

# Good practice in scientific programming

Robert Haase

October 2022

#OpenScience

#OpenSource

Accessible

Reusable

Sustainable

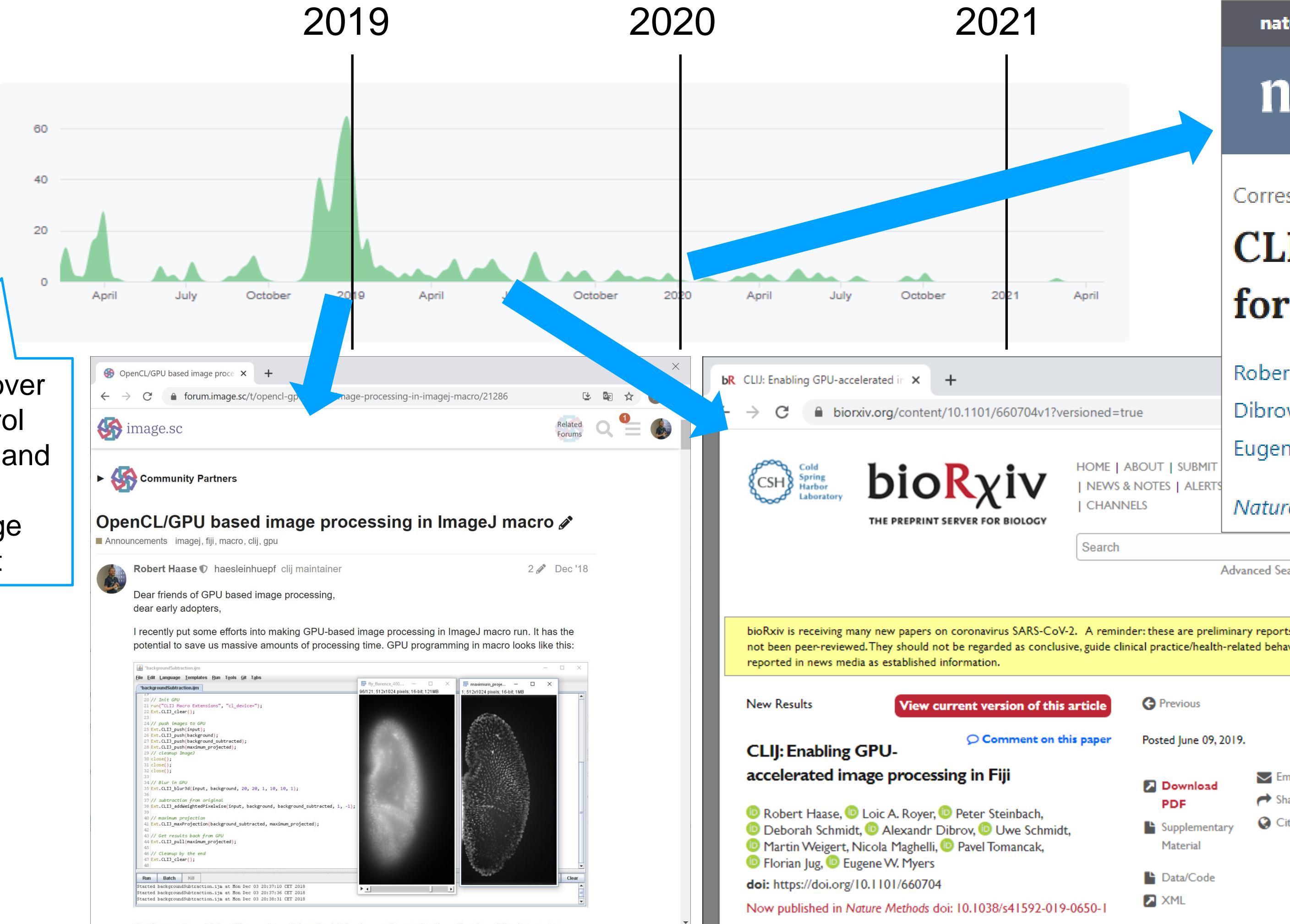
# An open science story



Nov. 2017: I took over microscopy control software from Loic and “found” a GPU-accelerated image processing part



Loic A. Royer  
(CZ Biohub)  
@loicaroyer



nature > nature methods > correspondence > article

## nature methods

Correspondence | Published: 18 November 2019

### CLIJ: GPU-accelerated image processing for everyone

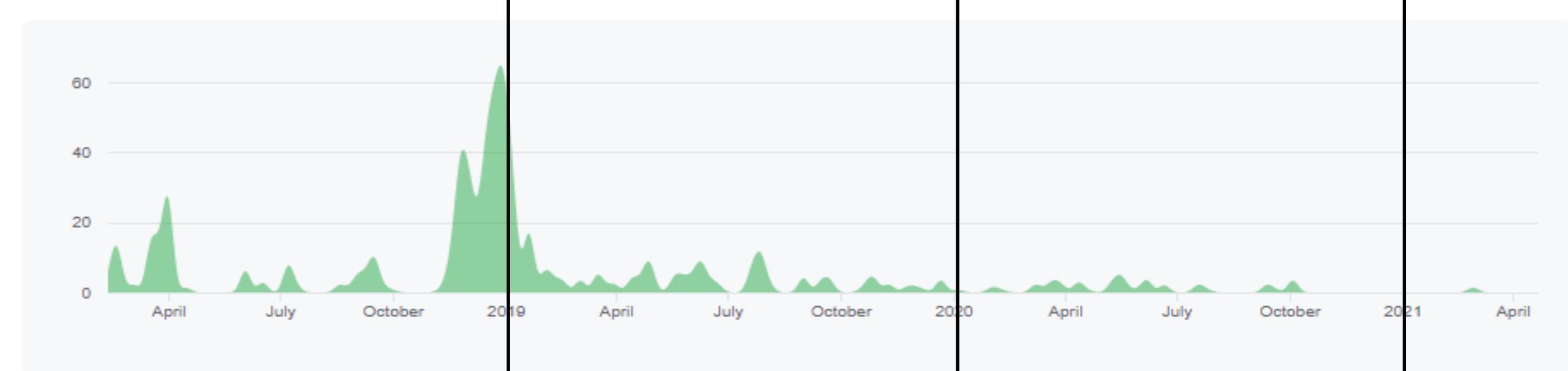
Robert Haase, Loic A. Royer, Peter Steinbach, Deborah Schmidt, Alexander Dibrov, Uwe Schmidt, Martin Weigert, Nicola Maghelli, Pavel Tomancak, Florian Jug & Eugene W. Myers

Nature Methods 17, 5–6(2020) | Cite this article

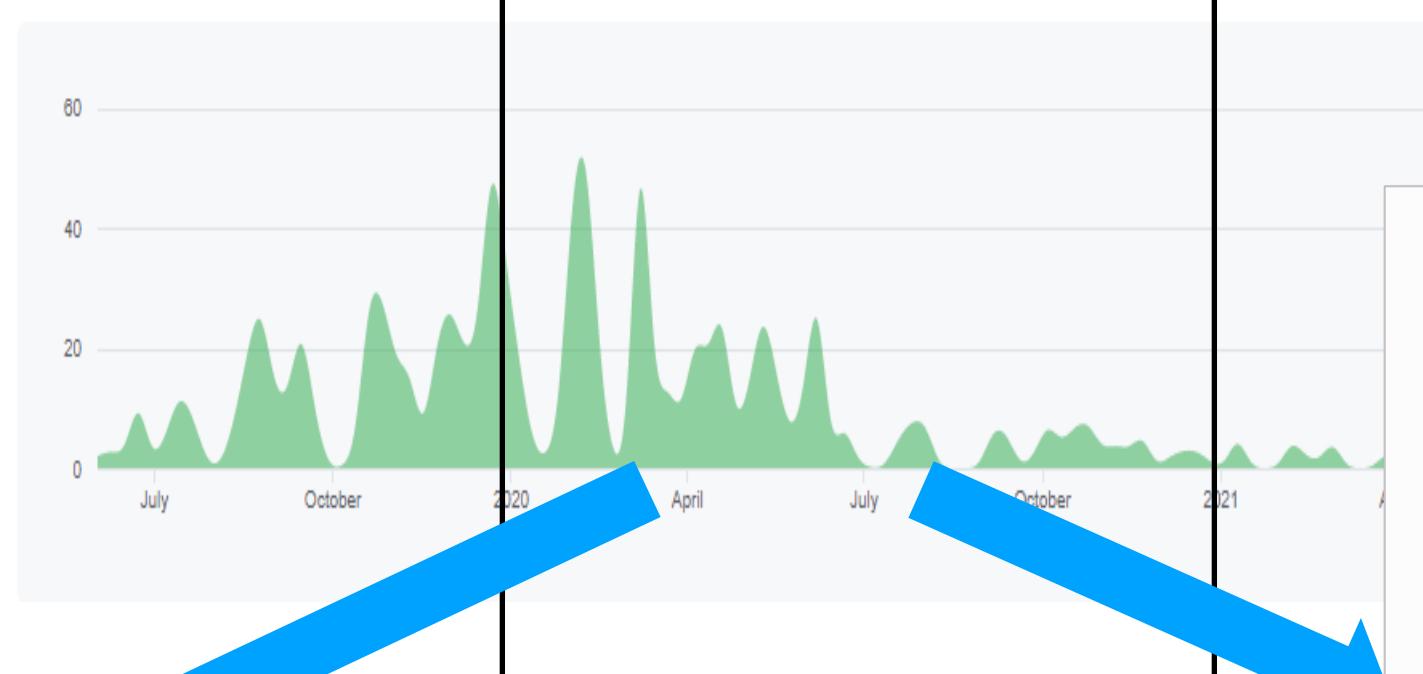
# An open science story



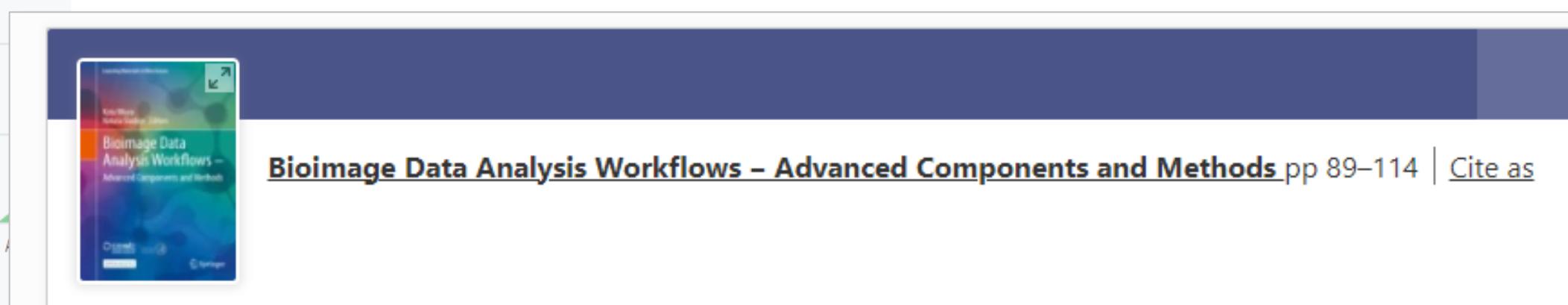
2019



2020



2021



Best co-author



Dani Vorkel  
(Myers lab)  
@happifocus

## GPU-Accelerating ImageJ Macro Image Processing Workflows Using CLIJ

[Daniela Vorkel & Robert Haase](#)

Chapter | [Open Access](#) | First Online: 29 September 2022

823 Accesses | 20 Altmetric

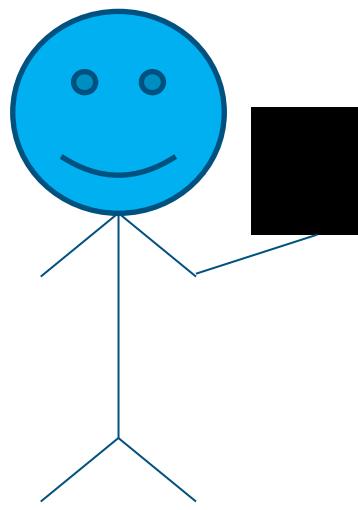
Part of the [Learning Materials in Biosciences](#) book series (LMB)

# Openness of software / projects

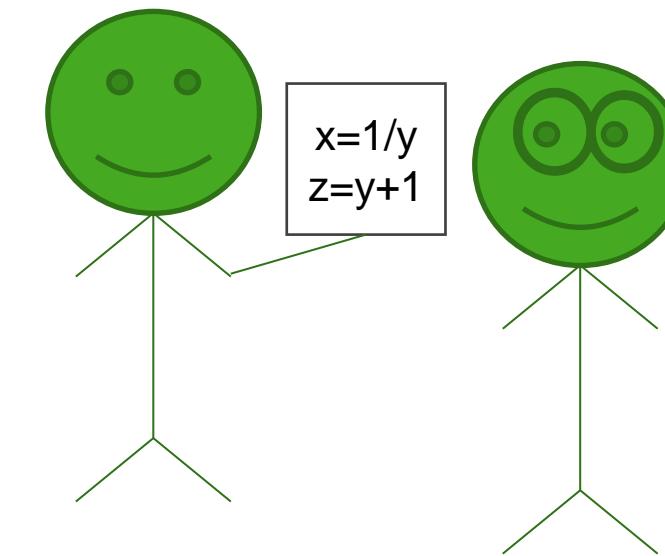
Choose your project's level wisely, and communicate it clearly

Communication  
is key!

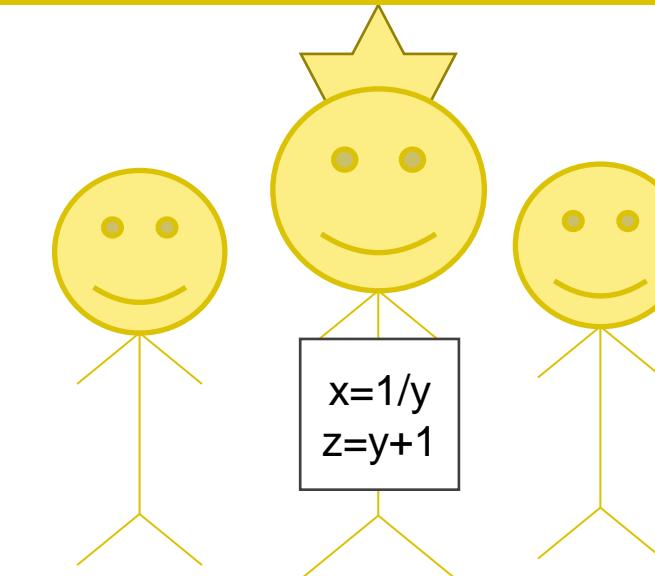
Closed source



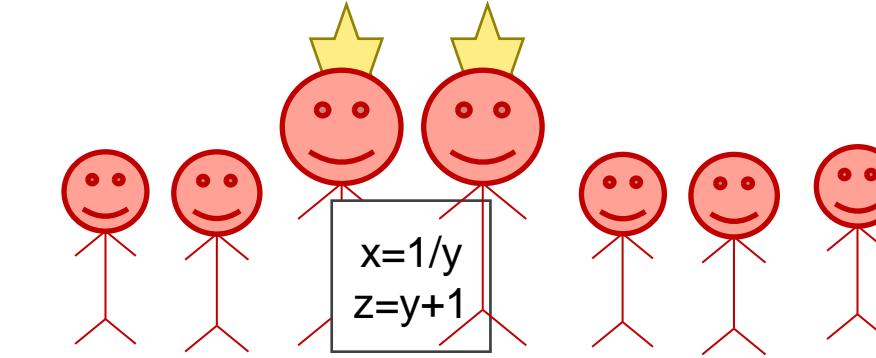
Open source



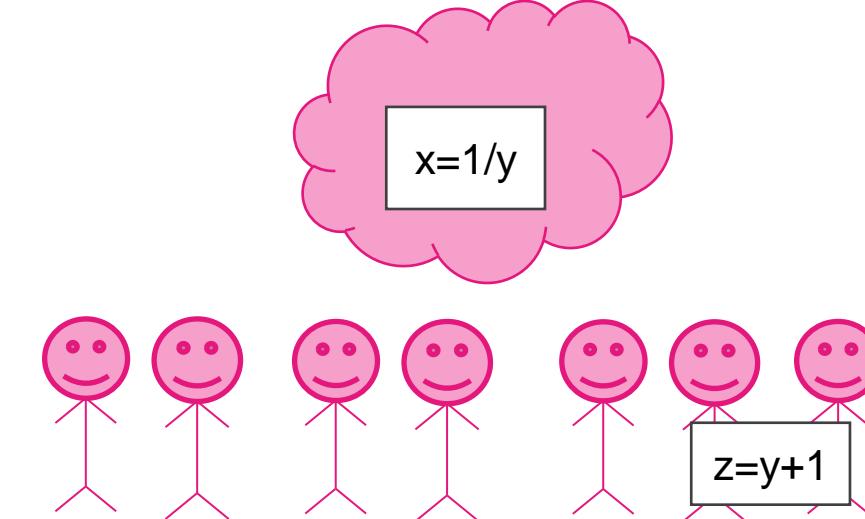
Benevolent  
dictatorship



Community driven



Openly extensible



- Open to collaborations
- “Black box”
- Compiled code (e.g. C/C++)
- Good for protecting intellectual properties (\$\$\$)

Hardware device drivers

- Code available to read
- Not necessarily executable code
- No maintenance / support efforts

Custom image analysis scripts

- Open to contributions
- Single maintainer, often overwhelmed
- Efficient decision making
- Bus factor  $\approx 1$

TrackMate, SNT, MorpholibJ, CLIJ

- Open to contributions
- Partially democratic
- Board of maintainers (core developers)
- Long-winded decision making

scikit-image, scipy, OpenCL

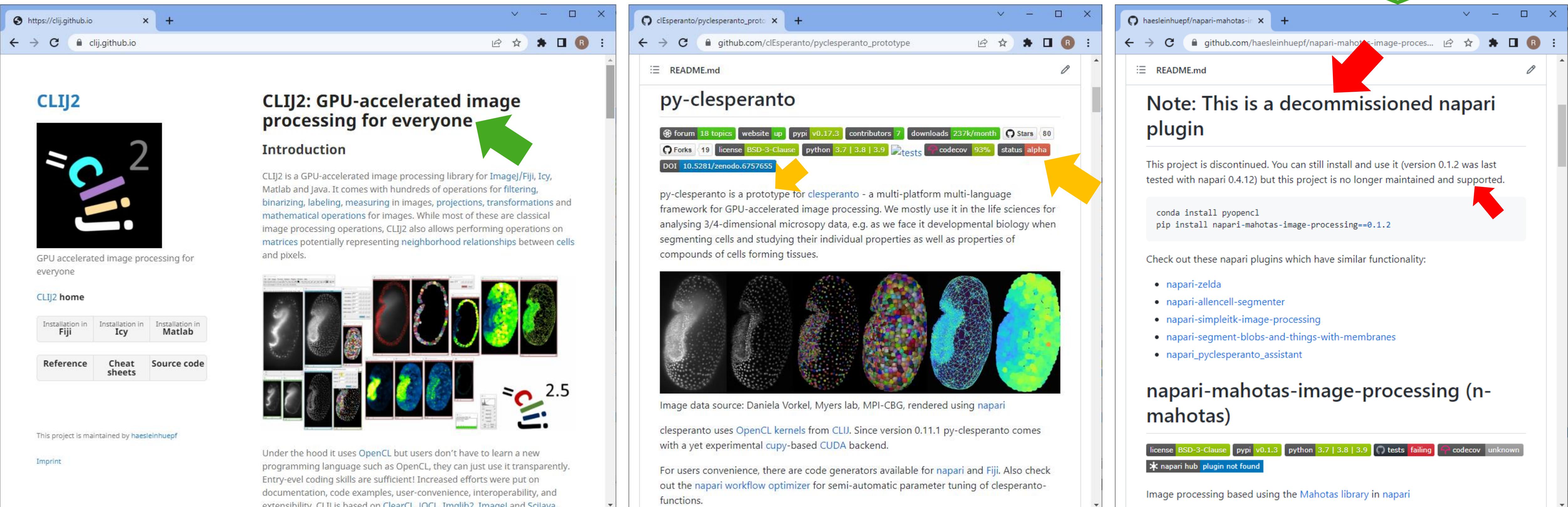
- Openly extensible; without maintainers involved
- Partially community driven

ImageJ, Python, numpy

# Target audience

Documentation should tell who is the target audience and how far it is developed

Communication is key!



