M. A., Swedlow, J. R., Huisken, J., Osten, P., Khanjani, N., Weiss, K., Bakalov, V., Engle, M., Gridley, L., Krzyzanowski, M., Madden, T., Maiese, D., Mandal, M., Waterfield, J., Williams, D., Hamilton, C. M., & Huggins, W. (2022). Standard metadata for 3D microscopy. *Scientific Data*, *9*(1), 449. <https://doi.org/10.1038/s41597-022-01562-5>
- Rozenblatt-Rosen, O., Regev, A., Oberdoerffer, P., Nawy, T., Hupalowska, A., Rood, J. E., Ashenberg, O., Cerami, E., Coffey, R. J., Demir, E., Ding, L., Esplin, E. D., Ford, J. M., Goecks, J., Ghosh, S., Gray, J. W., Guinney, J., Hanlon, S. E., Hughes, S. K., ... Human Tumor Atlas Network. (2020). The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. *Cell*, *181*(2), 236–249. <https://doi.org/10.1016/j.cell.2020.03.053>
- Ryan, J., Pengo, T., Rigano, A., Montero Llopis, P., Itano, M. S., Cameron, L. C., Marqués, G., Strambio-De-Castillia, C., Sanders, M. A., & Brown, C. M. (2021). MethodsJ2: A Software Tool to Capture and Generate Comprehensive Microscopy Methods Text and Improve Reproducibility. *Nature Methods*, *18*, 1414–1415. <https://doi.org/10.1038/s41592-021-01290-5>
- Sansone, S.-A., Rocca-Serra, P., Field, D., Maguire, E., Taylor, C. F., Hofmann, O., Fang, H., Neumann, S., Tong, W., Amaral-Zettler, L., Begley, K., Booth, T., Bougueleret, L., Burns, G., Chapman, B., Clark, T., Coleman, L.-A., Copeland, J., Das, S., ... Hide, W. (2012). Toward interoperable bioscience data. *Nature*

- Genetics*, 44(2), 121–126. <http://www.nature.com/ng/journal/v44/n2/full/ng.1054.html>
- Sarkans, U., Chiu, W., Collinson, L., Darrow, M. C., Ellenberg, J., Grunwald, D., Hériché, J.-K., Iudin, A., Martins, G. G., Meehan, T., Narayan, K., Patwardhan, A., Russell, M. R. G., Saibil, H. R., Strambio-De-Castillia, C., Swedlow, J. R., Tischler, C., Uhlmann, V., Verkade, P., ... Brazma, A. (2021). REMBI: Recommended Metadata for Biological Images-enabling reuse of microscopy data in biology. *Nature Methods*, 18(12), 1418–1422. <https://doi.org/10.1038/s41592-021-01166-8>
- Schapiro, D., Sokolov, A., Yapp, C., Chen, Y.-A., Muhlich, J. L., Hess, J., Creason, A. L., Nirmal, A. J., Baker, G. J., Nariya, M. K., Lin, J.-R., Maliga, Z., Jacobson, C. A., Hodgman, M. W., Ruokonen, J., Farhi, S. L., Abbondanza, D., McKinley, E. T., Persson, D., ... Sorger, P. K. (2021). MCMICRO: a scalable, modular image-processing pipeline for multiplexed tissue imaging. *Nature Methods*, 19(3), 311–315. <https://doi.org/10.1038/s41592-021-01308-y>
- Schapiro, D., Yapp, C., Sokolov, A., Reynolds, S. M., Chen, Y.-A., Sudar, D., Xie, Y., Muhlich, J., Arias-Camison, R., Arena, S., Taylor, A. J., Nikolov, M., Tyler, M., Lin, J.-R., Burlingame, E. A., Human Tumor Atlas Network, Chang, Y. H., Farhi, S. L., Thorsson, V., ... Sorger, P. K. (2022). MITI minimum information guidelines for highly multiplexed tissue images. *Nature Methods*, 19(3), 262–267. <https://doi.org/10.1038/s41592-022-01415-4>
- Schmied, C., Nelson, M. S., Avilov, S., Bakker, G.-J., Bertocchi, C., Bischof, J., Boehm, U., Brocher, J., Carvalho, M. T., Chiritescu, C., Christopher, J., Cimini, B. A., Conde-Sousa, E., Ebner, M., Ecker, R., Eliceiri, K., Fernandez-Rodriguez, J., Gaudreault, N., Gelman, L., ... Jambor, H. K. (2023). Community-developed checklists for publishing images and image analyses. *Nature Methods*. <https://doi.org/10.1038/s41592-023-01987-9>
- Sheen, M. R., Fields, J. L., Northan, B., Lacoste, J., Ang, L.-H., Fiering, S., & Reproducibility Project: Cancer Biology. (2019). Replication Study: Biomechanical remodeling of the microenvironment by stromal caveolin-1 favors tumor invasion and metastasis. *eLife*, 8. <https://doi.org/10.7554/eLife.45120>
- Shillum, C., Petro, J. A., Demeranville, T., Wijnbergen, I., Hershberger, S., & Simpson, W. (2021). *From Vision to Value: ORCID's 2022–2025 Strategic Plan*. ORCID. <https://doi.org/10.23640/07243.16687207.V1>
- Sickle Cell Disease Ontology Working Group. (2019). The Sickle Cell Disease Ontology: enabling universal

