#### **Supplementary information**

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

In the format provided by the authors and unedited



Supplemental Figure 1: Quality, rigor, reproducibility and sharing value for imaging experiments require the definition of community-driven Microscopy Metadata specifications and the adoption of easy-to-use metadata collection tools to facilitate the documentation and quality control tasks for experimental scientists. The establishment of FAIR (Wilkinson et al., 2016), community-driven Microscopy Image Data Standards implies parallel development on three interrelated fronts: (WHERE) Next-Generation File Formats (NGFF) where the ever-increasing scale and complexity of image data and metadata would be contained for exchange (Moore et al., 2021); blue bubble). (WHAT) Community-driven specifications for what 'data provenance' information (microscope hardware specifications, image acquisition settings and image structure metadata) and quality control metrics are essential for rigor, reproducibility, and reuse and should therefore be captured in Microscopy Metadata (magenta bubble). (HOW) Shared rules for how the (ideally) automated capture, representation and storage of Microscopy Metadata should be implemented in practice (yellow bubble). Micro-Meta App, MethodsJ2 and OMERO.mde are three highly interoperable tools and complementary that function to: 1) train users on the importance of documentation and guality control; 2) facilitate metadata extraction, collection, and storage; 3) automatically write Methods sections; and 4) facilitate the development of experimental metadata specifications in connection with local core facilities. To facilitate adoption by users with different use-styles and preferences, the three tools each work in a specialized environment: Micro-Meta App is used as stand-alone app or can be integrated in third-party image data portals. MethodsJ2 works as an ImageJ plugin. OMERO.mde works in the context of the OMERO image data repository. The different tools are based on different software platforms in order to appeal to the broadest community including microscope builders, imaging scientists working in core facilities and experimental scientists. The concept is to bring the tools to software platforms people are already using and lower the bar to enable broad uptake.

### MethodsJ2 step-by-step overview

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https://github.com/ABIF-McGill/MethodsJ2

### MethodsJ2 - Workflow



### MethodsJ2 - run



Drag and drop MethodsJ2.py on the main Fiji toolbar. Alternatively, click File > New > Script, then in the Script Editor, Click File > Open, and select MethodsJ2.py

Check language: click Language and select Python

Once the script is loaded is ready, click Run

It may take a few seconds to start.

### MethodsJ2 – select image

	MethodsJ2	
Welcome to Methods	J2 – a tool to help write materials and methods sections for imaging experime	ents
First, the script will e	xtract as much information as possible from the metadata of an image file.	Select an image to load and to source metadata.
Please select an image re	presentative of your imaging experiments Brov	Click on Browse and navigate to the image, or drag and drop in
🗹 Display original m	netadata (recommended)	image file into the text input field
✓ Display Bio-Form Save output:	ats OME-XML metadata (recommended)	Optional: display metadata windows (useful for filling out dialog boxes later)
Save methods dat	a in same folder as image 🛛 Select a folder to save methods data	, , , , , , , , , , , , , , , , , , ,
	Cancel	OKSelect where to save the csv file output of the script.

#### MethodsJ2 – select image

BPAE\_3color\_30p-200ms\_63xOil\_003\_diffExp\_Int\_.czi (50%)
 1/3 (c:1/3 - BPAE\_3color\_30p-200ms\_63xOil\_003\_diffExp\_Int\_\_.czi #); 145.86x



### MethodsJ2 – Sample Preparation

Sample Preparation Information					
Please describe your experiment, the sample, and how your sample was mounted					
Sample description:	BPAE cells				
Sample preparation:	fixed and stained with DAPI, Phalloidin-AF488 and Mitotracker				
Mounting medium:	Cytoseal				
Coverglass:	No. 1.5				
Sample holder:	Glass slide				
	Cancel OK				

Please provide information about the sample, and how it was prepared for imaging

Given the variety of samples and preparations, no text is generated for sample description. It is more of a reminder for users to provide complete sample information.