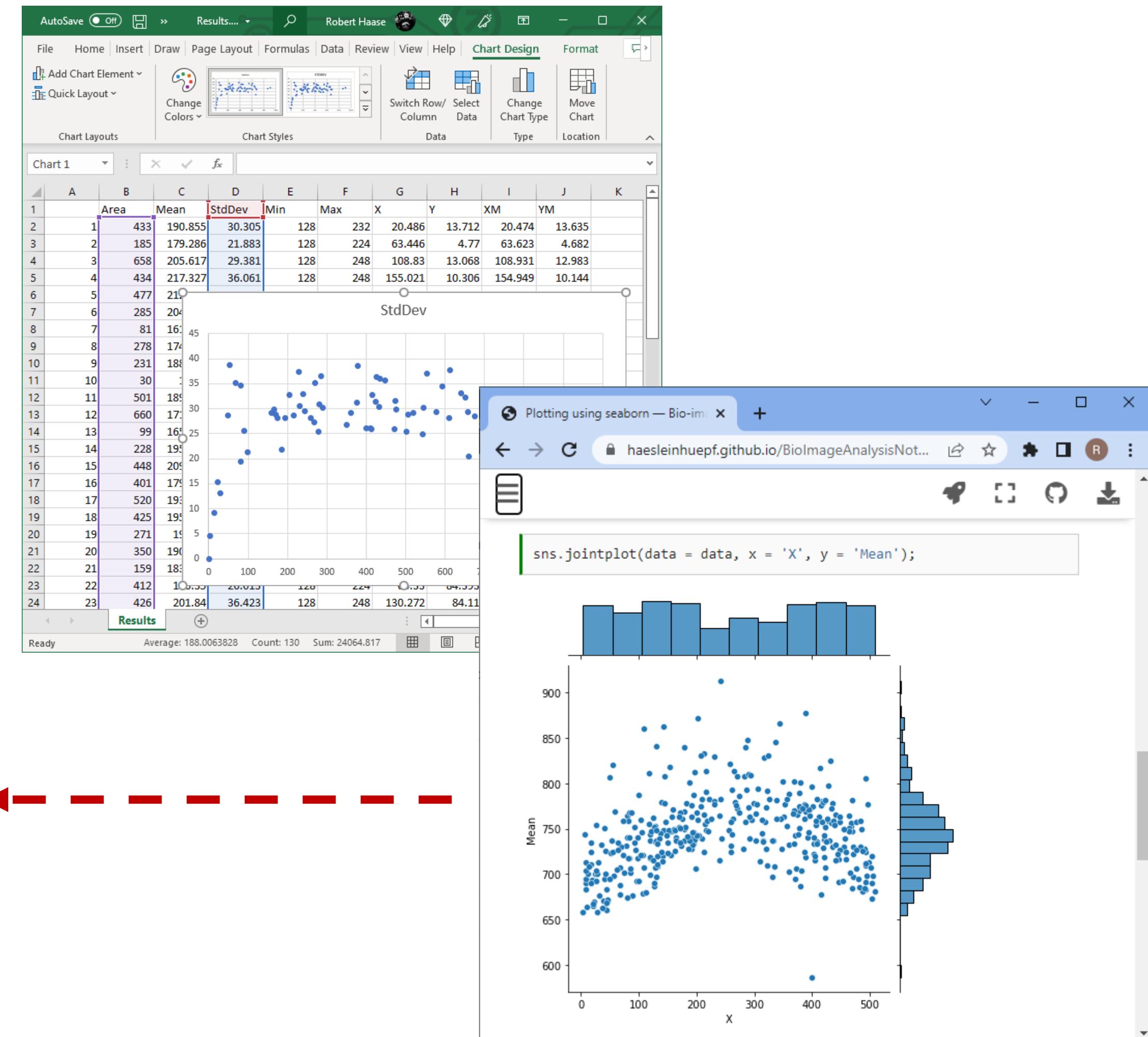
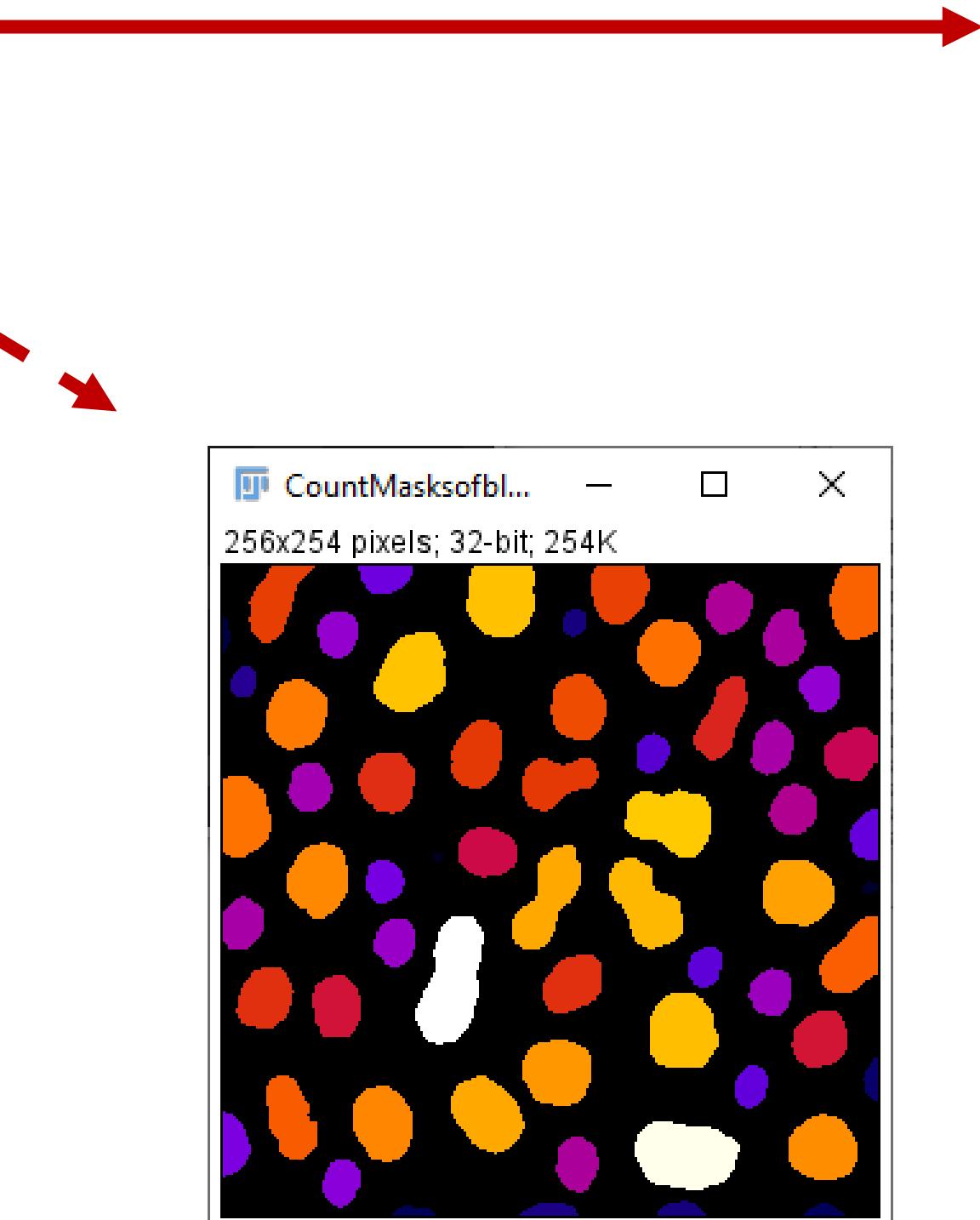
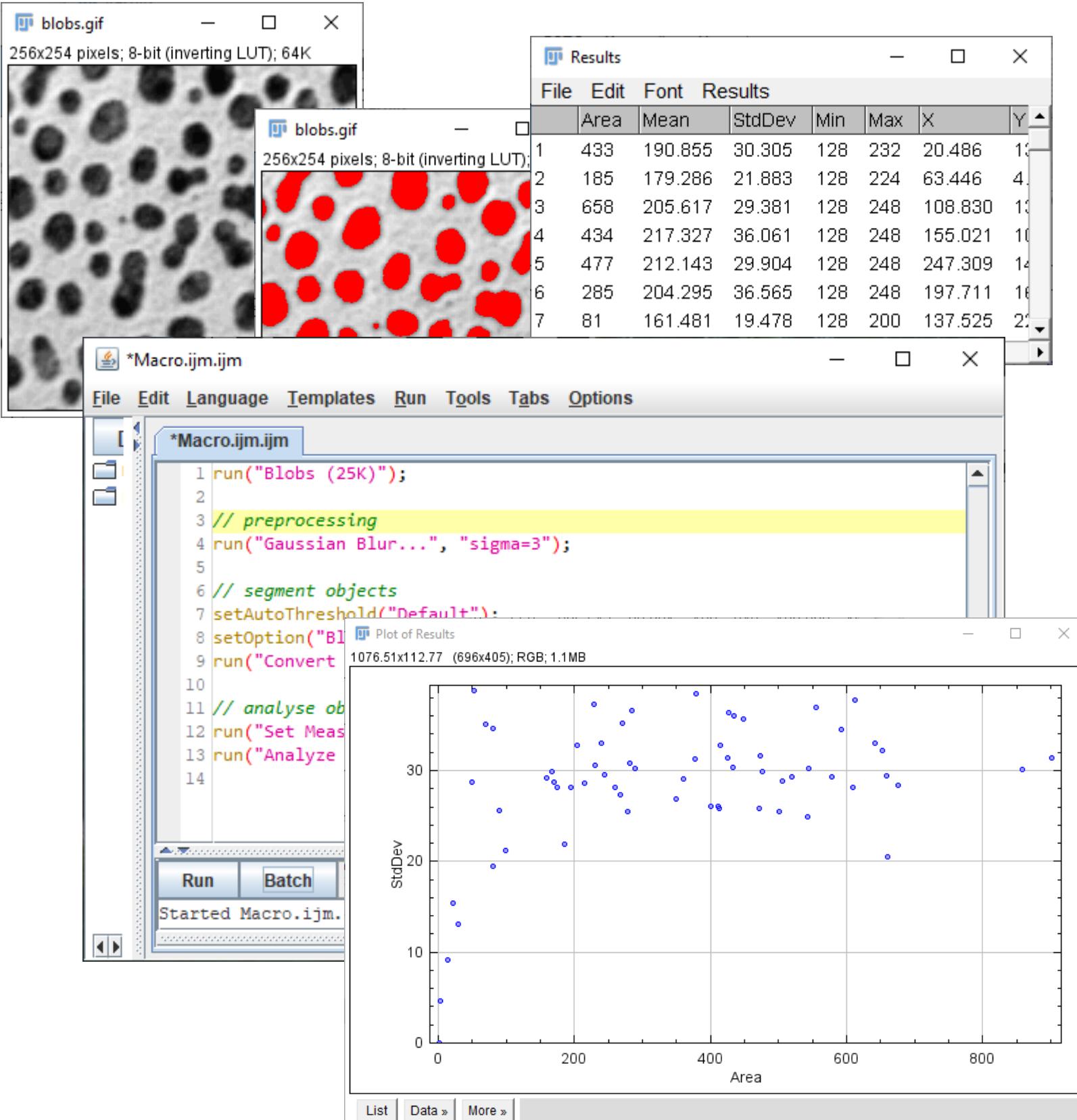
The figure displays three separate browser windows side-by-side, each showing a different GitHub project's README page.

- Left Window (CLIJ2):** Shows the main page for the CLIJ2 library. It features a large logo with the text "GPU accelerated image processing for everyone". Below the logo is a section titled "Introduction" which describes CLIJ2 as a GPU-accelerated image processing library for ImageJ/Fiji, Icy, Matlab and Java. A green arrow points from the text "GPU accelerated image processing for everyone" towards the "Introduction" section.
- Middle Window (py-clesperanto\_prototype):** Shows the README for the py-clesperanto prototype. It includes a screenshot of a microscopy image with various overlays. A yellow arrow points from the text "py-clesperanto is a prototype for clesperanto" towards the "Introduction" section.
- Right Window (napari-mahotas-image-processing):** Shows the README for the napari-mahotas-image-processing plugin. A red arrow points from the text "Note: This is a decommissioned napari plugin" towards the "Introduction" section. Below this note, a red arrow points from the text "This project is discontinued. You can still install and use it (version 0.1.2 was last tested with napari 0.4.12) but this project is no longer maintained and supported." towards the "Introduction" section.

**Common Features:** Each window includes a navigation bar at the top, a header with the project name, a "README.md" file icon, and a "pypi v0.17.3" badge. The middle and right windows also show GitHub statistics like forks, license, python versions, tests, codecov, and status.

