MethodsJ2

Joel Ryan, Thomas Pengo, Alex Rigano, Paula Montero Llopis,

Michelle S. Itano, Lisa Cameron, Guillermo Marqués,

Caterina Strambio-De-Castillia, Mark A. Sanders and Claire M. Brown

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

Problem to address

- Authors of research papers tend to write incomplete methods sections for microscopy data/experiments:

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- Global need for standardization of image metadata

Standardization of image/microscope metadata

- Common language:

  e.g.“*Light source*” vs “*Illumination*” vs “*incident light*”

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- Proper databasing

Standardization of image/microscope metadata

- Common language:

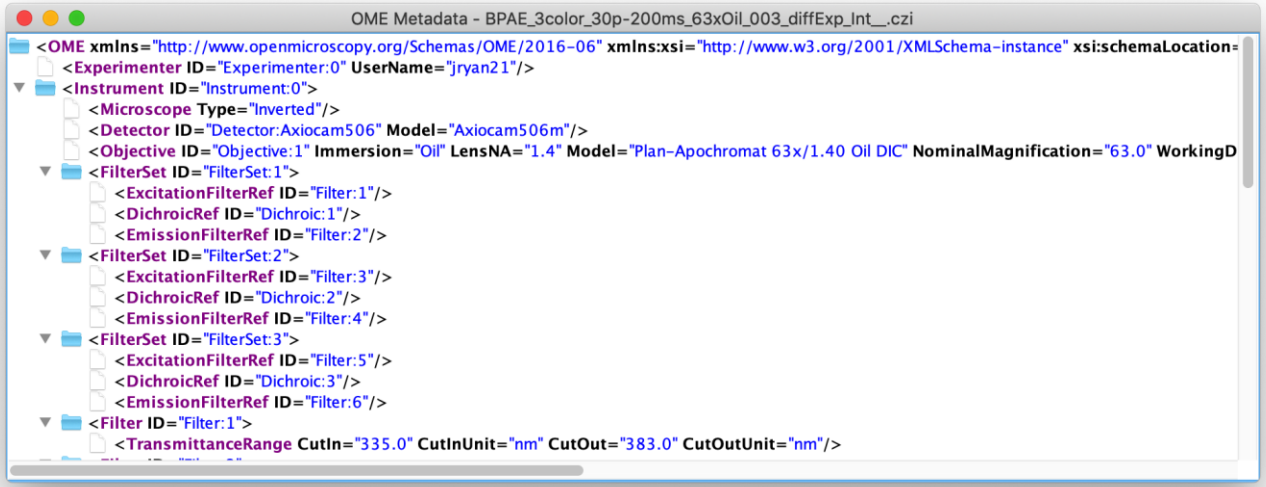
  e.g.“*Light source*” vs “*Illumination*” vs “*incident light*”

- Proper databasing

- Help users/authors determine what is crucial for reporting

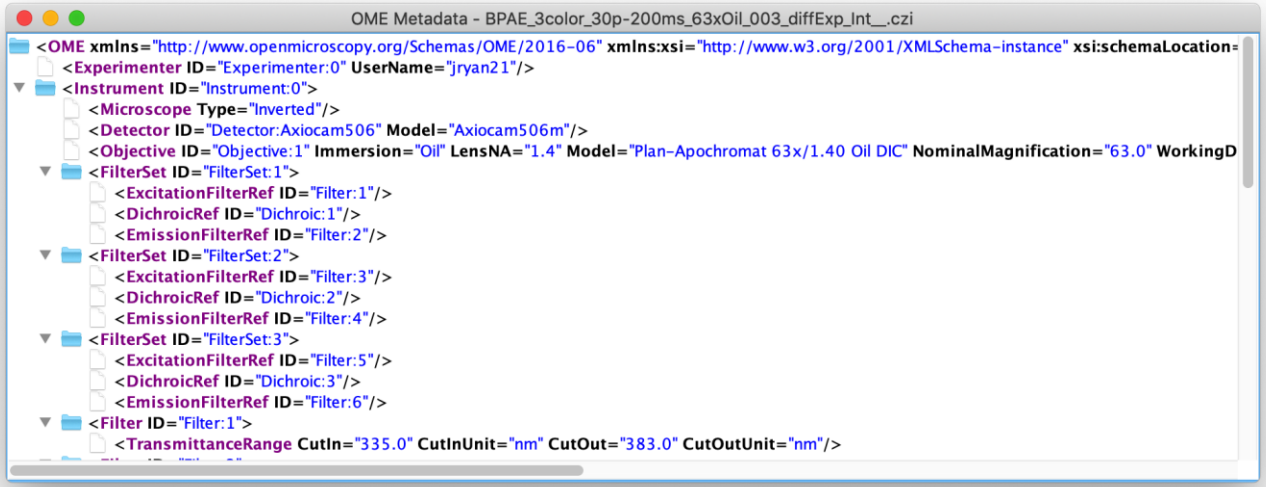
Standardization of image/microscope metadata

- Image metadata: Open Microscope Environment (OME)



Standardization of image/microscope metadata

- Image metadata: Open Microscope Environment (OME)

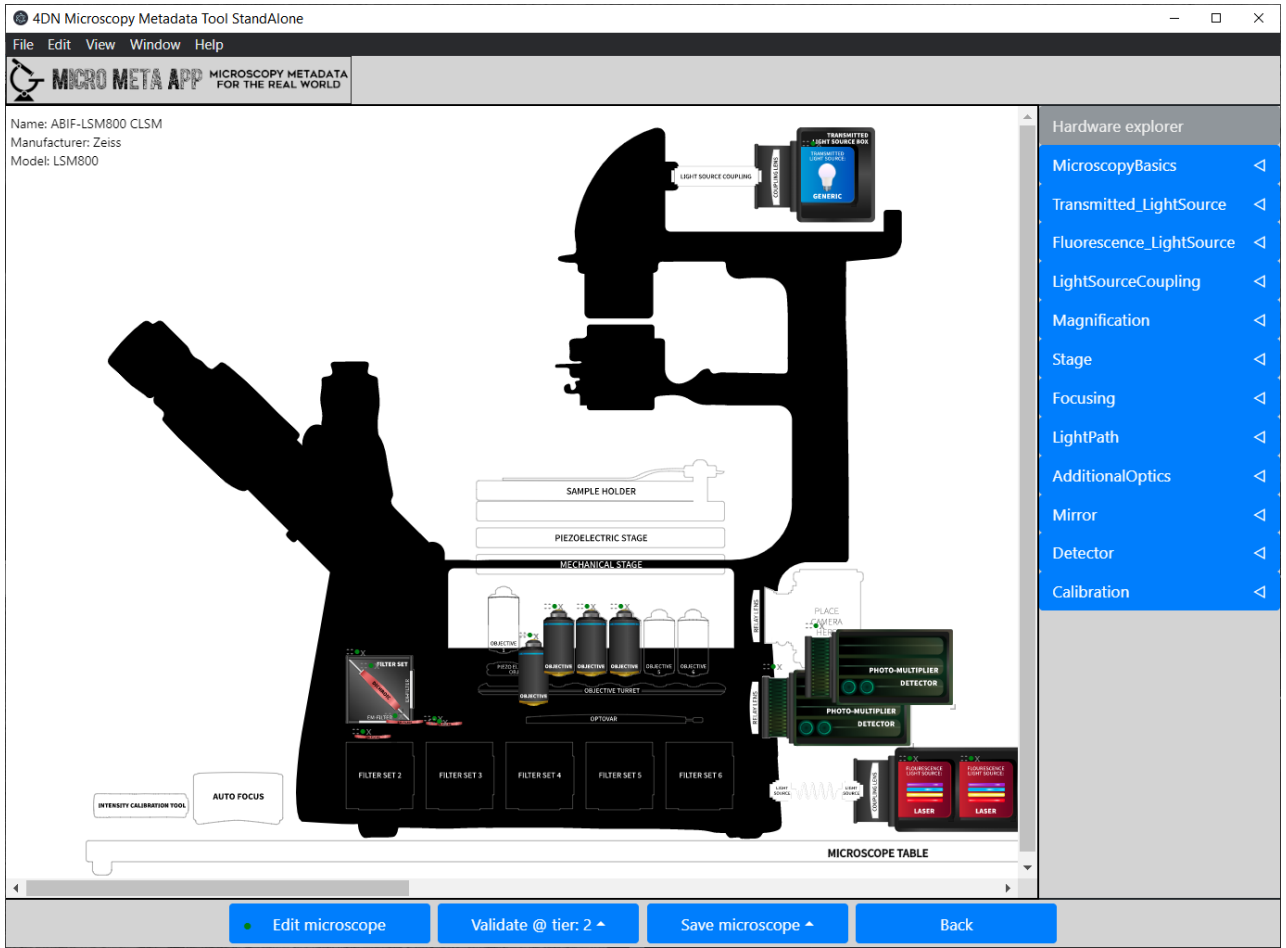


- Microscopy metadata: *4DN-BINA-OME Microscopy specifications*

----> Micro-Meta App

Micro-Meta App

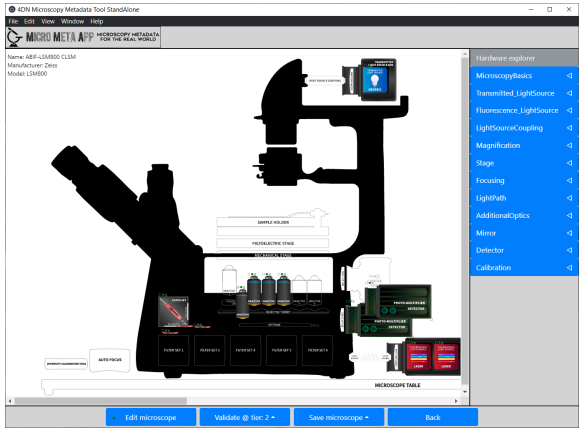
- GUI-based software to build a microscope hardware file using standardized metadata language



