



# Interacting with the bioimage analysis community

Virginie Uhlmann

virginie.uhlmann@mls.uzh.ch | @VirginieUhlmann

December 2024



A background grid of 12 microscopy images showing various cellular structures and patterns in shades of green, blue, and purple.

## Today's menu

1. How to get help on [image.sc](https://image.sc) and GitHub
2. How to share your image data and analysis
3. Good practices with image analysis



A grid of microscopy images in shades of green and blue, showing various cellular structures and patterns. The images are arranged in a regular grid across the entire slide.

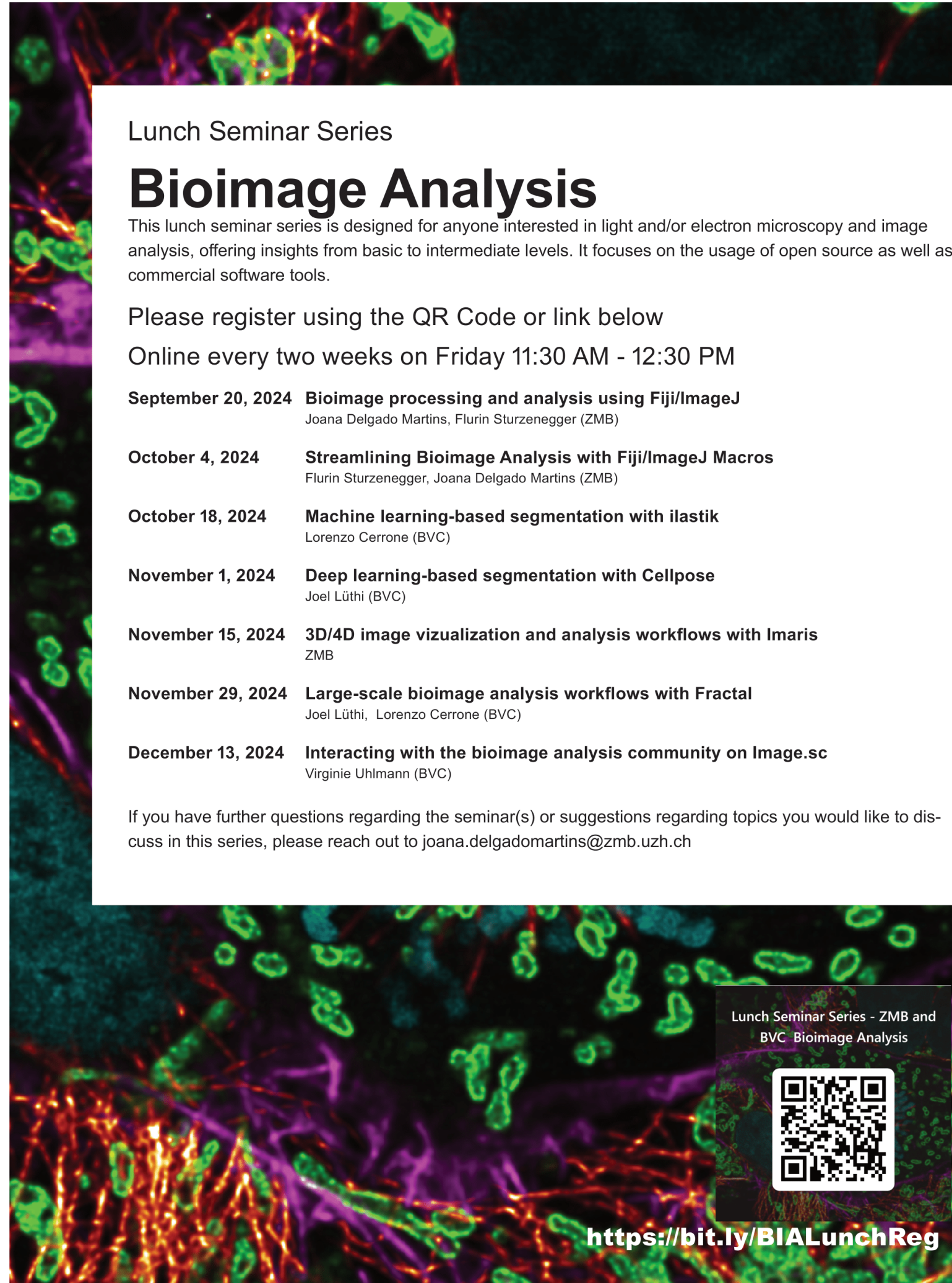
# How to get help on image.sc and GitHub



# Help! I need to analyse my images and I don't know where to start!



Center for Microscopy and Image Analysis (ZMB)  
Biovision Center (BVC)



Lunch Seminar Series

## Bioimage Analysis

This lunch seminar series is designed for anyone interested in light and/or electron microscopy and image analysis, offering insights from basic to intermediate levels. It focuses on the usage of open source as well as commercial software tools.


Please register using the QR Code or link below

Online every two weeks on Friday 11:30 AM - 12:30 PM

- September 20, 2024** **Bioimage processing and analysis using Fiji/ImageJ**  
Joana Delgado Martins, Flurin Sturzenegger (ZMB)
- October 4, 2024** **Streamlining Bioimage Analysis with Fiji/ImageJ Macros**  
Flurin Sturzenegger, Joana Delgado Martins (ZMB)
- October 18, 2024** **Machine learning-based segmentation with ilastik**  
Lorenzo Cerrone (BVC)
- November 1, 2024** **Deep learning-based segmentation with Cellpose**  
Joel Lüthi (BVC)
- November 15, 2024** **3D/4D image visualization and analysis workflows with Imaris**  
ZMB
- November 29, 2024** **Large-scale bioimage analysis workflows with Fractal**  
Joel Lüthi, Lorenzo Cerrone (BVC)
- December 13, 2024** **Interacting with the bioimage analysis community on Image.sc**  
Virginie Uhlmann (BVC)

If you have further questions regarding the seminar(s) or suggestions regarding topics you would like to discuss in this series, please reach out to [joana.delgadomartins@zmb.uzh.ch](mailto:joana.delgadomartins@zmb.uzh.ch)

Lunch Seminar Series - ZMB and BVC Bioimage Analysis



<https://bit.ly/BIALunchReg>

...to be continued!

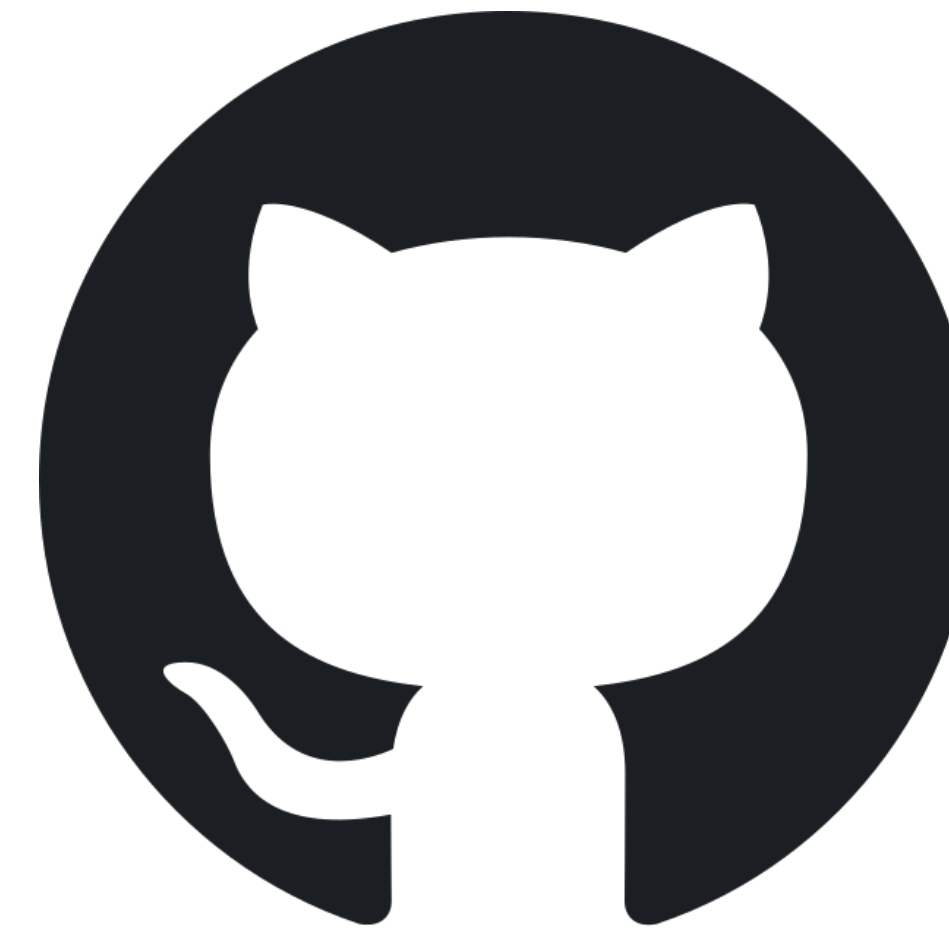


**Help! I need to analyse my images and ~~I don't know where to start~~ I've tried the nice things I was told about in the Bioimage Analysis Lunch Seminar Series but it's not working and I am stuck!**

Enter the two image analysis heroes:



image.sc



github.com



# The image.sc forum

image.sc is the online forum of the bioimaging scientific community



**Curtis Rueden**  ctrueden ImageJ2 and Fiji lead

10  Aug 2018

Welcome to the **Scientific Community Image Forum** at [forum.image.sc](https://forum.image.sc)!

This forum's focus is software-oriented aspects of scientific imaging, particularly (but not limited to) image analysis, processing, acquisition, storage, and management of digital scientific images.

**Everyone is welcome to ask questions.** It's for beginners and experts; life scientists and computer scientists; for practical questions and theoretical approaches to solving scientific problems with images. The primary objective is to [foster independent learning](#) <sup>235</sup> for everyone in the community.

Several open source software projects have pledged to use this forum as their recommended discussion channel; see the "Community Partners" dropdown on the [front page](#) <sup>403</sup>. Discussion of *any* software packages in the imaging ecosystem is equally welcome—the goal here is inclusivity. Our [mission](#) <sup>59</sup> is for people to be able to ask "how do I do X?" without prior knowledge of these various software programs. See the [Guidelines](#) <sup>307</sup> for further information.

***Tips for posting your first question:*** Please post a representative, original image file, as well as a brief explanation (avoiding science-specific "jargon" <sup>32</sup>) and/or an annotated version of the image to better indicate what solution you are after.

The image.sc community declares no financial interests in collecting personal data. You can find details on the [Terms of Service](#) <sup>21</sup> page.

The forum is jointly operated by the Broad Institute and UW-Madison via the [Center for Open Bioimage Analysis \(COBA\)](#) <sup>121</sup>.



# The image.sc forum


image.sc is the recommended discussion channel for most of the tools we talked about in this Seminar Series

The screenshot displays the image.sc forum interface. At the top, there is a navigation bar with the image.sc logo, a search icon, and buttons for 'Zulip chat', 'Related Forums', 'Sign Up', and 'Log In'. On the left, a sidebar menu includes 'Topics', 'Upcoming Events', 'More', 'CATEGORIES' (with sub-items: Announcements, Development, Image Analysis, Job Opportunities, Usage & Issues, All categories), and 'TAGS' (with sub-items: irods, ome-ngff, All tags). The main content area is titled 'Community Partners' and features a grid of 60 logos for various image analysis tools and projects, including AGAVE, AICSImageIO, Arkitect, Aydin, BAND, BIAFLOWS, BiaPy, BiofilmQ, Bio-Formats, Biomechanics, BrainGlobe, CAREamics, Cell-ACDC, Cellpose, CellProfiler, CLIJ, Cytomine, DAIM, DeepLabCut, Fiji, FLIMLib, GerBI, GloBIAS, Icy, IDR, ilastik, ImageJ, ImageJ2, ImgLib2, ImJoy, ImSwitch, iRODS, JIPipe, JuliaImages, Mars, MCMICRO, MIA, MIB, μManager, MoBIE, ModularImageAnalysis, MorphoGraphX, MorphoNet, napari, NEUBIAS, NFDI4BIOIMAGE, OME, OMERO, OmeSliCC, OpenIRIS, OpenSPIM, Orbit, Piximi, PolusAI, PYME, Python-Microscope, QUAREP-LiMi, QuPath, scenery, SCIFIO, scikit-image, sciview, SmartMicroscopy, SpotMAX, SR-Tesseler, StarDist, TeamTomo, TissUUmaps, vedo, VVDViewer, webKnossos, ZeroCostDL4Mic, and 'Your Icon Here'. At the bottom, there are sections for 'RELATED COMMUNITIES' (μforum, STK, KNIME) and 'SPONSORED BY' (COBA).



# Post categories on image.sc

Category	Topics
<b>Usage &amp; Issues</b> This category is for discussing technical questions and problems with scientific image software.	<b>182 / month</b>
<b>Image Analysis</b> This category is for questions about <a href="#">image processing and analysis</a> .	<b>174 / month</b>
<b>Development</b> This category is for development (i.e., programming) questions about scientific image software.	<b>29 / month</b>
<b>Announcements</b> This category is for announcements, such as new software releases and upcoming community events.	<b>14 / month</b>
<b>Data Management</b> This category is a complement of the “Image analysis” category for collecting questions and experiences about the structuring, storage, and curation of data. Whether you’re storing data locally on disk, in the cloud, or looking for a database solution, this category is probably a good place to post. ...	<b>9 / month</b>
<b>Job Opportunities</b> See here for postings about job positions relating to the field of scientific imaging.	<b>7 / month</b>

<b>Websites</b> Discussion about the websites of the software partners of the Image.sc forum, their organization, how they work, and how they can be improved.	<b>2 / month</b>
<b>Hello my name is</b>  This category is a place to encourage newcomers to all create at least one post here on image.sc.	<b>6 / month</b>
<b>Community Partners</b> This category contains topics describing the Community Partners being discussed on this forum. A Community Partner is an open-source software project or community organization that uses this forum as a primary recommended discussion channel.	<b>2 / month</b>
<b>Blog Posts</b> This category is a place where software partners can publish blog posts for the community.	<b>100</b>
<b>Positive Posts</b> This is a category for purely positive posts. It’s so easy to become overly focused on the problems that we’re facing in imaging.	<b>0</b>

A nice place to start (even in the absence of specific questions)





# What makes a good forum post?

I tried to open my images in ilastik  
but it doesn't work. Please help.





# What makes a good forum post?

I am using ilastik version 1.4.1b22 and creating a pixel classification workflow. In the “Input Data” section, when I click “Add New...” and select my images, I get the following error:

[error log or screenshot]

The images I am trying to load are [image file details, including format and size]. An example can be found here: [URL to a public repository with an example image].

I have already tried the solution proposed on this post by @thatfantasticuser, but the error persists.

Does anyone have an idea of what could be happening?





# What makes a good forum post?

Provide enough details to allow someone else to replicate your problem



I am using ilastik version 1.4.1b22 and creating a pixel classification workflow. In the “Input Data” section, when I click “Add New...” and select my images, I get the following error:

[error log or screenshot]



Post the error log

Provide an example dataset



The images I am trying to load are [image file details, including format and size]. An example can be found here: [URL to a public repository with an example image].

I have already tried the solution proposed on this post by @thatfantasticperson, but the error persists.



Say what you have already tried

Be kind :)



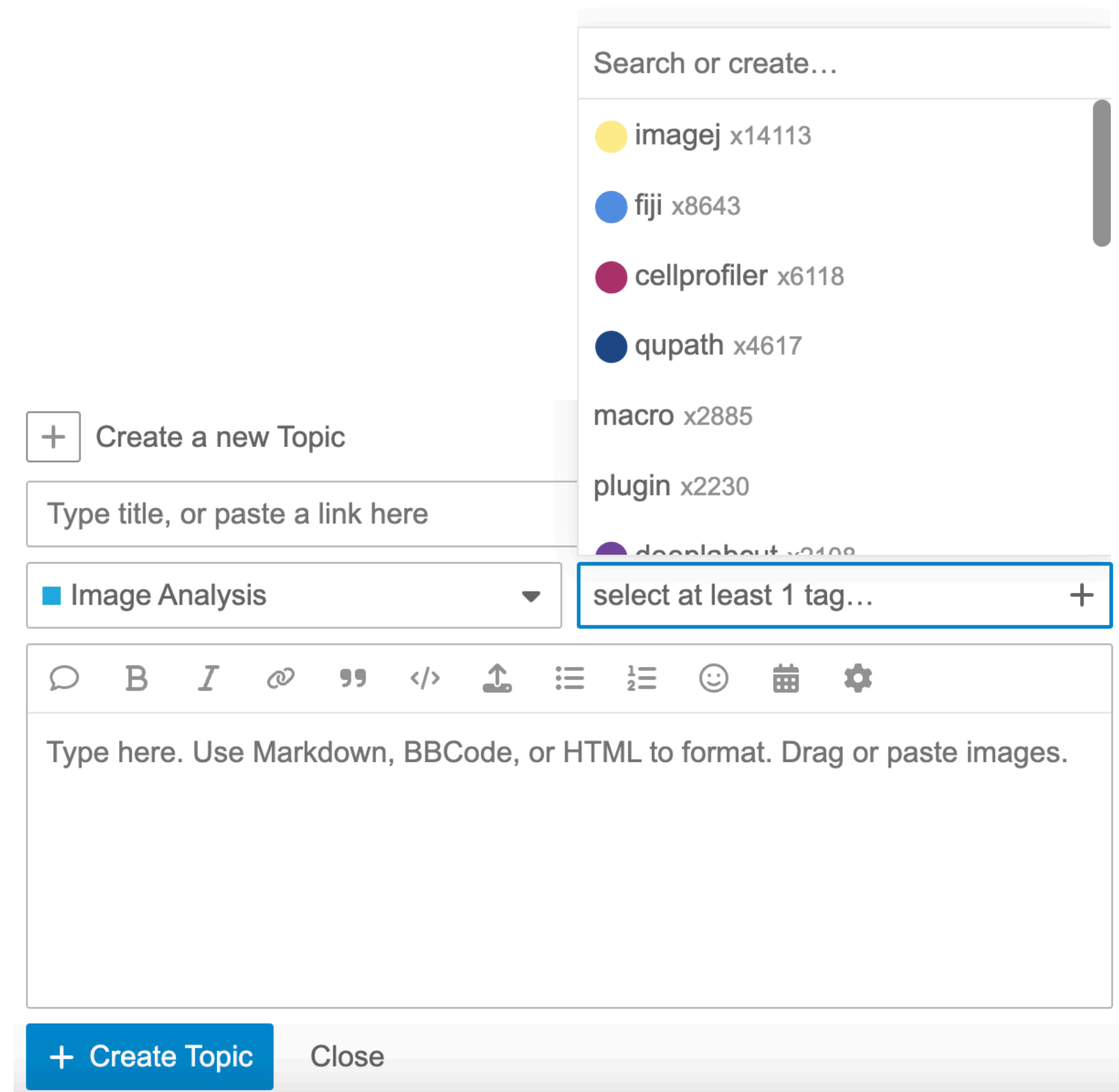
Does anyone have an idea of what could be happening?



