

# How to automatically generate Materials & Methods data using MethodsJ2

IGC Advanced Imaging Resource, 24.4.23

Before you start: you will need the following:

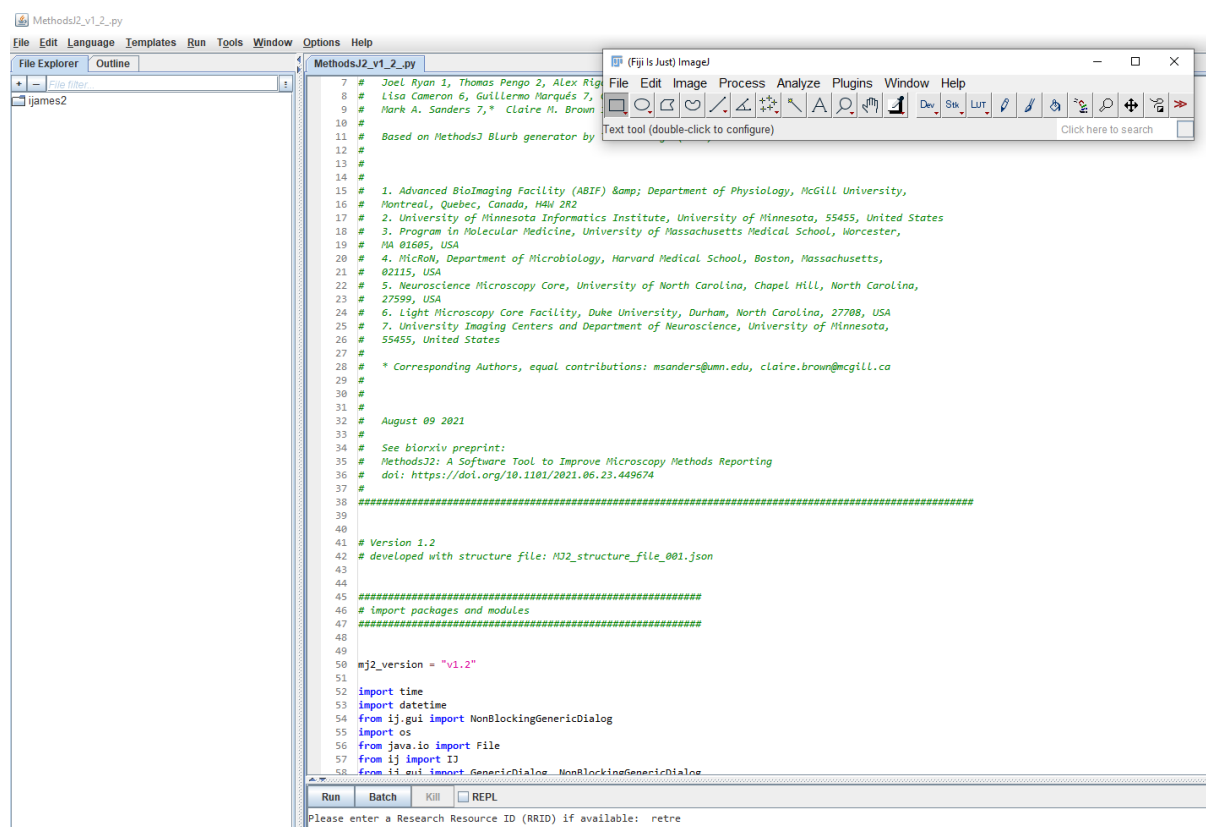
- ImageJ/FIJI <https://imagej.net/software/fiji/downloads>
- MethodsJ2 script (MethodsJ2\_v1\_2\_.py; found at <https://github.com/ABIF-McGill/MethodsJ2>)
- The .json file for the microscope you used. This can be found at the facility GitHub <https://github.com/IGC-Advanced-Imaging-Resource/MethodsJ2.git>
- An example image in its raw format

## Step 1:

Download the MethodsJ2 script (MethodsJ2\_v1\_2\_.py), this can be found at <https://github.com/ABIF-McGill/MethodsJ2>