Rigano et al, 2021

Micro-Meta App

“Building” your microscope generates a standardized configuration file for that microscope



```
{
  "Name": "ABIF Axiovert1",
  "Schema_ID": "Instrument.json",
  "ID": "93efaebd-1042-43aa-994e-2f5bc2a92fb1",
  "Tier": 3,
  "ValidationTier": 1,
  "ModelVersion": "2.01.0",
  "AppVersion": "1.2.2-b1",
  "MicroscopeStand": {
    "Name": "ABIF-Axiovert1",
    "Schema_ID": "InvertedMicroscopeStand.json",
    "ID": "370f843c-b4fb-4c75-a385-d4b6049eb3cb",
    "Tier": 1,
    "ModelVersion": "2.01.0",
    "Extension": "Basic",
    "Domain": "MicroscopeHardwareSpecifications",
    "Category": "MicroscopeStand",
    "Manufacturer": "Zeiss",
    "Model": "Axio Observer Z1",
    "CatalogNumber": "999",
    "Type": "Compound",
    "Origin": "Commercial-custom modified"
  },
  "components": [
    {
      "Name": "Zen",
      "ID": "df2a3244-27c4-4a2b-b0b4-6969509f64a5",
      "Tier": 1,
      "Schema_ID": "AcquisitionSoftware.json",
```

components › 3 › Name

Rigano et al, 2021

Micro-Meta App ---> MethodsJ2

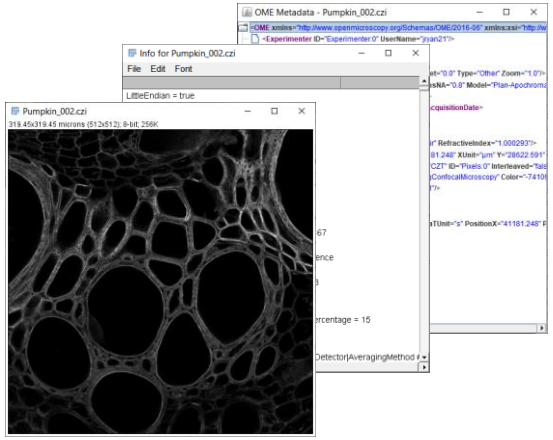
- Problem to address:

  Authors of research papers tend to write incomplete methods sections for microscopy data/experiments

- Solution:

  Build a Fiji script to help write methods sections

MethodsJ2 – Information input

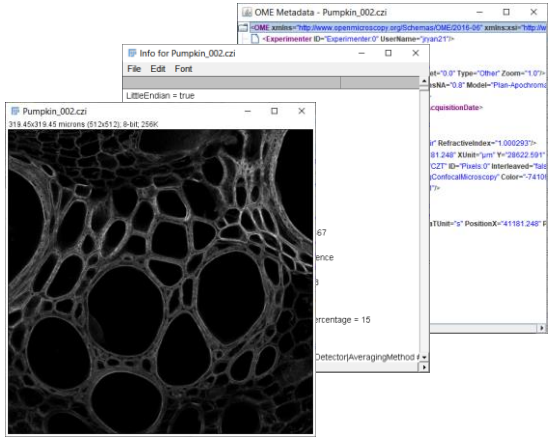


Image, metadata,
OME metadata

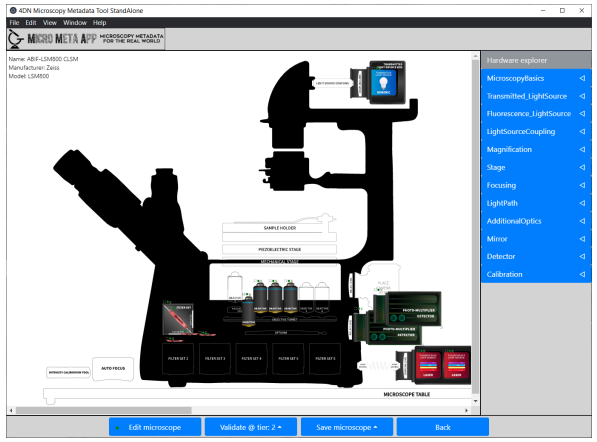
MethodsJ2

Python script
running in Fiji

MethodsJ2 – Information input



Image, metadata,
OME metadata



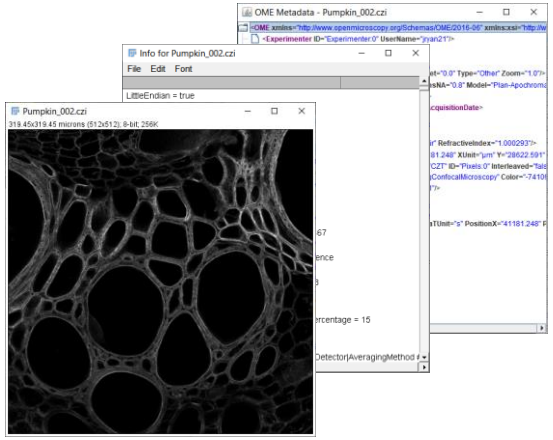
Micro-Meta App microscope
hardware specifications file

MethodsJ2

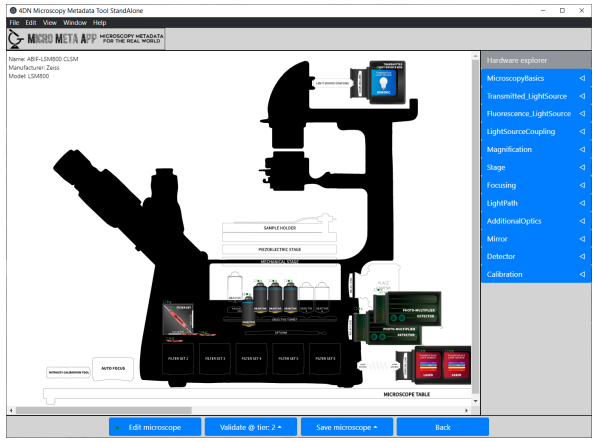
Python script
running in Fiji

Contains objectives,
filters, detectors, etc..

MethodsJ2 – Information input



Image, metadata,
OME metadata



Micro-Meta App microscope
hardware specifications file

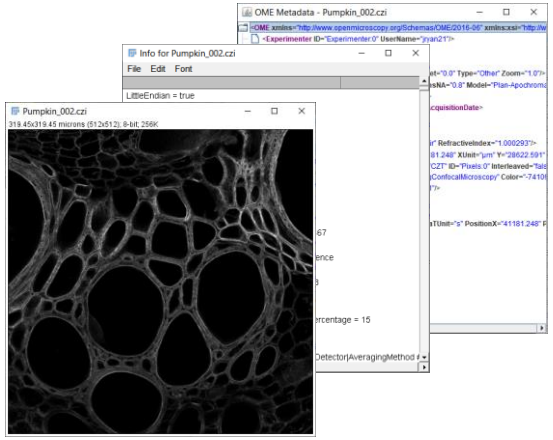
MethodsJ2

Python script
running in Fiji

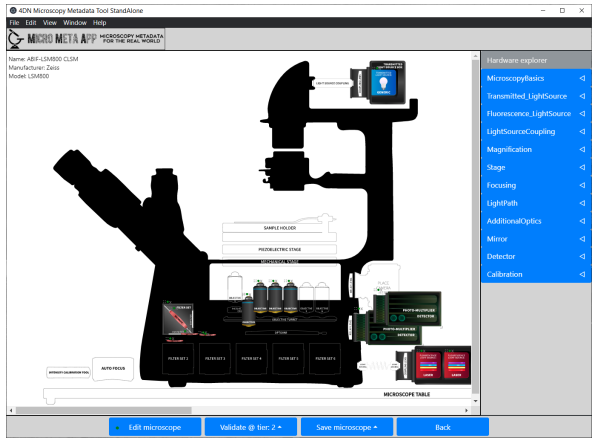
User input,
Data validation

e.g.:
- validate detected exposure time,
- choose objective from those available on the selected microscope