# Stepping up your image.sc game even further

## Use tags

This will ensure that the corresponding developers are notified of your post



## Provide screenshots

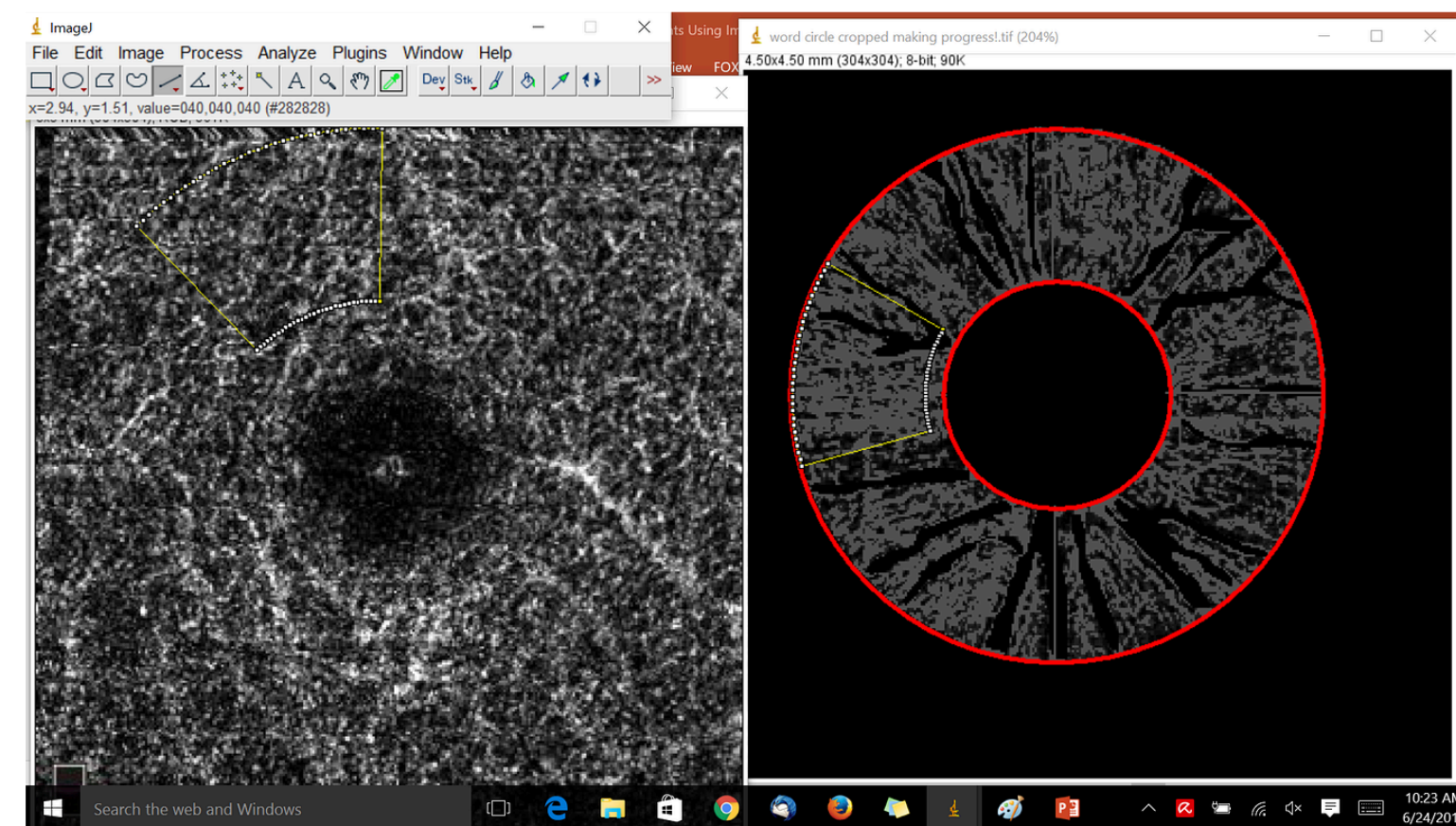
Pictures are worth a thousand words (if there are words accompanying them!!)

**A** **acha** 1 Jun 2016

Hello @oburri ,

Thank you for this macro! It seems like a great solution. I'm having just a few difficulties with running it, which likely may be related to my inexperience.

When I run it, as expected, it asks me to draw a line thru the image and then 2nd box asks for number of circles and quadrants. However, afterwards, a single quadrant (or 1/8 region) appears instead of a diagram like yours. Additionally, although the macro text includes radii of the circles, when I've run it, there has been no dialog box prompt for it (and thus the quadrant does not extend entirely to the rim of the inner circle). I also ran the macro in an empty window and got the same result. I appreciate your help. I've attached a sample of what I ended up with to the right. Thank you very much!





# How to image.sc

## DO

Tag people in your posts

Create one post per topic

Stay cordial, kind, and mindful of everyone's time

## DON'T

Send people private messages

Follow up on resolved posts

Assume that people are at your service



# GitHub

GitHub is an online platform that allows software developers to create, store, manage, and share their code

The screenshot shows the GitHub Trending page. At the top, there is a dark navigation bar with a menu icon, the GitHub logo, and a 'Sign in' button. Below this is a secondary navigation bar with links for 'Explore', 'Topics', 'Trending' (which is highlighted), 'Collections', 'Events', and 'GitHub Sponsors'. The main content area has a large 'Trending' heading and a sub-heading: 'See what the GitHub community is most excited about today.' Below this is a filter bar with 'Repositories' and 'Developers' tabs, and dropdown menus for 'Spoken Language: Any', 'Language: Any', and 'Date range: Today'. Three repository cards are visible: 1. 'soxoj / maigret' (Python) with 11,617 stars and 847 forks, built by several users, with a 'Sponsor' and 'Star' button, and '479 stars today'. 2. 'astral-sh / uv' (Rust) with 31,191 stars and 845 forks, built by several users, with a 'Star' button, and '1,707 stars today'. 3. 'ollama / ollama' with a 'Star' button.



# GitHub issues

GitHub issues is a “ticket system” for reporting and discussing bugs, usage problems, and improvement suggestions

User and repository names

Source code

Issues log

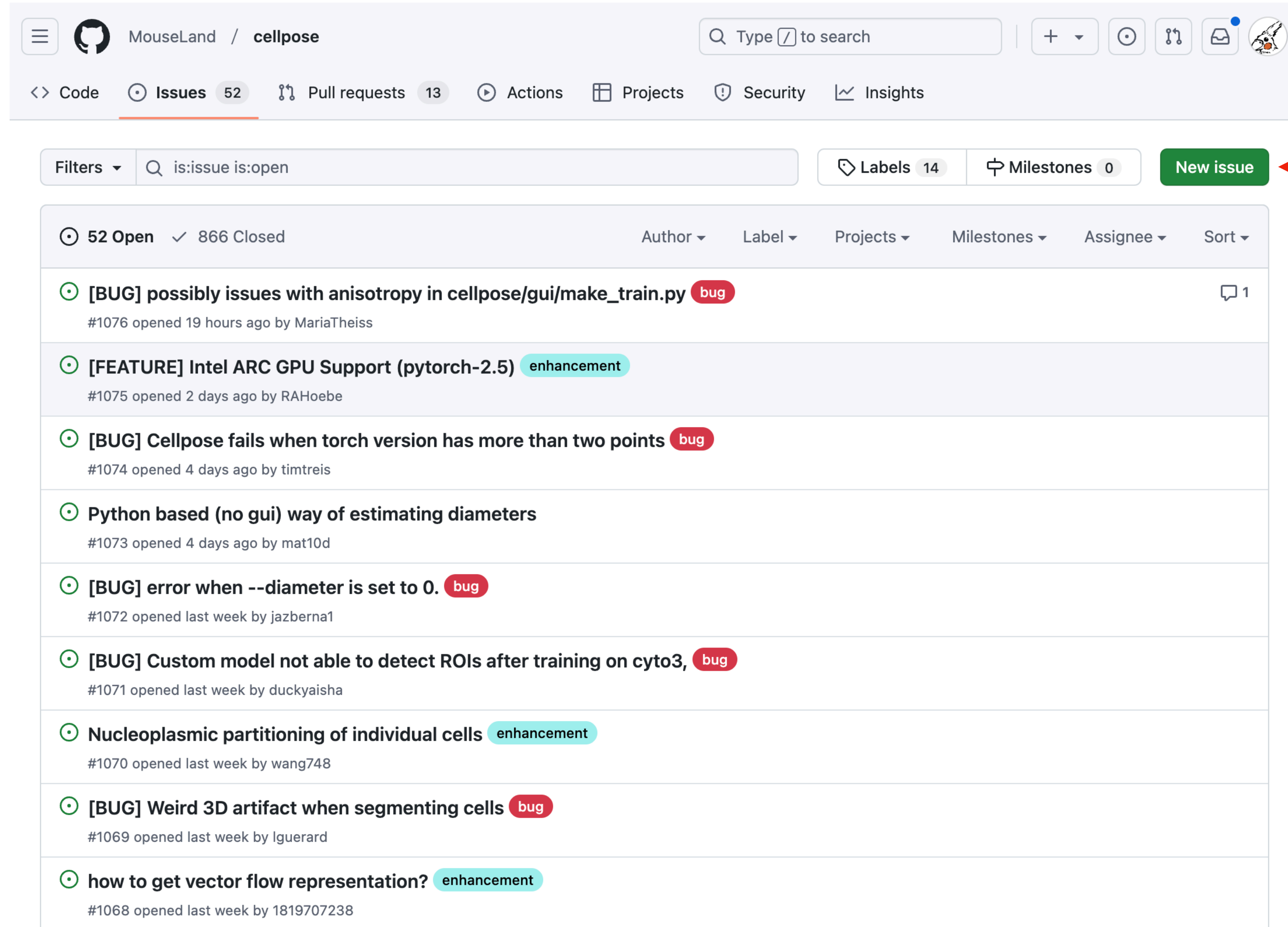
Compiled code

The screenshot displays the GitHub interface for the 'cellpose' repository. At the top, the repository name 'cellpose' and user 'MouseLand' are visible. Below this, navigation tabs include 'Code', 'Issues' (with 52 issues), 'Pull requests' (13), 'Actions', 'Projects', 'Security', and 'Insights'. Repository statistics show 29 watchers, 404 forks, and 1.4k stars. The commit log table lists recent commits by 'carsen-stringer', including updates to 'tox.ini', 'docs', and 'LICENSE'. The 'About' section on the right describes 'cellpose' as a generalist algorithm for cellular segmentation, with tags for 'segmentation', 'cell-segmentation', and 'cell-biology'. The 'Releases' section shows the latest version 'v3.1.0' released on Oct 29.

File	Commit Message	Time Ago
.github	update tox.ini	10 months ago
cellpose	adding other paper code	3 weeks ago
docs	updating docs	2 months ago
notebooks	adding train / test loss as output to train_s...	3 months ago
paper	adding other paper code	3 weeks ago
pyinstaller	adding cli files and envs	4 years ago
tests	updating to new mask creation on gpu	2 months ago
.gitignore	Initial commit	4 years ago
.readthedocs.yml	Update .readthedocs.yml	10 months ago
.style.yapf	adding yapf style	10 months ago
LICENSE	Update LICENSE	4 years ago
MANIFEST.in	init repo	4 years ago
README.md	Update README.md	2 months ago



# GitHub issues



MouseLand / **cellpose**  + 🔍 📧

<> Code **Issues 52** Pull requests 13 Actions Projects Security Insights

Filters  Labels 14 Milestones 0 **New issue**

52 Open ✓ 866 Closed Author Label Projects Milestones Assignee Sort

- [BUG] possibly issues with anisotropy in cellpose/gui/make\_train.py** **bug** 1  
#1076 opened 19 hours ago by MariaTheiss
- [FEATURE] Intel ARC GPU Support (pytorch-2.5)** **enhancement**  
#1075 opened 2 days ago by RAHoebe
- [BUG] Cellpose fails when torch version has more than two points** **bug**  
#1074 opened 4 days ago by timtreis
- Python based (no gui) way of estimating diameters**  
#1073 opened 4 days ago by mat10d
- [BUG] error when --diameter is set to 0.** **bug**  
#1072 opened last week by jazberna1
- [BUG] Custom model not able to detect ROIs after training on cyto3,** **bug**  
#1071 opened last week by duckyaisha
- Nucleoplasmic partitioning of individual cells** **enhancement**  
#1070 opened last week by wang748
- [BUG] Weird 3D artifact when segmenting cells** **bug**  
#1069 opened last week by Iguerard
- how to get vector flow representation?** **enhancement**  
#1068 opened last week by 1819707238

Open an  
new issue

# What makes a good issue?

What is the problem, in full



On what version of the software, operating system, or hardware did the problem occur



What was the output or error log



iamlll commented on Apr 16 • edited

**Install problem**  
I have tried installing cellpose and torch (GPU version) in several conda environments (deleting the original environment before trying again) without issue, following the README installation instructions. However, when I try running cellpose in a script it cannot detect / interface with my computer's GPU. Here is the setup of my latest attempt:

First, create an environment with  
`conda env create -f environment.yml`  
Next, uninstall torch: `pip uninstall torch`  
Install torch with  
`pip3 install torch --index-url https://download.pytorch.org/whl/cu118`  
(I've also tried using conda commands to install pytorch and installing older versions of cuda. The end result is always the same, i.e. that my torch version is not installed properly)

**Environment info**  
[pkglist.txt](#)  
I am using an Nvidia GeForce GTX Titan X.  
Package list when using the command  
`conda install pytorch pytorch-cuda=11.8 -c pytorch -c nvidia`  
to install pytorch instead of torch:  
[pkglist\\_pytorch.txt](#)

**Run log**  
Here's the test code I was using to check whether cellpose could access my GPU:

```
io.logger_setup()
core.use_gpu()
```

This code snippet returns the following output:

```
2024-04-15 19:20:12,179 [INFO] WRITING LOG OUTPUT TO /home/user/.cellpose/run.log
2024-04-15 19:20:12,179 [INFO]
cellpose version: 3.0.7
platform: linux
python version: 3.8.5
torch version: 2.2.2+cu118
(<Logger cellpose.io (INFO)>, PosixPath('/home/user/.cellpose/run.log'))
>>> core.use_gpu()
2024-04-15 19:20:25,852 [INFO] TORCH CUDA version not installed/working.
False
```