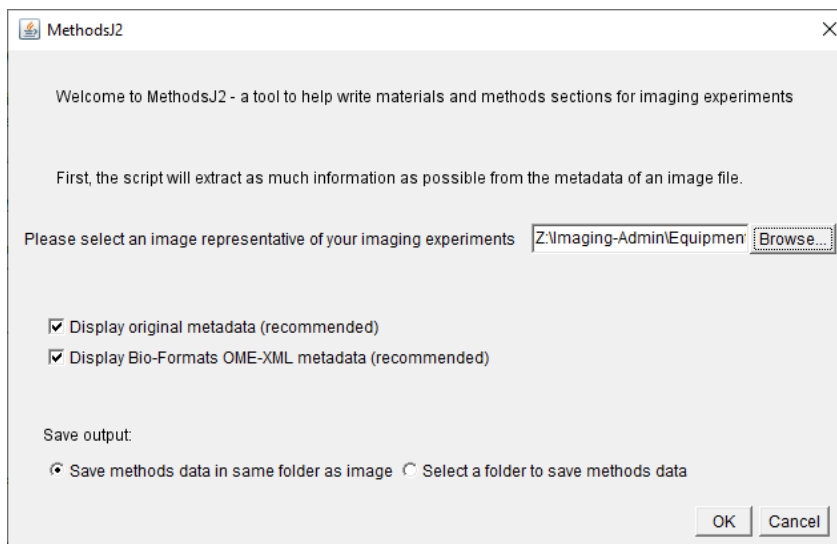
## Step 2:

Open ImageJ/FIJI. Drag and drop the above script onto the main console. A script editing window will appear. Click 'Run'



## Step 3:

You will be prompted to upload a representative image. Please use the raw data collected from the microscope in its native format (e.g. .czi for BriteMac, .nd2 for SoRa). Click 'Okay'



Welcome to MethodsJ2 - a tool to help write materials and methods sections for imaging experiments

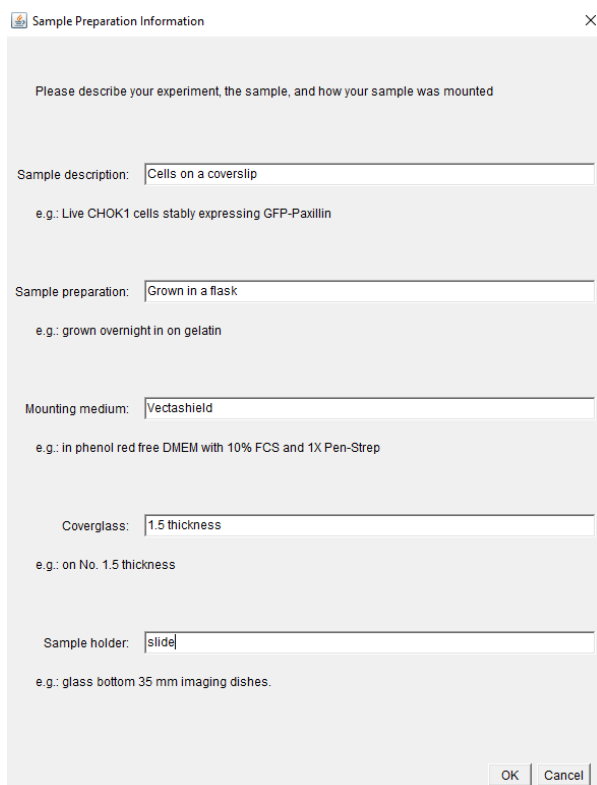
First, the script will extract as much information as possible from the metadata of an image file.

Please select an image representative of your imaging experiments

☒ Display original metadata (recommended)  
☒ Display Bio-Formats OME-XML metadata (recommended)

Save output:  
☒ Save methods data in same folder as image ☐ Select a folder to save methods data

You will be prompted to add some useful details of your experiment, e.g. sample holder, coverglass thickness. These are optional and do not appear in your materials & methods text. Click 'Okay' when done



Please describe your experiment, the sample, and how your sample was mounted

Sample description:   
e.g.: Live CHOK1 cells stably expressing GFP-Paxillin

Sample preparation:   
e.g.: grown overnight in on gelatin


Mounting medium:   
e.g.: in phenol red free DMEM with 10% FCS and 1X Pen-Strep

Coverglass:   
e.g.: on No. 1.5 thickness

Sample holder:   
e.g.: glass bottom 35 mm imaging dishes.