- sickle cell-based knowledge representation. *Database: The Journal of Biological Databases and Curation*, 2019. <https://doi.org/10.1093/database/baz118>
- Snyder, M. P., & HuBMAP Consortium. (2019). The human body at cellular resolution: the NIH Human Biomolecular Atlas Program. *Nature*, 574(7777), 187–192. <https://doi.org/10.1038/s41586-019-1629-x>
- Soiland-Reyes, S., Sefton, P., Crosas, M., Castro, L. J., Coppens, F., Fernández, J. M., Garijo, D., Grüning, B., La Rosa, M., Leo, S., Ó Carragáin, E., Portier, M., Trisovic, A., RO-Crate Community, Groth, P., & Goble, C. (2022). Packaging research artefacts with RO-Crate. *Data Science*, 5(2), 97–138. <https://doi.org/10.3233/ds-210053>
- Solbrig, H., Moxon, S., Unni, D., Vaidya, G., Hegde, H., Duncan, B., Patil, S., Winston, D., Wagner, A., Schafer, K., Putman, T., Haendel, M., & Mungall, C. (2023). *LinkML*. Zenodo. <https://doi.org/10.5281/ZENODO.8084083>
- Steeleworthy, M. (2014). Research Data Management and the Canadian Academic Library: An Organizational Consideration of Data Management and Data Stewardship. *NISTIR 8297*. https://scholars.wlu.ca/lib_pub/29/
- Stirling, D. R., Swain-Bowden, M. J., Lucas, A. M., Carpenter, A. E., Cimini, B. A., & Goodman, A. (2021). CellProfiler 4: improvements in speed, utility and usability. *BMC Bioinformatics*, 22(1), 433. <https://doi.org/10.1186/s12859-021-04344-9>
- Stocker, M., Darroch, L., Krahl, R., Habermann, T., Devaraju, A., Schwardmann, U., D'Onofrio, C., & Häggström, I. (2020). Persistent identification of instruments. *Data Science Journal*, 19. <https://doi.org/10.5334/dsj-2020-018>
- Strambio-De-Castillia, C., Bajcsy, P., Boehm, U., Chambers, J., Corbett, A. D., Faklaris, O., Gaudreault, N., Lacoste, J., Laude, A., Nelson, G., Nitschke, R., Pimentel, J. A., Sudar, D., Brown, C. M., & North, A. J. (2019). *BioImaging North America (BINA): Quality Control and Data Management WG (QC-DM-WG)*. Bioimaging North America Site. <https://www.bioimagingnorthamerica.org/qc-dm-wg/>
- Swedlow, J. R., Goldberg, I. G., Brauner, E., & Sorger, P. K. (2003). Informatics and Quantitative Analysis in Biological Imaging. *Science*, 300(5616), 100–102. <http://www.sciencemag.org/cgi/doi/10.1126/science.1082602>