What are the steps to reproduce the problem

What has been tried already



# Which resource should I use when?

image.sc



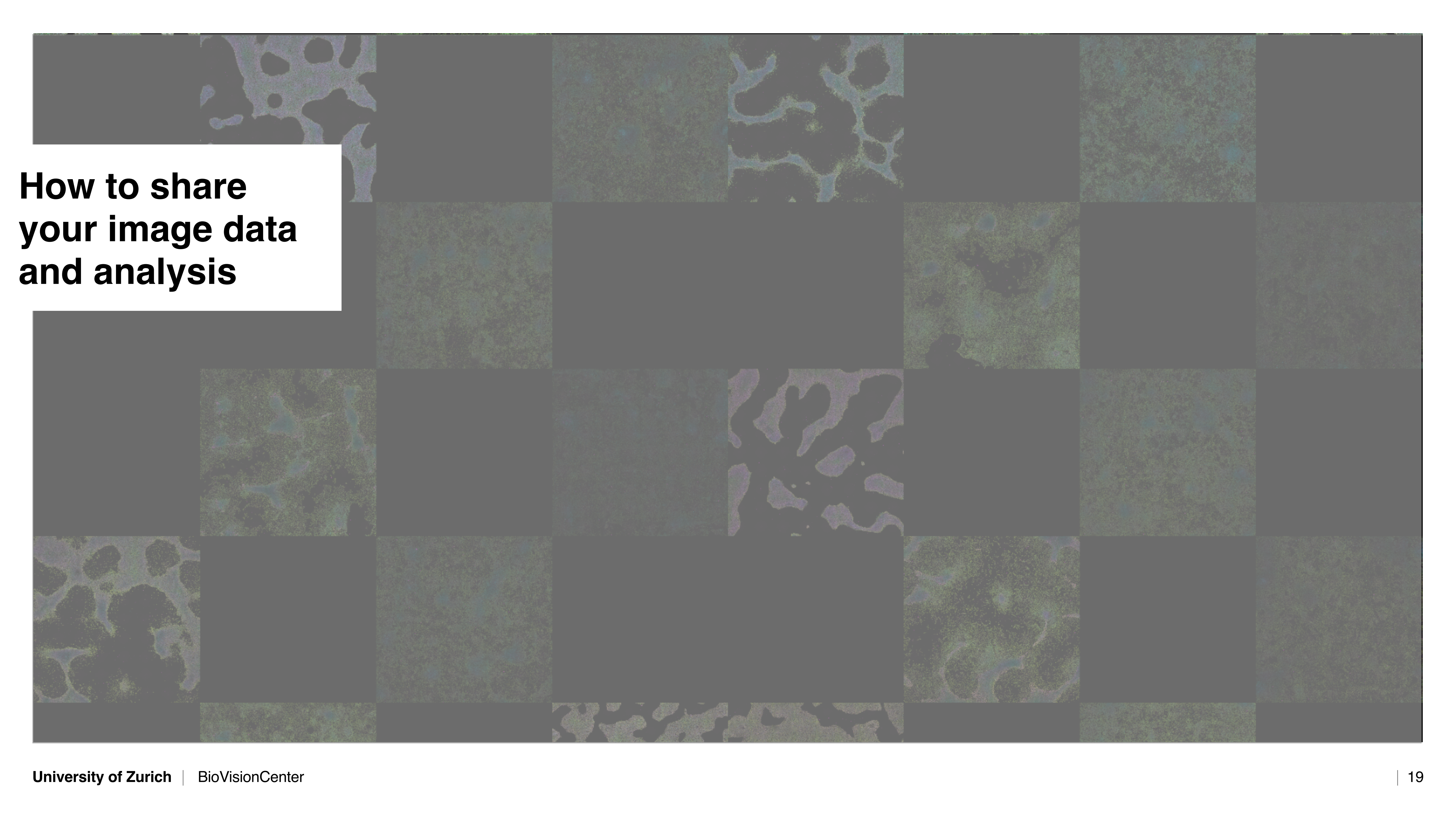
Usage problems  
General image analysis questions  
Installation issues  
Welcoming platform for everyone

github.com



Bugs and feature requests  
Highly specific questions  
Documentation/API issues  
Specialised platform for developers



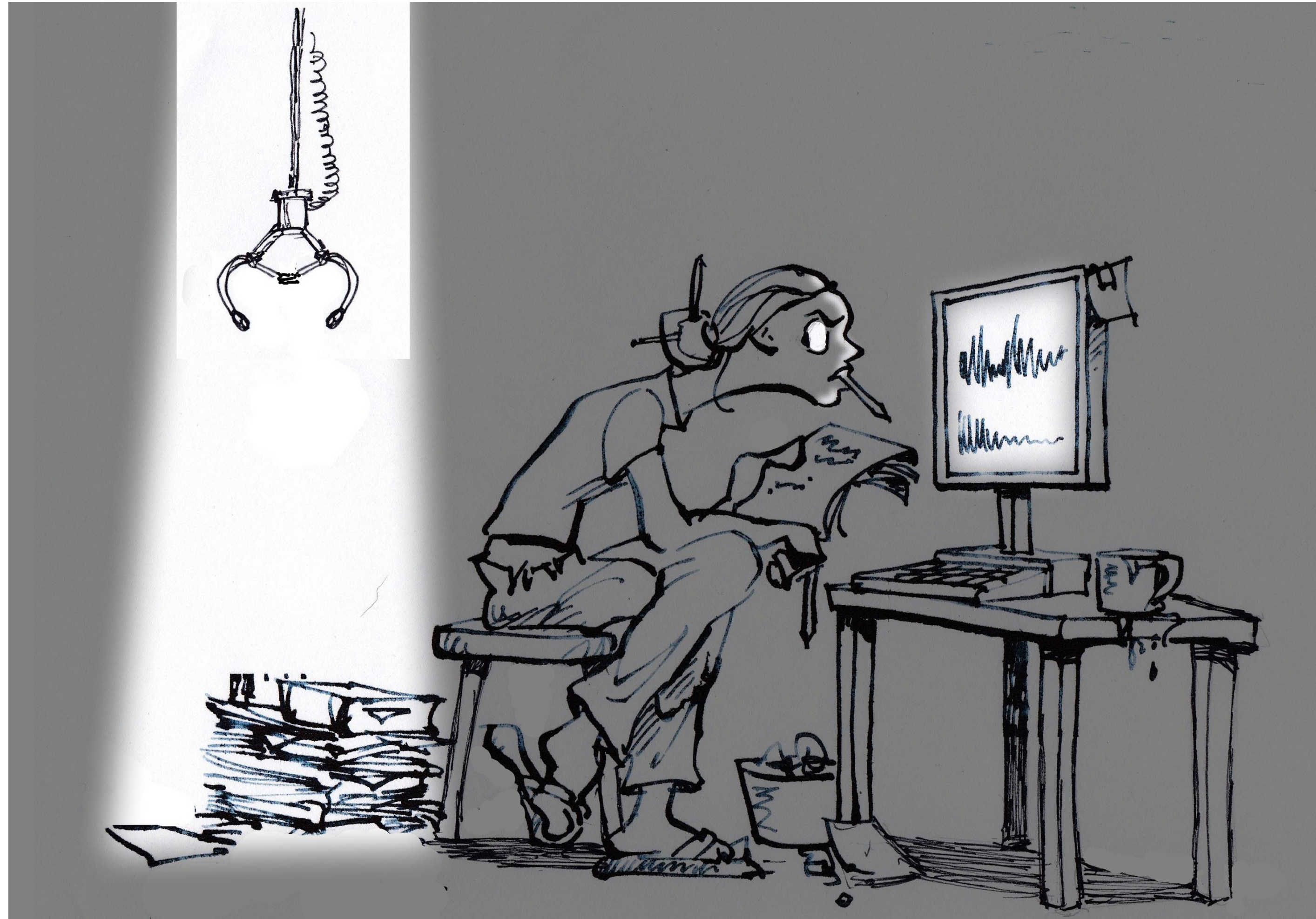
A grid of 24 microscopy images arranged in 4 rows and 6 columns. The images show various biological structures, including cell clusters, individual cells, and fibrous networks, rendered in shades of blue, green, and purple. A white text box is overlaid on the top-left corner.

# How to share your image data and analysis



# Why aren't all image data and analysis shared?

Mostly because of fear (of being scooped, of being wrong) and lack of awareness (“it’s not worth the effort”).



“Fear of being scooped”, cartoon by John R. McKiernan, licensed CC BY (<http://whyopenresearch.org/gallery.html>)



# Why sharing my image data and analysis?

Because it benefits you (visibility, funding, recognition), the rest of the scientific community (reuse, reanalysis, collaboration), and society at large.

Wilkinson *et al.*, *Sci Data*, 2016

Uhlmann *et al.*, *Journal of Cell Science*, 2024

The FAIR Guiding Principles for scientific data

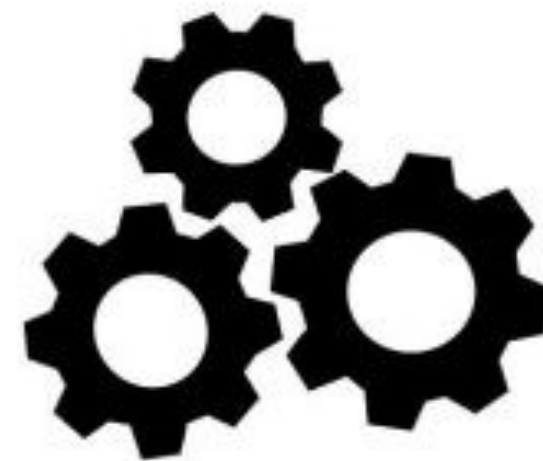
**F**  
Findable



**A**  
Accessible



**I**  
Interoperable



**R**  
Reusable





# Where can I share my image data and analysis?

On free, publicly-funded online infrastructures such as [zenodo.org](https://zenodo.org) (hosted at CERN, Switzerland)



The screenshot shows the Zenodo website interface. At the top is a blue header with the 'zenodo' logo and a menu icon. Below the header is a section titled 'Featured communities'. The first featured community is the 'EU Open Research Repository', which includes the European Union flag, a 'Browse' button, and a description: 'Open repository for EU-funded research outputs from Horizon Europe, Euratom, and earlier Framework Programmes.' Below this is a section titled 'Recent uploads'. The first upload is a dataset titled 'CEAD Cohort Study of Individuals with diabetes in Eloy Alfaro Health district, Esmeraldas: Interview data, Health records and Variable Code Equivalencies' from the CEAD project. It was uploaded on December 10, 2024, and is marked as 'Open'. The description mentions it is part of the 'UMH Global Health Research Group' and provides a link to a case study. At the bottom right of the upload card, there are icons for views (33) and downloads (25).

# Public data sharing with Zenodo



Author attribution



Published August 12, 2024 | Version v5 Dataset Open

## OME-Zarr 3D hiPSCs with 3D labels & 3D measurements, 2x2 field of views

Lüthi, Joel!

Show affiliations

These are 2 small OME-Zarr files of the data from [10.5281/zenodo.7057076](https://doi.org/10.5281/zenodo.7057076).

The images have been processed using [Fractal](#), the workflow is attached as a json file. It ran with `fractal-server==2.3.6`, `fractal-client==2.0.1`, `fractal-web==1.4.0` and `fractal-tasks-core==1.2.1`.

Both Zarr files are Zip-compressed to allow easier upload & download from Zenodo.

20200812-CardiomyocyteDifferentiation14-Cycle1.zarr contains 3 3D channels, a nuclear segmentation produced by [cellpose](#) as labels and 4 tables: A ROI table for the whole well, a ROI table for the 4 field of views, a masking ROI table for the nuclear segmentation, as well as measurements performed with [napari-skimage-regionprops](#).

20200812-CardiomyocyteDifferentiation14-Cycle1\_mip.zarr contains the same 3 channels, but as maximum intensity projections. It contains nuclear segmentation through [cellpose](#), as well as 3 more labels generated by [napari workflows](#) (different thresholds, less accurate segmentations). It also contains 7 tables: The region of interests like in the 3D data, as well as measurements performed with [napari-skimage-regionprops](#).

The tables are stored in the OME-Zarr file according to the [Fractal table specification spec](#) in AnnData.

The 3 channels are:

- 0: DAPI, nuclear stain
- 1: nanog, antibody staining with Bio-Techne AG, AF1997-SP, Lot KKJ0617121 for the stemness marker nanog
- 2: Lamin B1, antibody staining with Abcam, ab16048, Lot GR3244890-2 for the nuclear envelope marker Lamin B1

### Files

20200812-CardiomyocyteDifferentiation14-Cycle1.zarr.zip

20200812-CardiomyocyteDifferentiation14-Cycle1.zarr.zip

The previewer is not showing all the files.

- 20200812-CardiomyocyteDifferentiation14-Cycle1.zarr
  - .zattrs 540 Bytes
  - .zgroup 24 Bytes
    - B
      - .zgroup 24 Bytes
        - 03
          - .zattrs 135 Bytes
          - .zgroup 24 Bytes
            - 0
              - .zattrs 4.1 kB
              - .zgroup 24 Bytes
                - 0
                  - .zarray 420 Bytes

833 VIEWS

271 DOWNLOADS

Show more details

Metrics

### Versions

| Version       | Date         |
|---------------|--------------|
| Version v5    | Aug 12, 2024 |
| Version v4    | Dec 4, 2023  |
| Version 1.2.0 | Jun 28, 2023 |
| Version 1.1.0 | Feb 24, 2023 |
| Version 1.0.0 | Oct 4, 2022  |

View all 5 versions

Cite all versions? You can cite all versions by using the DOI [10.5281/zenodo.7144918](https://doi.org/10.5281/zenodo.7144918). This DOI represents all versions, and will always resolve to the latest one. [Read more](#).

Versioning

### External resources

Indexed in

OpenAIRE

### Keywords and subjects

immunofluorescence high content imaging image analysis

fractal OME-NGFF OME-Zarr

### Details

DOI [10.5281/zenodo.13305316](https://doi.org/10.5281/zenodo.13305316)

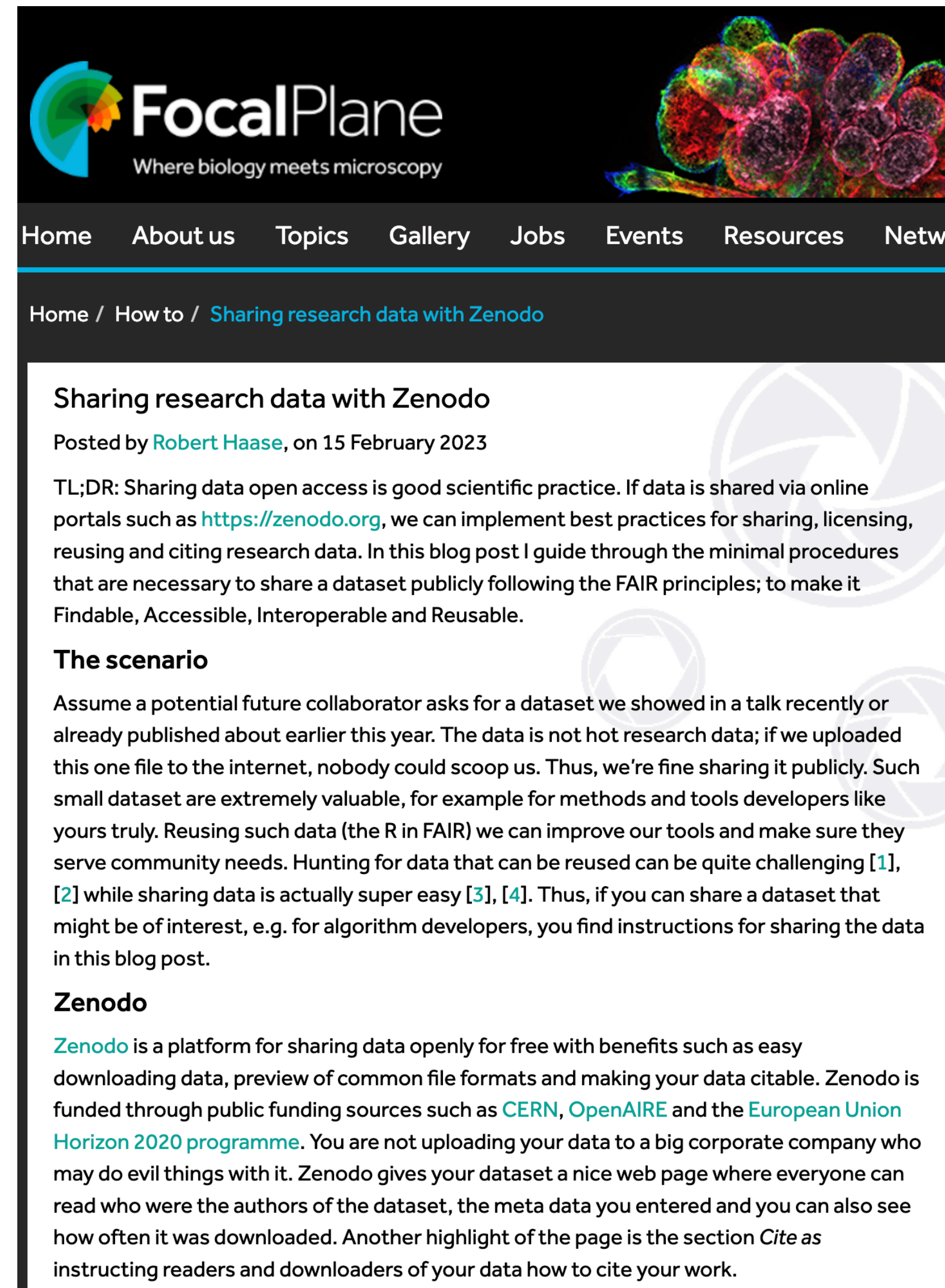
Resource type  
Dataset

Publisher  
Zenodo

Unique object identifier



# Public data sharing with Zenodo



The screenshot shows a web page from FocalPlane, a platform for biologists. The header features the FocalPlane logo with the tagline 'Where biology meets microscopy' and a navigation menu with links for Home, About us, Topics, Gallery, Jobs, Events, Resources, and Network. Below the navigation is a breadcrumb trail: Home / How to / Sharing research data with Zenodo. The main content area is titled 'Sharing research data with Zenodo' and is dated February 15, 2023, by Robert Haase. The text discusses the importance of open access and the FAIR principles (Findable, Accessible, Interoperable, and Reusable). It describes a scenario where a dataset is shared publicly and explains the benefits of using Zenodo as a platform for data sharing, including easy access, citation, and public funding support.