#### Step 4:

The image dimensions will appear (these are read from your image using Bioformats) – check over them and click 'Okay'


 Image dimensions ✕

According to the metadata, you have selected an image with the following dimensions:

Image width in pixels (X):	<input type="text" value="1012"/>
Image height in pixels (Y):	<input type="text" value="1020"/>
Number of slices (Z):	<input type="text" value="1"/>
Number of channels (C):	<input type="text" value="3"/>
Number of frames (T):	<input type="text" value="1"/>
Dimension order:	<input type="text" value="XYCZT"/>
Pixel size XY (micron):	<input type="text" value="0.14"/>
Voxel size Z (micron):	<input type="text" value="n/a"/>
Time interval:	<input type="text" value="n/a"/>

### Step 5:

You now need to tell MethodsJ2 which microscope was used for the acquisition. Select the .json relating to the microscope you used (e.g. Britemac.json). If you can't find the microscope you are looking for, please contact the facility (AIR-support@igc.ed.ac.uk)

 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.

This image appears to have been acquired on a:

Zeiss wide field

Please select a Micro-Meta App json file corresponding to this system

Confirm that the details of this system are correct (e.g. Zeiss widefield) and click 'Okay'

 Microscope system overview ✕

According to the metadata, this image was acquired on a:

Zeiss wide field

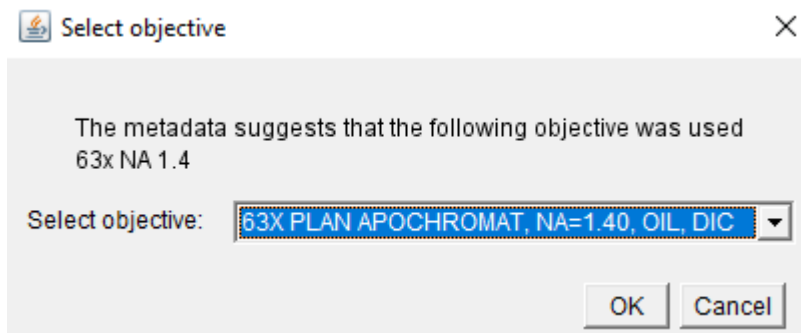
You have selected a Micro-Meta App file for a  
ABIF Axiovert1,  
an Compound system made by Zeiss.

Please select the best descriptor for this system

Acquisition software:

### Step 6:

Check that the objective has been recorded correctly (e.g. 63x in the example below). If not, choose the correct objective from the dropdown list. Click 'Okay'



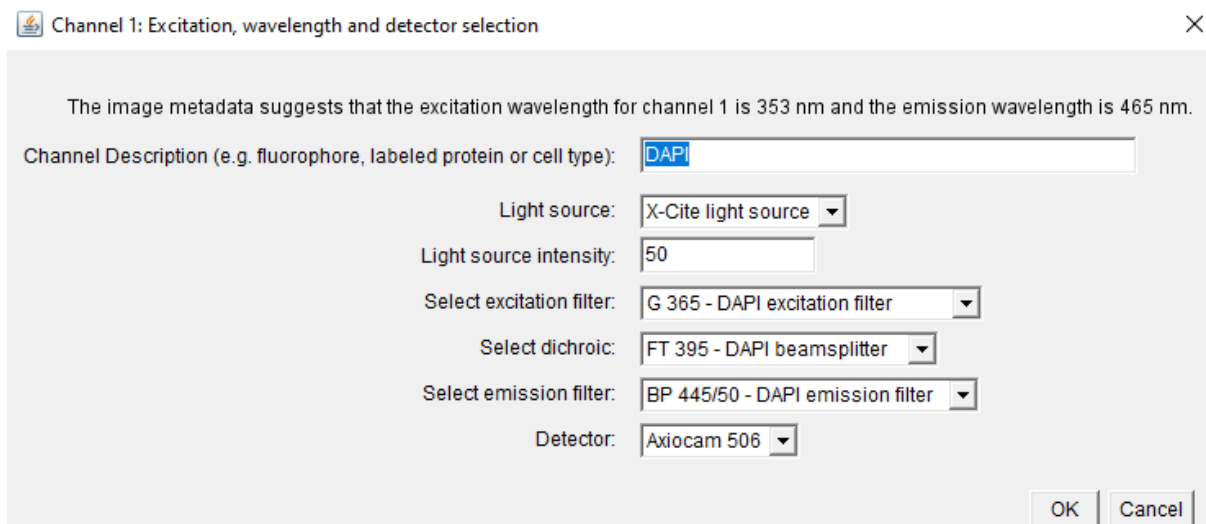
The metadata suggests that the following objective was used  
63x NA 1.4