- Swedlow, J. R., Kankaanpää, P., Sarkans, U., Goscinski, W., Galloway, G., Sullivan, R. P., Brown, C. M., Wood, C., Keppler, A., Loos, B., Zullino, S., Longo, D. L., Aime, S., & Onami, S. (2021). A Global View of Standards for Open Image Data Formats and Repositories. *Nature Methods* (<https://doi.org/10.1038/s41592-021-01113-7>), 18, 1440–1446.
<https://doi.org/10.1038/s41592-021-01113-7>
- Swedlow, J. R., Lewis, S. E., & Goldberg, I. G. (2006). Modelling data across labs, genomes, space and time. *Nature Cell Biology*, 8(11), 1190–1194. <http://www.nature.com/doi/10.1038/ncb1496>
- TensorFlow Development Team. (2023). *TensorFlow _ Configures TensorFlow ops to run deterministically (ConfigExperimentalEnable_op_determinism)* (Version v2.8.4).
https://www.tensorflow.org/versions/r2.8/api_docs/python/tf/config/experimental/enable_op_determinism
- Tromans-Coia, C., Jamali, N., Abbasi, H. S., Giuliano, K. A., Hagimoto, M., Jan, K., Kaneko, E., Letzsch, S., Schreiner, A., Sexton, J. Z., Suzuki, M., Trask, O. J., Yamaguchi, M., Yanagawa, F., Yang, M., Carpenter, A. E., & Cimini, B. A. (2023). Assessing the performance of the Cell Painting assay across different imaging systems. *Cytometry. Part A: The Journal of the International Society for Analytical Cytology*.
<https://doi.org/10.1002/cyto.a.24786>
- UNESCO. (2022). *UNESCO Recommendation on Open Science*. Unesco.
<https://www.unesco.org/en/open-science/about?hub=686>
- UNESCO, & Canadian Commission for UNESCO. (2022). *An introduction to the UNESCO Recommendation on Open Science*. 11. <https://unesdoc.unesco.org/ark:/48223/pf0000383771>
- Vandereyken, K., Sifrim, A., Thienpont, B., & Voet, T. (2023). Methods and applications for single-cell and spatial multi-omics. *Nature Reviews. Genetics*, 24(8), 494–515.
<https://doi.org/10.1038/s41576-023-00580-2>
- Viana, M. P., Chen, J., Knijnenburg, T. A., Vasan, R., Yan, C., Arakaki, J. E., Bailey, M., Berry, B., Borensztein, A., Brown, E. M., Carlson, S., Cass, J. A., Chaudhuri, B., Cordes Metzler, K. R., Coston, M. E., Crabtree, Z. J., Davidson, S., DeLizo, C. M., Dhaka, S., ... Rafelski, S. M. (2023). Integrated intracellular organization and its variations in human iPS cells. *Nature*, 613(7943), 345–354.
<https://doi.org/10.1038/s41586-022-05563-7>

- Vierdag, W.-M. A. M., & Saka, S. K. (2024). A perspective on FAIR quality control in multiplexed imaging data processing. *Frontiers in Bioinformatics*, 4, 1336257. <https://doi.org/10.3389/fbinf.2024.1336257>
- Wilkinson, M. D., Dumontier, M., Aalbersberg, I. J. J., Appleton, G., Axton, M., Baak, A., Blomberg, N., Boiten, J.-W., da Silva Santos, L. B., Bourne, P. E., Bouwman, J., Brookes, A. J., Clark, T., Crosas, M., Dillo, I., Dumon, O., Edmunds, S., Evelo, C. T., Finkers, R., ... Mons, B. (2016). The FAIR Guiding Principles for scientific data management and stewardship. *Scientific Data*, 3, 160018. <https://doi.org/10.1038/sdata.2016.18>
- Wollmann, T., Erfle, H., Eils, R., Rohr, K., & Gunkel, M. (2017). Workflows for microscopy image analysis and cellular phenotyping. *Journal of Biotechnology*, 261, 70–75. <https://doi.org/10.1016/j.jbiotec.2017.07.019>
- Wollmann, T., Hiltmann, S., & Kostykin, L. (2023). *Introduction to image analysis using Galaxy*. <https://training.galaxyproject.org/training-material/topics/imaging/tutorials/imaging-introduction/tutorial.html>
- Wolstencroft, K., Owen, S., Goble, C., Nguyen, Q., Krebs, O., & Muller, W. (2012, October). RightField: Semantic enrichment of Systems Biology data using spreadsheets. *2012 IEEE 8th International Conference on E-Science*. 2012 IEEE 8th International Conference on E-Science (e-Science), Chicago, IL, USA. <https://doi.org/10.1109/escience.2012.6404412>