**FocalPlane**  
Where biology meets microscopy

Home About us Topics Gallery Jobs Events Resources Network

Home / How to / [Sharing research data with Zenodo](#)

## Sharing research data with Zenodo

Posted by [Robert Haase](#), on 15 February 2023

TL;DR: Sharing data open access is good scientific practice. If data is shared via online portals such as <https://zenodo.org>, we can implement best practices for sharing, licensing, reusing and citing research data. In this blog post I guide through the minimal procedures that are necessary to share a dataset publicly following the FAIR principles; to make it Findable, Accessible, Interoperable and Reusable.

### The scenario

Assume a potential future collaborator asks for a dataset we showed in a talk recently or already published about earlier this year. The data is not hot research data; if we uploaded this one file to the internet, nobody could scoop us. Thus, we're fine sharing it publicly. Such small dataset are extremely valuable, for example for methods and tools developers like yours truly. Reusing such data (the R in FAIR) we can improve our tools and make sure they serve community needs. Hunting for data that can be reused can be quite challenging [1], [2] while sharing data is actually super easy [3], [4]. Thus, if you can share a dataset that might be of interest, e.g. for algorithm developers, you find instructions for sharing the data in this blog post.

### Zenodo

[Zenodo](#) is a platform for sharing data openly for free with benefits such as easy downloading data, preview of common file formats and making your data citable. Zenodo is funded through public funding sources such as [CERN](#), [OpenAIRE](#) and the [European Union Horizon 2020 programme](#). You are not uploading your data to a big corporate company who may do evil things with it. Zenodo gives your dataset a nice web page where everyone can read who were the authors of the dataset, the meta data you entered and you can also see how often it was downloaded. Another highlight of the page is the section *Cite as* instructing readers and downloaders of your data how to cite your work.

# Where ELSE can I share my image data?

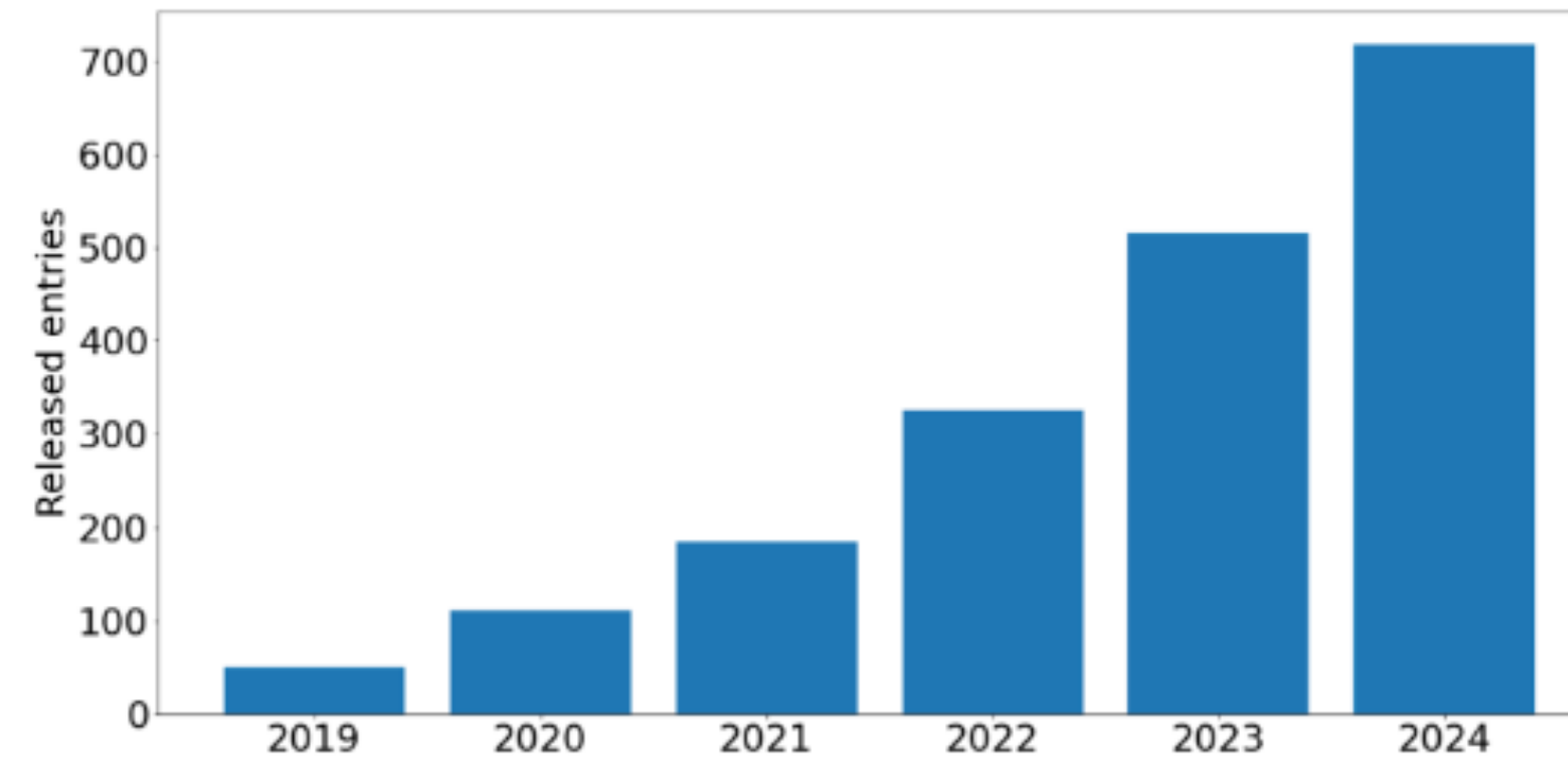
On free, publicly-funded online resource specifically dedicated to bioimages such as the Bioimage Archive (hosted at EMBL-EBI, UK)



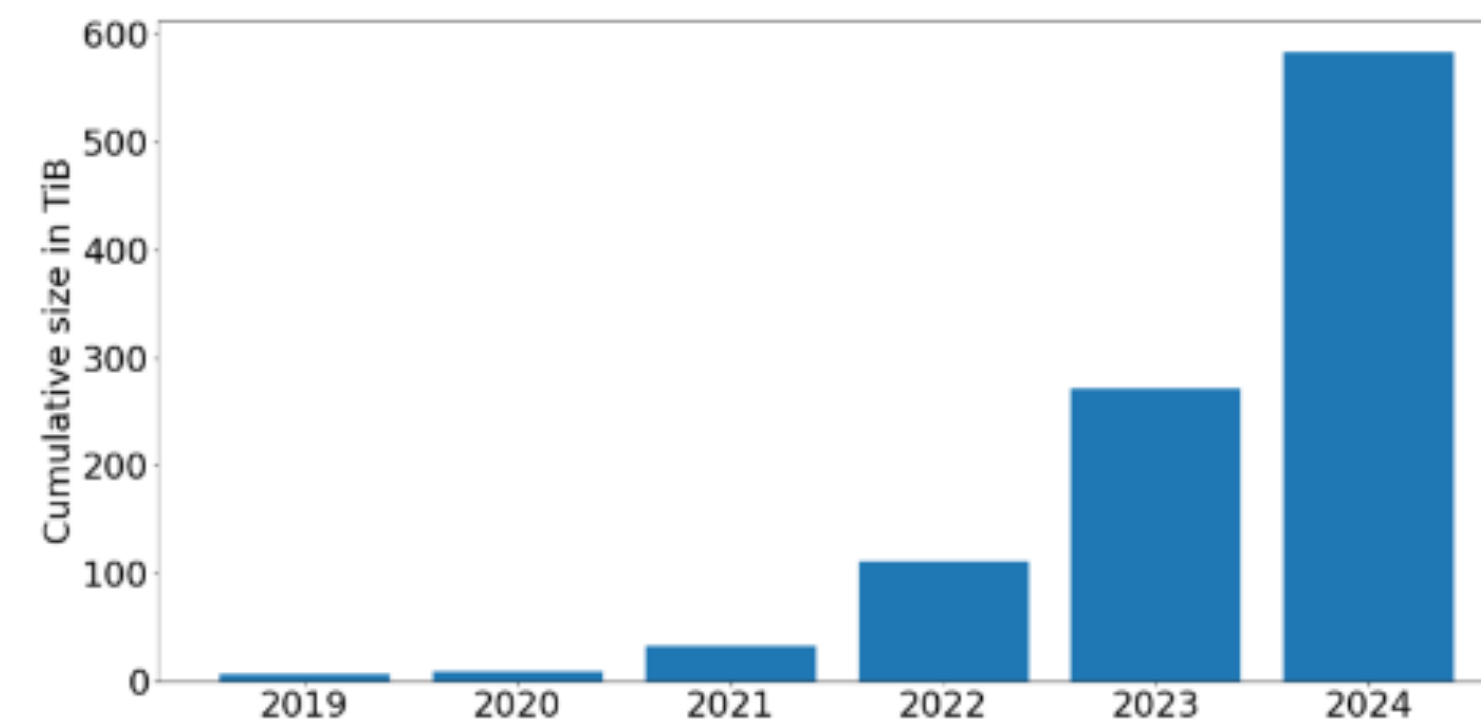
BioImage Archive

As of 20th September, 2024, the archive provides access to 721 individual datasets. Deposition rates are approaching one per day, with the 1000th entry expected sometime in the first half of 2025.

Growth rate - released entries



Growth rate - data volumes





# Public bioimage data sharing on the Bioimage Archive



## ALPHA S-BIAD599

An image-based data-driven analysis of cellular architecture in a developing tissue

Released: 2022-12-13

By: Jonas Hartmann, Mie Wong, Elisa Gallo, Darren Gilmour

### On this page

[Study Information](#) ▾

[Images](#) ▾

[Annotations](#) ▾

[Models used](#) ▾

### In a nutshell

584 images

196 annotations

Study size: 130.1GiB

Filetype breakdown:

- .tif: 584 (130.1GiB)

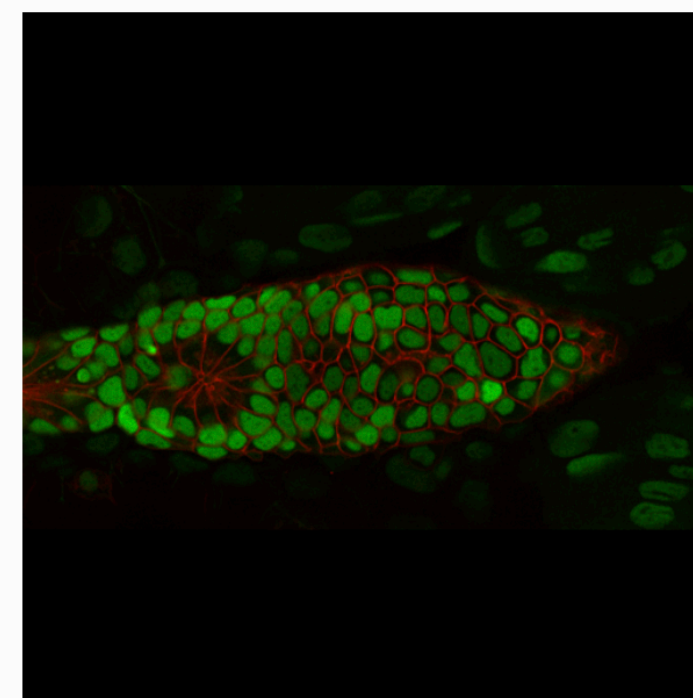
License : CC BY 4.0

### This dataset has

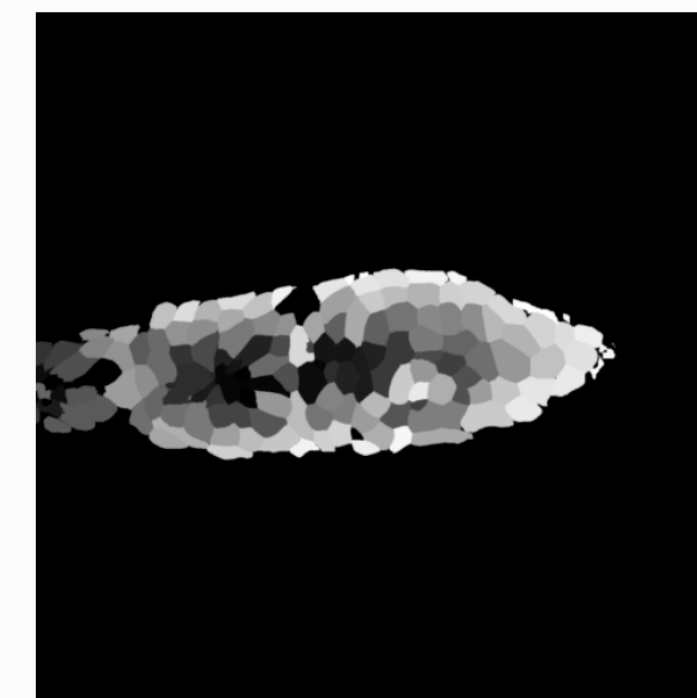
segmentation masks

3D

Super valuable for  
method developers!



Example image for this dataset



Example annotation for this dataset

### Study Information

[Original submission page](#)

### Study Summary

3D zebrafish embryo images with single-cell segmentation and point cloud-based morphometry

Organism

Danio rerio (zebrafish)

# Where can I share my code?

On version-controlled, collaborative software development platforms such as GitHub

The screenshot shows the GitHub interface for the repository 'fractal-tasks-core'. The repository is public and has 4 watchers, 6 forks, and 14 stars. The main content area displays a commit history table with columns for commit message, commit hash, and time ago. The commit history table is as follows:

| Commit Message   | Commit Hash | Time Ago     |
|--|-------------|--------------|
| tcompa bump version 1.3.2 -> 1.3.3 ✓                               | 9e4efc4     | 2 weeks ago  |
| .github add 3.12 to tasks CI                                       |             | 2 months ago |
| docs Use logos from fractal-logos                                  |             | last month   |
| examples Rename maximum intensity projection to projection         |             | 4 months ago |
| fractal_tasks_core bump version 1.3.2 -> 1.3.3                     |             | 2 weeks ago  |
| tests Add upper and lower quantile rescaling to calculate_regis... |             | 2 months ago |
| .gitignore Extract prepare_label_group function from write.py      |             | last year    |
| .mypy.ini Add .mypy.ini  |             | 2 years ago  |
| .pre-commit-config.yaml Update Cellpose tests                      |             | 6 months ago |
| CHANGELOG.md CHANGELOG [skip ci]                                   |             | 2 weeks ago  |
| LICENSE Create LICENSE   |             | 2 years ago  |
| README.md Use logos from fractal-logos                             |             | last month   |
| mkdocs.yml Use logos from fractal-logos                            |             | last month   |
| poetry.lock Bump notebook from 7.0.7 to 7.2.2                      |             | last month   |
| pyproject.toml bump version 1.3.2 -> 1.3.3                         |             | 2 weeks ago  |

On the right side of the repository page, there are several sections: 'About' (Main tasks for the Fractal analytics platform), 'License' (BSD-3-Clause license), 'Contributors' (10 contributors), 'Releases' (94 tags), 'Deployments' (368 deployments), and 'Languages' (Python 100.0%).

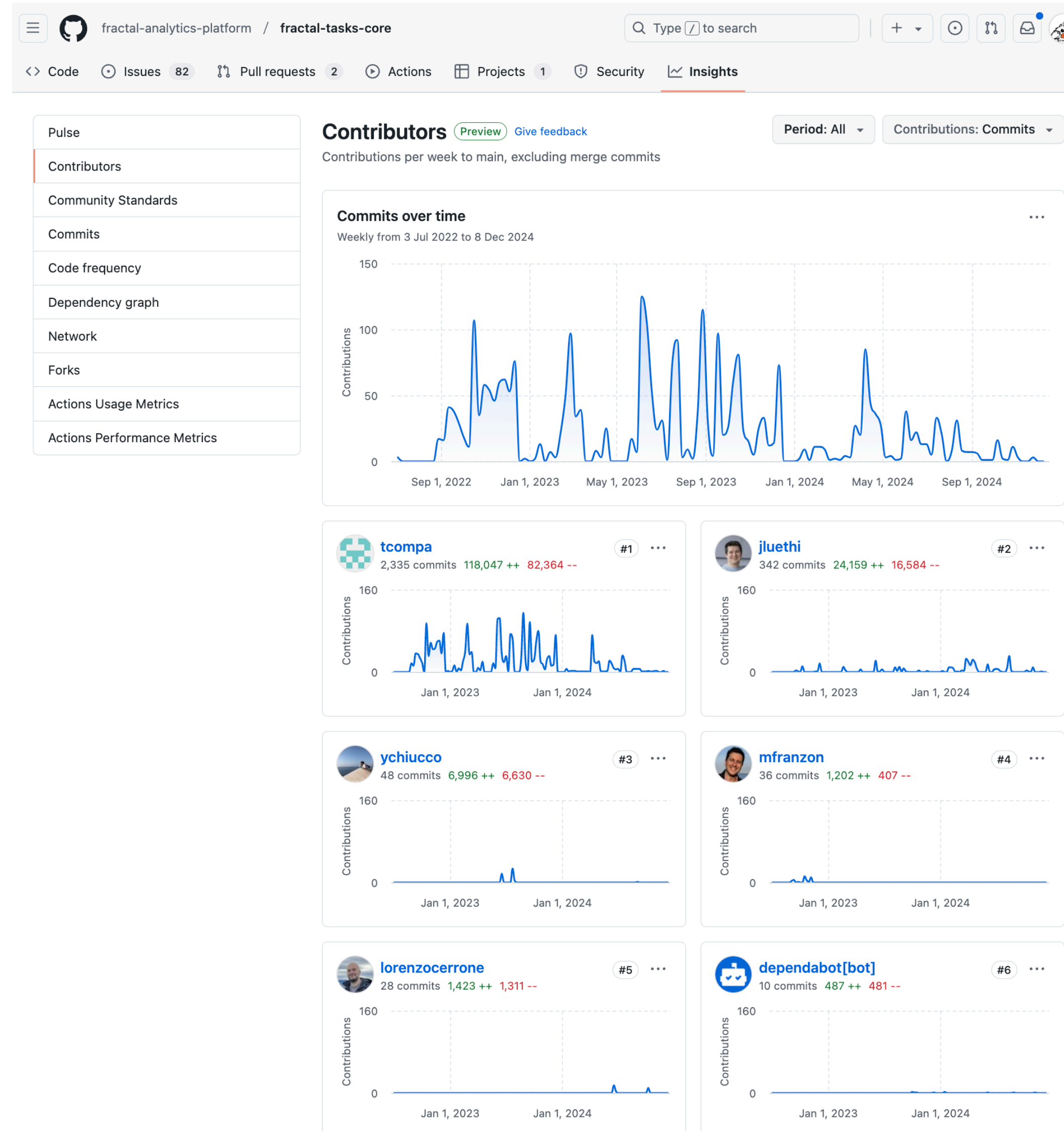
Red arrows point to the following elements:

- Metrics:** Points to the 'Star 14' button in the repository header.
- License:** Points to the 'BSD-3-Clause license' link in the 'About' section.
- Contributors:** Points to the 'Contributors 10' section showing the avatars of the contributors.