MethodsJ2 – input / output



Image, metadata, OME metadata



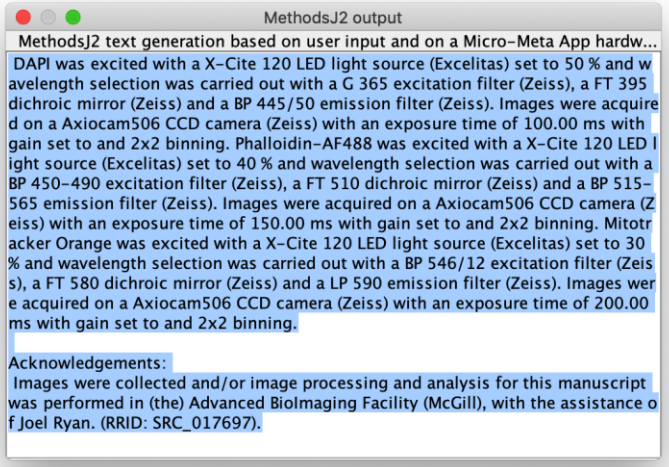
Micro-Meta App microscope hardware specifications file

MethodsJ2

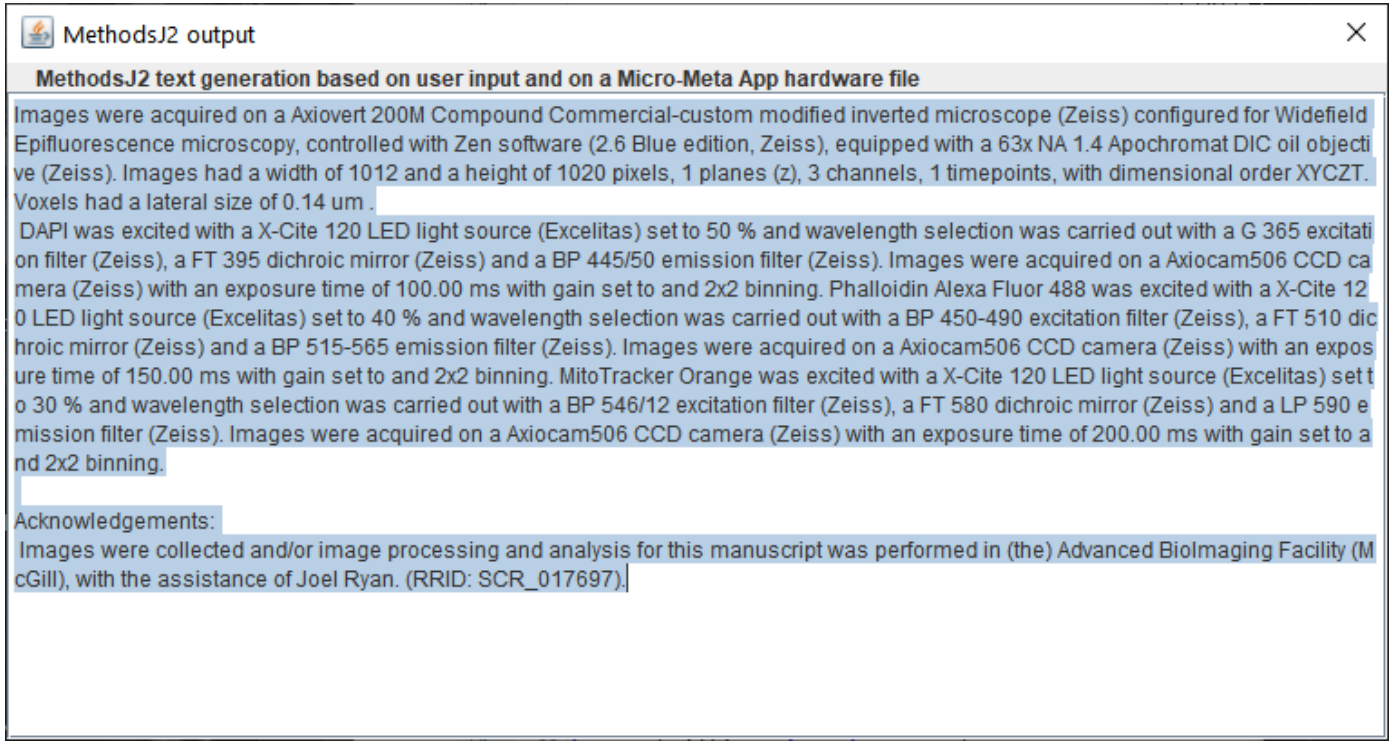
Python script running in Fiji

User input, guided by core facility staff

Generates materials and methods section for imaging experiments, based on community guidelines



MethodsJ2 – text output



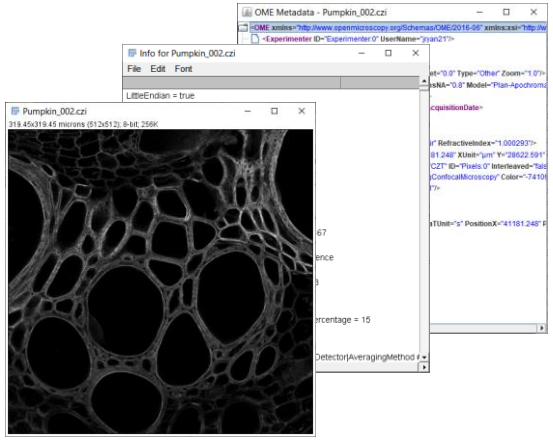
A draft of an experimental section text is displayed in a popup window and copied to the clipboard, to be pasted into a manuscript for revision.

MethodsJ2 – csv output

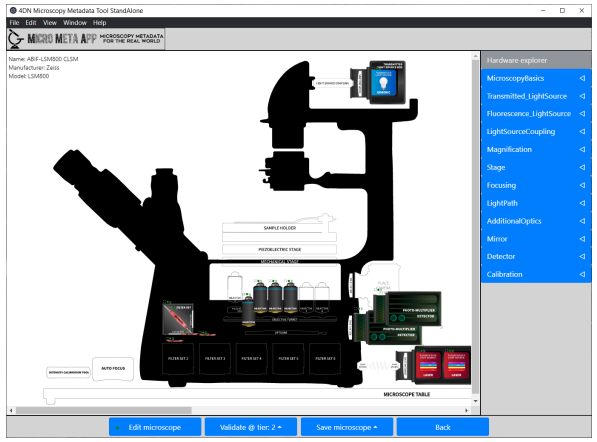
	A	B	C
1	Label	Image metadata value	User input value
2	Script		MethodsJ2 v1.2
3	Date		8/9/2021 11:40:58 AM
4	Image file:		C:\Users\joelr\Documents\GitHubRepositories\MethodsJ2\BPAE_3color_30p-200ms_63xO
5	MJ2 structure file:		https://raw.githubusercontent.com/ABIF-McGill/MethodsJ2/main/MJ2_structure_files/MJ2
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:		C:\Users\joelr\Documents\GitHubRepositories\MethodsJ2\abif_axiovert1_.json
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 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 – how it works…



Image, metadata, OME metadata



Micro-Meta App microscope hardware specifications file

MethodsJ2

Python script running in Fiji

- "asks the questions"
- Downloaded by users

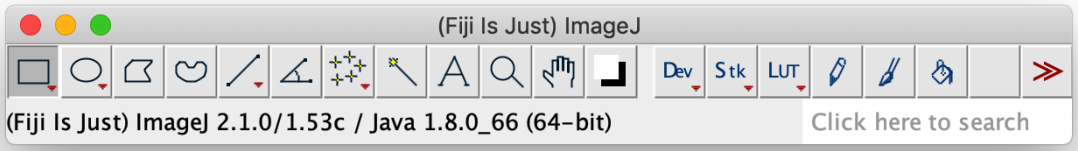
MJ2 structure file

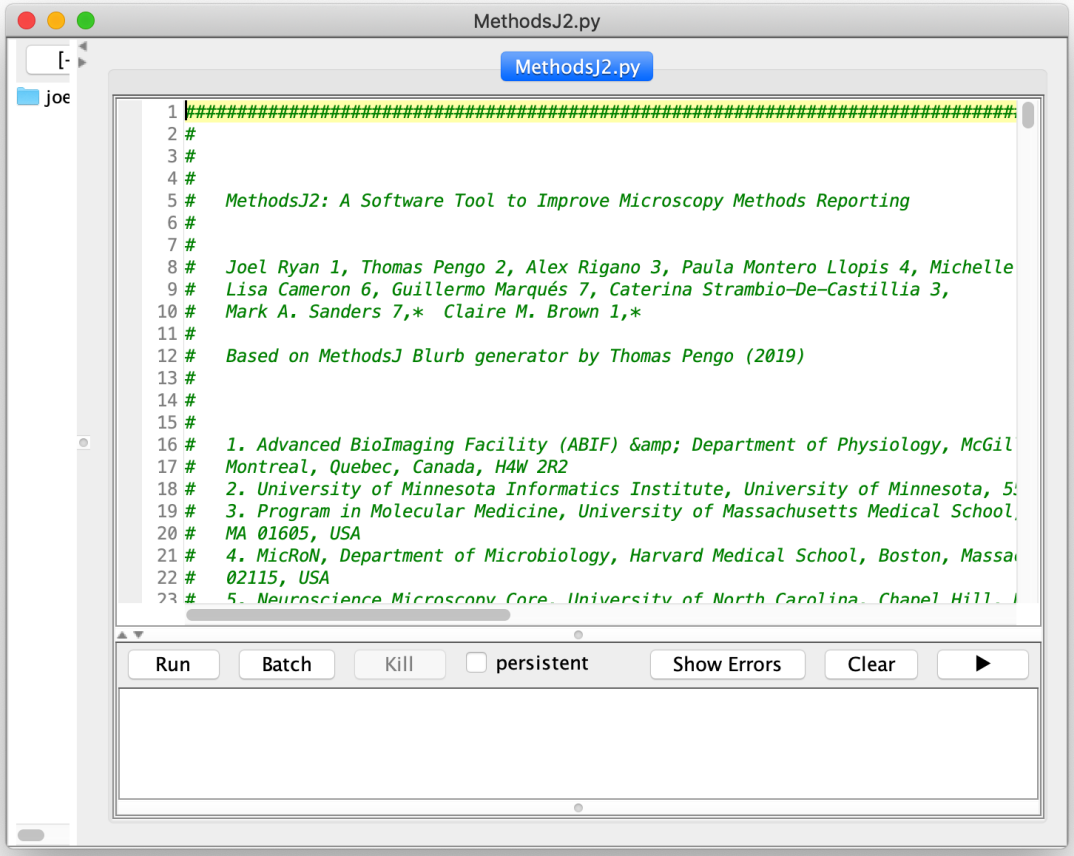
- "defines the questions"
- Stored online

