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

To the Editor — Proper reporting of metadata is essential to reproduce microscopy experiments, interpret results and share images[1,2]. The lack of methods reporting in microscopy is evident in that few research articles pass a test for the minimal information required to reproduce experiments[1] (about 17% of 240 articles containing 1,500 figures with images). The problem is compounded by the number and variety of microscope modalities, options and associated components. Automation has distanced researchers from the technical parameters, so it can be difficult for them to know what information needs to be reported. MethodsJ2 is an ImageJ/Fiji-based software tool that aims to improve reproducibility in microscopy by capturing image metadata from multiple sources, consolidating it and automatically generating methods text for publication.

To properly evaluate and reproduce microscopy images, information about sample preparation, experimental conditions, microscope hardware, image acquisition settings and image analysis parameters is required. This information is called metadata and is defined as 'a set of data that describes and gives information about other data'. Researchers involved in the 4D Nucleome initiative[3] and Bioimaging North America (BINA) (https://www.bioimagingna.org/) have developed extensive community-driven specifications for microscopy metadata[4,5]. These specifications build on a previous Open Microscopy Environment (OME) model[6] and include an in-depth community-driven microscopy metadata model for light microscopy called 4DN-BINA-OME[4]. The model scales with experimental design, instrument complexity and the degree to which image processing and quantitative image analysis are required for interpreting results. This ensures that essential information is included while minimizing the burden on experimental scientists to collect and report metadata[7].

Microscope metadata guidelines[8–10], examples of what can go wrong if metadata are not reported[11] and descriptions of the importance of measuring and reporting microscope quality control[12] have been published. Increased awareness and education around microscopy metadata and straightforward accessible tools are vital for successful implementation of such guidelines. MethodsJ2 is an extensible, open-source microscopy methods reporting software tool that runs in ImageJ/Fiji and builds on MethodsJ[1,13,14]. Integration with ImageJ/Fiji should make it broadly available to experimental scientists.

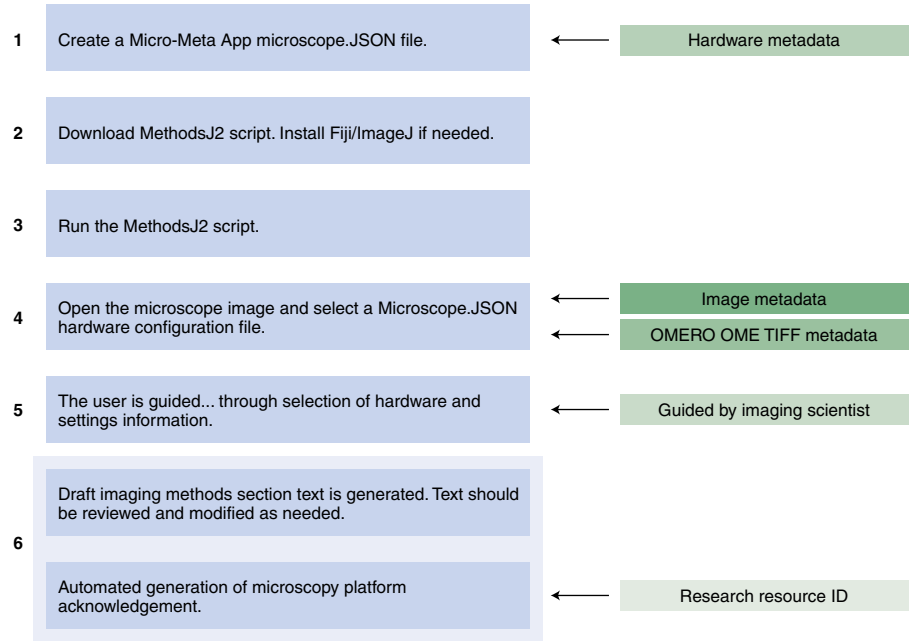

Fig. 1 | MethodsJ2 workflow overview. Steps required to automatically generate microscopy methods text. Image metadata are collected from the microscope image acquisition software metadata in the image file using the OME TIFF tools. Hardware metadata are collected from a Micro-Meta App Microscope.JSON file.

MethodsJ2 automatically gathers metadata from the image using OME BioFormats (for example, pixel size, magnification) and captures microscopy metadata from a Microscope.JSON file generated using Micro-Meta App[5,15]. Micro-Meta App is a companion software tool that guides researchers step-by-step in the collection of community-standardized microscopy metadata for a specific microscope[4]. MethodsJ2 also guides the user to enter specific experimental and sample metadata (for example, cell type, dyes). Finally, the software guides the user through a step-by-step validation of the metadata. To improve tracking of imaging facility impact, acknowledgement text, including a facility Research Resource ID (RRID, https://scicrunch.org/resources) can be added to the script. The methods text is then automatically generated but must be reviewed and edited.