# Image data science is cross-disciplinary

... and uses diverse toolsets

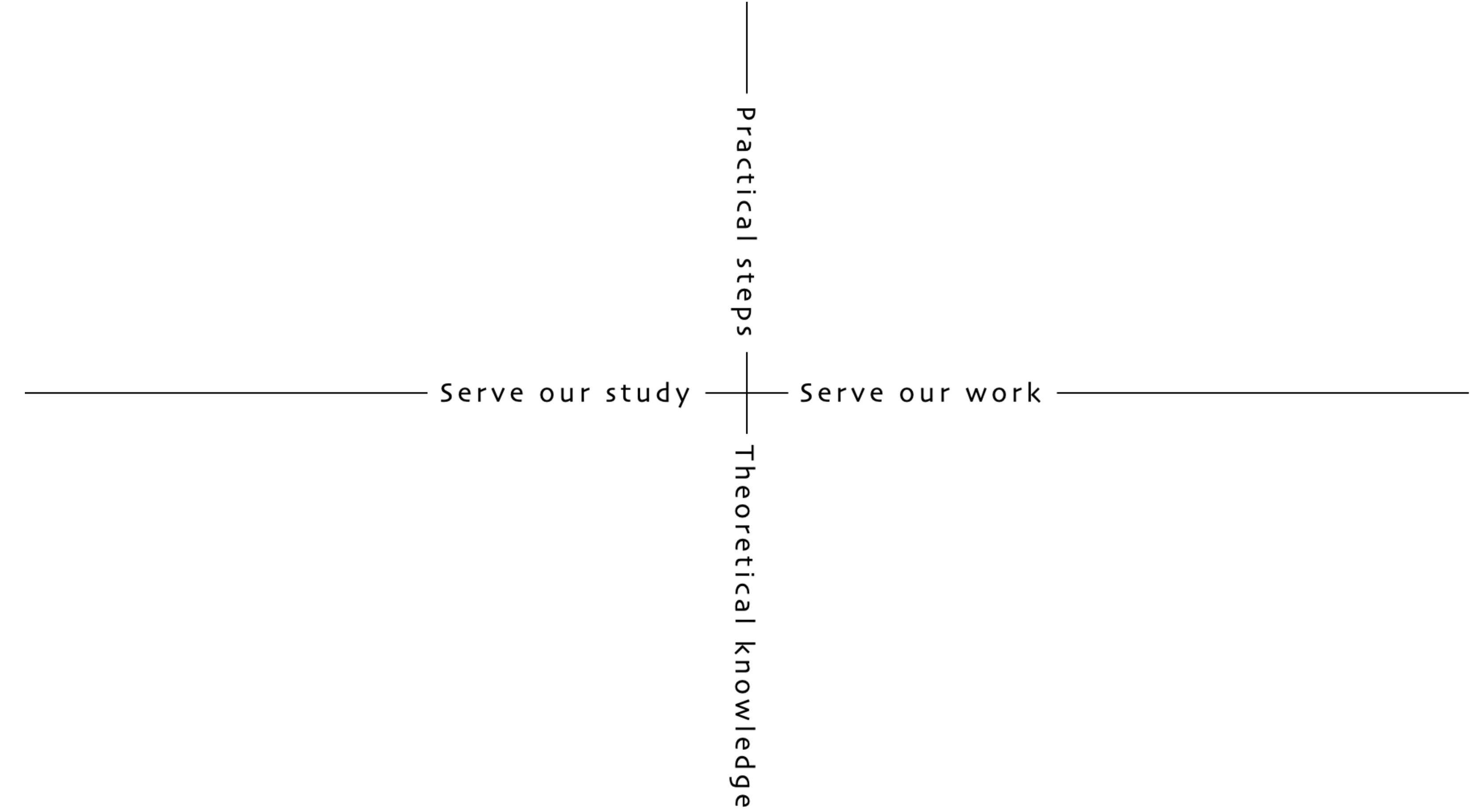


# Documentation is key

... to make code reusable

# Documentation best-practices

## The four modes of documentation



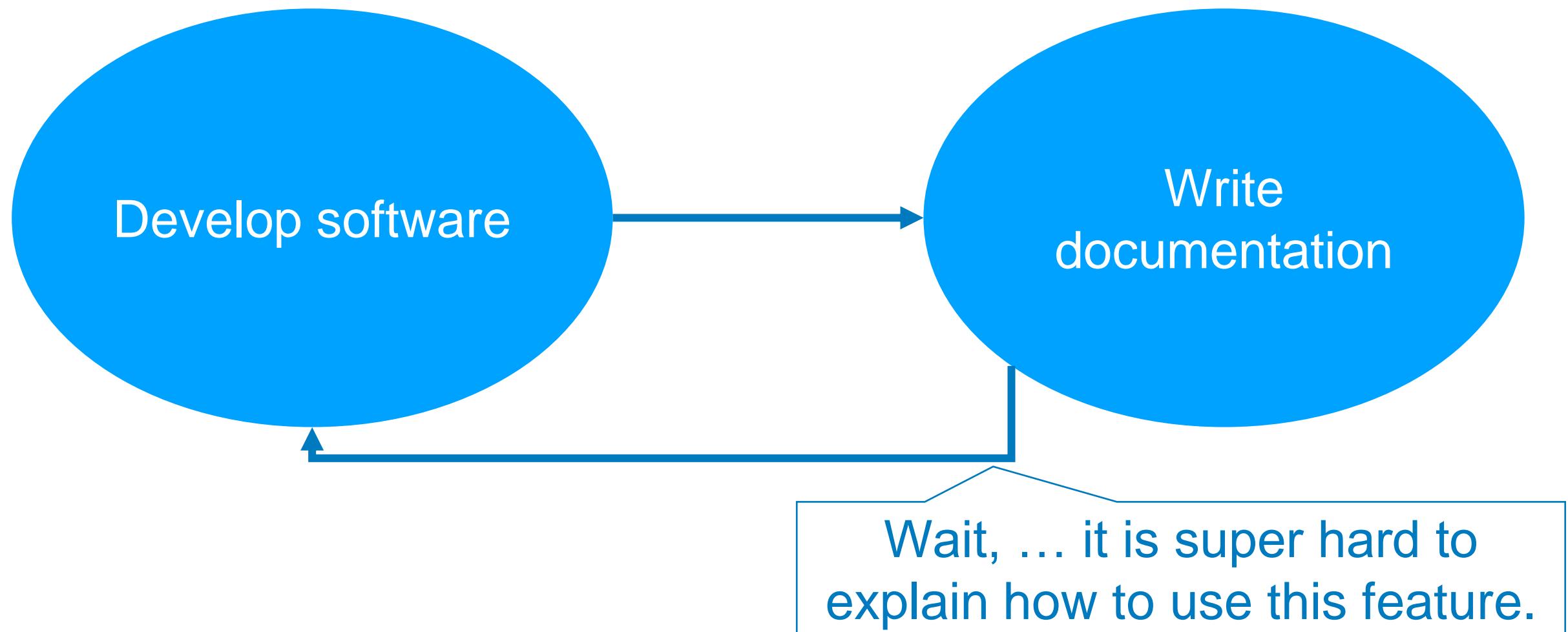
# Documentation best-practices

## The four modes of documentation



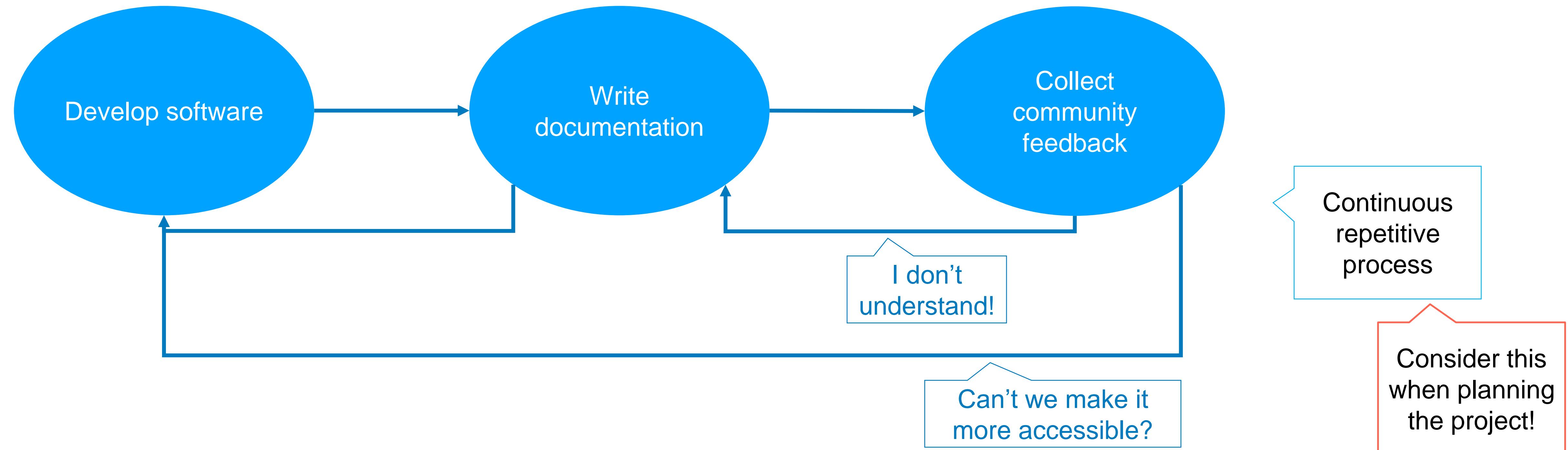
# Documentation best-practices

Documentation is a process, not a final step



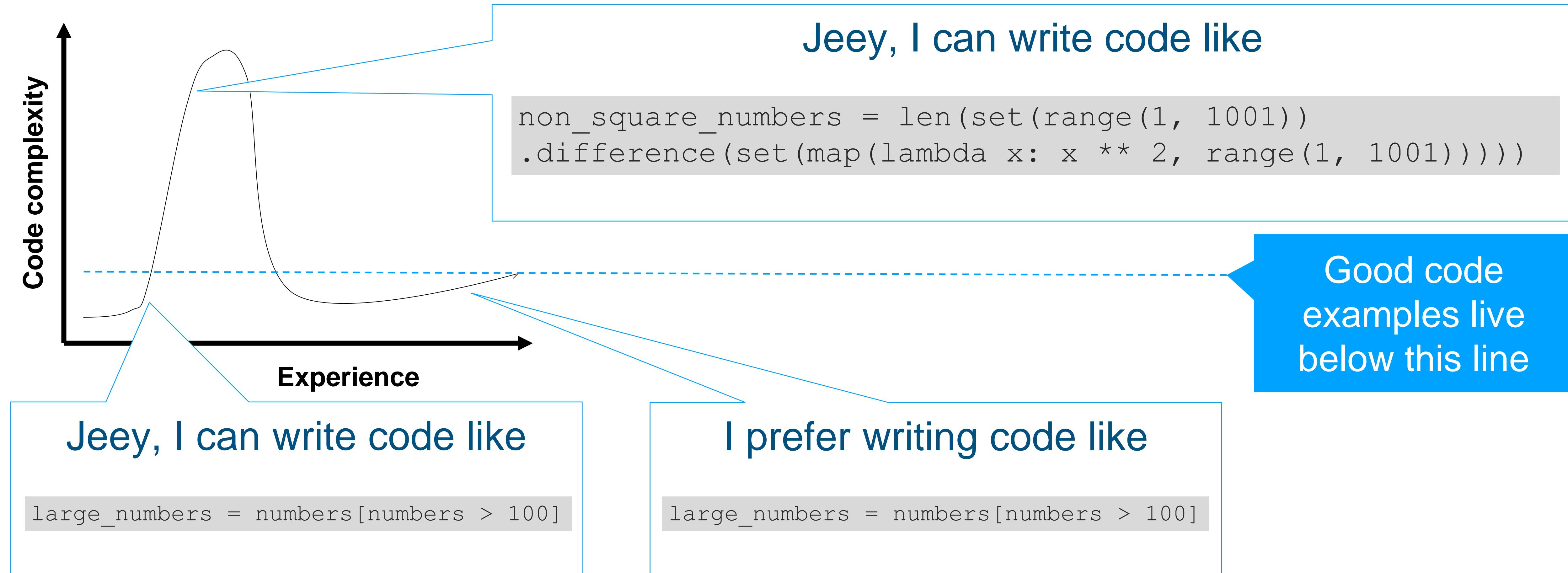
# Documentation best-practices

Documentation is a process, not a final step



# Documentation best-practices

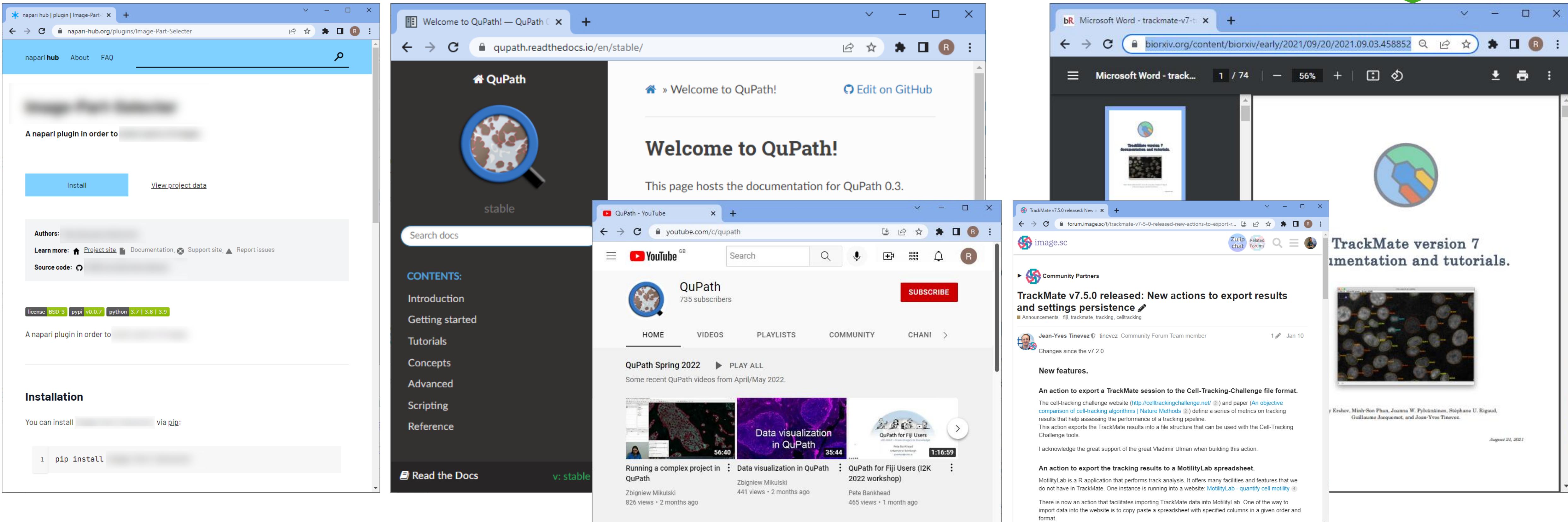
Interpretation of “High quality code” changes with experience



# Documentation best-practices

Use your project's website to show others how to use your software.  
Otherwise, they may not use it.

Communication  
is key!



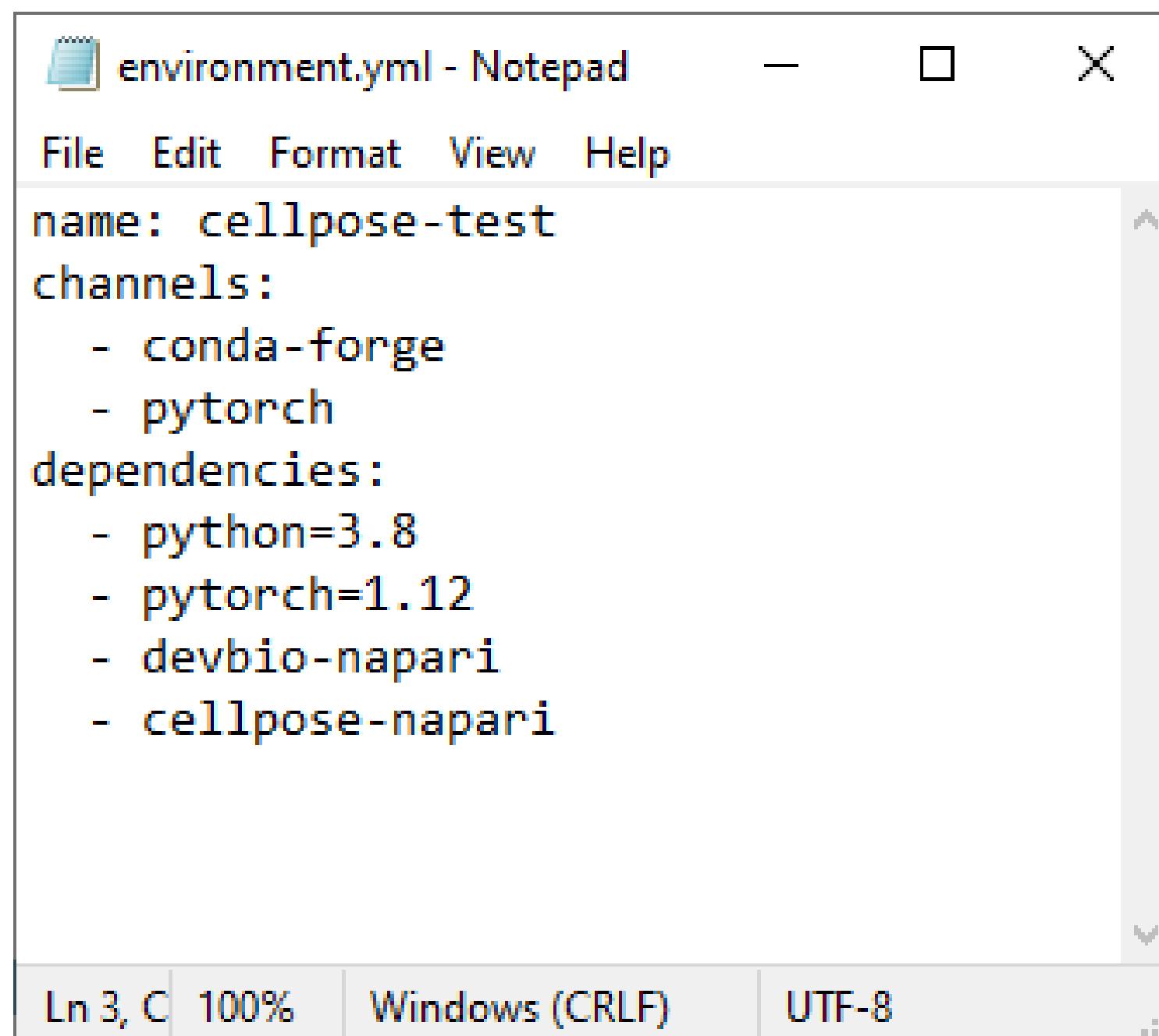
The image displays five browser windows side-by-side, each representing a different project's documentation and communication strategy:

- napari hub**: A screenshot of a plugin page on napari-hub.org, showing a "Install" button and a "View project data" link.
- Welcome to QuPath!**: A screenshot of the QuPath documentation site on qupath.readthedocs.io, featuring a magnifying glass icon and a "Welcome to QuPath!" heading.
- Microsoft Word - track...**: A screenshot of a Microsoft Word document titled "TrackMate version 7 documentation and tutorials.", showing a thumbnail of a cell image.
- QuPath - YouTube**: A screenshot of the QuPath YouTube channel page on youtube.com/c/qupath, showing a subscriber count of 735 and several video thumbnails related to QuPath usage.
- TrackMate v7.5.0 released: New actions to export results and settings persistence**: A screenshot of the TrackMate v7.5.0 release announcement on forum.image.sc, including a "Community Partners" section and details about new features like "An action to export a TrackMate session to the Cell-Tracking-Challenge file format".

# Documenting dependencies

Maintain a document with the dependencies (and versions) you need in your project!