MethodsJ2 – structure file (online)

```
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), "
305         },
```

MethodsJ2 - usage





- Download MethodsJ2 python script from Github
- Open in macro/script editor in Fiji.

AUTOMATED-INTUITIVE-INTERACTIVE

- Visual documentation guide
- Automate
- Teach/Train
- Web-integration

Micro-Meta App

MethodsJ2

- Extract
- Consolidate
- Automate
- Methods text

- Model extension
- Experimental metadata
- Link to imaging facility

OMERO.mde

OMERO

BIO-FORMATS

MethodsJ2

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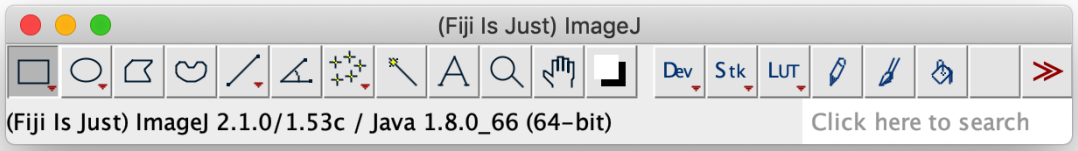
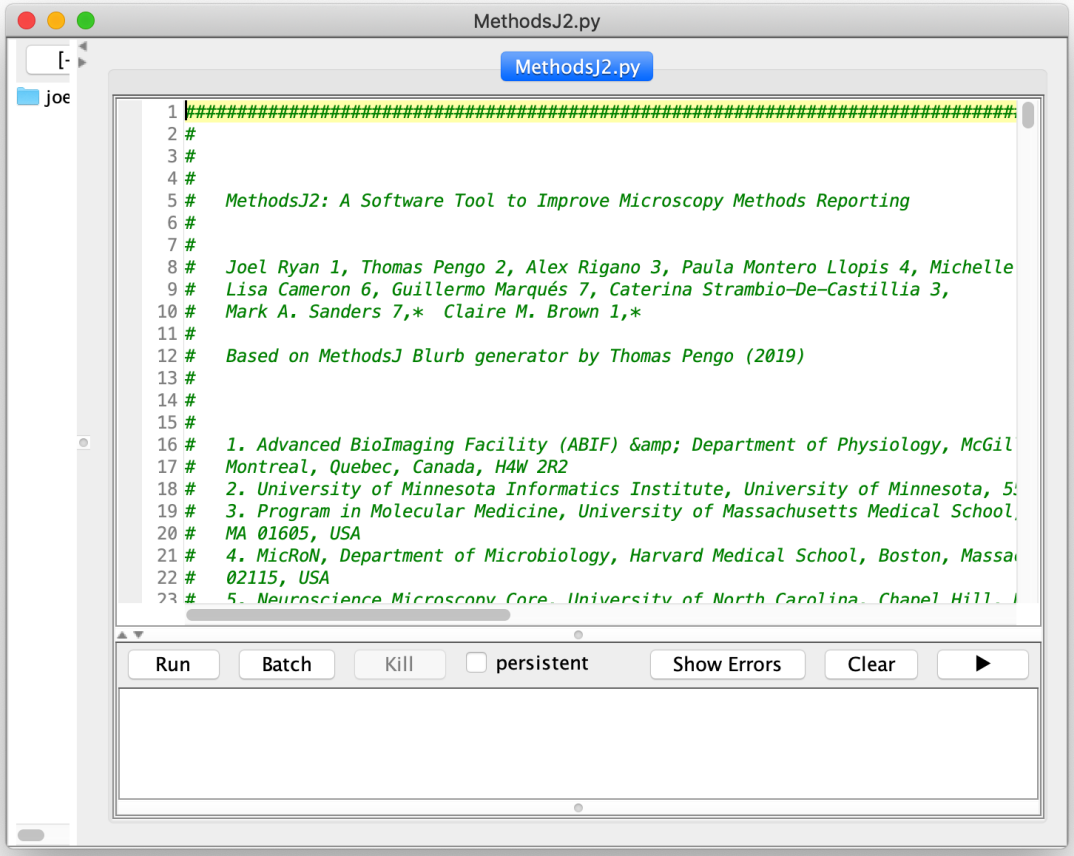
https://github.com/ABIF-McGill/MethodsJ2

https://www.biorxiv.org/content/10.1101/2021.06.23.449674v1

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

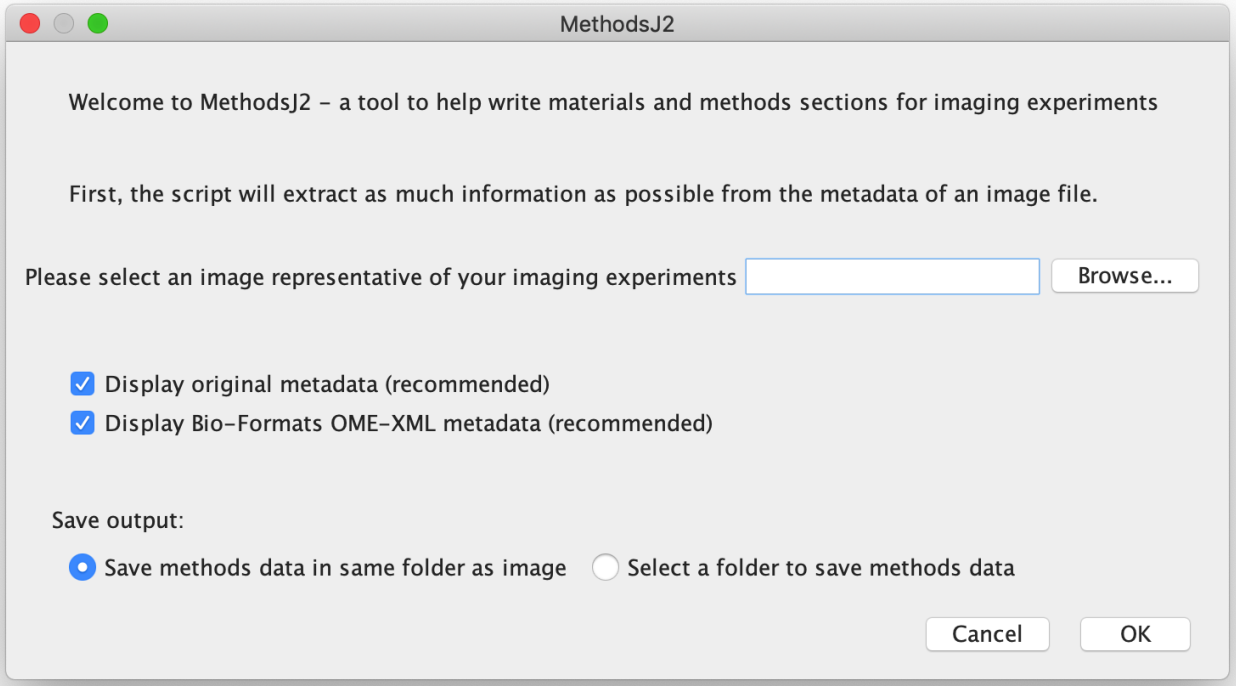


Check language: click Language and select Python

Once the script is loaded is ready, click Run

It may take a few seconds to start.