Comprehensive methods reporting is essential for reporting imaging data, sharing images and emerging new methods[16–22]. Progress along the path of rigor and reproducibility is essential for high quality microscope-based science and is a shared responsibility. Experimental scientists must use due diligence to understand the fundamentals of the technologies and required microscope metadata on which their research relies. Imaging scientists need to educate experimental scientists, so that they understand what metadata need to be reported and why. Microscope manufacturers ought to integrate, automate and report microscope metadata. Scientific publishers and reviewers have a duty to promote community-based guidelines[4,6,23]

and to ensure that published microscope images meet a minimum standard. Funding agencies need to uphold high-quality reproducible microscope images and ensure that detailed microscope metadata are available when images are publicly shared.

MethodsJ2 and two companion software tools — Micro-Meta App[15] and OMERO.mde[23] — advance rigor and reproducibility in microscopy (Supplementary Fig. 1), but there are still challenges. Microscopy metadata are often limited, not in standard formats, not accessible owing to the use of proprietary microscope manufacturer software and/or lost when images are saved and opened with third-party software[4]. Microscope manufacturers need to work with the global community through organizations such as Quality Assessment and Reproducibility for Instruments & Images in Light Microscopy (QUAREP-LiMi)[24,25] to automate the collection of metadata, ensure they conform to community standards[4,6,23] and make them readily available. The implementation and evolution of MethodsJ2, Micro-Meta App[15] and OMERO.mde[23], will promote transparency and reproducibility and help stakeholders to ensure that microscopy metadata are documented and reported.

The following list describes the MethodsJ2 workflow (summarized in Fig. 1); a more detailed workflow and sample microscope metadata are available in the Supplementary Information.

1. Use Micro-Meta App to create and save a Microscope.JSON file. Give components detailed names, as this text populates the methods text. For example, put '63×/1.4 NA Plan-Apochromatic oil immersion' rather than '63×'.
2. Download the MethodsJ2 script (file named: MethodsJ2_v1_2_.py), an example Microscope.JSON file and an example image file from GitHub (https://github.com/ABIF-McGill/MethodsJ2). Download and install ImageJ/Fiji (https://fiji.sc/).
3. Drag the MethodsJ2 script file and drop it onto the ImageJ/Fiji toolbar. The script editor will open, then press 'Run'.
4. Select an image file. The image metadata are automatically extracted. Sample information can be added manually. Select a Microscope.JSON file for the corresponding microscope.
5. Follow the step-by-step guidance to validate the metadata and input critical hardware and settings information. Note: have an experienced microscope user or imaging scientist help with this step.
6. Click 'OK'. Draft methods text and any custom facility acknowledgment statement are automatically generated and appear in a popup window, are copied to the clipboard and can be pasted into a manuscript. A.csv file of the microscope metadata is generated and saved (see the sample.csv file in the Supplementary Information and on the GitHub portal). Note: it is the responsibility of the experimental scientists to review the draft text and ensure that it is accurate.

Reporting summary

Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at https://doi.org/10.1038/s41592-021-01290-5.

Data availability

Data in the form of a sample image and Microscope.JSON file are available at https://github.com/ABIF-McGill/MethodsJ2.

Code availability

Full source code and step-by-step instructions are available at https://github.com/ABIF-McGill/MethodsJ2 and https://doi.org/10.5281/zenodo.5172827. ❐

Joel Ryan[1,2], Thomas Pengo[3], Alex Rigano[4], Paula Montero Llopis[5], Michelle S. Itano[6,7,8,9], Lisa A. Cameron[10], Guillermo Marqués[11,12], Caterina Strambio-De-Castillia[4], Mark A. Sanders[11,12] and Claire M. Brown[1,2] ✉

[1]Advanced BioImaging Facility (ABIF), McGill University, Montreal, Quebec, Canada. [2]Department of Physiology, McGill University, Montreal, Quebec, Canada. [3]University of Minnesota Informatics Institute, University of Minnesota, Minneapolis, MN, USA. [4]Program in Molecular Medicine, University of Massachusetts Chan Medical School, Worcester, MA, USA. [5]MicRoN, Department of Microbiology, Harvard Medical School, Boston, MA, USA. [6]Neuroscience Microscopy Core, University of North Carolina, Chapel Hill, NC, USA. [7]Department of Cell Biology & Physiology, University of North Carolina, Chapel Hill, NC, USA. [8]Carolina Institute for Developmental Disabilities, University of North Carolina, Chapel Hill, NC, USA. [9]UNC Neuroscience Center, University of North Carolina, Chapel Hill, NC, USA. [10]Light Microscopy Core Facility, Duke University, Durham, NC, USA. [11]University Imaging Centers, University of Minnesota, Minneapolis, MN, USA. [12]Department of Neuroscience, University of Minnesota, Minneapolis, MN, USA.
✉*e-mail: claire.brown@mcgill.ca*