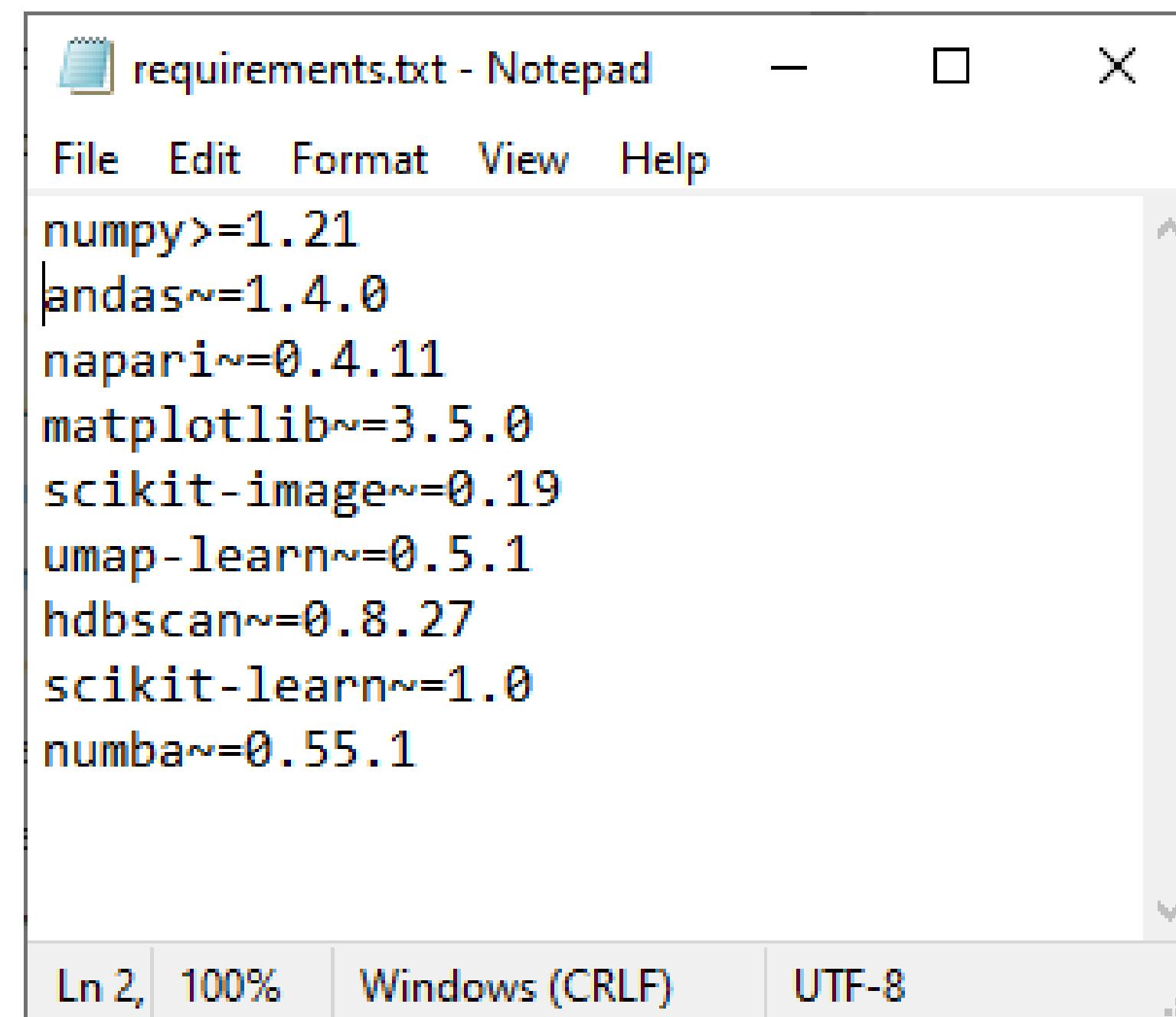
- The conda way



```
environment.yml - Notepad
File Edit Format View Help
name: cellpose-test
channels:
- conda-forge
- pytorch
dependencies:
- python=3.8
- pytorch=1.12
- devbio-napari
- cellpose-napari
```

conda env create -f environment.yml

- The pip way



```
requirements.txt - Notepad
File Edit Format View Help
numpy>=1.21
andas~=1.4.0
napari~=0.4.11
matplotlib~=3.5.0
scikit-image~=0.19
umap-learn~=0.5.1
hbscan~=0.8.27
scikit-learn~=1.0
numba~=0.55.1
```

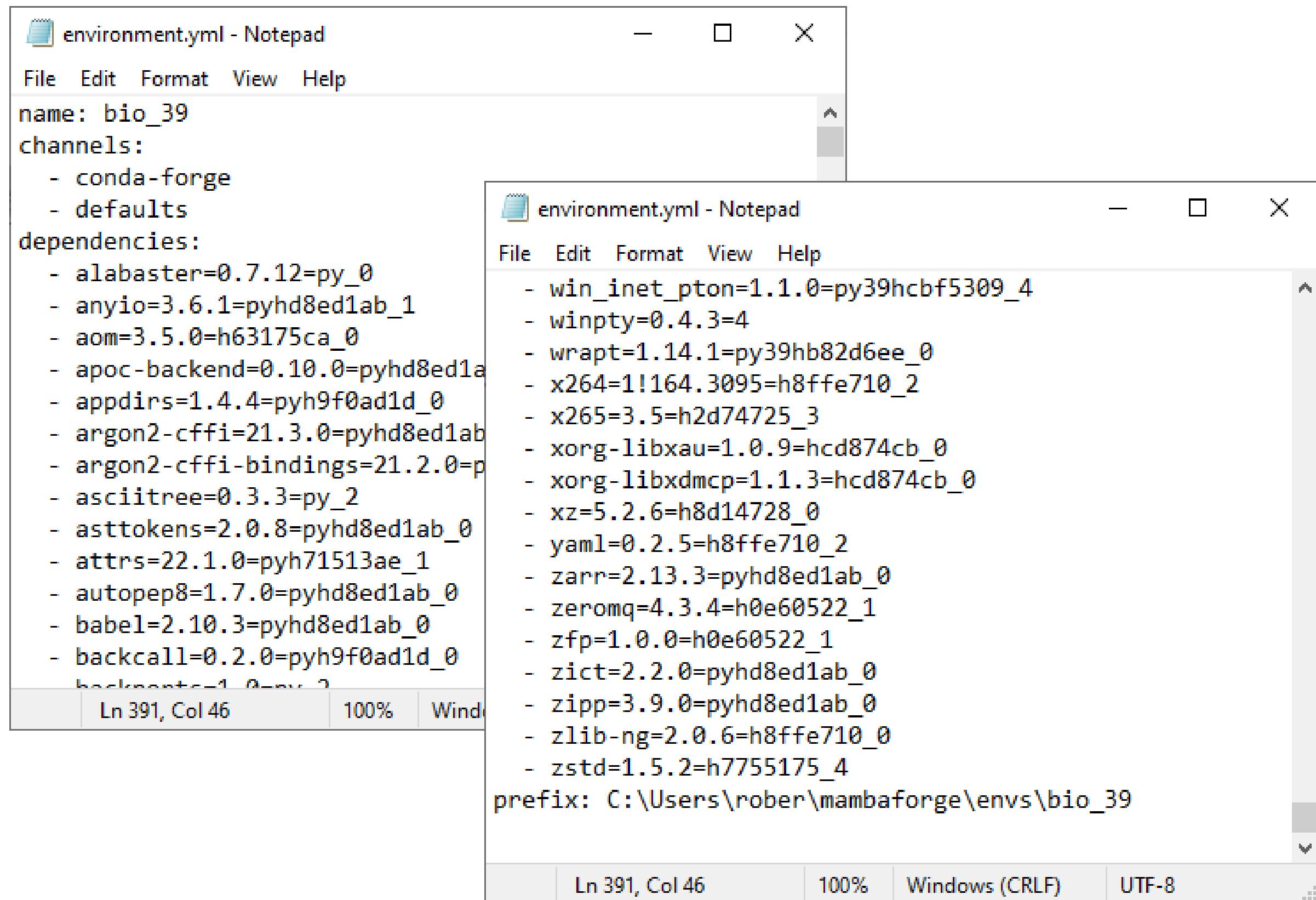
pip install -r requirements.txt

In case your  
environment is  
screwed up, you can  
rebuild it any time.

# Documenting dependencies

... the complete way.

```
conda env export > environment.yml
```



```
environment.yml - Notepad
File Edit Format View Help
name: bio_39
channels:
- conda-forge
- defaults
dependencies:
- alabaster=0.7.12=py_0
- anyio=3.6.1=pyhd8ed1ab_1
- aom=3.5.0=h63175ca_0
- apoc-backend=0.10.0=pyhd8ed1a
- appdirs=1.4.4=pyh9f0ad1d_0
- argon2-cffi=21.3.0=pyhd8ed1ab
- argon2-cffi-bindings=21.2.0=p
- asciitree=0.3.3=py_2
- asttokens=2.0.8=pyhd8ed1ab_0
- attrs=22.1.0=pyh71513ae_1
- autopenp8=1.7.0=pyhd8ed1ab_0
- babel=2.10.3=pyhd8ed1ab_0
- backcall=0.2.0=pyh9f0ad1d_0
backports=1.0.1=py_2
Ln 391, Col 46 100% Wind...
```

```
environment.yml - Notepad
File Edit Format View Help
- win_inet_pton=1.1.0=py39hcbf5309_4
- winpty=0.4.3=4
- wrapt=1.14.1=py39hb82d6ee_0
- x264=1!164.3095=h8ffe710_2
- x265=3.5=h2d74725_3
- xorg-libxau=1.0.9=hcd874cb_0
- xorg-libxdmcp=1.1.3=hcd874cb_0
- xz=5.2.6=h8d14728_0
- yaml=0.2.5=h8ffe710_2
- zarr=2.13.3=pyhd8ed1ab_0
- zeromq=4.3.4=h0e60522_1
- zfp=1.0.0=h0e60522_1
- zict=2.2.0=pyhd8ed1ab_0
- zipp=3.9.0=pyhd8ed1ab_0
- zlib-ng=2.0.6=h8ffe710_0
- zstd=1.5.2=h7755175_4
prefix: C:\Users\rober\mambaforge\envs\bio_39
Ln 391, Col 46 100% Windows (CRLF) UTF-8
```

Excellent way to document which dependencies were *actually* used...

It is *questionable* if re-creating an environment from this yml file works.

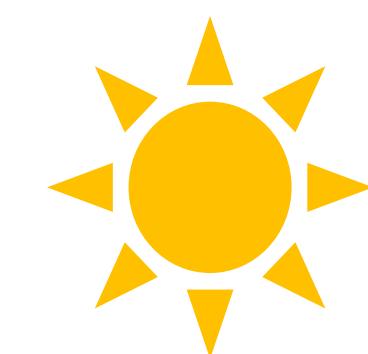
# Shipping scientific software

... so that others can reuse it

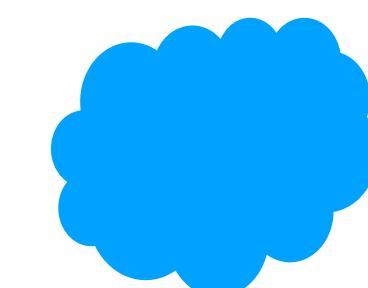
# Deployment

Method / algorithm / software developers live from making things that are useful for others.

“... is available as user-friendly standalone software.”



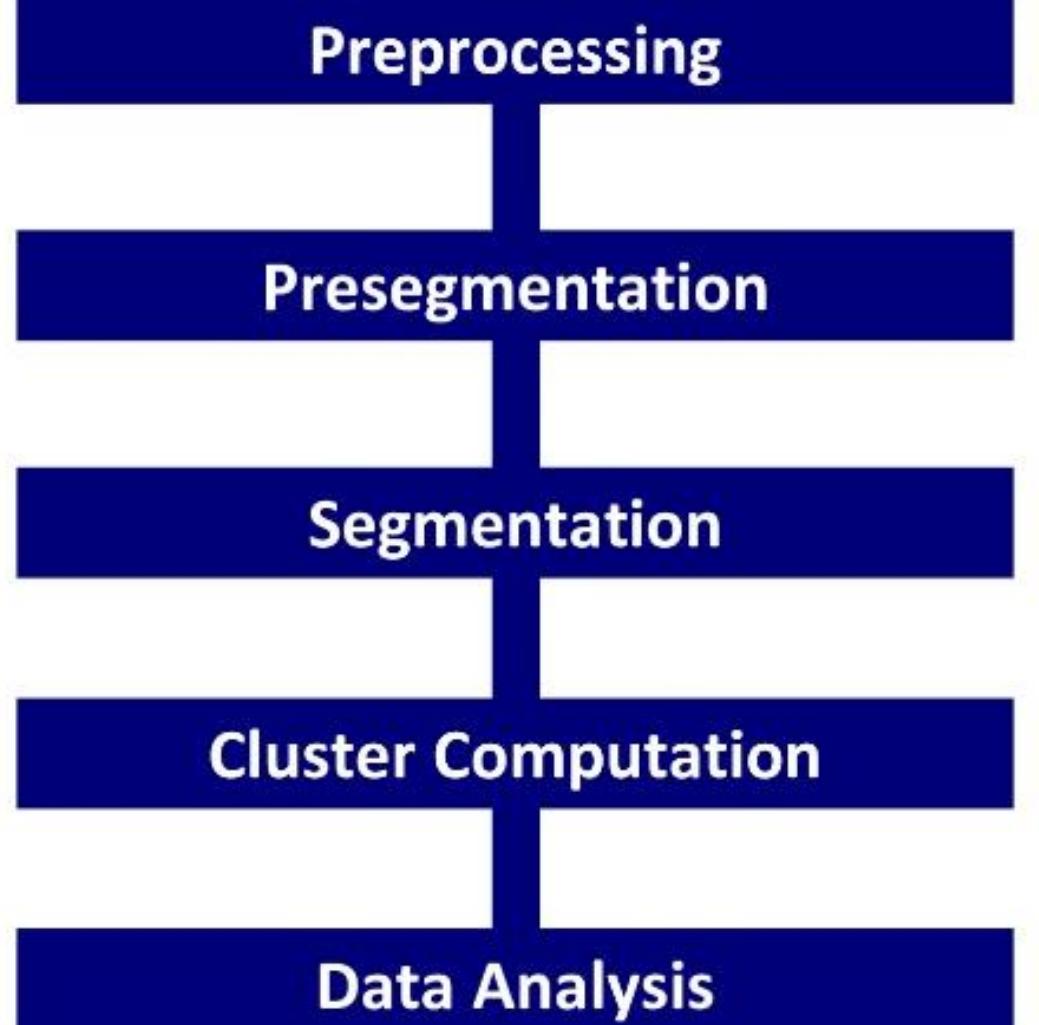
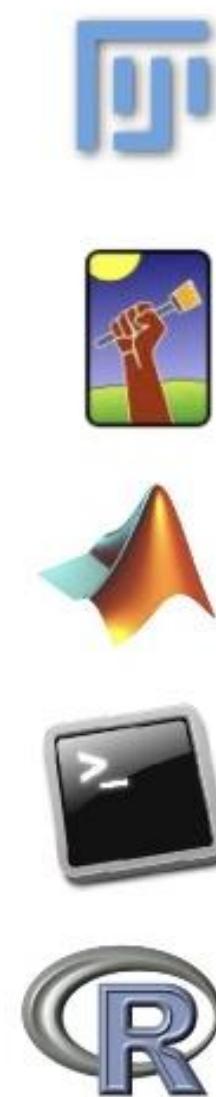
Installation can be made easy.



Ensuring interoperability with other software comes with high effort.



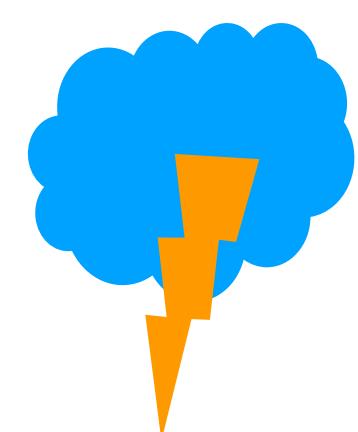
Combining standalone software is often painful and not *user-friendly*.



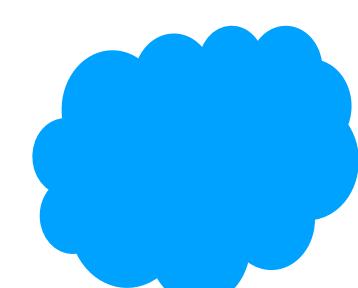
Think of workflow developers,  
a.k.a. “users”.



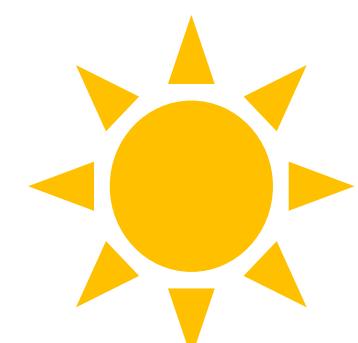
“... is available as user-friendly Python library.”



In life-sciences, a Python library may not be perceived as *user-friendly*.



Installation and dependency management is often tricky.



Interoperability comes basically for free.