MethodsJ2 – select image



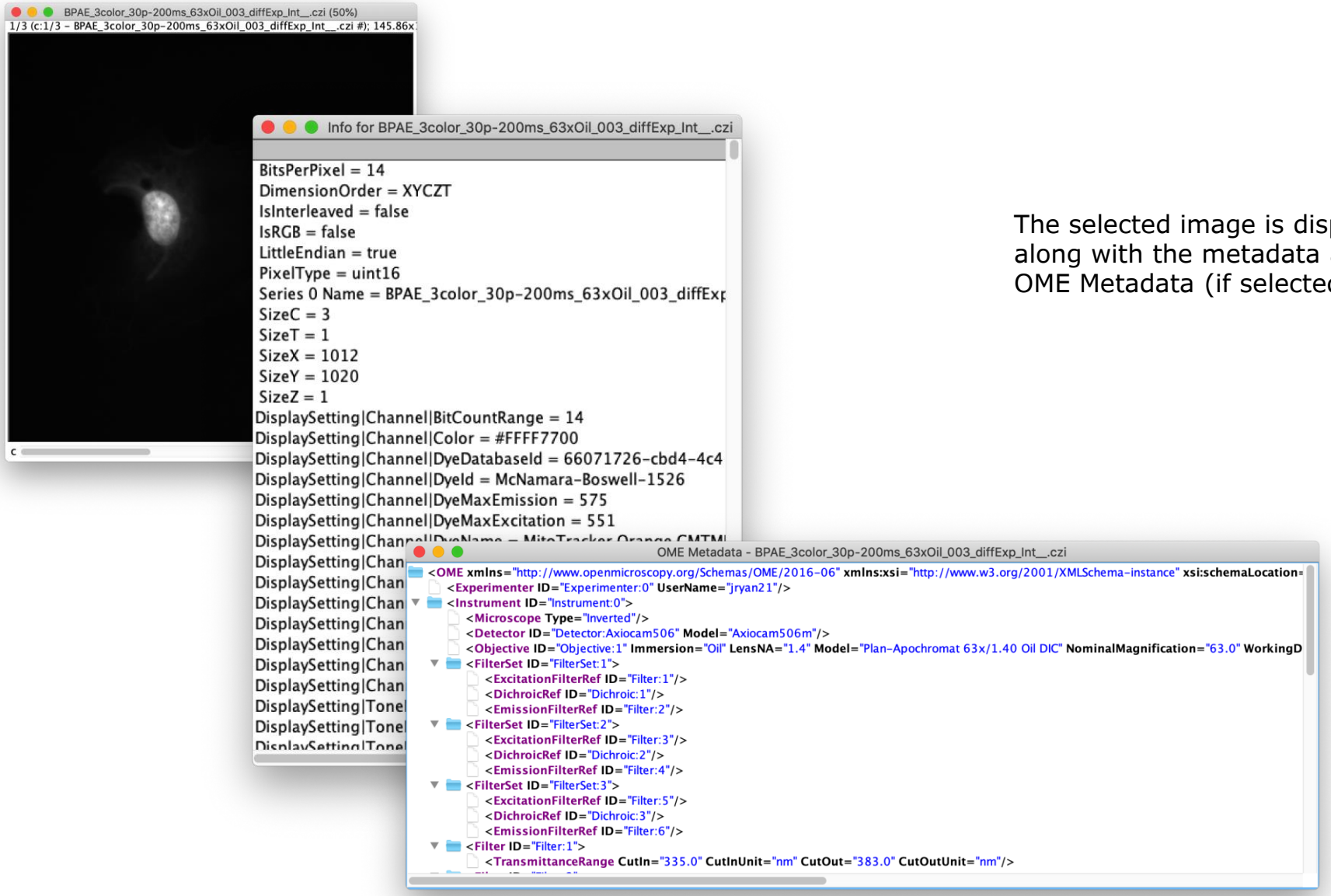
Select an image to load and to source metadata.

Click on Browse and navigate to the image, or drag and drop in image file into the text input field

Optional: display metadata windows (useful for filling out dialog boxes later)

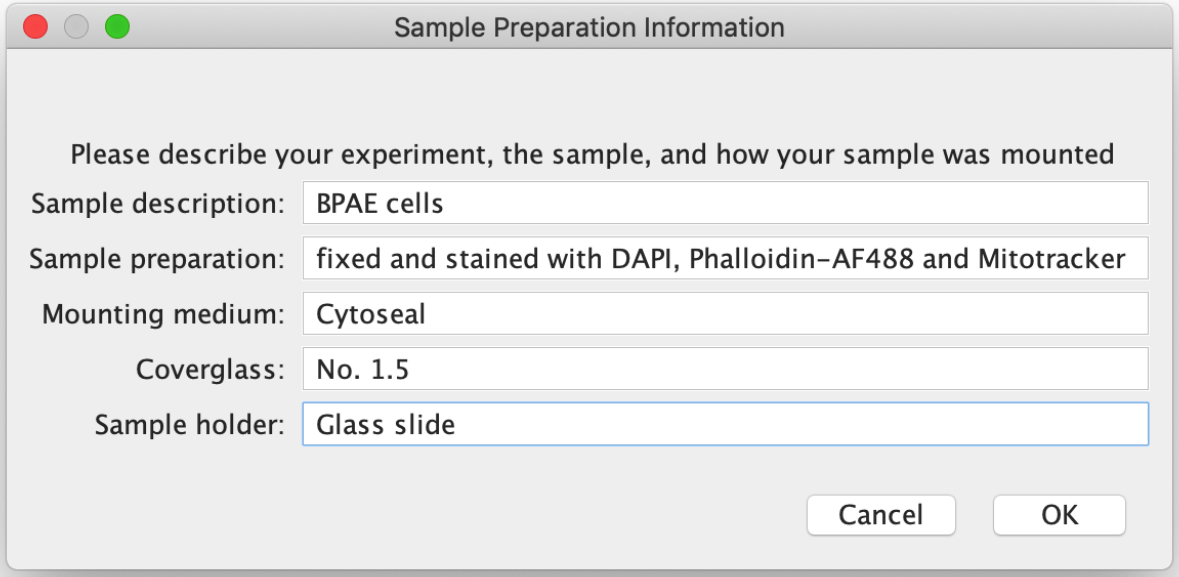
Select where to save the csv file output of the script.

MethodsJ2 – select image



The selected image is displayed, along with the metadata and OME Metadata (if selected)