### MethodsJ2 – Image dimensions

	Image o	dimensions	Please ver
According to the metac	lata, you have sel	ected an image with the following dimensions:	image me
Image width in pixels (X):	1012	]	
Image height in pixels (Y):	1020		
Number of slices (Z):	1		
Number of channels (C):	3		
Number of frames (T):	1		
Dimension order:	XYCZT		
Pixel size XY (micron):	0.14		
Voxel size Z (micron):	n/a		
Time interval:	n/a		
		Cancel OK	

Please verify image dimensions. Values are sourced from the image metadata

### MethodsJ2 – select Microscope.json file

Microscope hardware: select the Micro-Meta App Microscope.json file	
According to the metadata: The selected image has a width of 1012 pixels, a height of 1020 pixels, 3 channel(s), 1 slice(s), and 1 frame(s), with a dimensional order of XYCZT. The latera	al pixel size is 0.14 microns.
This image appears to have been acquired on a:	
Zeiss wide field	
Please select a Micro-Meta App json file corresponding to this system -2//abif_axiovert1json Browse	
	Cancel OK

Choose Micro-Meta App hardware specifications file for the microscope used to acquire the selected image

## MethodsJ2 – choose descriptor and software

Microscope system overview			
According to	the metadata, this image was ac	quired on a:	
Zeiss wide field			
You have sel ABIF Axiover an Compour	ected a Micro-Meta App file for a t1, id system made by Zeiss.	a	
Please select the	best descriptor for this system	Widefield Epifluorescence	<b>\$</b>
	Acquisition software:	Zen 🗘	
		Cancel	ОК

Please select the best descriptor for the selected microscope, as well as the acquisition software.

### MethodsJ2 – select objective

	Select objective			
The metadata 63x NA 1.4	suggests that the following objective was used			
Select objective:	63X PLAN APOCHROMAT, NA=1.40, OIL, DIC			
	Cancel OK			
	Select objective			
The metadata suggests that the following objective was used 63x NA 1.4				
Select objective:	<ul> <li>✓ 10X PLAN NEOFLUAR, NA= 0.30, Ph 1</li> <li>20X PLAN APOCHROMAT, NA=0.80</li> <li>40X LD ACHROPLAN, NA=0.60, Ph2, Korr</li> </ul>			

Select the objective used for this experiment.

A suggestion is made based on the metadata, and the list of objectives to choose from is sourced from the microscope configurations file.

The drop-down menu is populated from objectives available in the Micro-Meta app hardware specifications file.

# MethodsJ2 – Channel acquisition settings

•	Channel 1: Excitation, wavelen	gth and detector selection	
The image metadata s	uggests that the excitation wavelength fo	or channel 1 is 353 nm and the emis	ssion wavelength is 465 nm.
Channel Description (e.g. f	luorophore, labeled protein or cell type):	DAPI	
	Light source:	X-Cite light source	
	Light source intensity:	50 %	
	Select excitation filter:	G 365 - DAPI excitation filter	
	Select dichroic:	FT 395 – DAPI beamsplitter	
	Select emission filter:	BP 445/50 – DAPI emission filter	r 😒
	Detector:	Axiocam 506	
			Cancel OK
🛑 🔵 🔵 Channe	el 1: camera settings		Please fill in information for the
E	xposure time: 100.00 ms		first channel
Gain (if adjustable a	nd available):		
Ca	mera Binning: 2x2 ᅌ		Options in drop-down menus ar sourced from the microscope configuration file.
	Cancel OK		Detector settings are based on

Detector settings are based on whether a camera or point detector is selected

## MethodsJ2 – Channel acquisition settings loop

Channel 1: Excitation, wavelength and	d detector selection
Channel 2: Excitation, waveleng	gth and detector selection
The image metadata suggests that the excitation wavelength fo	or channel 2 is 488 nm and the emission wavelength is 509 nm.
Channel Description (e.g. fluorophore, labeled protein or cell type):	Phalloidin-AF4:
Light source:	X-Cite light source
Light source intensity:	40 %
Select excitation filter:	BP 450–490 – GFP excitation filter
Select dichroic:	FT 510 – GFP beamsplitter
Select emission filter:	BP 515–565 – GFP emission filter ᅌ
Channel 1: camera settings	Avison FOC
	Cancel OK
Gai Exposure time:	150.00 ms
Gain (if adjustable and available):	
Camera Binning:	2x2 Channel menus will loop through the channels in the selected
Cancol	I OK image.
	Channel 1: Excitation, wavelength ar Channel 2: Excitation, wavelength for Channel Description (e.g. fluorophore, labeled protein or cell type): Light source: Light source intensity: Select excitation filter: Select dichroic: Select emission filter: Channel 1: camera settings Channel 2: camera settings Gai Gain (if adjustable and available): Camera Binning:

### MethodsJ2 – select optional devices

<u> </u>				
Enviroi	Environmental conditions maintained by device (temperature, CO2, humidity) Focus Stabilization:			
			Canaal	
			Cancel	UK

Choose whether optional devices from the microscope hardware specifications file were used for the selected image.