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Author contributions
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Check for updates

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

To the Editor — Although today the majority of scientific data, including microscopy and imaging data, are available in digital format, a real benefit from easy sharing and reuse of digital data according to the FAIR (findability, accessibility, interoperability and reusability) principles[1] exists only if data are understandable and unambiguously interpretable. Collecting and maintaining the relevant metadata is key to ensuring that data are reliable and reusable and can be found and accessed by the scientific community. Imaging data are usually extremely rich data files, as they report on various parameters in a multidimensional space and are acquired with complex microscopy instruments. The metadata or data models are very diverse due to the wide range of, for example, modalities, scales, experimental setups and file formats. Therefore, the appropriate use of suitable standardized metadata and data models is a challenge[2,3]. Accordingly, flexible tools for capturing a complete

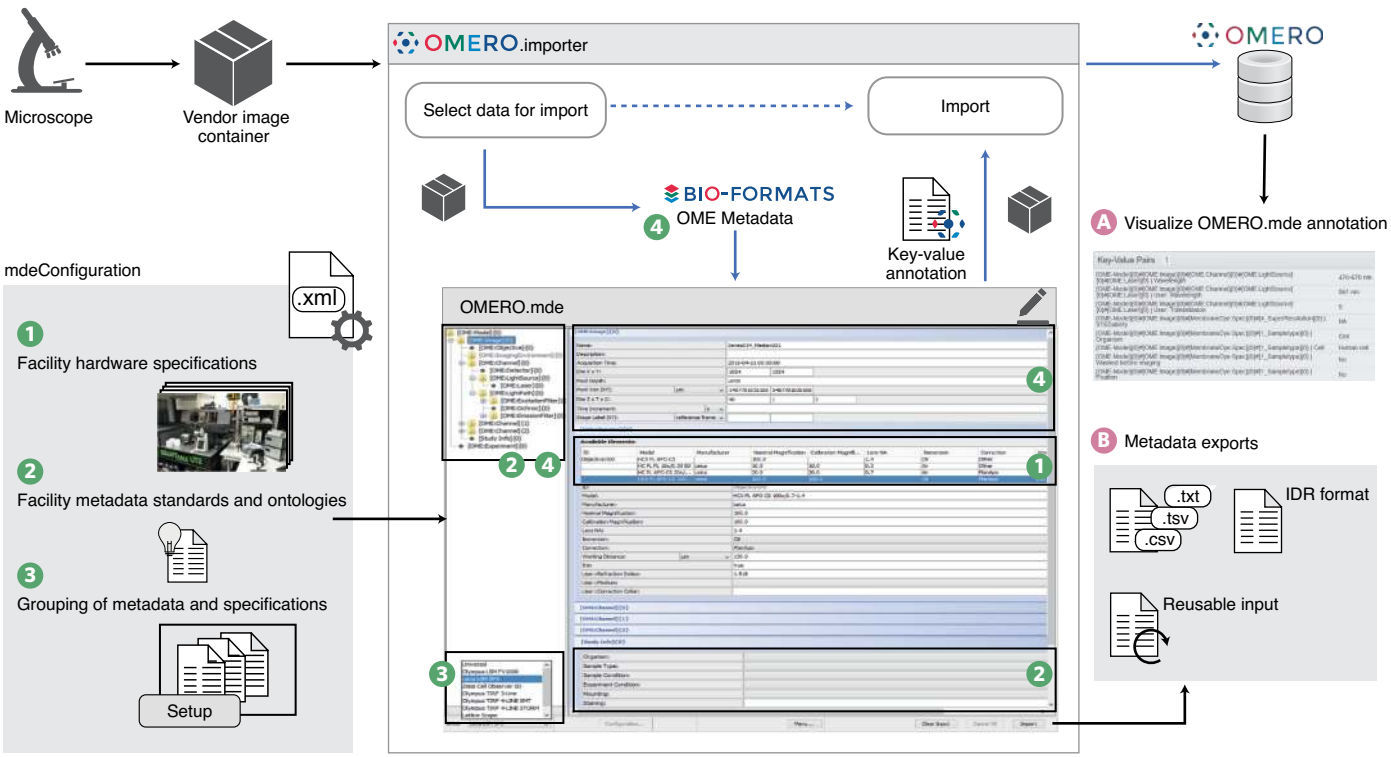

Fig. 1 | OMERO.importer with integrated MDEmic as OMERO.mde. In OMERO.importer, the MDEmic tool is integrated as an intermediate step for the selection of data for import and for the import itself. Metadata can then be added, which is transferred to the repository together with the image data (**A**); or the annotations can be exported in different formats in this step (**B**). MDEmic can be customized via a configuration file and loads the specifications from this file dynamically when the OMERO.importer is started (1, 2, 3). All technical metadata of the images marked in the previous step of data selection are read out by Bio-Format (4) and provided as values in MDEmic.