# Deployment

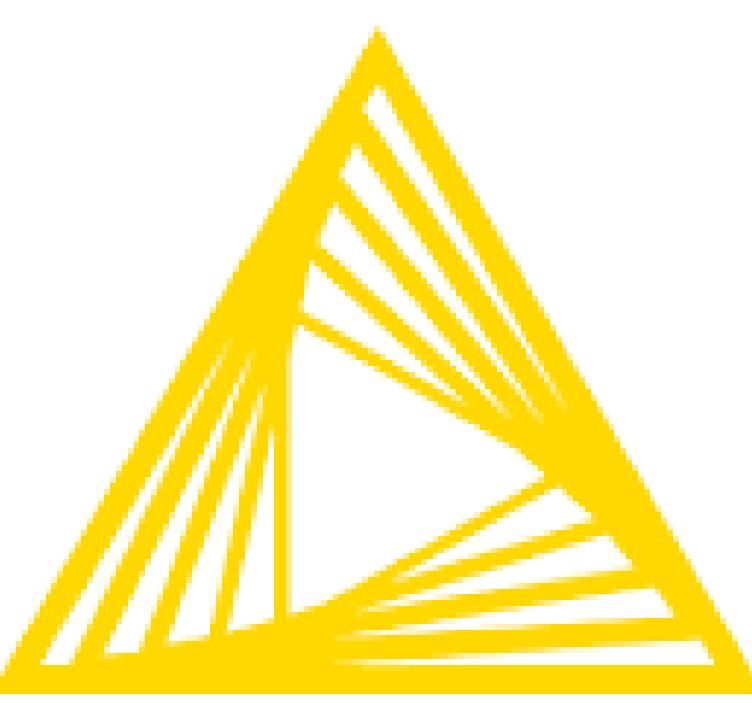
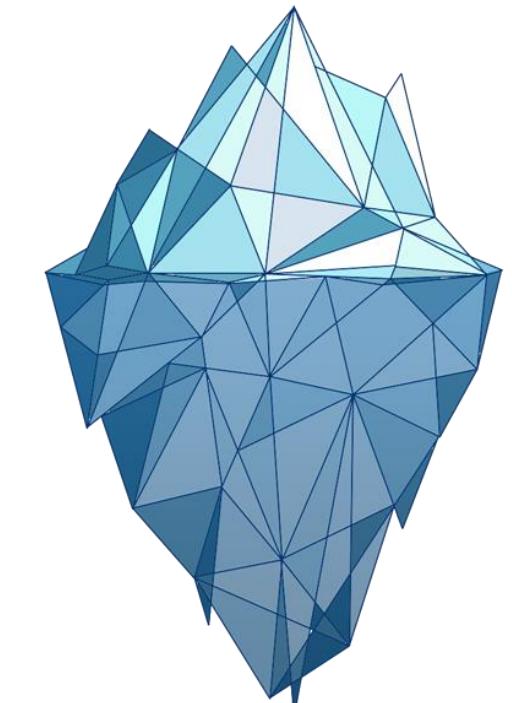
Ship new methods as plugins for established platforms

minimizing and

- effort to ensure interoperability with other tools and file-formats,
- entrance-level burden for new users and
- installation efforts.

maximizing

- visibility,
- accessibility,
- community support and finally,
- adoption.

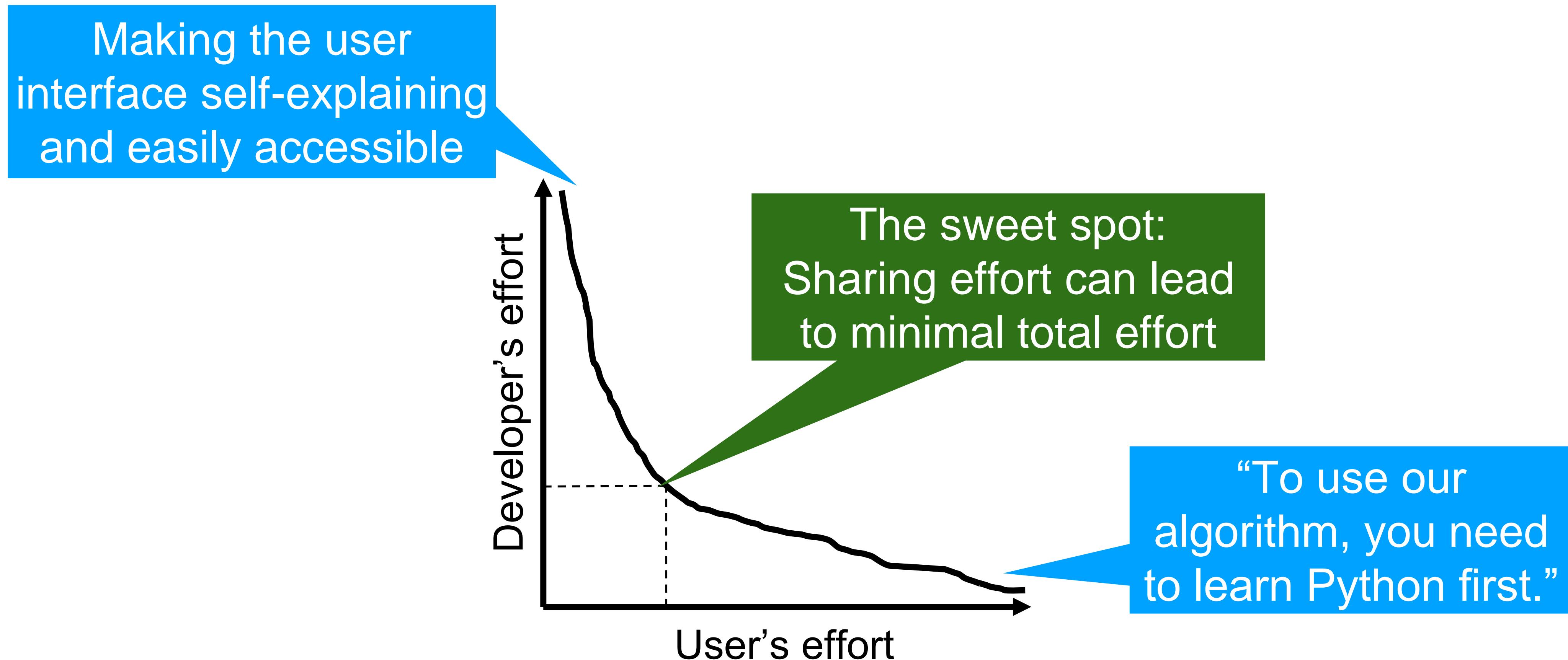


# Interdisciplinary collaboration

... of life scientists and developers joining forces.

# Why we need to work together

- ... to minimize effort



# Why we need to work together

- ... to be successful in our projects (and grant applications)

Computer scientist: “I would like to develop software that allows to unravel the underlying principles of embryo development.”

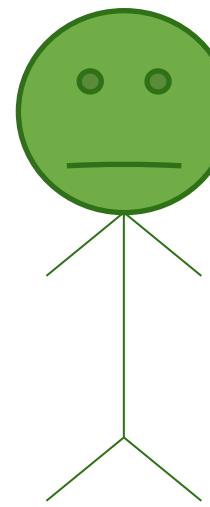
Funding agency: “But you’re lacking the developmental biology skills to make this happen.”

Biologist: “I would like to do quantitative image data science unravel the underlying principles of embryo development.”

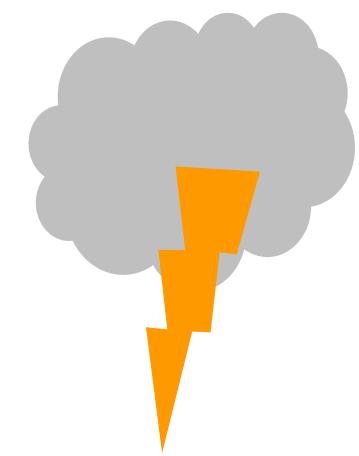
Funding agency: “But you’re lacking the bioinformatics skills to make this happen.”

# Matching expectations

... and *meeting in the middle* for successful collaborations

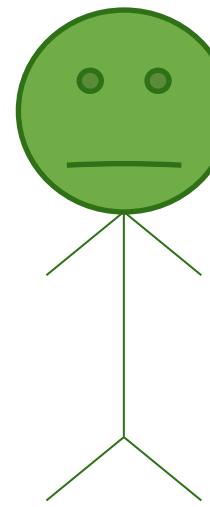


I need somebody who just analyzes the image data. I'm happy to pay for it but can't offer co-authorship.

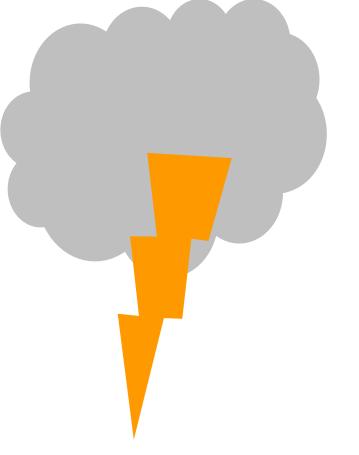


I need to advance my academic career

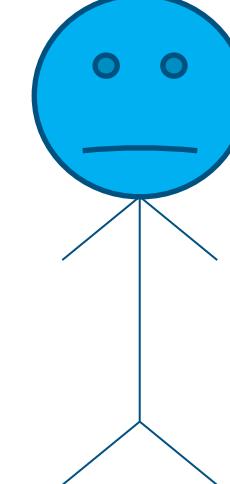
Is it ok to ask for payment and co-authorship?



I need somebody who analyzes the image data for us. I can't pay but I'm happy to offer co-authorship.



I need to make sure my core-facility has some income.

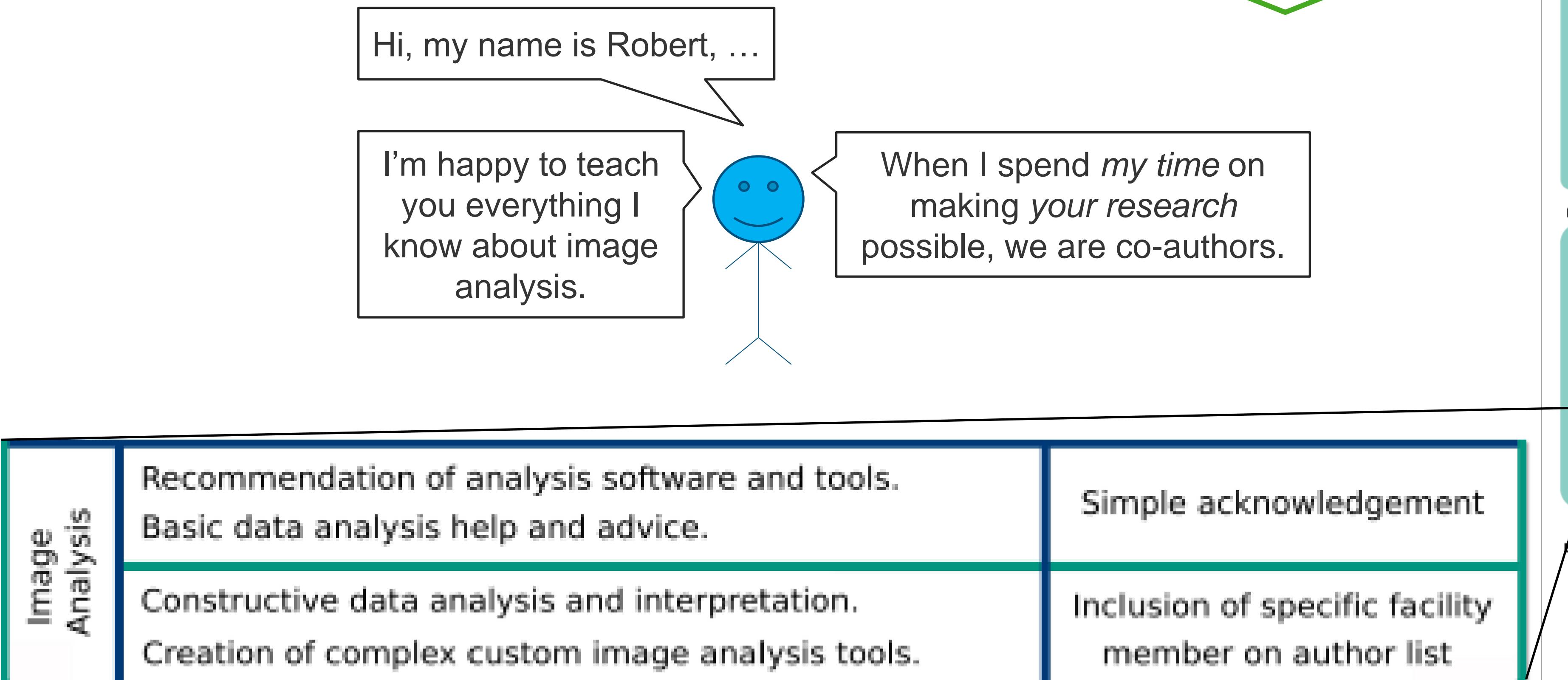


I wish I was a member of their group. They are paid and co-authors.

# Matching expectations

Speak out your expectations and conditions early.

Communication  
is key!



## Imaging Facility Guidelines for Acknowledgement

- 1 All publications resulting from the use of instruments within the facility should acknowledge the facility as a whole, e.g. 'the authors gratefully acknowledge the [core facility name] for their support & assistance in this work' and the facility should be informed of the publication.
- 2 Specific grants that have funded the facility instruments used for the work to be published must be acknowledged if the data was acquired during the active period of that grant. Facility staff will advise users of such grant codes.
- 3 Assistance above the technical or routine level, with any facility staff providing scientific input and expertise in experimental set-up, acquisition or analysis, should be recognised through co-authorship on resulting publications. Please discuss acknowledgements with facility staff prior to manuscript submission.

### Example scenarios with baseline recommendations:

Sample Preparation	Fast, routine sample preparation with standard protocol.	Simple acknowledgement
Development of new sample preparation protocols. Optimisation of existing protocols for specific samples.	Inclusion of specific facility member on author list	
Image Acquisition	Training of users to acquire images themselves. Simple acquisition of raw data.	Simple acknowledgement
Operational image acquisition with input and decisions dependent on expertise. Design or re-design of experimental conditions.	Inclusion of specific facility member on author list	
Image Analysis	Recommendation of analysis software and tools. Basic data analysis help and advice.	Simple acknowledgement
Constructive data analysis and interpretation. Creation of complex custom image analysis tools.	Inclusion of specific facility member on author list	

Based on the publication policy compiled by Natasha Stephen, Plymouth Electron Microscopy Centre, after discussions with the RMS EM-UK community



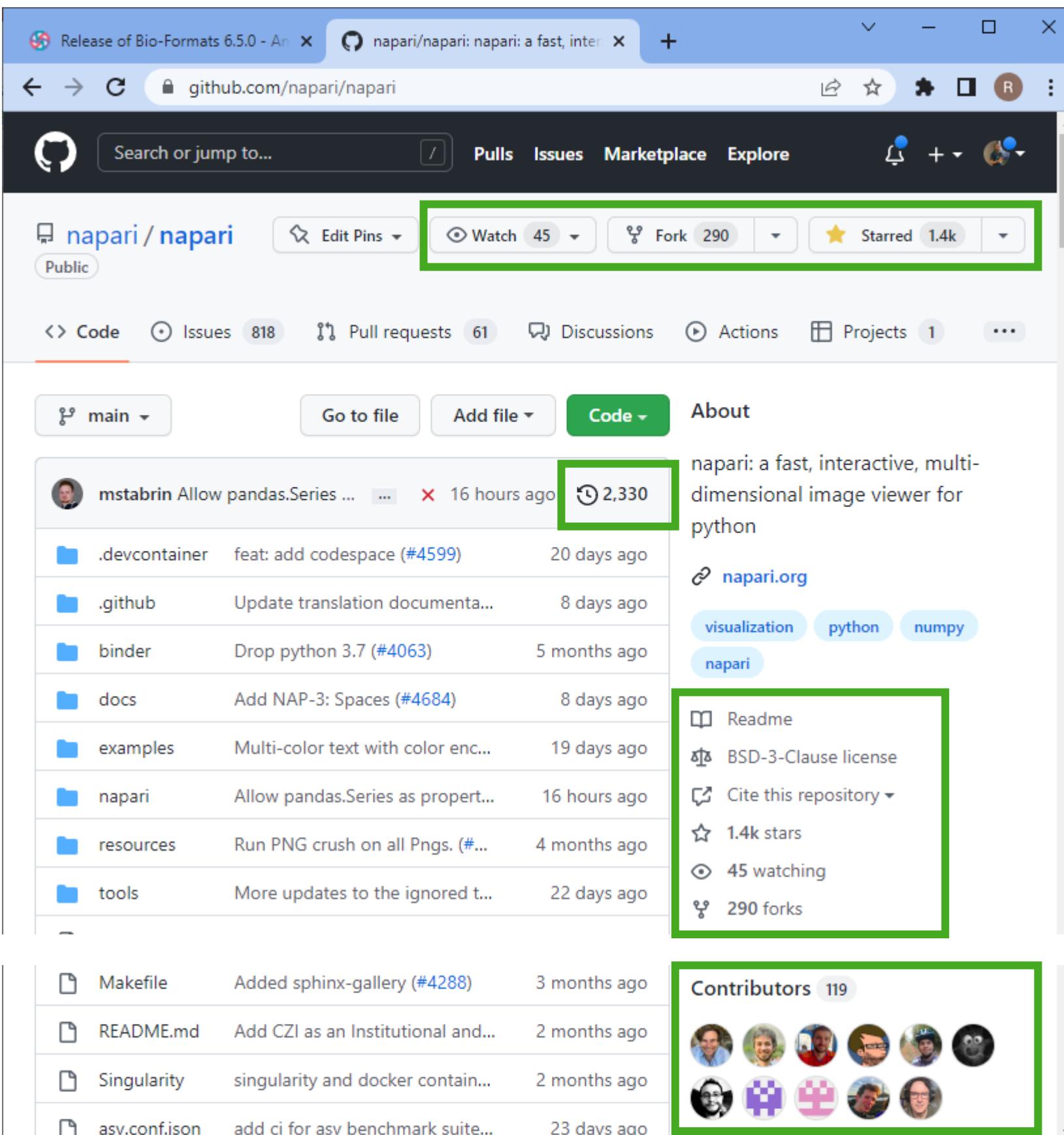
# Software quality indicators

... to differentiate the good stuff from the bad.

# Software quality indicators

Visit the project's github or gitlab page and review indicators.