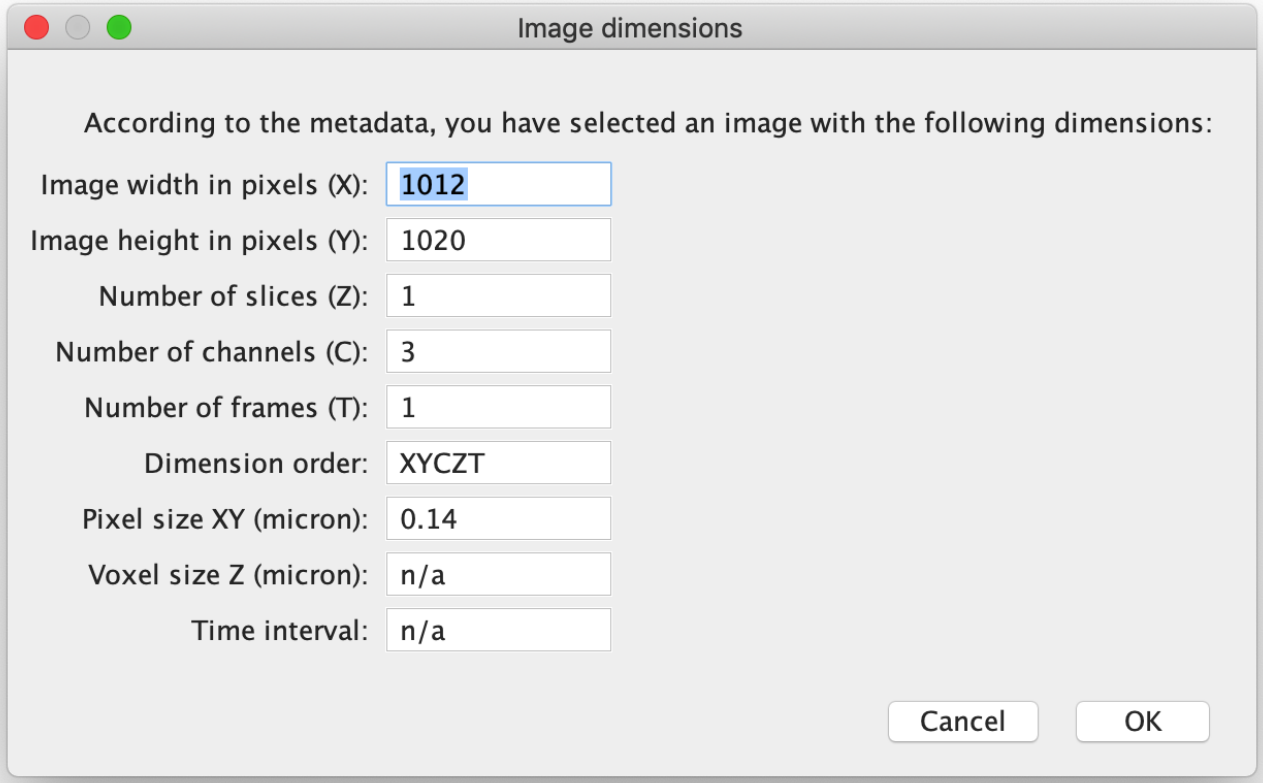
MethodsJ2 – Sample Preparation



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

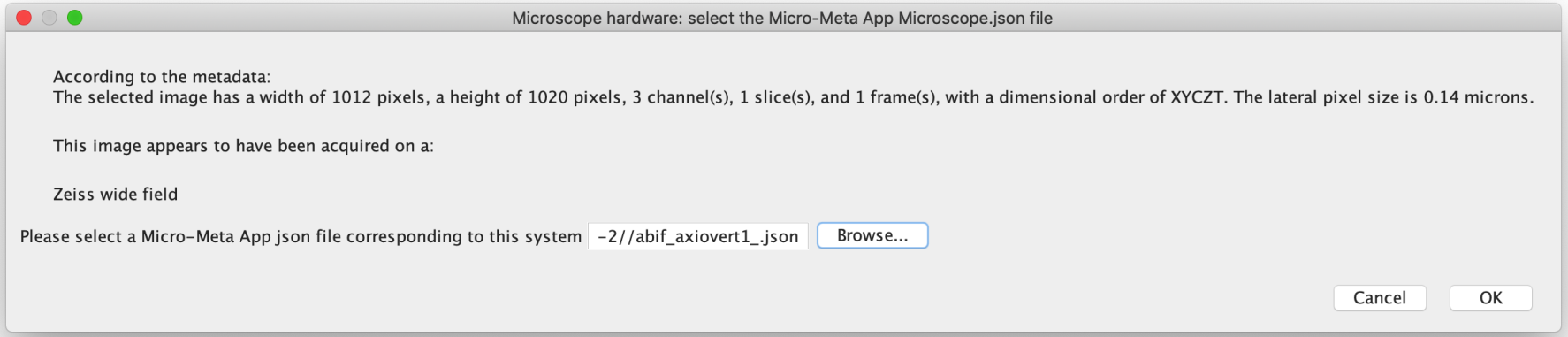
Given the variety of samples and preparations, no text is generated for sample description. It is more of a reminder for users to provide complete sample information.

MethodsJ2 – Image dimensions



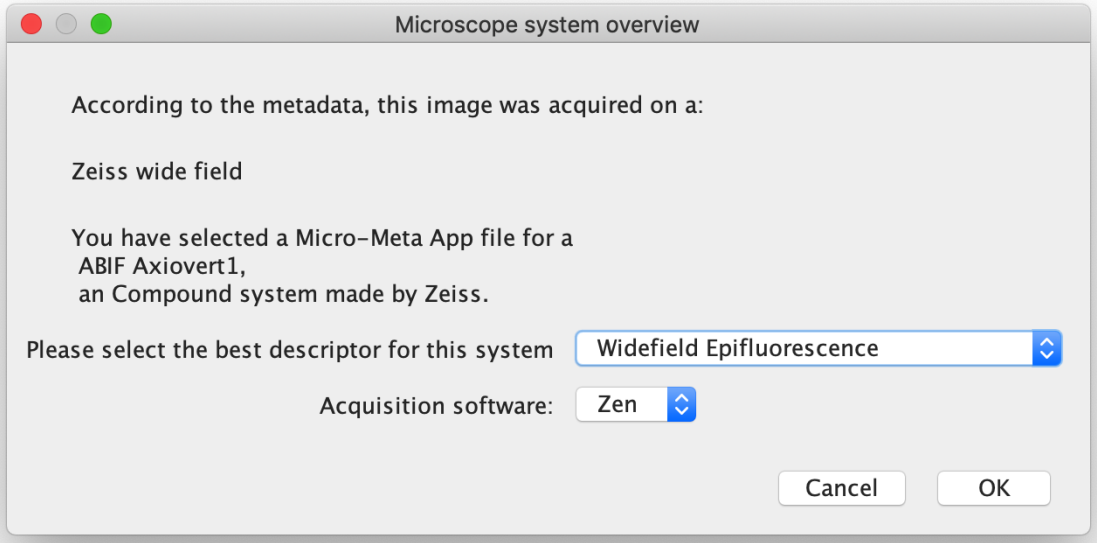
Please verify image dimensions. Values are sourced from the image metadata

MethodsJ2 – select Microscope.json file



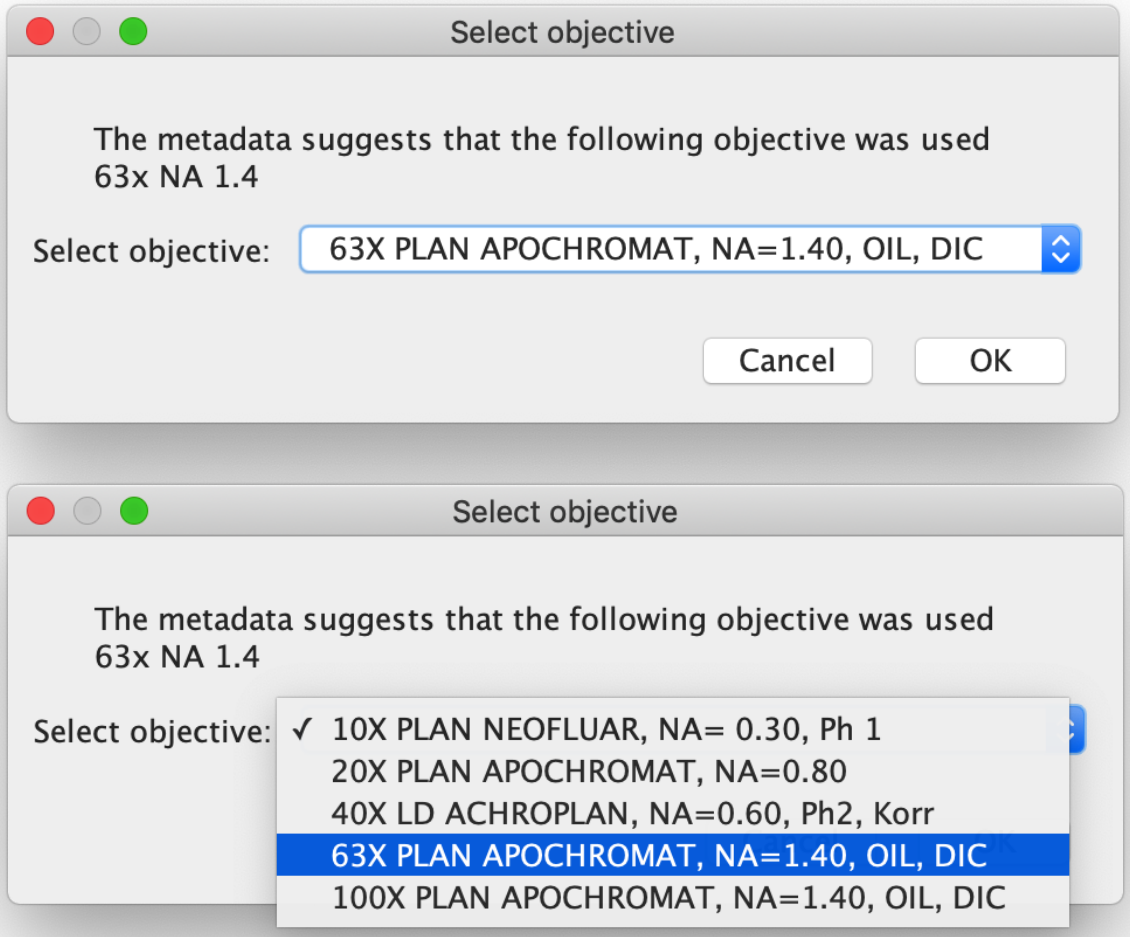
Choose Micro-Meta App hardware specifications file for the microscope used to acquire the selected image