Select objective:

OK Cancel

### Step 7:

Add the channel information. For each channel, you will need to add a name (e.g. DAPI) and add/confirm details such as the filters and light source intensities used



The image metadata suggests that the excitation wavelength for channel 1 is 353 nm and the emission wavelength is 465 nm.

Channel Description (e.g. fluorophore, labeled protein or cell type):

Light source:

Light source intensity:

Select excitation filter:

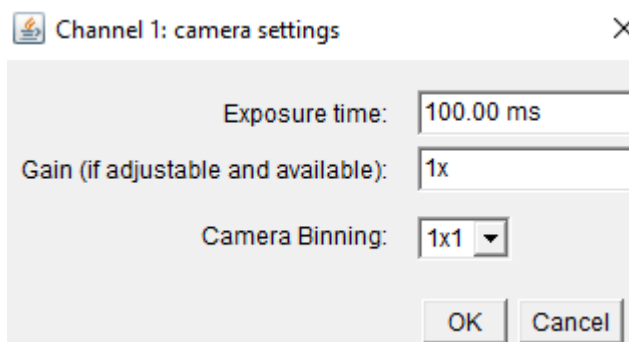
Select dichroic:

Select emission filter:

Detector:

OK Cancel

You will also be prompted to check that the recorded exposure time is correct:



Exposure time:


Gain (if adjustable and available):

Camera Binning:

OK Cancel

### Step 8:

If relevant, select any other devices that were used (e.g. incubation equipment used for live imaging, etc), click 'Okay'


Select optional devices
✕


☐ Environmental conditions maintained by device (temperature, CO2, humidity)

☐ Focus Stabilization:

OK
Cancel

### Step 9:

Add necessary details to acknowledge the facility. Add the name of technical staff if they have provided particular help with the acquisition (beyond normal expected training/troubleshooting). It is not necessary to fill in an RRID


Acknowledgements
✕

Please remember to acknowledge the imaging core facility and staff in your publications

To facilitate this, please enter the name of the core facility:


Please enter the name of a core facility staff member, if appropriate:

Please enter a Research Resource ID (RRID) if available:

OK
Cancel

### Step 10:

The resultant materials and methods blurb will be appear in a separate window. These can be saved as a .txt or copied and pasted into a Word document. Make sure that you read over this text for accuracy


MethodsJ2 output
✕

**MethodsJ2 text generation based on user input and on a Micro-Meta App hardware**

binning. FITC was excited with a X-Cite 120 LED light source (Excelitas) set to 100 and wavelength selection was carried out with a BP 450-490 excitation filter (Zeiss), a FT 10 dichroic mirror (Zeiss) and a BP 515-565 emission filter (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) with an exposure time of 150.00 ms with gain set to and 1x1 binning. AF555 was excited with a X-Cite 120 LED light source (Excelitas) set to 100 and wavelength selection was carried out with a BP 546/12 excitation filter (Zeiss), a FT 580 dichroic mirror (Zeiss) and a LP 590 emission filter (Zeiss). Images were acquired on a Axiocam506 CCD camera (Zeiss) with an exposure time of 200.00 ms with gain set to and 1x1 binning.

Acknowledgements:

Images were collected and/or image processing and analysis for this manuscript was