- **Stars:** People like software, similarly to tweets on Twitter
- **Watching:** People receive updates for new releases
- **Forks:** People made a copy of the code, e.g. to contribute to the project
- **Contributors:** People who contributed to the code
- **Commits:** Changes to the code



Release of Bio-Formats 6.5.0 - An napari/napari: napari: a fast, inter... +  
github.com/napari/napari

Search or jump to... Pulls Issues Marketplace Explore

napari / napari Public

Watch 45 Fork 290 Starred 1.4k

Code Issues 818 Pull requests 61 Discussions Actions Projects 1 ...

main Go to file Add file Code

About

mstabin Allow pandas.Series ... 16 hours ago 2,330

.devcontainer feat: add codespace (#4599) 20 days ago

.github Update translation documenta... 8 days ago

binder Drop python 3.7 (#4063) 5 months ago

docs Add NAP-3: Spaces (#4684) 8 days ago

examples Multi-color text with color enc... 19 days ago

napari Allow pandas.Series as propert... 16 hours ago

resources Run PNG crush on all Pngs. (#... 4 months ago

tools More updates to the ignored t... 22 days ago

Makefile Added sphinx-gallery (#4288) 3 months ago

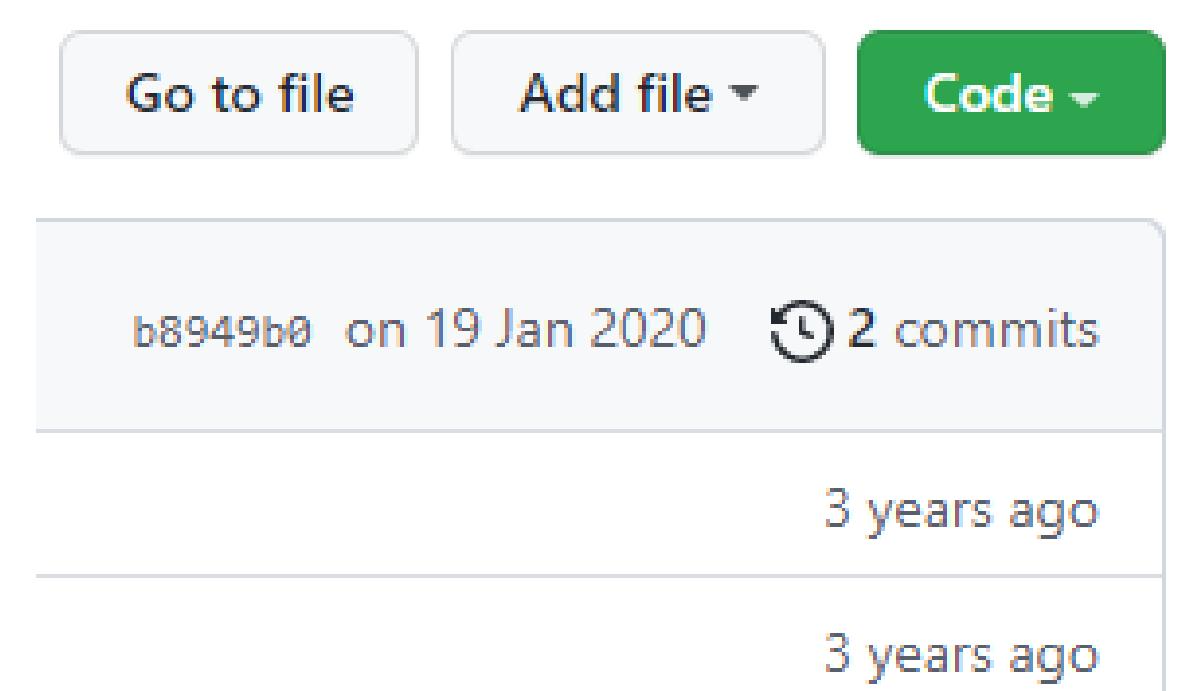
README.md Add CZI as an Institutional and... 2 months ago

Singularity singularity and docker contain... 2 months ago

asv.conf.json add ci for asv benchmark suite... 23 days ago

Readme BSD-3-Clause license Cite this repository 1.4k stars 45 watching 290 forks

Contributors 119



Go to file Add file Code

b8949b0 on 19 Jan 2020 2 commits

3 years ago

3 years ago

About

No description, website, or topics provided.

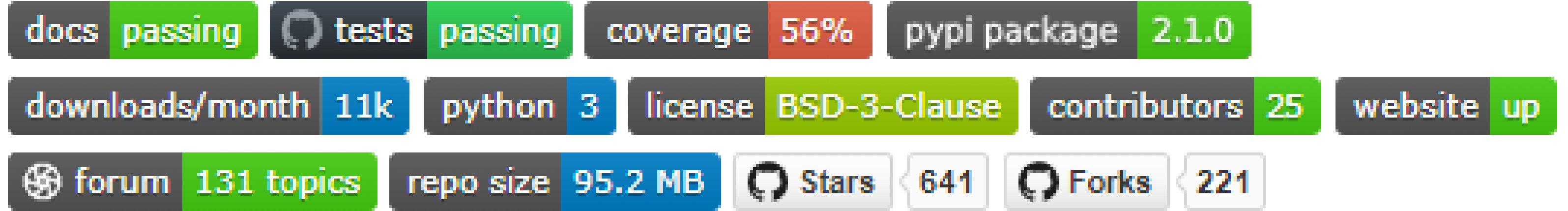
1 star

2 watching

0 forks

# Software quality indicators

Visit the project's github or gitlab page and review indicators.



Note, github badges cannot be deserved.  
Developers put them there



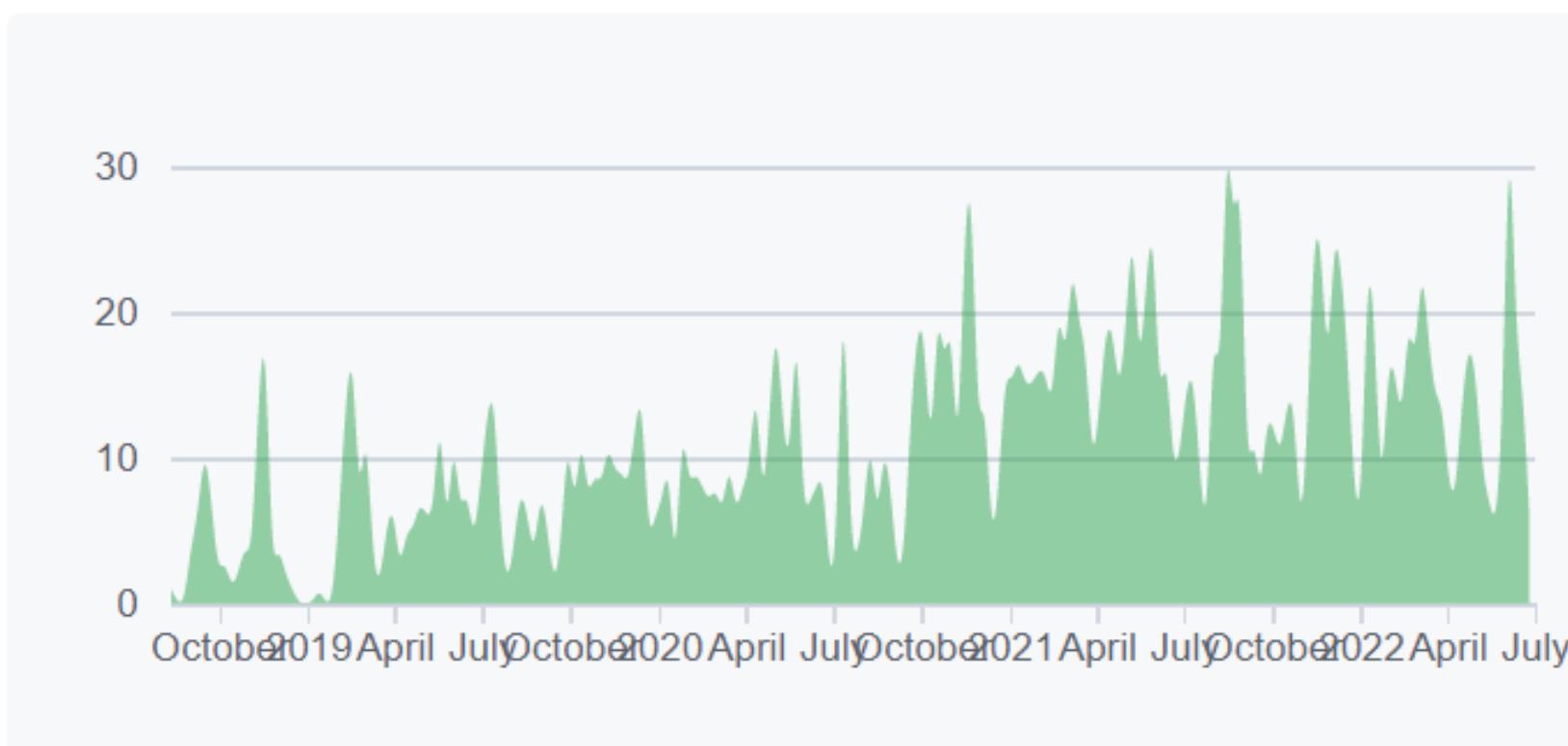
# Software quality indicators

Visit the project's github or gitlab page and review indicators.

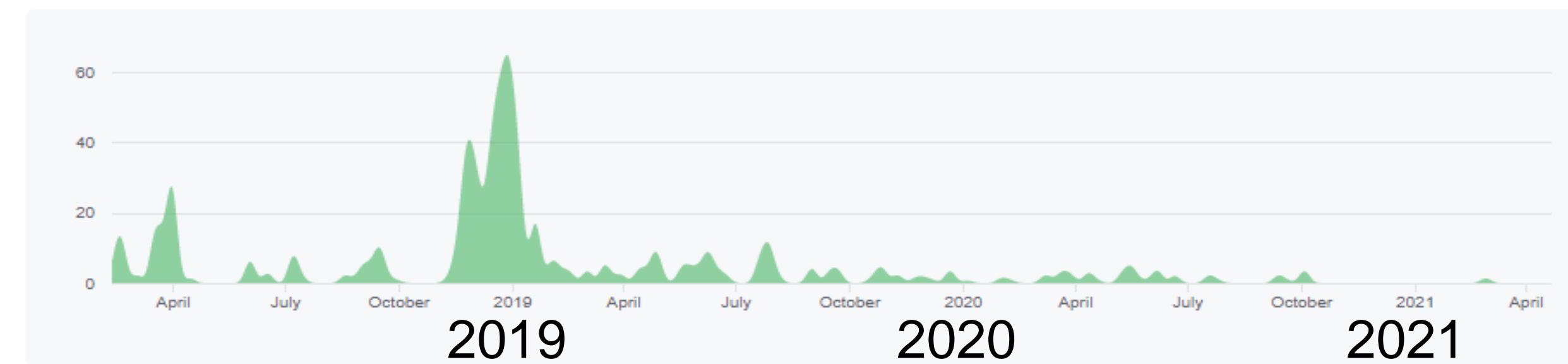
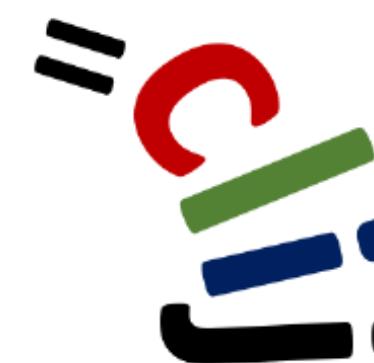
Aug 12, 2018 – Jul 1, 2022

Contributions: Commits ▾

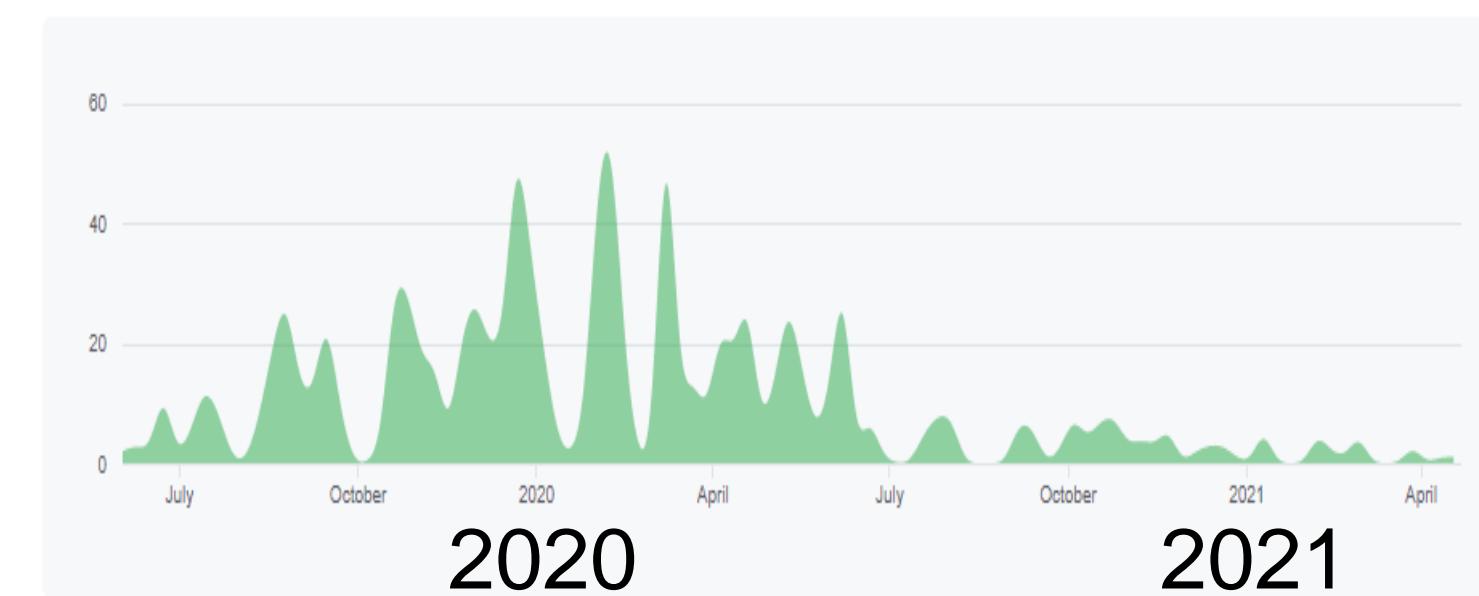
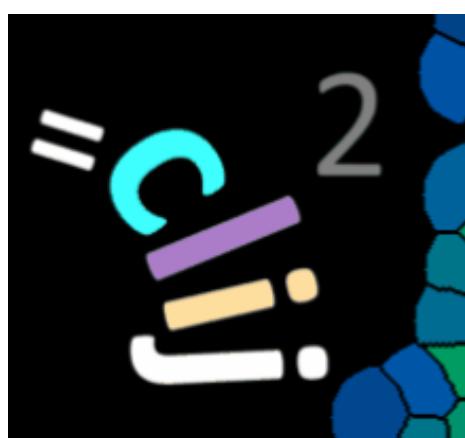
Contributions to main, excluding merge commits and bot accounts



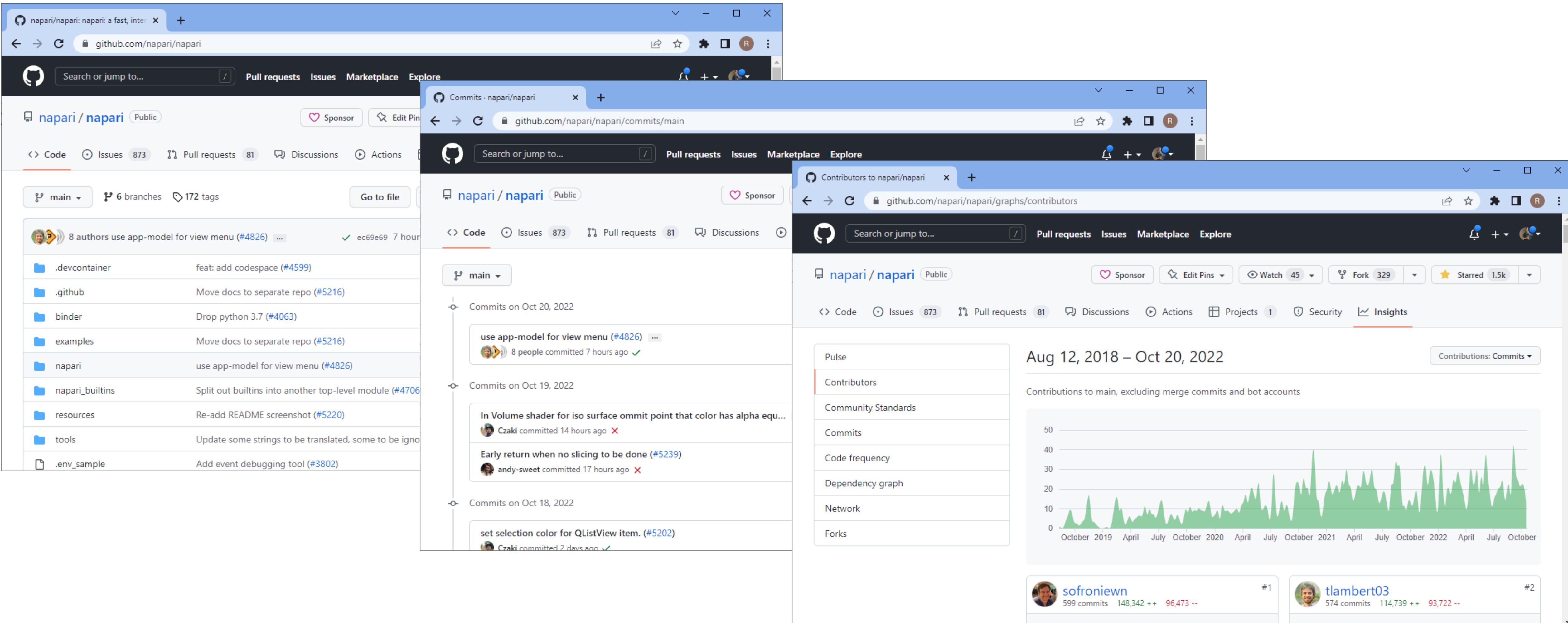
Be a bit careful when development appears to have halted



And check related projects



# Demo



The image shows three separate browser tabs from GitHub, each displaying different aspects of the napari repository:

- Left Tab:** Shows the main repository page for napari/napari. It displays 873 issues, 81 pull requests, and 172 tags. A list of recent commits is shown, including:
  - feat: add codespace (#4599)
  - Move docs to separate repo (#5216)
  - Drop python 3.7 (#4063)
  - Move docs to separate repo (#5216)
  - use app-model for view menu (#4826)
  - Split out builtins into another top-level module (#4706)
  - Re-add README screenshot (#5220)
  - Update some strings to be translated, some to be ignored (#4826)
  - Add event debugging tool (#3802)
- Middle Tab:** Shows the commit history for the main branch. It highlights commits from October 20, 2022, including:
  - use app-model for view menu (#4826) - 8 people committed 7 hours ago
  - In Volume shader for iso surface omit point that color has alpha equ... - Czaki committed 14 hours ago
  - Early return when no slicing to be done (#5239) - andy-sweet committed 17 hours ago
- Right Tab:** Shows the 'Contributors' section for the napari/napari repository. It includes a timeline from Aug 12, 2018, to Oct 20, 2022, and a chart showing contributions over time. Top contributors listed are:
  - sofroniewn (599 commits, 148,342 ++, 96,473 --)
  - tlambert03 (574 commits, 114,739 ++, 93,722 --)