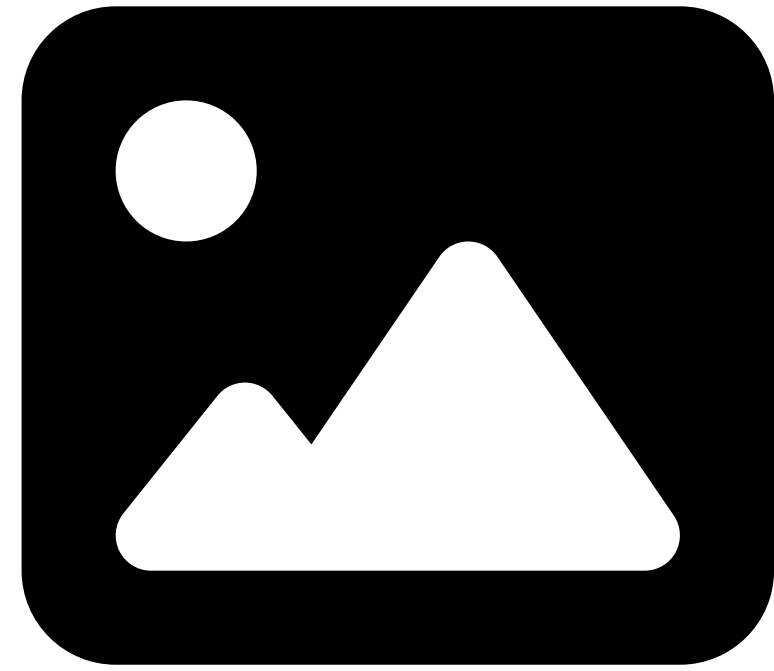
# Code sharing on GitHub

Version control makes it possible to unambiguously track contributions, and ensure that credit is given where credit is due.



# What should I care about when sharing my data?

Image data

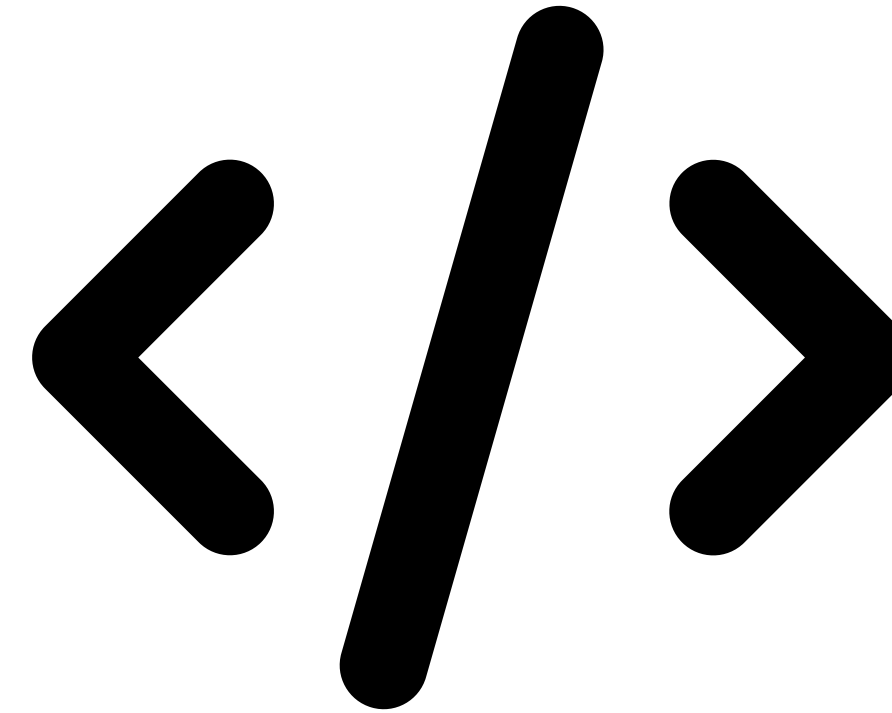


DOI

Only substantial modifications are archived

Hosted on publicly-funded platform

Code



Version control

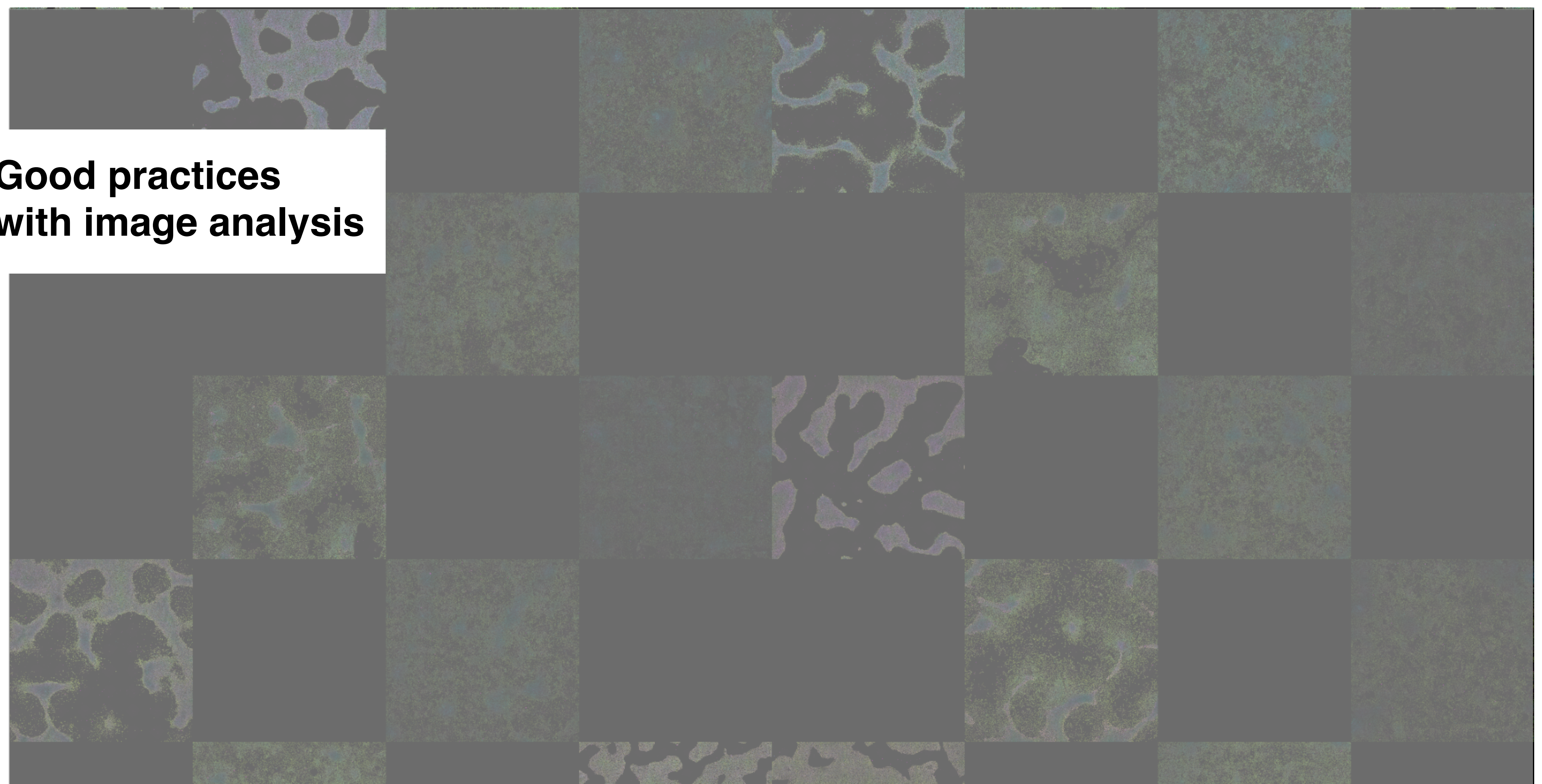
Full history of changes is available

Hosted on collaborative platforms

For both: appropriate licensing!



# Good practices with image analysis

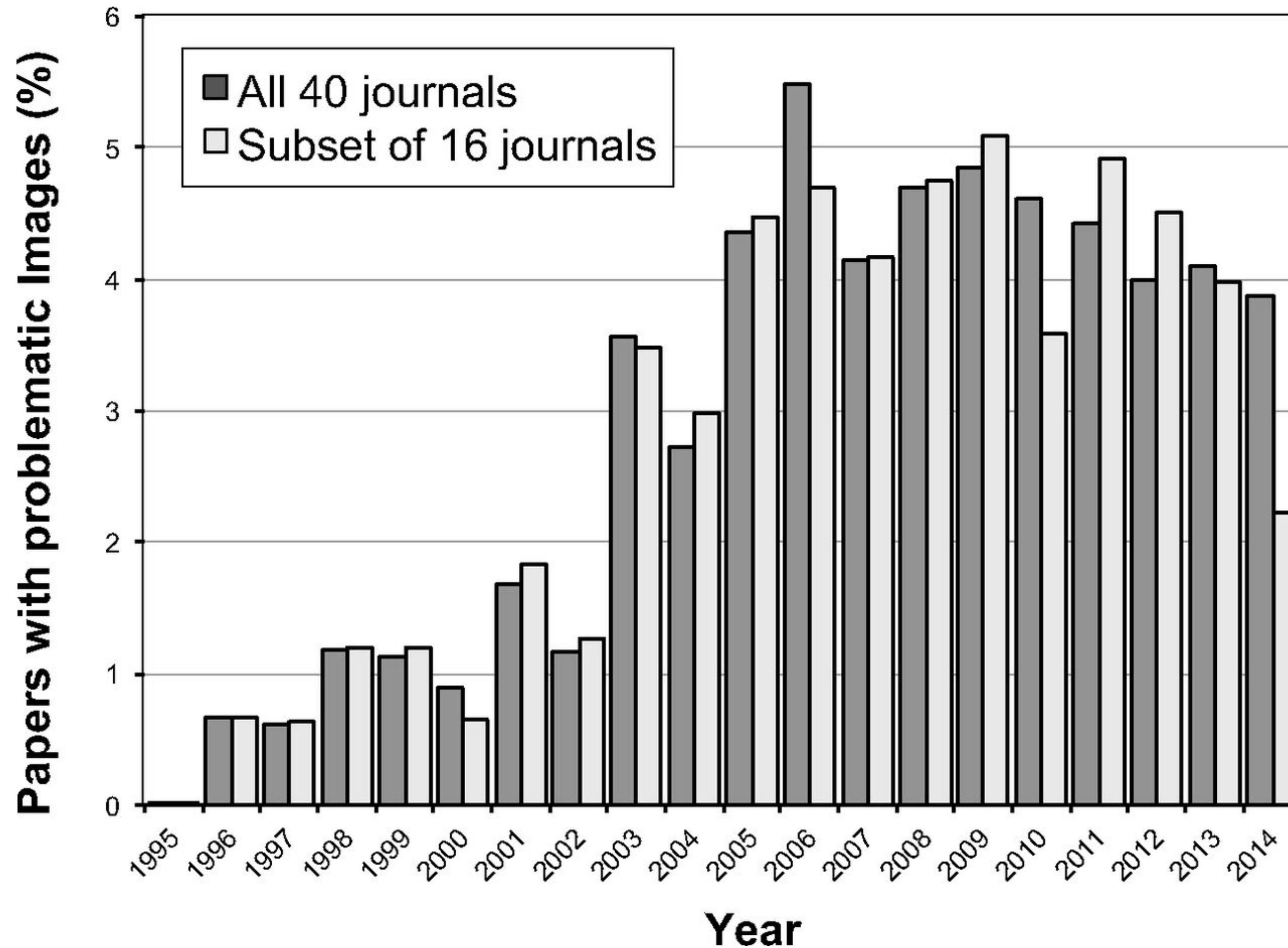




# Images are data, and should be treated as such

Surveying >20'000 papers published in 40 scientific journals over 1995-2014, 4% of published papers appeared to contain problematic figures (mishandling) with ~2% suggesting deliberate manipulation (misconduct)

Bik *et al.*, mBio, 2016





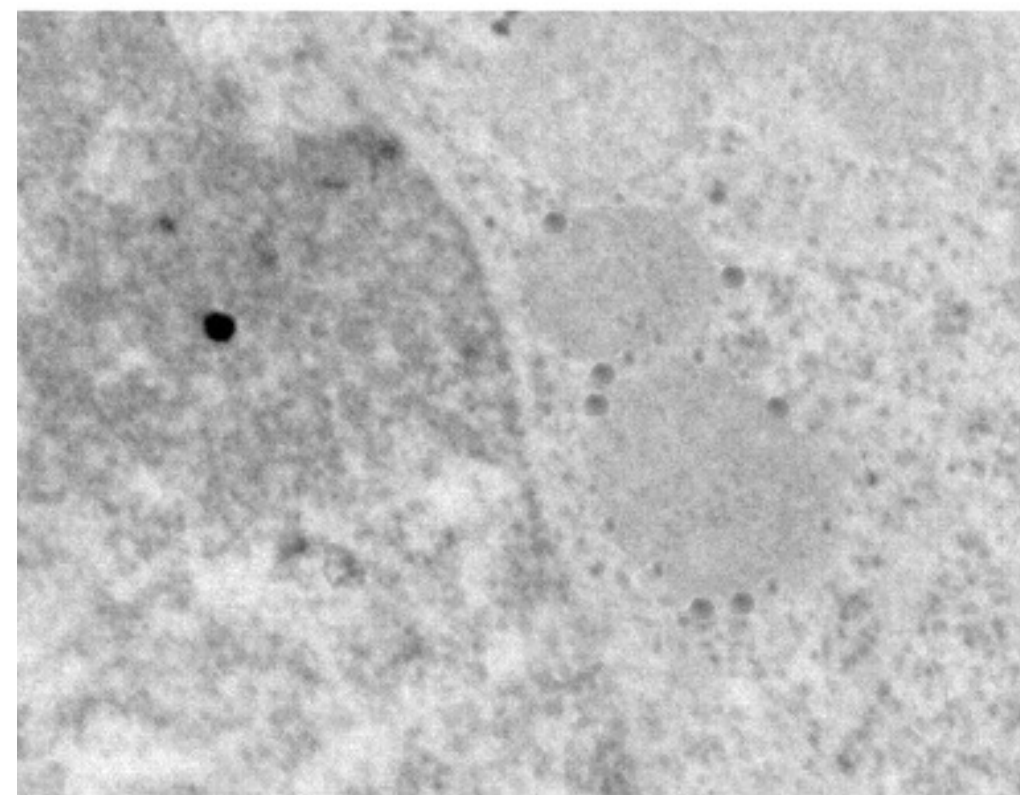
# Beware of image data mishandling: visualisation

Changes to the visual rendering of image data may alter the message they convey - that includes intensity adjustments, cropping, duplications, changes of bit depth, ...