List of Contributors

Name	Email	ORCID	Affiliation	Funding Statement	Contribution*
Nikki Bialy	nbialy@morgridge.org	https://orcid.org/0000-0001-9681-9632	Biolmaging North America (BINA RRID: SCR_024409), Morgridge Institute for Research, 330 North Orchard Street, Madison, WI 53715, USA.	NB is supported through a grant from the Chan Zuckerberg Initiative DAF, an advised fund of Silicon Valley Community Foundation, to the Morgridge Institute for Research for Biolmaging North America (BINA).	Resources, Writing - Original Draft, Writing - Review & Editing, Endorsement, Supervision, Project Administration
Frank Alber	falber@g.ucla.edu	https://orcid.org/0000-0003-1981-8390	Department of Microbiology, Immunology & Molecular Genetics, University of California Los Angeles, USA		Endorsement
Brenda Andrews	brenda.andrews@utoronto.ca	https://orcid.org/0000-0001-6427-6493	The Donnelly Centre, University of Toronto, Toronto Canada M5S 3E1	Work in the Andrews lab is supported by the NIH (R01HG005853) and the Canadian Institutes of Health Research (CIHR). BA holds at Tier 1 Canada Research Chair in Systems Genetics and Cell Biology	Writing - Original Draft, Endorsement
Michael Angelo	mangelo0@stanford.edu		Stanford University School of Medicine, Palo Alto, CA, USA		Writing - Original Draft
Brian Beliveau	beliveau@uw.edu	https://orcid.org/0000-0003-1314-3118	University of Washington	BJB acknowledges support from the National Institutes of Health under grant 1R35GM137916 (NIGMS).	Writing - Original Draft
Lacramioara (Lacra) Bintu	lbintu@stanford.edu	https://orcid.org/0000-0001-5443-6633	Stanford University, Stanford, CA, USA		Endorsement
Alistair Boettiger	aboettig@stanford.edu	https://orcid.org/0000-0002-3	Stanford University,		Writing - Review & Editing, Endorsement

		554-5196	Stanford, CA, USA		
Ulrike Boehm	ulrike.boehm@gmail.com	https://orcid.org/0000-0001-7471-2244	Carl Zeiss AG, Oberkochen, Germany		Writing - Review & Editing, Endorsement
Claire M. Brown	claire.brown@mcgill.ca	https://orcid.org/0000-0003-1622-663X	Advanced Bioluminescence Imaging Facility (ABIF), McGill University, Montreal, Quebec, H3G 0B1, Canada	This project has been made possible in part by grant number 2020-225398 from the Chan Zuckerberg Initiative DAF, an advised fund of Silicon Valley Community Foundation.	Endorsement
Mahmoud Bukar Maina	M.Bukar-Maina@sussex.ac.uk	https://orcid.org/0000-0002-7421-3813	University of Sussex, Sussex, UK & Biomedical Science Research and Training Centre, Yobe State University, Nigeria		Writing - Review & Editing, Endorsement
James J. Chambers	jjchambe@umass.edu	https://orcid.org/0000-0003-3883-8215	Institute for Applied Life Sciences, University of Massachusetts, Amherst, MA 01003, USA		Endorsement
Beth A. Cimini	bcimini@broadinstitute.org	https://orcid.org/0000-0001-9640-9318	Broad Institute of MIT and Harvard, Imaging Platform, Cambridge, MA, USA	This publication has been made possible in part by CZI grant 2020-225720 (DOI:10.37921/977328 pjbca) from the Chan Zuckerberg Initiative DAF, an advised fund of Silicon Valley Community Foundation (funder DOI 10.13039/100014989. This work was also supported by the Center for Open Bioimage Analysis (COBA) funded by the National Institute of	Writing - Review & Editing, Endorsement