# Crowd sourcing

... ideas, feedback, improvements

# Market research

## Engage with the community

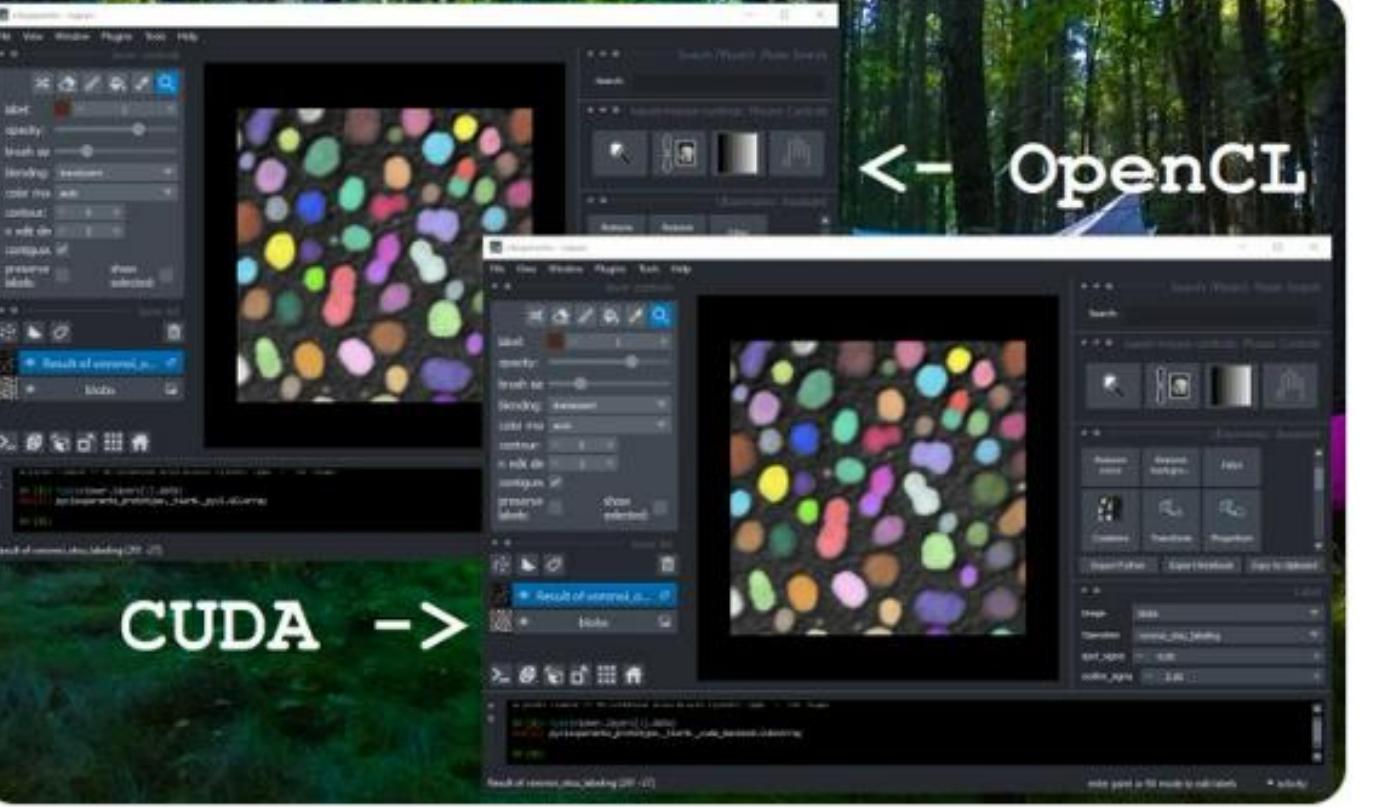
- Use twitter to reach out
- Learn about who needs what

Robert Haase  
@haesleinhuepf

... and we will incorporate **#CUDA**/**@CuPy\_Team** with **#OpenCL**/**#clesperanto** to find new friends who use GPUs differently and learn from them. 🧑💻🚀

You wonder what will be different between **#clesperanto**-OpenCL and **#clesperanto**-CUDA based image processing? 😊

I hope not a single bit 😎



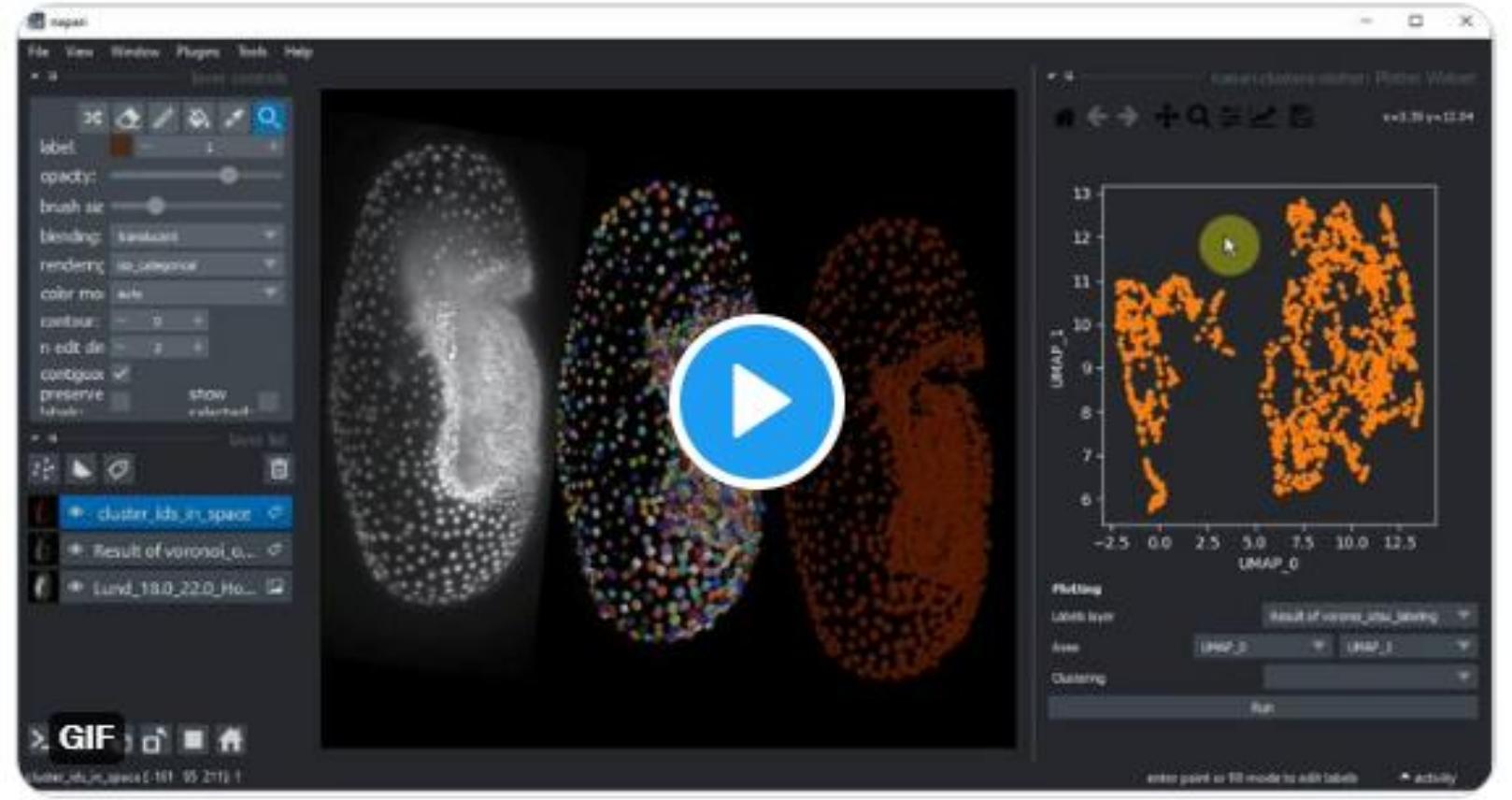
5:55 PM · Nov 15, 2021 · Twitter Web App

2 Retweets 32 Likes

Laura Žigutytė  
@zigutyte

My first **@napari\_imaging** plugin is out now! It can measure region properties, plot them, perform k-means or manual clustering. Huge thanks to **#biapol** group members for amazing teamwork and all the help **@RyanSavill4**, **@zoccolermarcelo** and **@haesleinhuepf** 😊

[napari-hub.org/plugins/napari...](https://napari-hub.org/plugins/napari...)

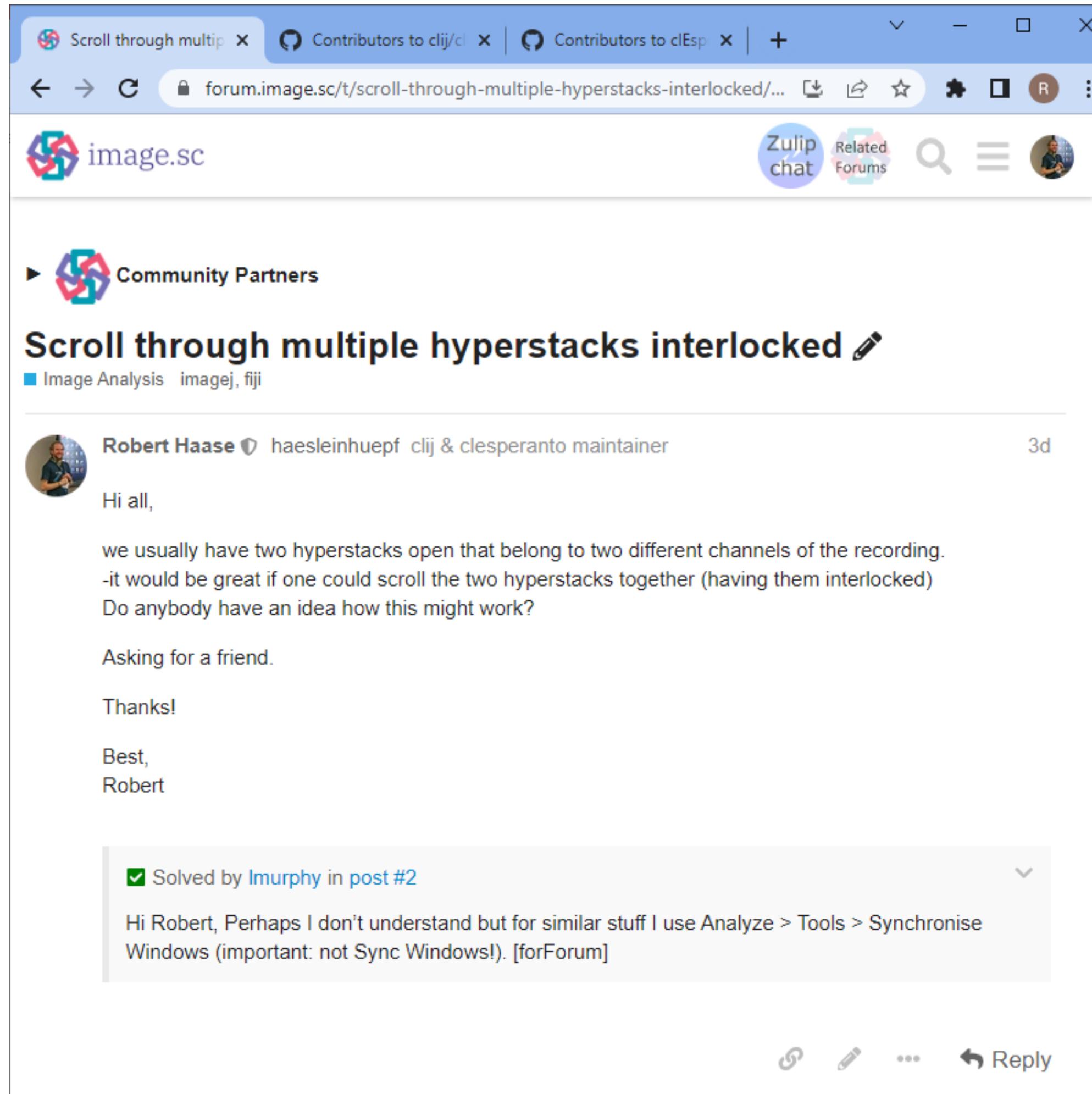


2:56 PM · Nov 15, 2021 · Twitter Web App

74 Retweets 12 Quote Tweets 403 Likes

Communication is key!

# Community involvement



The screenshot shows a forum post titled "Scroll through multiple hyperstacks interlocked" by Robert Haase. Robert asks if it's possible to scroll two interlocked hyperstacks together. He receives a reply from lmurphy suggesting the "Synchronise Windows" feature in Fiji. A screenshot of Fiji showing two channels (C1-mitosis.tif and C2-mitosis.tif) with the "Synchronise Windows" dialog open is included.

Robert Haase haesleinhuepf clij & clesperanto maintainer

Hi all,

we usually have two hyperstacks open that belong to two different channels of the recording.  
-it would be great if one could scroll the two hyperstacks together (having them interlocked)  
Do anybody have an idea how this might work?

Asking for a friend.

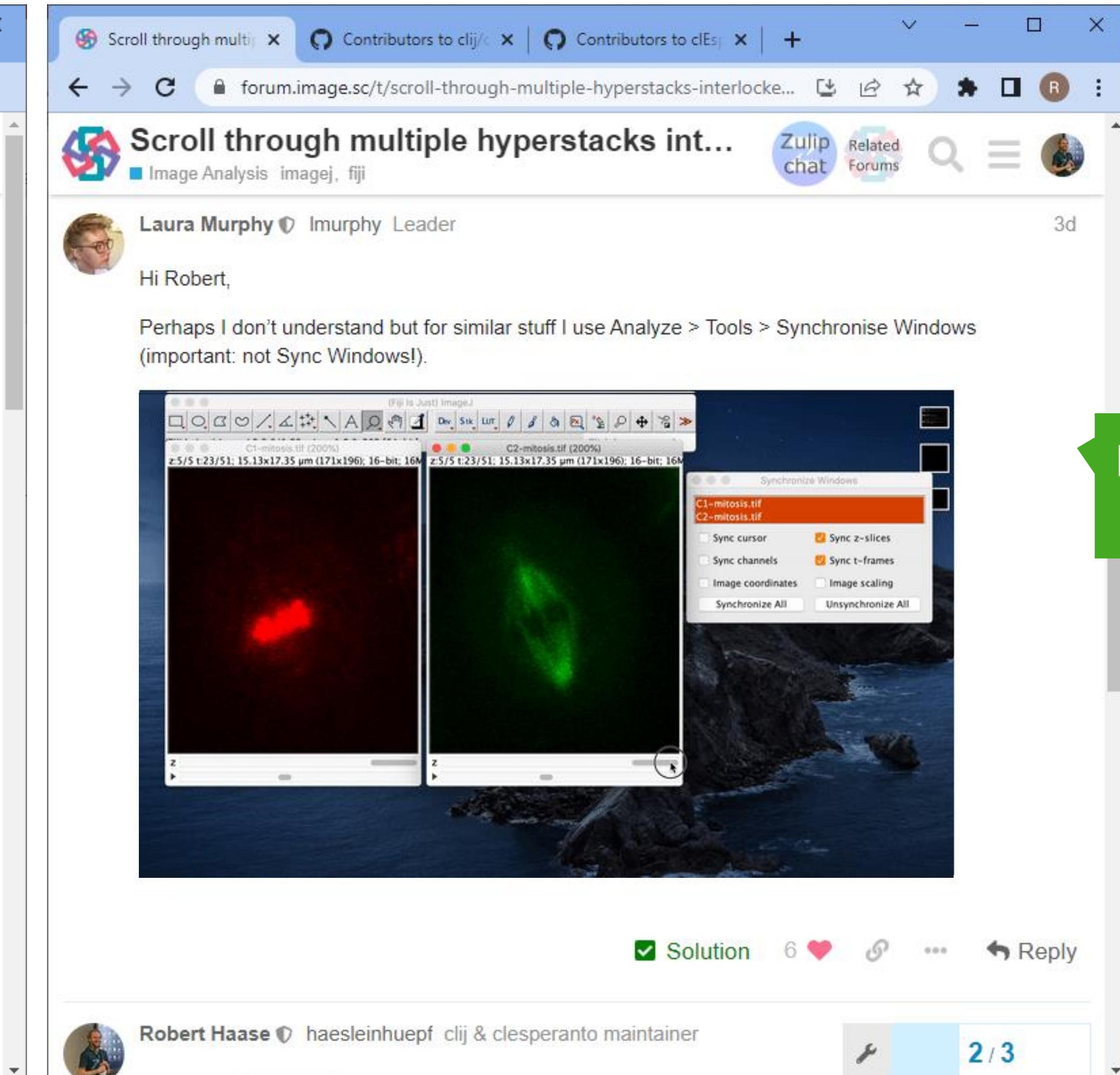
Thanks!