## MethodsJ2 – Sample text for acknowledgement

Acknowledgements			
Please remember to	acknowledge the imaging core facility and sta	ff in your publications	
To facilitate th	nis, please enter the name of the core facility:	Advanced BioImaging Facility at McGill	
lease enter the name	of a core facility staff member, if appropriate:	Joel Ryan	
Please en	ter a Research Resource ID (RRID) if available:	SCR_017697	
		Cancel	ОК

Please enter the name of the core facility or laboratory which manages the microscope used for the acquisition of the selected image, as well as any imaging scientist who was helpful in the imaging experiment, and if available a Research Resource ID

#### MethodsJ2 – text output

MethodsJ2 output ×	🕌 MethodsJ2 output	×
MethodsJ2 text generation based on user input and on a Micro-Meta App hardware file	MethodsJ2 text generation based on user input and on a Micro-Meta App hardware file	
Images were acquired on a Axiovert 200M Compound Commercial-custom modified inverted microscope (Zeiss) configured for Widefield Epifluorescence microscopy, controlled with Zen software (2.6 Blue edition, Zeiss), equipped with a 63x NA 1.4 Apochromat DIC oil object ve (Zeiss). Images had a width of 1012 and a height of 1020 pixels, 1 planes (z), 3 channels, 1 timepoints, with dimensional order XYCZT. Voxels had a lateral size of 0.14 um.	Images were acquired on a Axiovert 200M Compound Commercial-custom modified inverted microscope (Zeiss) of Epifluorescence microscopy, controlled with Zen software (2.6 Blue edition, Zeiss), equipped with a 63x NA 1.4 Aprove (Zeiss). Images had a width of 1012 and a height of 1020 pixels, 1 planes (z), 3 channels, 1 timepoints, with din Voxels had a lateral size of 0.14 um. DAPI was excited with a X-Cite 120 LED light source (Excelitas) set to 50 % and wavelength selection was carried	s) configured for Widefield Apochromat DIC oil objecti dimensional order XYCZT. ed out with a G 365 excitati
on filter (Zeiss), a FT 395 dichroic mirror (Zeiss) and a BP 445/50 emission filter (Zeiss). Images were acquired on a Axiocam506 CCD ca mera (Zeiss) with an exposure time of 100.00 ms with gain set to and 2x2 binning. Phalloidin Alexa Fluor 488 was excited with a X-Cite 12 0 LED light source (Excelitas) set to 40 % and wavelength selection was carried out with a BP 450-490 excitation filter (Zeiss), a FT 510 di hroic mirror (Zeiss) and a BP 515-565 emission filter (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) with an exposure ure time of 150.00 ms with gain set to and 2x2 binning. MitoTracker Orange was excited with a X-Cite 120 LED light source (Excelitas) set o 30 % and wavelength selection was carried out with a BP 546/12 excitation filter (Zeiss), a FT 580 dichroic mirror (Zeiss) and a LP 590 e mission filter (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) with an exposure mission filter (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) and a LP 590 e mission filter (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with gain set to an Axiocam506 CCD camera (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with gain set to an Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with gain set to an Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with gain set to an Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with gain set to an Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with gain set to an	on filter (Zeiss), a FT 395 dichroic mirror (Zeiss) and a BP 445/50 emission filter (Zeiss). Images were acquired or mera (Zeiss) with an exposure time of 100.00 ms with gain set to and 2x2 binning. Phalloidin Alexa Fluor 488 was 0 LED light source (Excelitas) set to 40 % and wavelength selection was carried out with a BP 450-490 excitation fil hroic mirror (Zeiss) and a BP 515-565 emission filter (Zeiss). Images were acquired on a Axiocam506 CCD came ure time of 150.00 ms with gain set to and 2x2 binning. MitoTracker Orange was excited with a X-Cite 120 LED light o 30 % and wavelength selection was carried out with a BP 546/12 excitation filter (Zeiss). Images were acquired on a Axiocam506 CCD came ure time of 150.00 ms with gain set to and 2x2 binning. MitoTracker Orange was excited with a X-Cite 120 LED light o 30 % and wavelength selection was carried out with a BP 546/12 excitation filter (Zeiss), a FT 580 dichroic mirror mission filter (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with a 200.00 ms with	on a Axiocam506 CCD ca as excited with a X-Cite 12 n filter (Zeiss), a FT 510 dic mera (Zeiss) with an expos ght source (Excelitas) set t ror (Zeiss) and a LP 590 e 00.00 ms with gain set to a
Acknowledgements: Images were collected and/or image processing and analysis for this manuscript was performed in (the) Advanced BioImaging Facility (k cGill), with the assistance of Joel Ryan. (RRID: SCR_017697).	Acknowledgements: Images were collected and/or image processing and analysis for this manuscript was performed in (the) Advance cGill), with the assistance of Joel Ryan. (RRID: SCR_017697).	iced Biolmaging Facility (M