				General Medical Sciences P41 GM135019	
Kevin Eliceiri	eliceiri@wisc.edu	https://orcid.org/0000-0001-8678-670X	Morgridge Institute for Research and the University of Wisconsin-Madison	This work was supported by the Center for Open Bioimage Analysis (COBA) funded by the National Institute of General Medical Sciences P41 GM135019 (Cimini and Eliceiri)	Writing - Review & Editing, Endorsement
Rachel Errington	ErringtonRJ@cardiff.ac.uk		School of Medicine, Cardiff University, Cardiff, UK		Writing - Original Draft, Writing - Review & Editing
Orestis Faklaris	orestis.faklaris@mri.cnrs.fr	https://orcid.org/0000-0001-5965-5405	BCM, Univ. Montpellier, CNRS, INSERM, Montpellier 34293, France	OF is supported by the French National Research Agency (ANR-10-INBS-04).	Writing - Review & Editing, Endorsement
Nathalie Gaudreault	nathalieg@alleninstitute.org	https://orcid.org/0000-0002-9220-5366	Allen Institute for Cell Science, Seattle, WA, USA	We wish to thank the Allen Institute for Cell Science Founder, Paul G. Allen, for his vision, encouragement, and support.	Writing - Review & Editing, Endorsement
Ronald N. Germain	rgermain@niaid.nih.gov	https://orcid.org/0000-0003-1495-9143	Laboratory of Immune System Biology, NIAID, NIH	Intramural Program of NIAID, NIH.	Writing - Review & Editing, Endorsement
Wojtek Goscinski	w.goscinski@anif.org.au	https://orcid.org/0000-0001-6587-1016	National Imaging Facility, Brisbane, Australia	The authors acknowledge the facilities and scientific and technical assistance of the National Imaging Facility, a National Collaborative Research Infrastructure Strategy (NCRIS) capability	Endorsement
David Grunwald	David.Grunwald@umassmed.edu	https://orcid.org/0000-0001-9067-804X	RNA Therapeutics Institute, UMass Chan Medical School, Worcester MA		Writing - Review & Editing, Endorsement

			01605, USA		
Michael Halter	michael.halter@nist.gov	https://orcid.org/0000-0002-1628-324X	National Institute of Standards and Technology, Gaithersburg, MD, USA		Writing - Review & Editing, Endorsement
Dorit Hanein	dorit@ucsb.edu	https://orcid.org/0000-0002-6072-4946	Departments of Biochemistry and Chemistry, of Biological Engineering, University of California, Santa Barbara, CA, USA	DH research is in part sponsored by the U.S. Army Research Office and accomplished under contract W911NF-19-D-0001 for the Institute for Collaborative Biotechnologies.	Writing - Original Draft, Writing - Review & Editing, Endorsement
John W. Hickey	john.hickey@duke.edu	https://orcid.org/0000-0001-9961-7673	Department of Biomedical Engineering, Duke University Durham, North Carolina, USA		Writing - Original Draft, Endorsement
Judith Lacoste	jlacoste@miacellavie.com	https://orcid.org/0000-0002-8783-8599	MIA Cellavie Inc., Montreal, Quebec, H1K 4G6, Canada		Endorsement
Alex Laude	alex.laude@newcastle.ac.uk	https://orcid.org/0000-0002-3853-1187	Biolmaging Unit, Newcastle University, UK	Newcastle University	Endorsement
Emma Lundberg	emmalu@stanford.edu		Stanford University, California, USA and SciLifeLab, KTH Royal Institute of Technology, Stockholm, Sweden		Endorsement
Jian Ma	jianma@cs.cmu.edu	https://orcid.org/0000-0002-4202-5834	Carnegie Mellon University, Pittsburgh, PA, USA		Endorsement
Leonel Malacrida	lmalacrida@pasteur.edu.uy	https://orcid.org/0000-0001-6253-9229	Institut Pasteur de Montevideo, & Universidad de la República, Montevideo, Uruguay		Endorsement

Josh Moore	josh@openmicroscopy.org	https://orcid.org/0000-0003-4028-811X	German Bioimaging-Gesellschaft für Mikroskopie und Bildanalyse e.V., Constance, Germany	JM is supported by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) – 501864659 as part of NFDI4BIOIMAGE.	Writing - Review & Editing, Endorsement
Glyn Nelson	glyn.nelson@ncl.ac.uk	http://orcid.org/0000-0002-1895-4772	Bioimaging Unit, Newcastle University, Newcastle upon Tyne, NE2 4HH, UK	Newcastle University, UK	Writing - Review & Editing, Endorsement
Elizabeth Kathleen Neumann	ekneumann@ucdavis.edu	https://orcid.org/0000-0002-6078-3321	Department of Chemistry, University of California, Davis, Davis, California, USA	University of California, Davis	Endorsement
Roland Nitschke	Roland.Nitschke@biologie.uni-freiburg.de	https://orcid.org/0000-0002-9397-8475	Life Imaging Center, Signalling Research Centres CIBSS and BIOS, University of Freiburg, 79104 Freiburg, Germany	R.N. was supported by grant NI 451/10-1 from the German Research Foundation and grant 03TN0047B 'FluMiKal' from the German Federal Ministry for Economic Affairs and Climate Action	Writing - Review & Editing, Endorsement
Shuichi Onami	sonami@riken.jp	https://orcid.org/0000-0002-8255-1724	RIKEN Center for Biosystems Dynamics Research, Kobe, Japan		Endorsement
Jaime A. Pimentel	arturo.pimentel@ibt.unam.mx	https://orcid.org/0000-0001-8569-0466	Laboratorio Nacional de Microscopía Avanzada, Instituto de Biotecnología, Universidad Nacional Autónoma de México, Cuernavaca, Morelos, 62210, México		Writing - Review & Editing, Endorsement
Anne L. Plant	anne.plant@nist.gov	https://orcid.org/0000-0002-8538-401X	National Institute of Standards and Technology,		Writing - Review & Editing, Endorsement