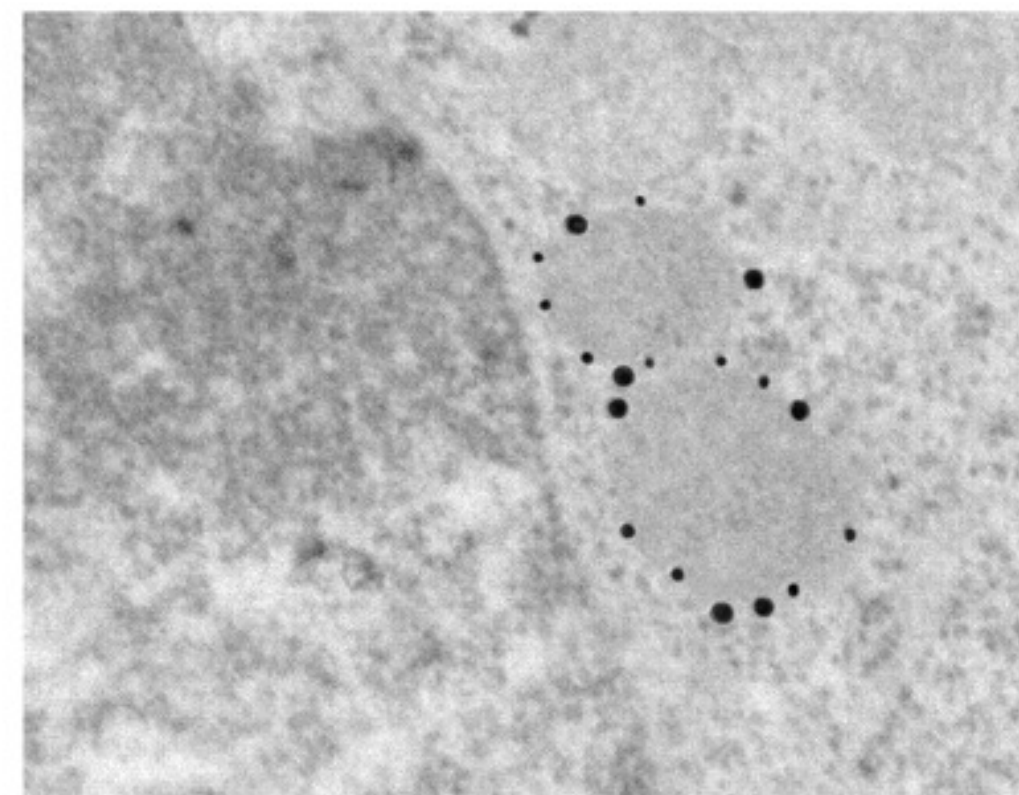
Miura & Nørrelykke, The EMBO Journal, 2021

## Selective contrast enhancement

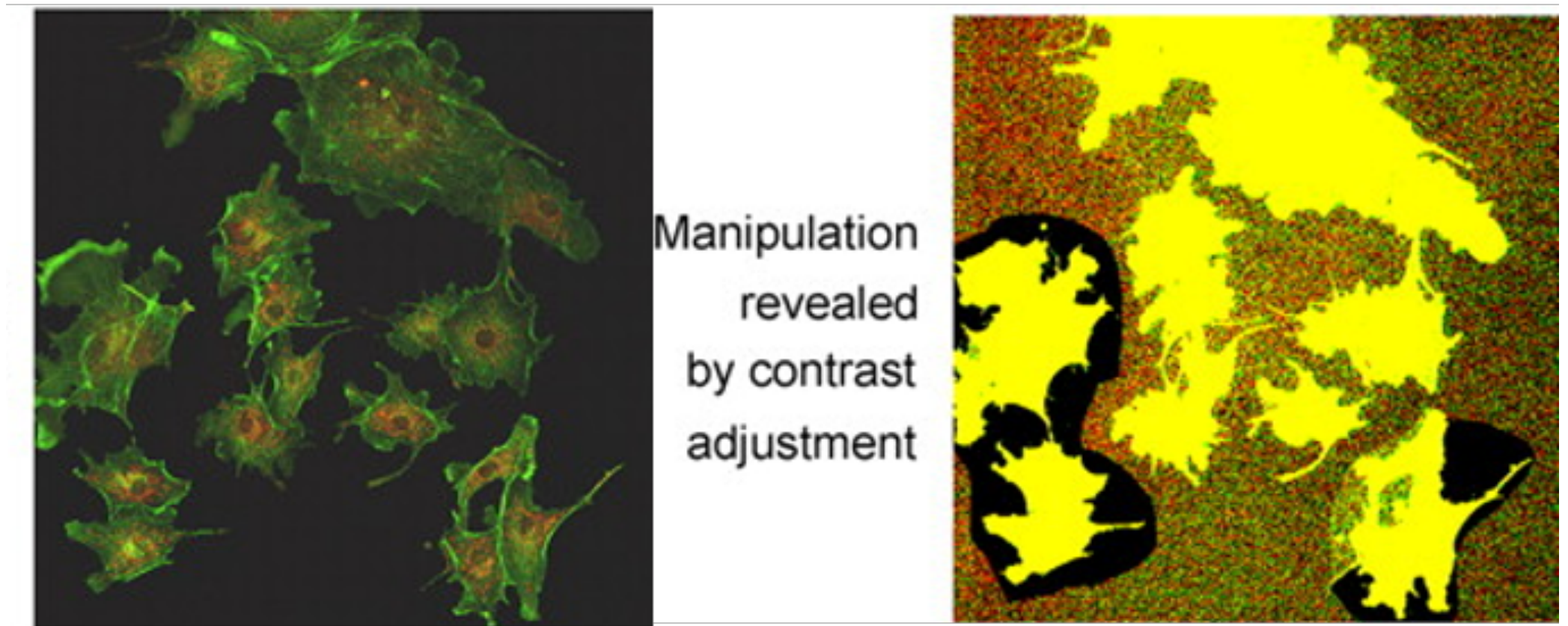
Original image



Manipulated image



## Selective cropping



Examples provided by Joana Delgado Martins, ZMB

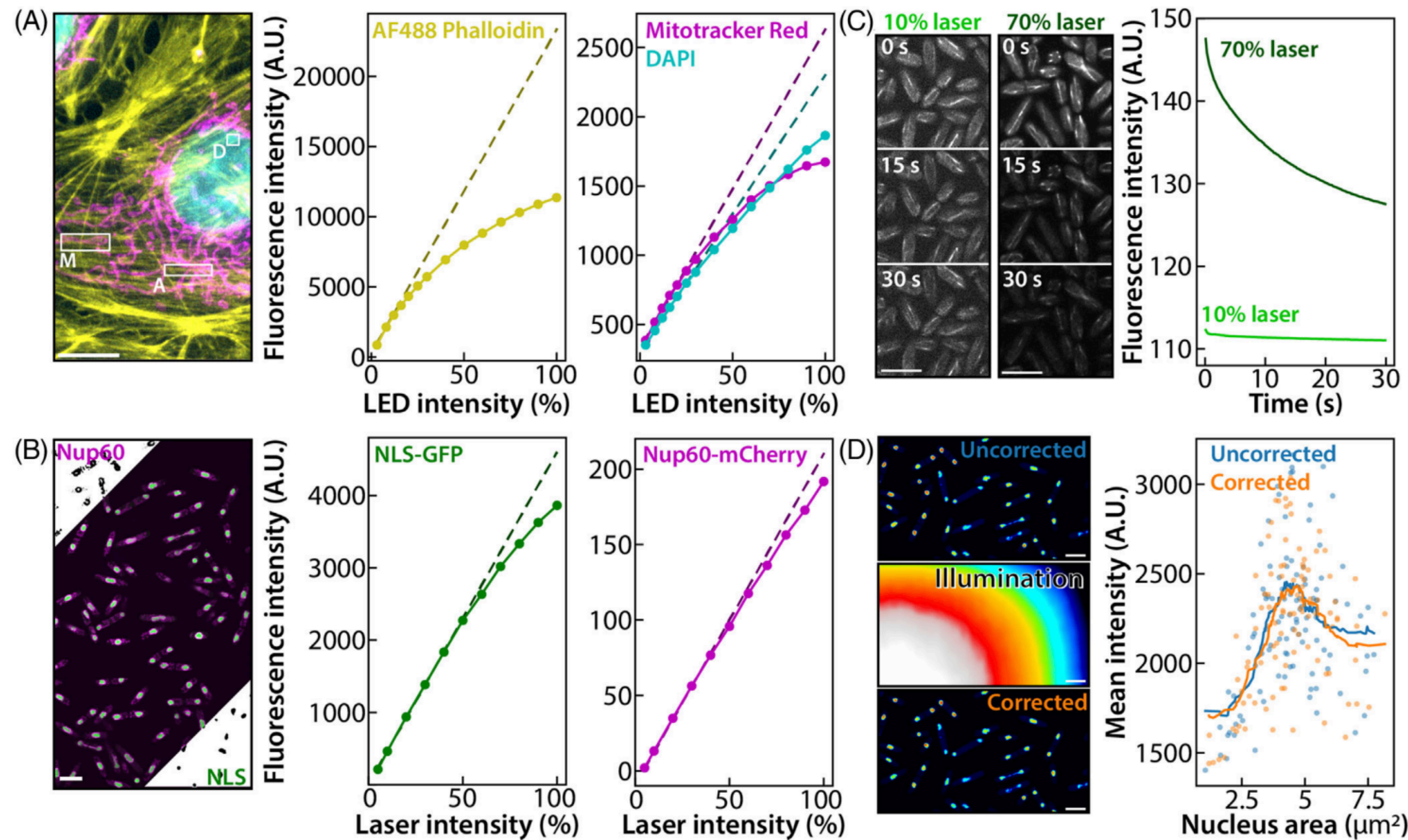


# Beware of image data mishandling: quantitative analysis

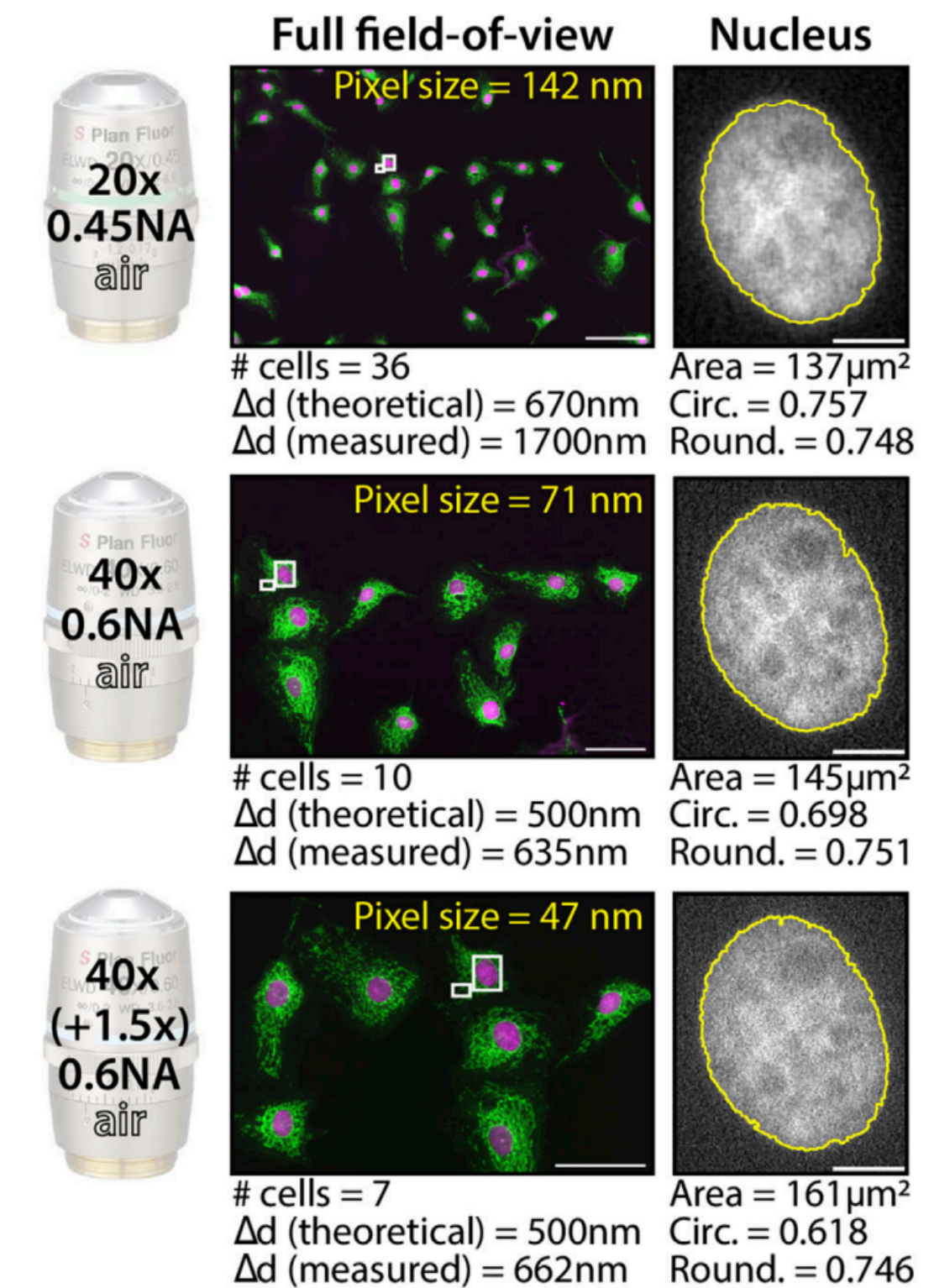
The imaging process (what happens at the microscope) has an impact on the downstream analysis (what happens at the computer) - understanding how to acquire a “measurable” image is therefore essential

Culley *et al.*, Journal of Microscopy, 2023

Illumination impacts intensity measurements



Acquisition parameters impact morphology measurements

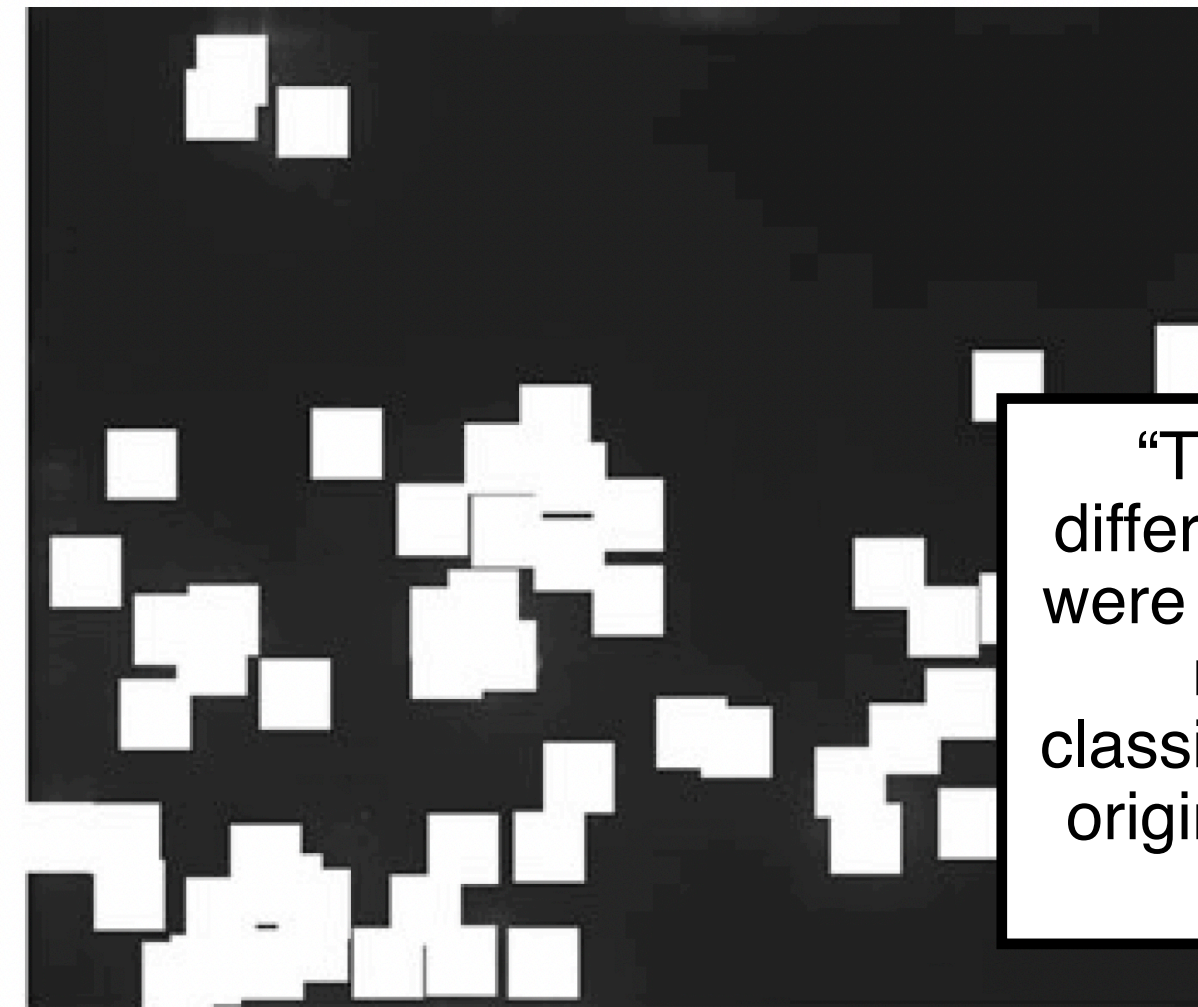
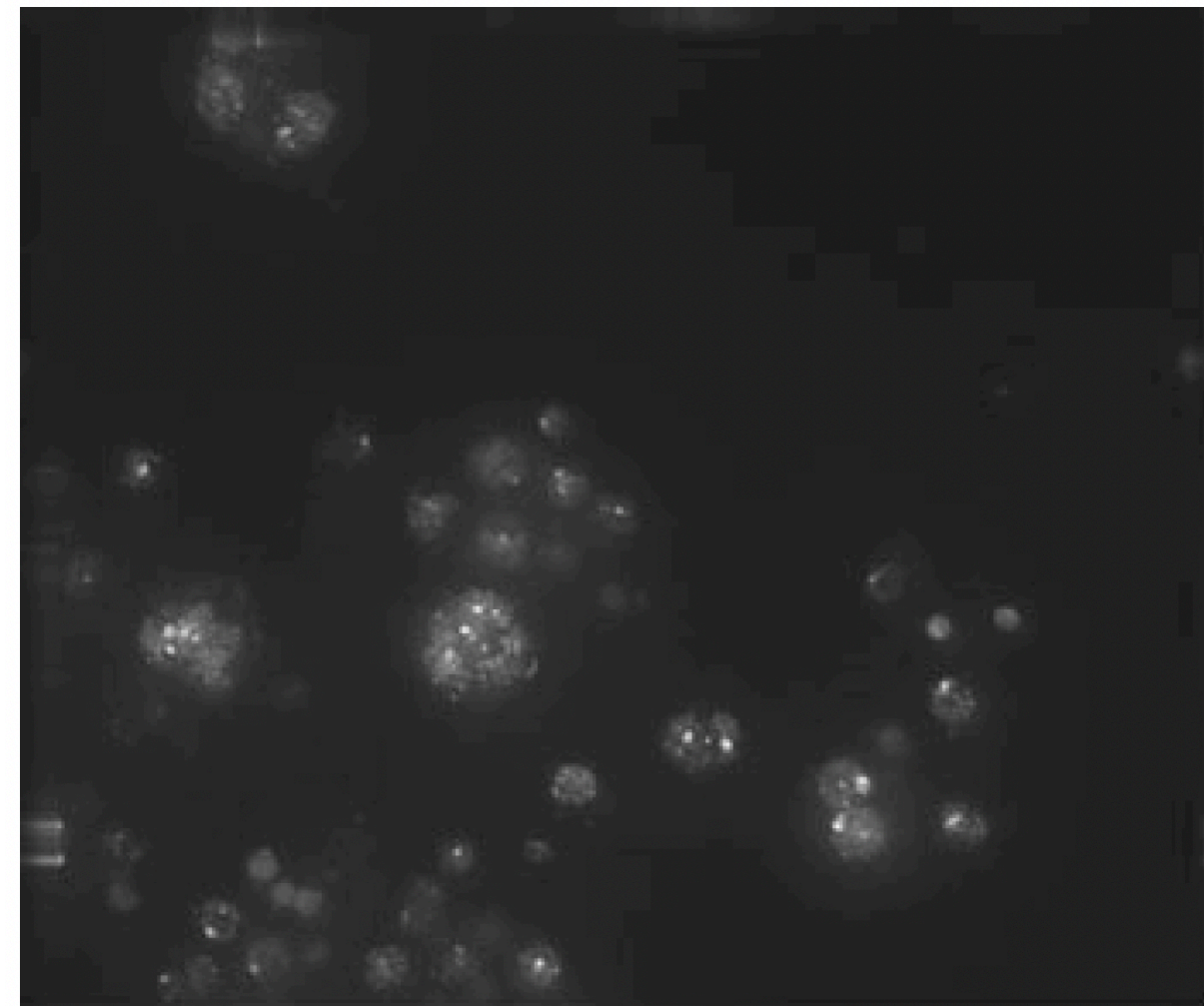