MethodsJ2 – choose descriptor and software



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

MethodsJ2 – select objective

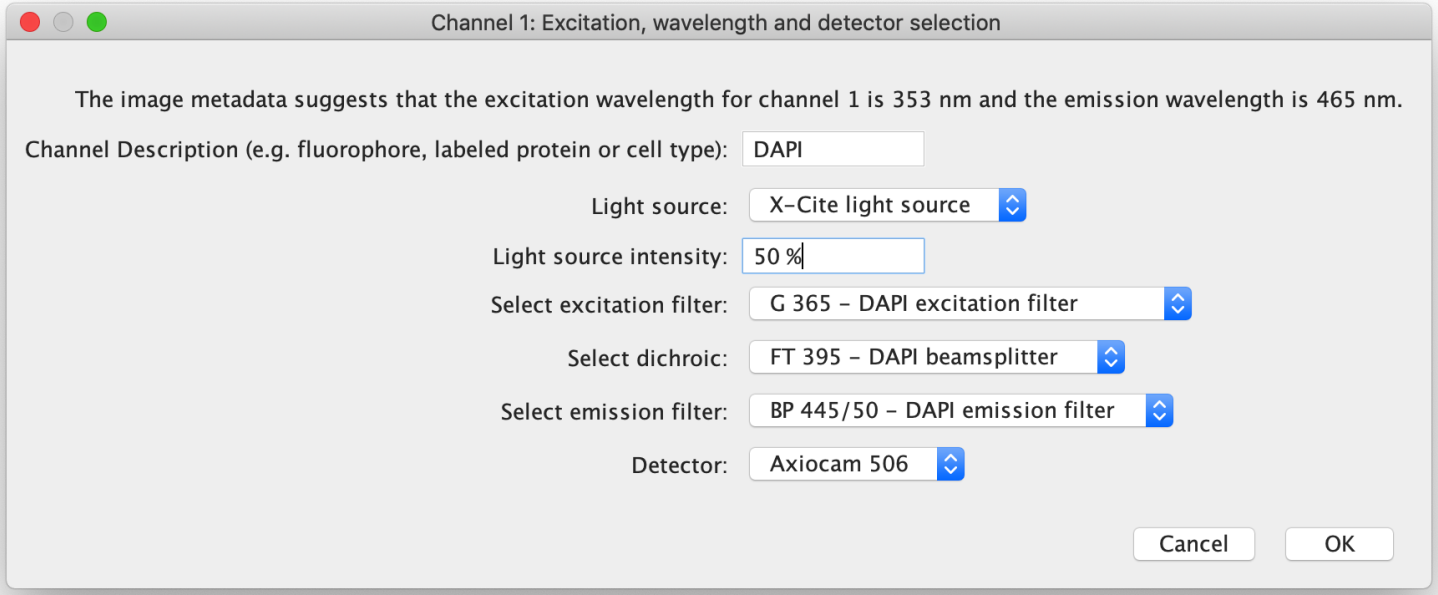


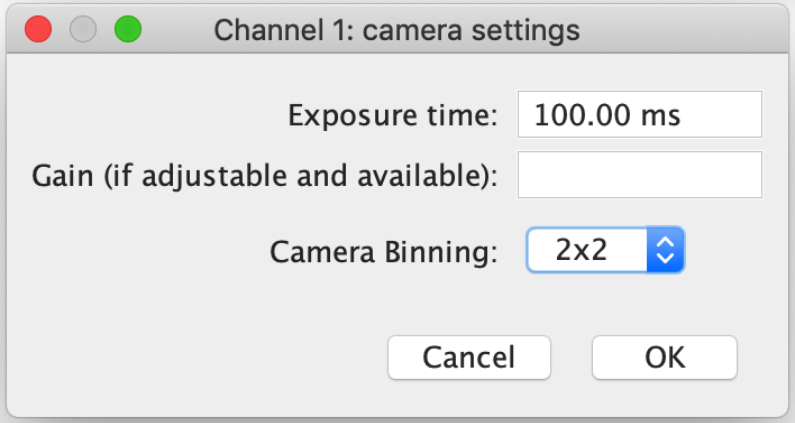
Select the objective used for this experiment.

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



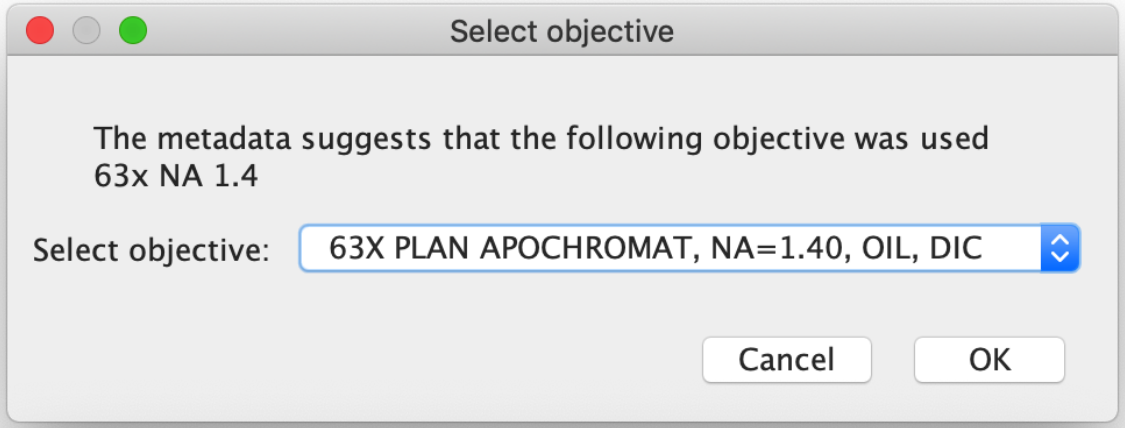


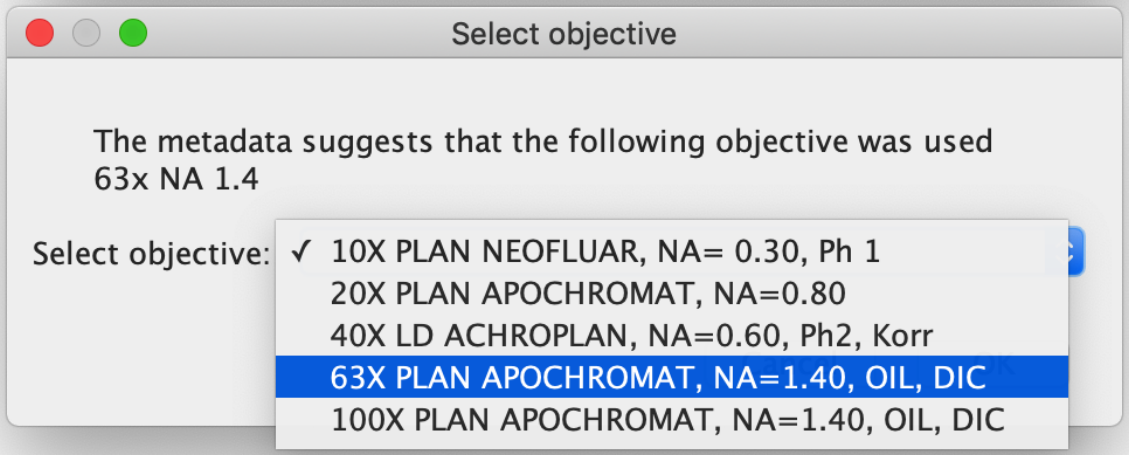
Please fill in information for the first channel

Options in drop-down menus are sourced from the microscope configuration file.

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

MethodsJ2 – select objective

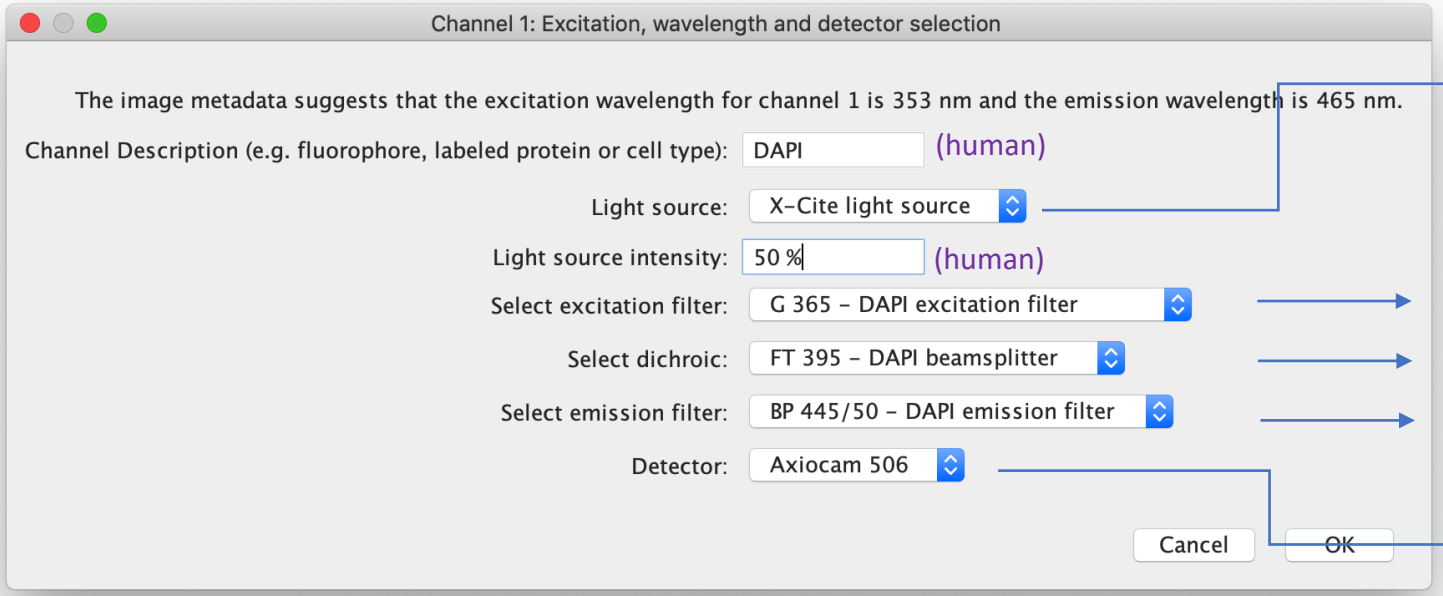




'Schema_ID': '"Objective.json", make dropdown menu with 'Name'

```
return "Magnification",
       "LensNA",
       "Correction",
       "ContrastModulation",
       "DIC",
       "ImmersionType",
       "CorrectionCollar",
       "Manufacturer"
```