			Gaithersburg, MD, USA		
Andrea J. Radtke	andrea.radtke@nih.gov	https://orcid.org/0000-0003-4379-8967	Laboratory of Immune System Biology, Lymphocyte Biology Section and Center for Advanced Tissue Imaging, NIAID, NIH, Bethesda, MD, USA	AJR is supported by the Intramural Research Program of the NIH, National Institute of Allergy and Infectious Diseases (NIAID) and National Cancer Institute (NCI)	Writing - Original Draft, Writing - Review & Editing, Endorsement
Bikash Sabata	bsabata@altoslabs.com	NA	Altos Labs, Redwood City, CA, USA	NA	Writing - Review & Editing, Endorsement
Denis Schapiro	Denis.Schapiro@uni-heidelberg.de	https://orcid.org/0000-0002-9391-5722	Institute for Computational Biomedicine, Heidelberg University Hospital, Heidelberg, Germany; Institute of Pathology, Heidelberg University Hospital, Heidelberg, Germany; Translational Spatial Profiling Center (TSPC), Heidelberg, Germany	DS is supported by the German Federal Ministry of Education and Research (BMBF 01ZZ2004); the Ministry for Science, Research and Science Baden-Württemberg „AI Health Innovation Cluster“ and "MULTI-SPACE"; Bruno und Helene Joester Stiftung and research funding from Cellzome, a GSK company.	Writing - Original Draft, Writing - Review & Editing, Endorsement
Johannes Schöneberg	jschoeneberg@health.ucsd.edu	https://orcid.org/0000-0001-7083-1828	University of California, San Diego, CA, USA	JS is supported by the Hartwell Foundation, the W.M.Keck Foundation, the Brain Research Foundation, The Chan Zuckerberg Foundation, and the NIH (1DP2GM150022-01, 1R01GM148765-01).	Writing - Review & Editing, Endorsement

Jeffrey M. Spraggins	jeff.spraggins@Vanderbilt.Edu	https://orcid.org/0000-0001-9198-5498	Department of Cell & Developmental Biology, Vanderbilt University School of Medicine, Nashville, TN, USA	J.M.S. is supported by the National Institutes of Health U01DK133766 (NIDDK), U54DK134302 (NIDDK), U54EY032442 (NEI), R01AG078803 (NIA), R01AI145992 (NIAID), and R01AI138581 (NIAID).	Writing - Review & Editing
Damir Sudar	dsudar@qitissue.com	https://orcid.org/0000-0002-2510-7272	Quantitative Imaging Systems LLC, Portland, OR, USA	DS is supported by the National Institutes of Health U2CCA23380 (NCI) and 1 R44 CA250861 (NCI).	Endorsement
Wouter-Michiel Adrien Maria Vierdag	michiel.vierdag@embl.de	https://orcid.org/0000-0003-1666-5421	Genome Biology Unit, European Molecular Biology Laboratory, Heidelberg, Baden-Württemberg, Germany	WMV receives research funding from Cellzome, a GSK company.	Writing - Original Draft, Writing - Review & Editing
Niels Volkmann	nvo@ucsb.edu	https://orcid.org/0000-0003-1328-6426	Departments of Bioengineering, of Biological Engineering, Electrical and Computer Engineering, and Biomolecular Science and Engineering Program, University of California, Santa Barbara, CA, USA		Writing - Original Draft, Writing - Review & Editing, Endorsement
Carolina Wahlby	carolina.wahlby@it.uu.se	https://orcid.org/0000-0002-4139-7003	Dept. Information Technology and Science for LifeLaboratory, Uppsala University, Uppsala, Sweden		Writing - Review & Editing, Endorsement