A draft of an experimental section text is displayed in a popup window and copied to the clipboard, to be pasted into a manuscript for revision.

### MethodsJ2 – csv output

	A	В	C
1	Label	Image metadata value	User input value
2	Script		MethodsJ2 v1.2
3	Date		8/9/2021 11:40:58 AM
4	Image file:		C:\Users\joelr\Documents\GitHubRepositories\MethodsJ2\BPAE_3color_30p-200ms_63xO
5	MJ2 structure file:		https://raw.githubusercontent.com/ABIF-McGill/MethodsJ2/main/MJ2_structure_files/MJ2
6	Sample description:		Cultured BPAE cells
7	Sample preparation:		grown on No. 1.5 glass coverslips, fixed with 4% PFA and stained with DAPI, Phalloidin Alex
8	Mounting medium:		mounted in Cytoseal
9	Coverglass:		
10	Sample holder:		on glass slides
11	Image width in pixels (X):	1012	1012
12	Image height in pixels (Y):	1020	1020
13	Number of slices (Z):	1	1
14	Number of channels (C):	3	3
15	Number of frames (T):	1	1
16	Dimension order:	XYCZT	XYCZT
17	Pixel size XY (micron):	0.14	0.14
18	Voxel size Z (micron):	n/a	n/a
19	Time interval:	n/a	n/a
20	Micro-Meta App json file:		$\label{eq:linear} C:\label{eq:linear} C:\lab$
21	Microscope:	Zeiss wide field	Zeiss Axiovert 200M Compound (ABIF Axiovert1)
22	Please select the best descriptor for this system		Widefield Epifluorescence
23	Acquisition software:		Zen
24	Select objective:	63x NA 1.4	63X PLAN APOCHROMAT, NA=1.40, OIL, DIC
25	Channel Description (e.g. fluorophore, labeled protein o	or cell type):	DAPI
26	Light source:		X-Cite light source
27	Light source intensity:		30%
28	Select excitation filter:		G 365 - DAPI excitation filter
29	Select dichroic:		FT 395 - DAPI beamsplitter

A csv file is generated and saved containing the data collected from the image metadata as well as the data input by the user (either manually or selected from options sourced from the microscope.json file), and the methods text generated.

### MethodsJ2 – extensibility

282	{		
283		"Dialog_Box": "Channel Settings",	
284		"category": "general",	
285		"Setting": "Light source intensity: ",	
286		"Add_to_same_row": 0,	
287		"CheckHardwareJSON": 0,	Dial
288		"Dialog_Type": "addStringField",	σοης
289		"blurb": "set to %s"	core
290			stru
291	},		onlir
292	{		
293		"Dialog_Box": "Channel Settings",	
294		"category": "general",	
295		"Dialog_Type": "addChoice",	
296		"Setting": "Select excitation filter: ",	
297		"Add_to_same_row": 0,	
298		"CheckHardwareJSON": 1,	
299		"Schema_ID": "ExcitationFilter.json",	
300		"attributes": [	
301		"Model",	
302		"Manufacturer"	
303		],	
304		"blurb": "and wavelength selection was carried out with a %s excitation filter (%s	s), "
305	},		

Dialog boxes, drop-down menus, text generation can be added or modified by core facility staff, by modifying a MJ2 structure file and storing it locally or online (e.g. on Github)