# Beware of image data mishandling: quantitative analysis

Automated image analysis methods can fail, regardless of how complex they are

Shamir, Journal of Microscopy, 2011



“The classification accuracy of the different genes was 47% when the cells were covered by white squares, which is marginally lower than the 52% classification accuracy achieved with the original images, but significantly higher than random, which is ~7%.”

|              | Actin | DNA | TfR | ER  | Giantin | GPP130 | Lamp2 | Tubulin | Mitochondria | Nucleolin |
|--------------|-------|-----|-----|-----|---------|--------|-------|---------|--------------|-----------|
| Actin        | 176   | 3   | 5   | 8   | 2       | 1      | 0     | 3       | 0            | 2         |
| DNA          | 0     | 174 | 1   | 15  | 5       | 1      | 1     | 2       | 1            | 0         |
| TfR          | 2     | 11  | 103 | 3   | 2       | 2      | 41    | 12      | 22           | 2         |
| ER           | 0     | 8   | 6   | 155 | 2       | 1      | 4     | 3       | 21           | 0         |
| Giantin      | 2     | 3   | 0   | 9   | 145     | 27     | 3     | 0       | 9            | 2         |
| GPP130       | 1     | 0   | 13  | 7   | 43      | 116    | 8     | 0       | 9            | 3         |
| Lamp2        | 1     | 0   | 32  | 1   | 5       | 5      | 139   | 3       | 13           | 1         |
| Tubulin      | 2     | 4   | 8   | 7   | 1       | 0      | 5     | 165     | 6            | 2         |
| Mitochondria | 1     | 4   | 12  | 26  | 6       | 0      | 8     | 7       | 133          | 3         |
| Nucleolin    | 4     | 2   | 4   | 0   | 3       | 6      | 4     | 5       | 2            | 170       |



# What can we do to minimise the risk of mishandling?

Educate ourselves on what can and cannot be done with our data and the methods we use - and remain curious!

Schmied *et al.*, Nature Methods, 2023

nature methods

Perspective

<https://doi.org/10.1038/s41592-023-01987-9>

## Community-developed checklists for publishing images and image analyses

Received: 17 February 2023

Accepted: 26 July 2023

Published online: 14 September 2023

Check for updates

Christopher Schmied<sup>1,53</sup>✉, Michael S. Nelson<sup>2</sup>, Sergiy Avilov<sup>3</sup>, Gert-Jan Bakker<sup>4</sup>, Cristina Bertocchi<sup>5,6</sup>, Johanna Bischof<sup>7</sup>, Ulrike Boehm<sup>8</sup>, Jan Brocher<sup>9</sup>, Mariana T. Carvalho<sup>10</sup>, Catalin Chiritescu<sup>11</sup>, Jana Christopher<sup>12</sup>, Beth A. Cimini<sup>13</sup>, Eduardo Conde-Sousa<sup>14</sup>, Michael Ebner<sup>15</sup>, Rupert Ecker<sup>16,17,18</sup>, Kevin Eliceiri<sup>19</sup>, Julia Fernandez-Rodriguez<sup>20</sup>, Nathalie Gaudreault<sup>21</sup>, Laurent Gelman<sup>22</sup>, David Grunwald<sup>23</sup>, Tingting Gu<sup>24</sup>, Nadia Halidi<sup>25</sup>, Mathias Hammer<sup>23</sup>, Matthew Hartley<sup>26</sup>, Marie Held<sup>27</sup>, Florian Jug<sup>1</sup>, Varun Kapoor<sup>28</sup>, Ayse Aslihan Koksoy<sup>29</sup>, Judith Lacoste<sup>30</sup>, Sylvia Le Dévédec<sup>31</sup>, Sylvie Le Guyader<sup>32</sup>, Penghuan Liu<sup>33</sup>, Gabriel G. Martins<sup>34</sup>, Aastha Mathur<sup>7</sup>, Kota Miura<sup>35</sup>, Paula Montero Llopis<sup>36</sup>, Roland Nitschke<sup>37</sup>, Alison North<sup>38</sup>, Adam C. Parslow<sup>39</sup>, Alex Payne-Dwyer<sup>40</sup>, Laure Plantard<sup>22</sup>, Rizwan Ali<sup>41</sup>, Britta Schroth-Diez<sup>42</sup>, Lucas Schütz<sup>43</sup>, Ryan T. Scott<sup>44</sup>, Arne Seitz<sup>45</sup>, Olaf Selchow<sup>46</sup>, Ved P. Sharma<sup>38</sup>, Martin Spitaler<sup>47</sup>, Sathya Srinivasan<sup>48</sup>, Caterina Strambio-De-Castillia<sup>49</sup>, Douglas Taatjes<sup>50</sup>, Christian Tischer<sup>51</sup>✉ & Helena Klara Jambor<sup>52</sup>✉

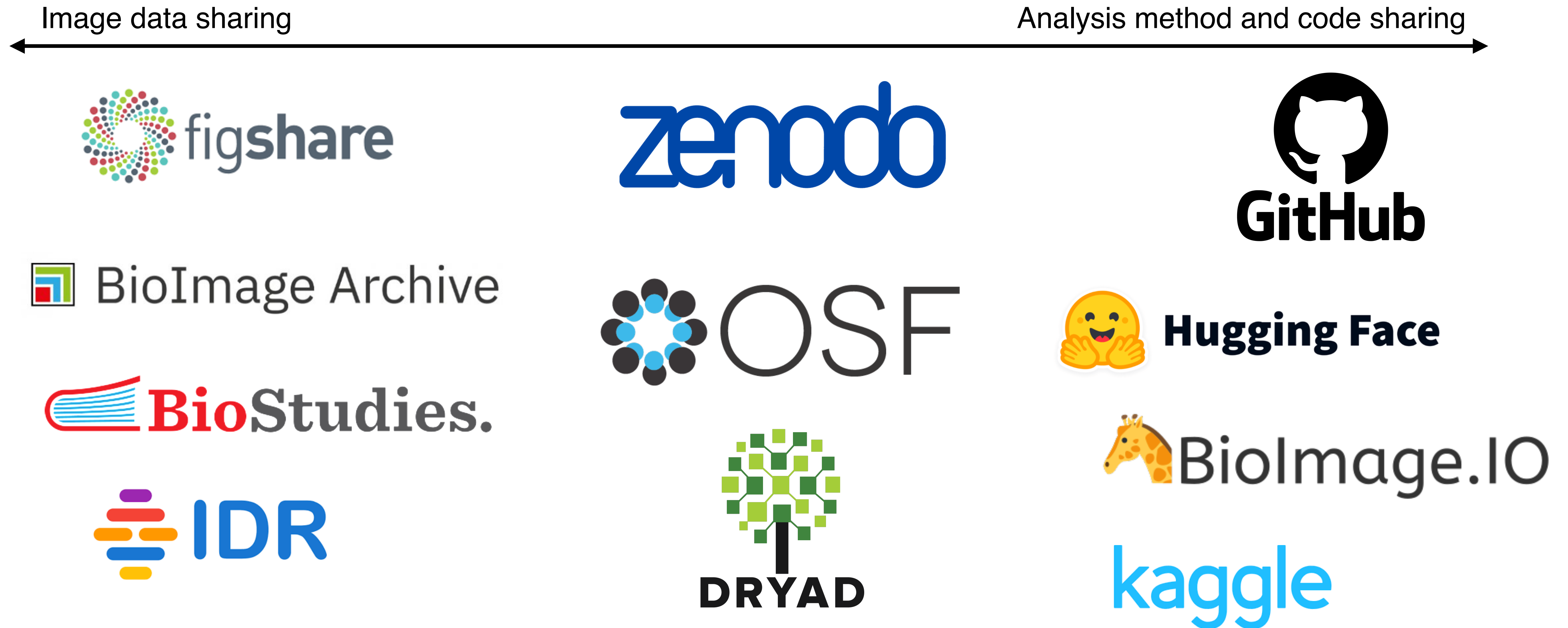
| Checklist for image publishing   |                          |             |
|--|--------------------------|-------------|
| <b>Image format</b>  |                          |             |
| Focus on relevant image content (e.g., crop, rotate, resize)   | <input type="checkbox"/> | Minimal     |
| Separate individual images   | <input type="checkbox"/> |             |
| Show example image used for quantifications  | <input type="checkbox"/> |             |
| Indicate position of zoom view/inset in full-view/original image   | <input type="checkbox"/> |             |
| Show images of the range of the described phenotype  | <input type="checkbox"/> |             |
| <b>Image colors and channels</b>   |                          |             |
| Annotation of channels (staining, marker, etc.) visible  | <input type="checkbox"/> | Minimal     |
| Adjust brightness/contrast, report adjustments, use uniform color scales   | <input type="checkbox"/> |             |
| Image comparison: use the same adjustments   | <input type="checkbox"/> |             |
| Channel colors: high visibility on the background<br>Best visibility: grayscale  | <input type="checkbox"/> |             |
| Multicolors: provide grayscale for each color channel  | <input type="checkbox"/> |             |
| Multicolor: if channels are merged, make accessible to color-blind individuals   | <input type="checkbox"/> |             |
| Provide intensity scales (calibration bar) for grayscale, color, pseudocolor etc.  | <input type="checkbox"/> | Recommended |
| Pseudocolored images: additionally provide grayscale version for comparison  | <input type="checkbox"/> | Ideal       |
| Gamma adjustments: additionally provide linear-adjusted image for comparison   | <input type="checkbox"/> |             |
| <b>Image annotation</b>  |                          |             |
| Add scale information (scale bar, image length in figure/figure legend)  | <input type="checkbox"/> | Minimal     |
| Explain all annotations (in figure/figure legend)  | <input type="checkbox"/> |             |
| Annotations should be legible (line width, size/point size, color)   | <input type="checkbox"/> |             |
| Annotations should not obscure key data  | <input type="checkbox"/> |             |
| Annotate imaging details important for interpreting the figure (depending on the main message and imaging technique, this may be, e.g., image pixel size, imaging intervals (time-lapse in movies), exposure time or anatomical section) | <input type="checkbox"/> | Recommended |
| <b>Image availability</b>  |                          |             |
| Images are shared (lossless compression/microscope images)   | <input type="checkbox"/> |             |
| Image files are freely downloadable (public database)  | <input type="checkbox"/> | Recommended |
| Image files are in dedicated image database (added-value database or image archive)  | <input type="checkbox"/> | Ideal       |

| Checklists for publication of image-analysis workflows |                          |   |
|--|--------------------------|---|
| <b>Established workflows</b>                           |                          |   |
| Cite workflow and platform                             | <input type="checkbox"/> | Minimal                                 |
| Key settings   | <input type="checkbox"/> |   |
| Example data   | <input type="checkbox"/> |   |
| Manual ROI   | <input type="checkbox"/> |   |
| 193  | <input type="checkbox"/> |   |
| All settings   | <input type="checkbox"/> | Recommended                             |
| Public example   | <input type="checkbox"/> |   |
| Document usage (e.g., screen recording or tutorial)    | <input type="checkbox"/> | Ideal                                   |
| Cloud hosted or container                              | <input type="checkbox"/> |   |
| <b>New workflows</b>                                   |                          |   |
| Cite components and platform                           | <input type="checkbox"/> | Minimal                                 |
| Describe sequence                                      | <input type="checkbox"/> |   |
| Key settings   | <input type="checkbox"/> |   |
| Example data and code                                  | <input type="checkbox"/> |   |
| Manual ROI   | <input type="checkbox"/> |   |
| 193  | <input type="checkbox"/> |   |
| All settings   | <input type="checkbox"/> | Recommended                             |
| Public example data and code                           | <input type="checkbox"/> |   |
| Rationale  | <input type="checkbox"/> |   |
| Limitations  | <input type="checkbox"/> |   |
| Screen recording or tutorial                           | <input type="checkbox"/> | Ideal                                   |
| Easy install and usage, container                      | <input type="checkbox"/> |   |
| <b>Machine learning workflows</b>                      |                          |   |
| Cite original method                                   | <input type="checkbox"/> | Minimal (all models)                    |
| Access to model  | <input type="checkbox"/> |   |
| Example or validation data                             | <input type="checkbox"/> |   |
| Training and testing data and metadata                 | <input type="checkbox"/> | Recommended (pretrained and new models) |
| Code available   | <input type="checkbox"/> |   |
| Limitations  | <input type="checkbox"/> |   |
| Cloud hosted or container                              | <input type="checkbox"/> |   |
| Standardized format                                    | <input type="checkbox"/> | Ideal (new models)                      |



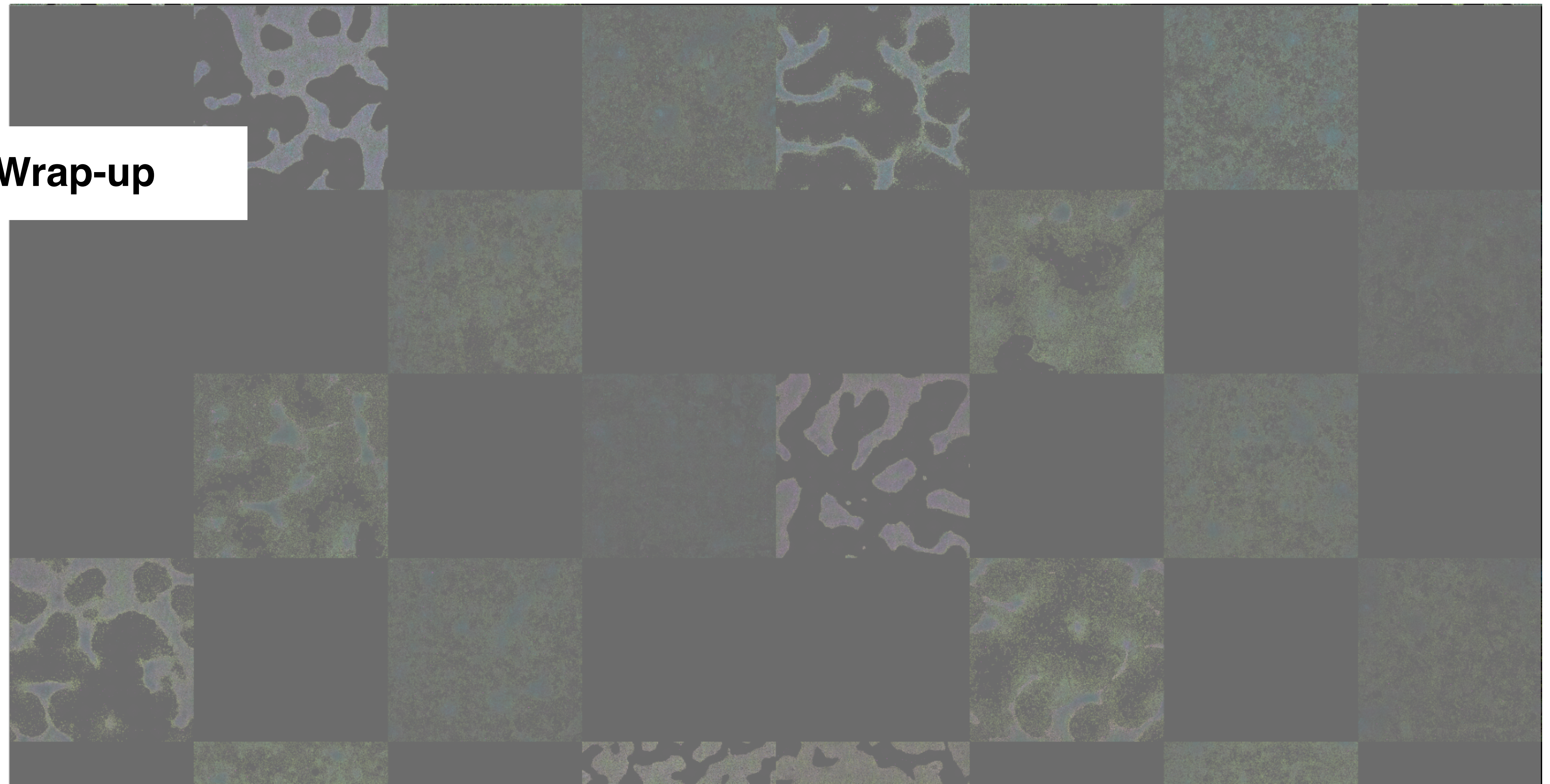
# What can we do to minimise the risk of mishandling?