Siyuan (Steven) Wang	siyuan.wang@yale.edu	https://orcid.org/0000-0001-6550-4064	Yale University		Endorsement
Ziv Yaniv	zivyaniv@nih.gov	https://orcid.org/0000-0003-0315-7727	Bioinformatics and Computational Bioscience Branch, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD, USA	Z.Y. is supported by the Bioinformatics and Computational Biosciences Branch (BCBB) Support Services Contract HHSN316201300006 W/75N93022F00001 to Guidehouse Inc.	Writing - Original Draft, Writing - Review & Editing, Endorsement
Caterina Strambio-De-Castillia	caterina.strambio@umassmed.edu	https://orcid.org/0000-0002-1069-1816	Program in Molecular Medicine, UMass Chan Medical School, Worcester MA 01605, USA		Conceptualization, Methodology Resources, Writing - Original Draft, Writing - Review & Editing, Endorsement, Supervision, Funding acquisition

* Author contributions categories comply with the CRediT initiative (Allen et al., 2019)

Acknowledgements

Disclaimer: Commercial products are identified in this document in order to specify the experimental procedure adequately. Such identification is not intended to imply recommendation or endorsement by the National Institute of Standards and Technology, nor is it intended to imply that the products identified are necessarily the best available for the purpose. The Authors thank Darryl Conte Jr., Ph.D., for insightful comments and suggested revisions to the manuscript.

Conflict of Interest Statements

Below are the statements shared by contributors indicating potential conflict of interest.

Name	Statement
Ulrike Boehm	UB's contribution to this manuscript is a result of her voluntary involvement with QUAREP-LiMi and BINA, and does not reflect the position of Carl Zeiss AG on this matter.

Josh Moore	holds equity in Glencoe Software.
Denis Schapiro	DS reports funding from GSK and received honorariums from Immunai, Noetik, Alpenglow and Lunaphore.
Damir Sudar	DSu is employed by Quantitative Imaging Systems, a commercial entity developing imaging software.
Siyuan (Steven) Wang	Founder, shareholder, consultant of Translura, Inc

Supplemental Materials

Supplemental Table 1

A non-exhaustive list of relevant communities and initiatives.

Type	Name	Link
European FAIR data and service infrastructure	European Open Science Cloud	https://www.eosc.eu/
European imaging data initiative	EUCAIM: European Federation for CAncer IMages	https://www.eibir.org/projects/eucaim/
Federation of Scientific Societies	FASEB Dataworks	https://www.faseb.org/data-management-and-sharing
German National Scientific Data Infrastructure	Multi Disciplinary (Data Science, BioImage, etc. etc.)	https://www.nfdi.de/
International community	ABRF: Association of Biomolecular Resource Facilities - Committee on Core Rigor and Reproducibility (CCoRRe)	https://www.abrf.org; https://www.abrf.org/core-rigor-and-reproducibility-ccorre-
International community	African BioImaging Consortium (ABIC)	https://www.africanbioimaging.org/
International community	AI4Life: AI models and methods for the life sciences (image data)	https://ai4life.eurobioimaging.eu/
International community	BioImaging North America (BINA) Quality Control and Data Management working group and AIMM interest working group	https://www.bioimagingnorthamerica.org/
International community	Global BioImaging	https://globalbioimaging.org
International Community	Human BioMolecular Atlas Program	https://portal.hubmapconsortium.org/
International	IBEX Imaging Community	https://ibeximagingcommunity.github.io/ibex_imaging

Community		knowledge base/
International community	Latin American Bioimaging (LABI)	https://labi.lat/
International community	NEUBIAS - Network of European BioImage Analysts/SoBIAS - Society for Bioimage Analysis	https://eubias.org/NEUBIAS/
International community	Open Microscopy Environment (OME)	https://www.openmicroscopy.org/
International community	QUAREP-LiMi	https://quarep.org/ https://quarep.org/working-groups/wg-7-metadata/
International community	vEM: Volume Electron Microscopy	https://www.volumeem.org/#/
International imaging infrastructure (open access)	Euro-BioImaging ERIC	www.eurobioimaging.eu
National/International community	Canada BioImaging	https://www.canadabioimaging.org/
National/International community	I3D:bio - Information Infrastructure for BioImage Data initiative (Germany)	https://www.i3dbio.de
National imaging data initiative	NCI Imaging Data Commons (USA)	https://portal.imaging.datacommons.cancer.gov/
National imaging data initiative	NFDI4BIOIMAGE (Germany)	https://nfdi4bioimage.de
National image data initiative	RDM4mic (Germany)	https://german-bioimaging.github.io/RDM4mic.github.io/