MethodsJ2 – Channel settings



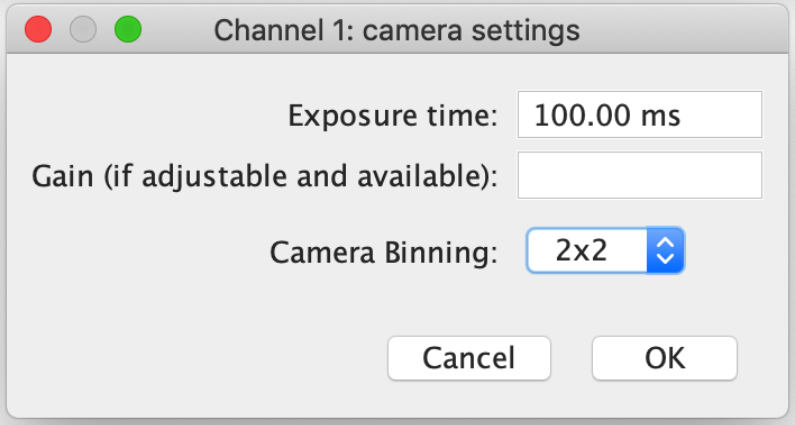
‘Schema_ID’: ‘"Fluorescence_LightSource_LightEmittingDiode.json“, or "Fluorescence_LightSource_Laser.json"

‘Schema_ID’: "ExcitationFilter.json"

‘Schema_ID’: "StandardDichroic.json"

‘Schema_ID’: "EmissionFilter.json"

‘Schema_ID’: "CCD.json", "IntensifiedCamera.json" or "CMOS.json"

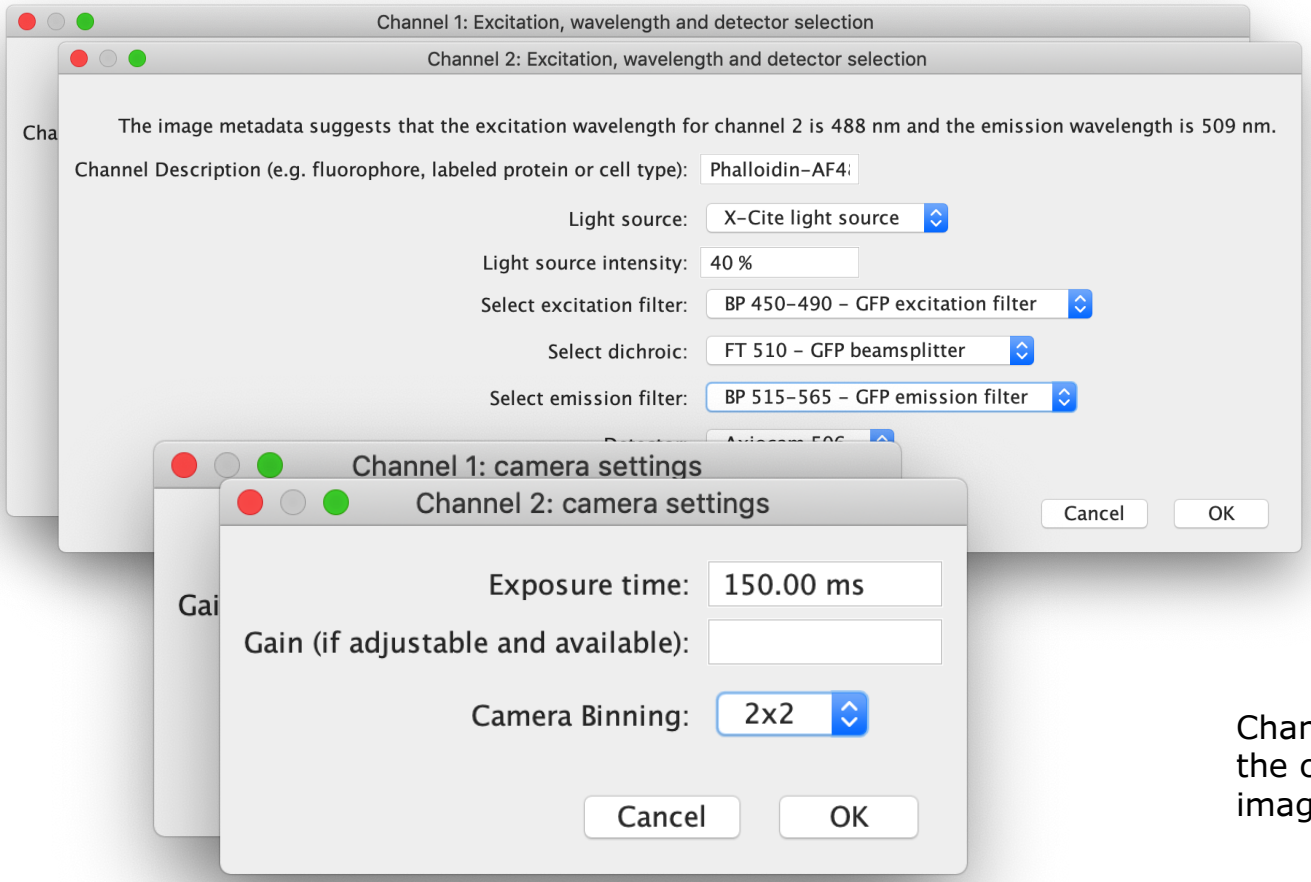


(human)

(human)

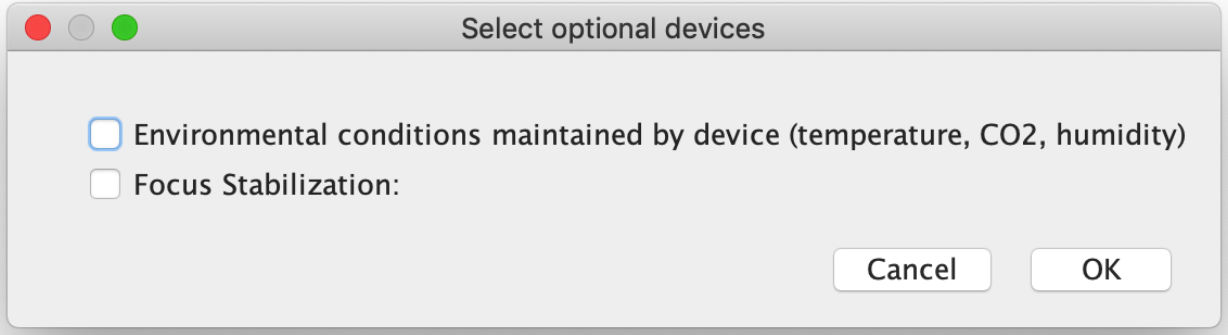
(human, Dropdown choices: [“1x1, “2x2”, “4x4”]

MethodsJ2 – Channel acquisition settings loop



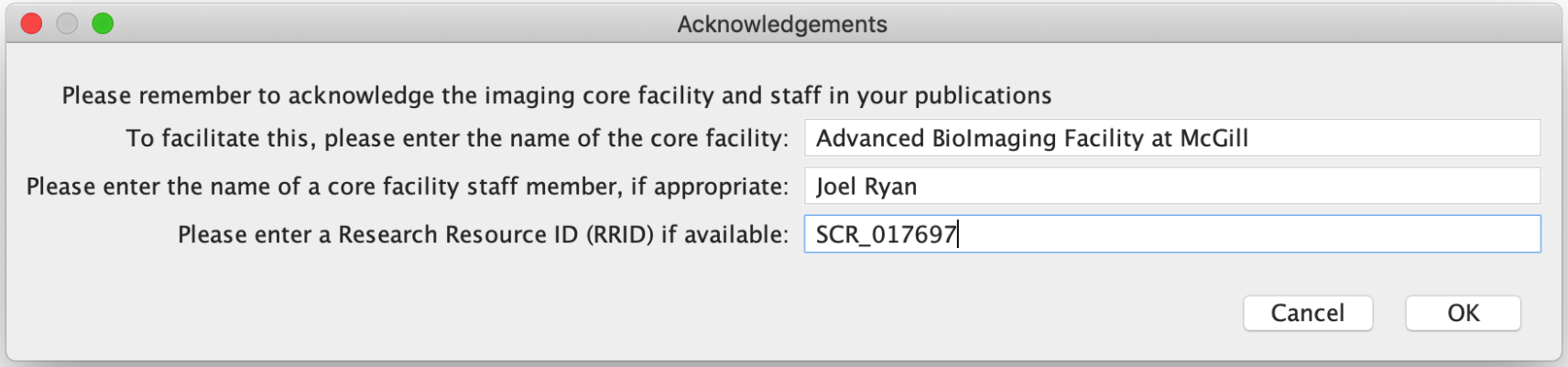
Channel menus will loop through the channels in the selected image.

MethodsJ2 – select optional devices



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

MethodsJ2 – Sample text for acknowledgement



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 – extensibility

```
282          {
283              "Dialog_Box": "Channel Settings",
284              "category": "general",
285              "Setting": "Light source intensity: ",
286              "Add_to_same_row": 0,
287              "CheckHardwareJSON": 0,
288              "Dialog_Type": "addStringField",
289              "blurb": "set to %s"
290
291          },
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), "
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)

https://raw.githubusercontent.com/ABIF-McGill/MethodsJ2/main/MJ2_structure_files/MJ2_structure_file_001.json