Be fully transparent about our work by openly sharing the data and the analysis methods we used - and not be afraid to stand corrected, it is better than being wrong forever!





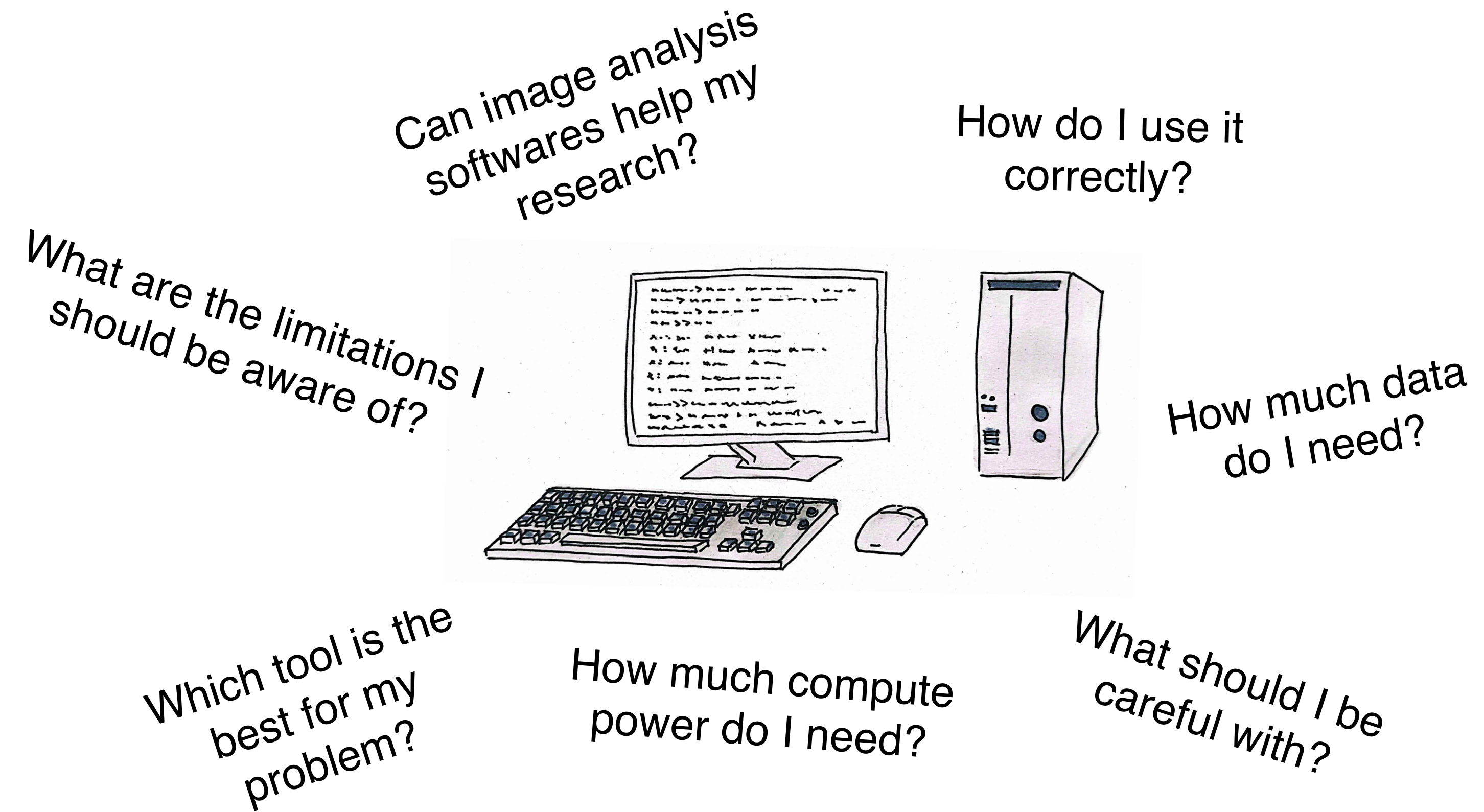
# Wrap-up





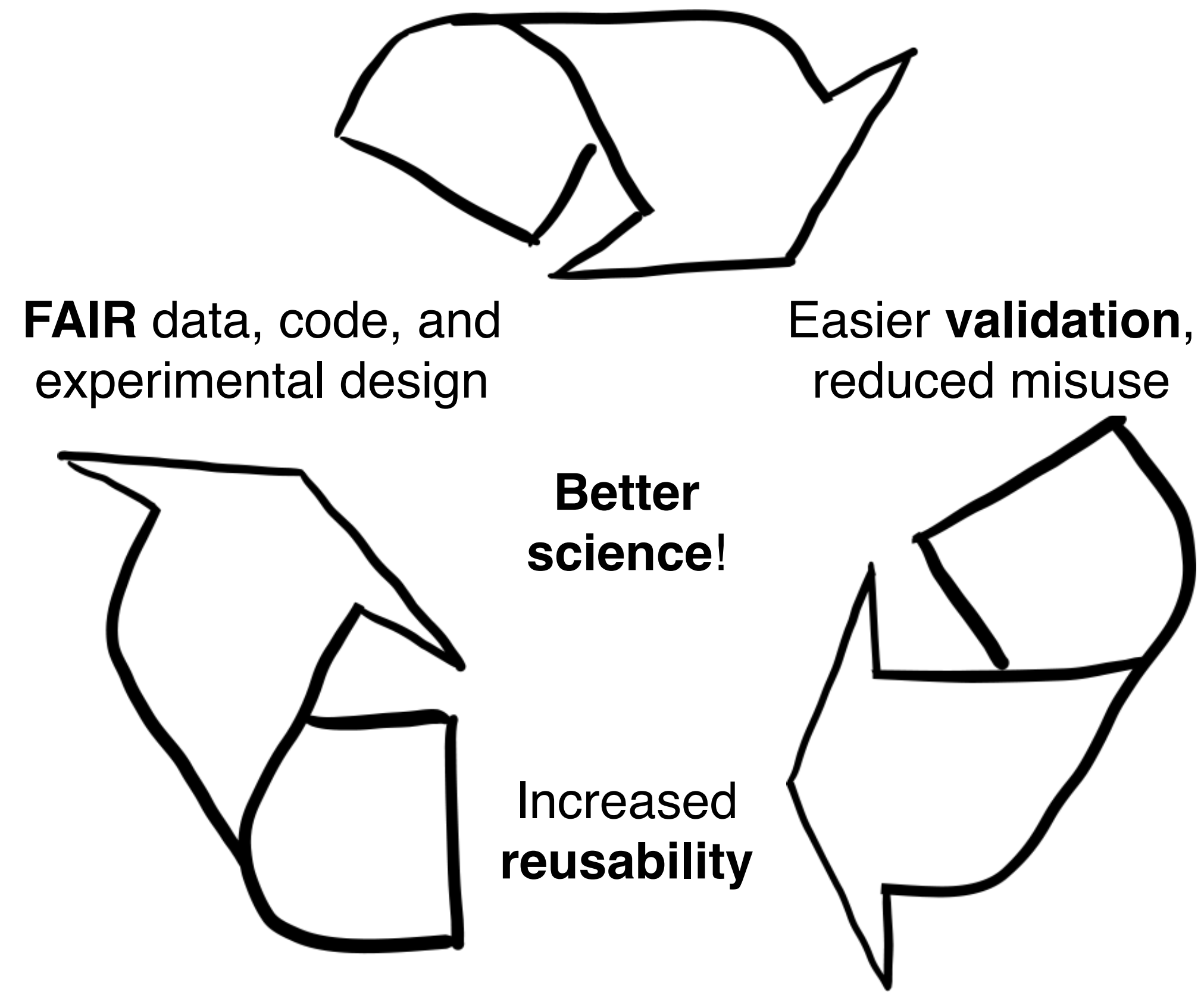
# Take-home message #1

Computer-based image analysis has already transformed the way we use microscopy in biology, and is not done breaking the limit of what can be achieved - it is here to stay and its potential in everyday work should not be ignored



# Take-home message #2

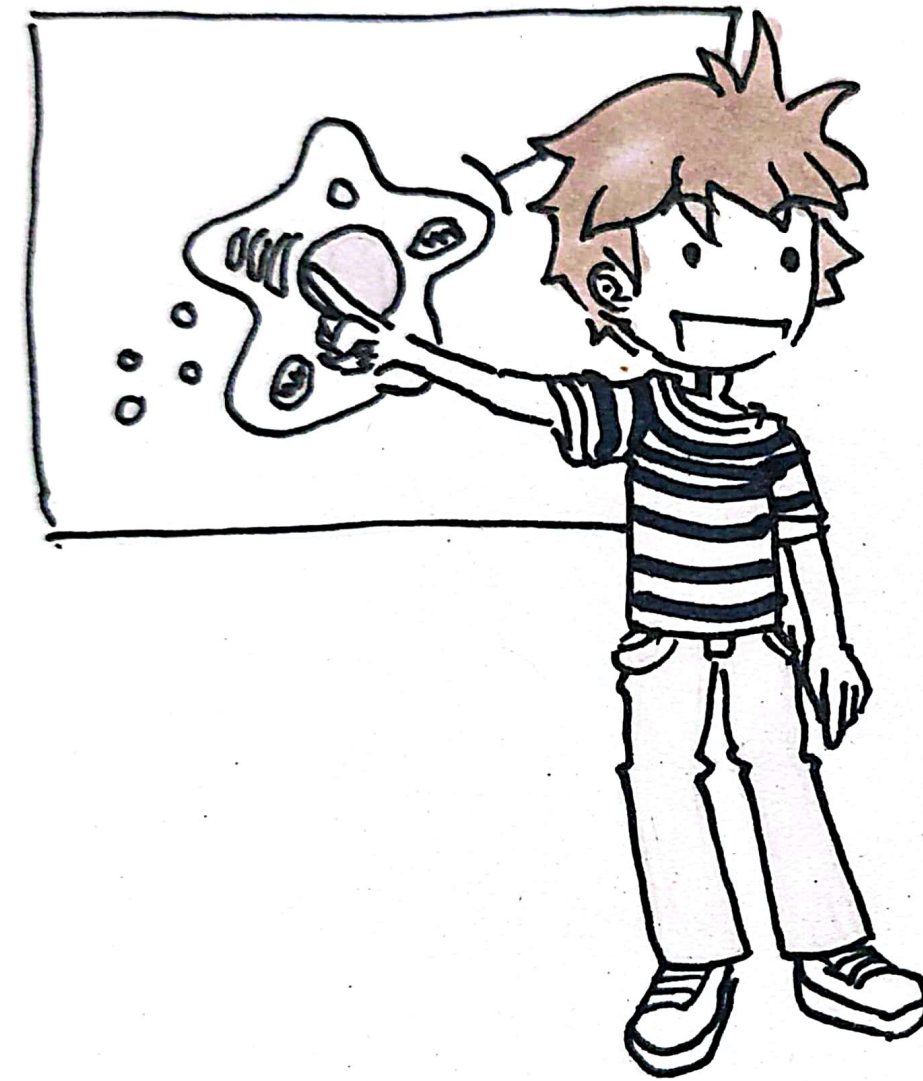
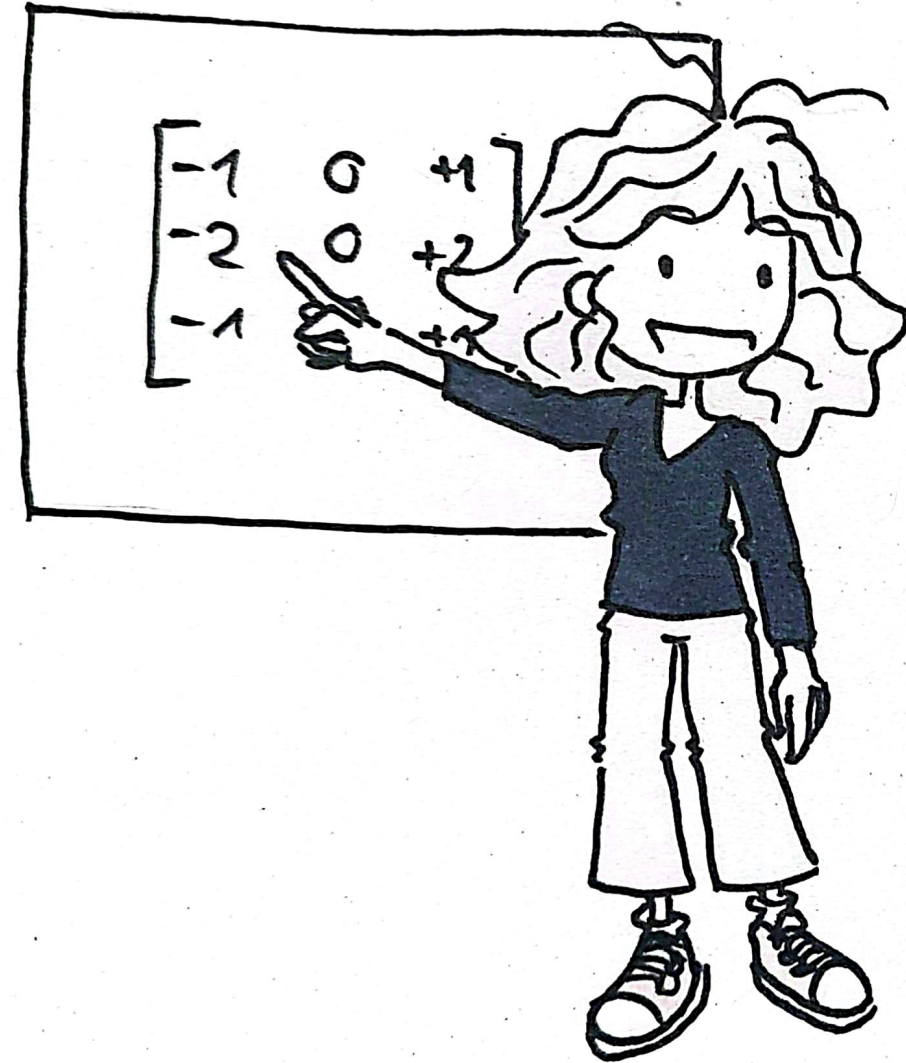
Computer-based image analysis brings additional challenges to the appropriate use of imaging data and of their analysis in biology...but is also a great opportunity to force us to improve as a community!





# Take-home message #3

None of us can be an expert at everything, and that's ok! Our job as scientists is to ask, study, read, and constantly question why and how we do things - errors are part of the process and become valuable experiences if we embrace them as part of our learning process





The background of the slide is a grid of 24 microscopy images arranged in 4 rows and 6 columns. The images show various cellular structures, likely neurons, with different staining patterns. Some images show bright, punctate structures, while others show more diffuse staining or specific cellular components.

**Thank you for  
your attention!**

**More questions?**  
virginie.uhlmann@mls.uzh.ch  
Y55-K56



# Resources to go further

- <https://doi.org/10.15252/emj.2020105889>
- <https://doi.org/10.1111/jmi.13208>
- <https://doi.org/10.1038/s41592-023-01987-9>
- <https://doi.org/10.1242/jcs.262139>
- <https://doi.org/10.1016/j.jmb.2022.167505>
- <https://doi.org/10.1007/s00418-023-02203-7>
- <https://doi.org/10.1111/jmi.13288>
- <https://doi.org/10.1038/s41592-023-02151-z>
- <https://doi.org/10.31219/osf.io/2zgmc>
- <https://doi.org/10.1038/s41592-023-02150-0>
- <https://doi.org/10.1371/journal.pbio.3002167>
- <https://doi.org/10.1371/journal.pbio.3000340>