Best,  
Robert

Solved by lmurphy in post #2

Hi Robert, Perhaps I don't understand but for similar stuff I use Analyze > Tools > Synchronise Windows (important: not Sync Windows!). [forForum]

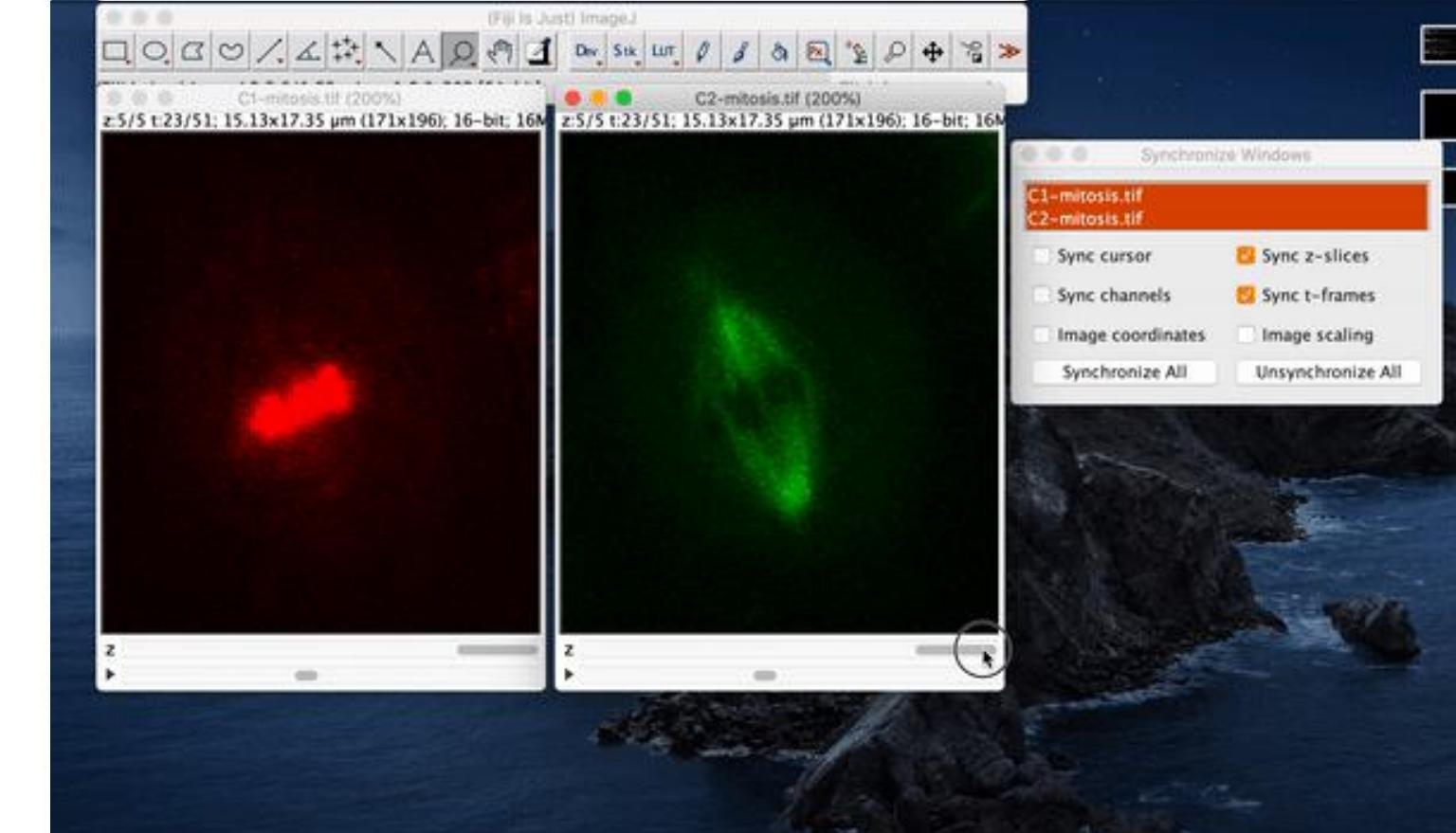
Reply



lmurphy lmurphy Leader

Hi Robert,

Perhaps I don't understand but for similar stuff I use Analyze > Tools > Synchronise Windows (important: not Sync Windows!).



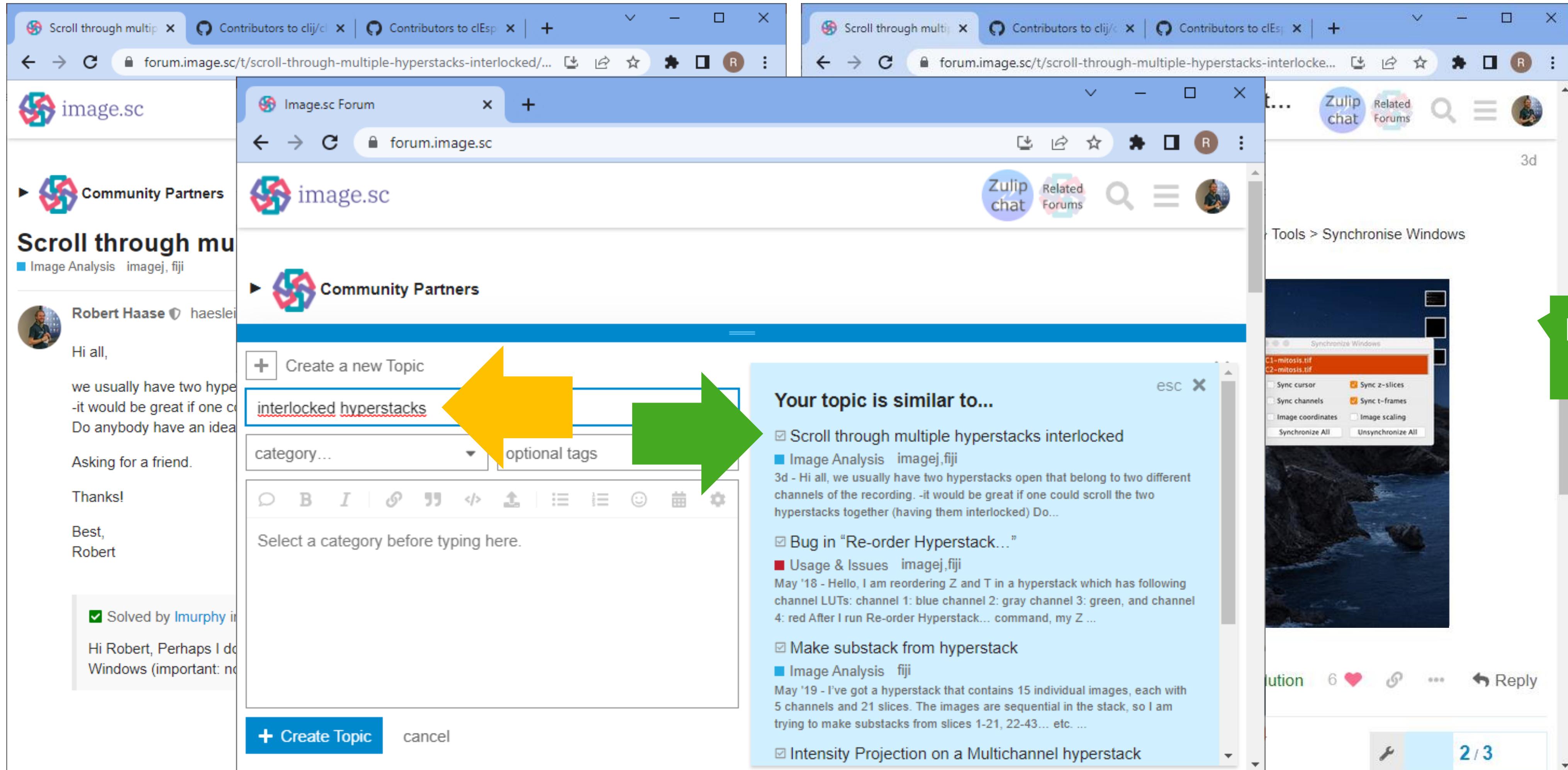
Solution 6 ❤️ ⚡ ... ↗ Reply

Robert Haase haesleinhuepf clij & clesperanto maintainer

2 / 3

Reply after 18 minutes!

# Community involvement



forum.image.sc/t/scroll-through-multiple-hyperstacks-interlocked/68862/2

**Image.sc Forum**

**Community Partners**

**Scroll through mu**

Hi all,  
we usually have two hyperstacks open that belong to two different channels of the recording. -it would be great if one could scroll the two hyperstacks together (having them interlocked) Do anybody have an idea?  
Asking for a friend.  
Thanks!  
Best,  
Robert

Solved by lmurphy

Hi Robert, Perhaps I do not understand Windows (important: no

**Create a new Topic**

interlocked hyperstacks

category... optional tags

+ Create Topic cancel

Your topic is similar to...

- Scroll through multiple hyperstacks interlocked
- Image Analysis imagej,fiji

3d - Hi all, we usually have two hyperstacks open that belong to two different channels of the recording. -it would be great if one could scroll the two hyperstacks together (having them interlocked) Do...

- Bug in "Re-order Hyperstack..."
- Usage & Issues imagej,fiji

May '18 - Hello, I am reordering Z and T in a hyperstack which has following channel LUTs: channel 1: blue channel 2: gray channel 3: green, and channel 4: red After I run Re-order Hyperstack... command, my Z ...

- Make substack from hyperstack
- Image Analysis fiji

May '19 - I've got a hyperstack that contains 15 individual images, each with 5 channels and 21 slices. The images are sequential in the stack, so I am trying to make substacks from slices 1-21, 22-43... etc. ...

- Intensity Projection on a Multichannel hyperstack

Tools > Synchronise Windows

Synchronise Windows

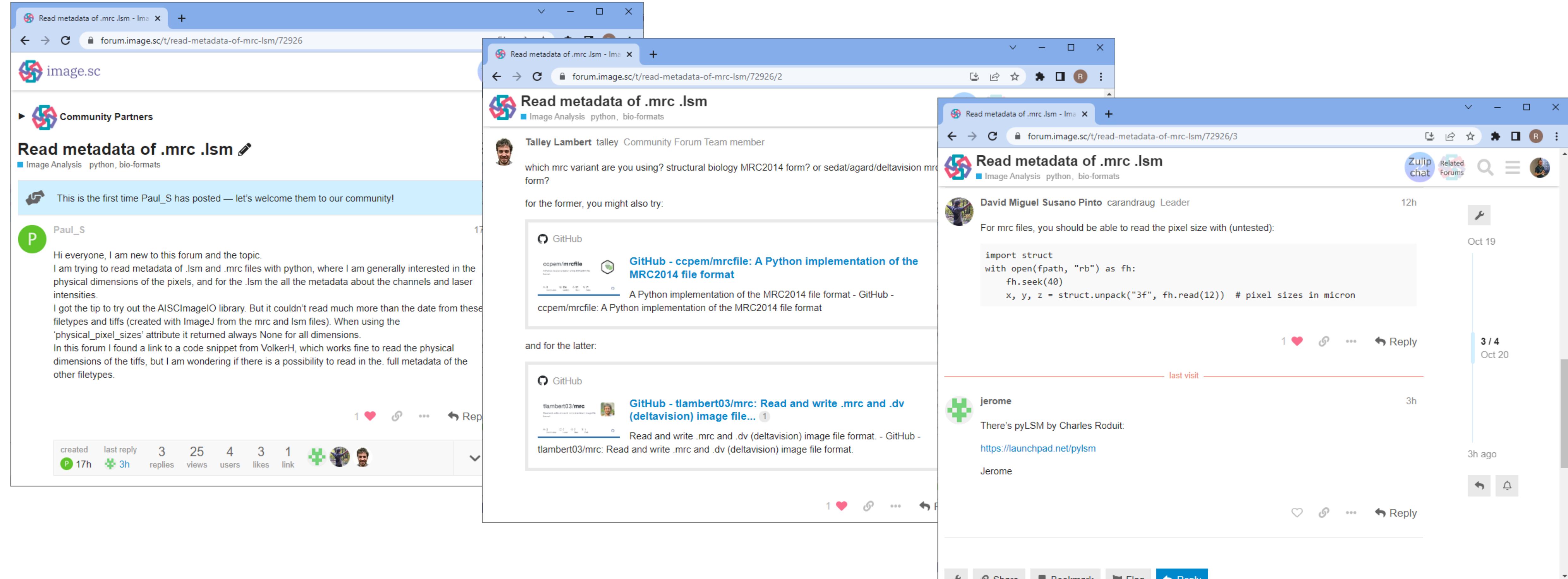
C1+mirosis.tif C2+mirosis.tif

- Sync cursor
- Sync z-slices
- Sync channels
- Sync t-frames
- Image coordinates
- Image scaling
- Synchronise All
- Unsynchronise All

Reply after 18 minutes!

# Community involvement

Yesterday...



Read metadata of .mrc .lsm

This is the first time Paul\_S has posted — let's welcome them to our community!

Paul\_S

Hi everyone, I am new to this forum and the topic. I am trying to read metadata of .lsm and .mrc files with python, where I am generally interested in the physical dimensions of the pixels, and for the .lsm the all the metadata about the channels and laser intensities. I got the tip to try out the AISCImageIO library. But it couldn't read much more than the date from these filetypes and tiffs (created with ImageJ from the mrc and lsm files). When using the 'physical\_pixel\_sizes' attribute it returned always None for all dimensions. In this forum I found a link to a code snippet from VolkerH, which works fine to read the physical dimensions of the tiffs, but I am wondering if there is a possibility to read in the full metadata of the other filetypes.

Talley Lambert

which mrc variant are you using? structural biology MRC2014 form? or sedat/agard/deltavision mrc form?

for the former, you might also try:

[GitHub - ccpem/mrcfile: A Python implementation of the MRC2014 file format](#)

David Miguel Susano Pinto

For mrc files, you should be able to read the pixel size with (untested):

```
import struct
with open(fpath, "rb") as fh:
    fh.seek(40)
    x, y, z = struct.unpack("3f", fh.read(12)) # pixel sizes in micron
```

jerome

There's pyLSM by Charles Roduit:

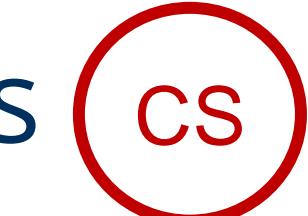
<https://launchpad.net/pylsm>

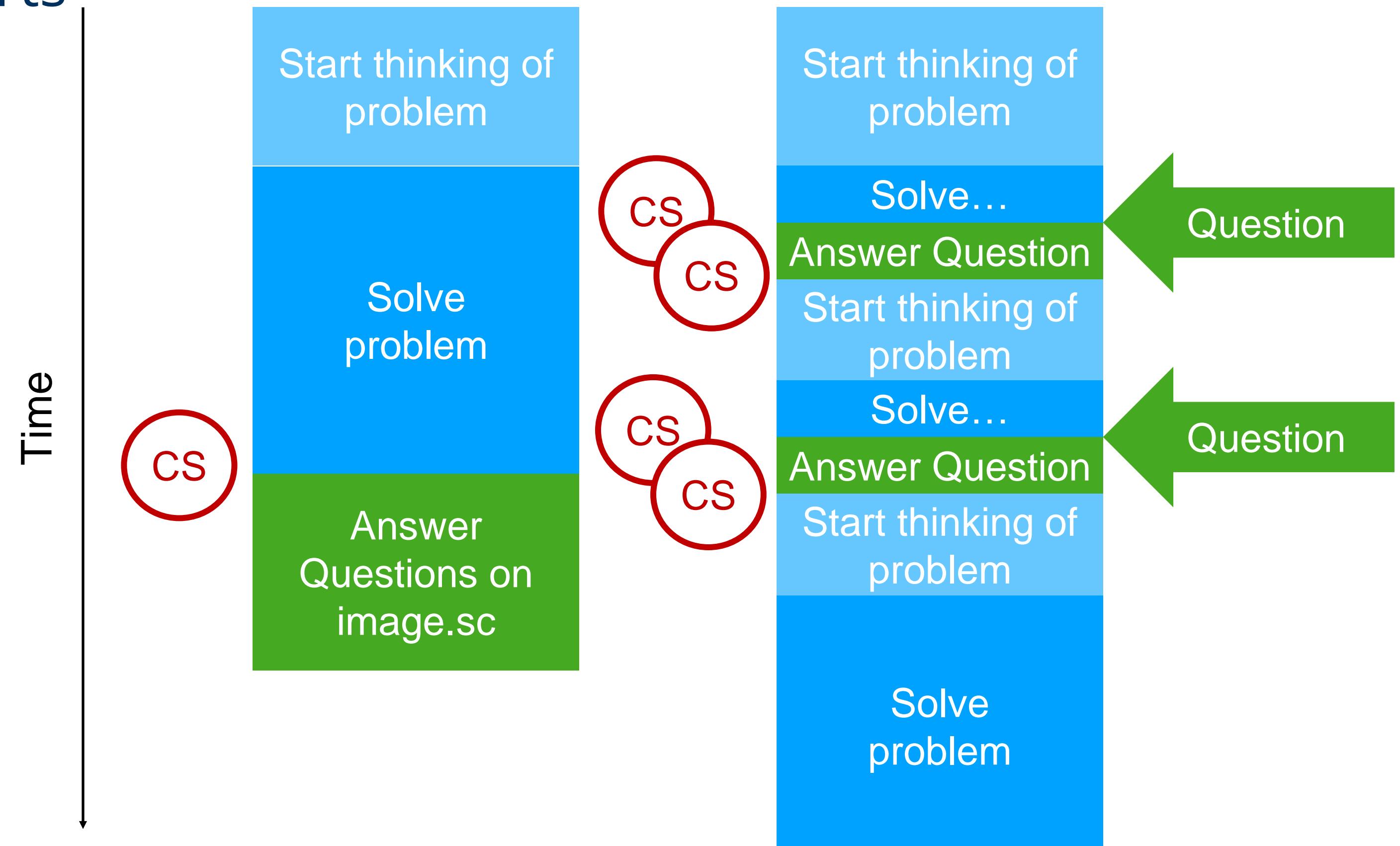
# Why public support channels

## User's perspective

- Receive feedback from multiple experts
- Also if one expert is on vacation

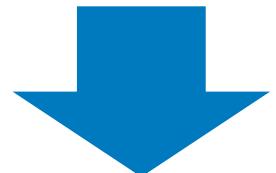
## Developer's perspective

- Reduce repetitive basic questions
- Distribute workload
- Distribute knowledge
- Asynchronous Q&A
- Minimize context-switches 



# Collaboration as a service

General questions



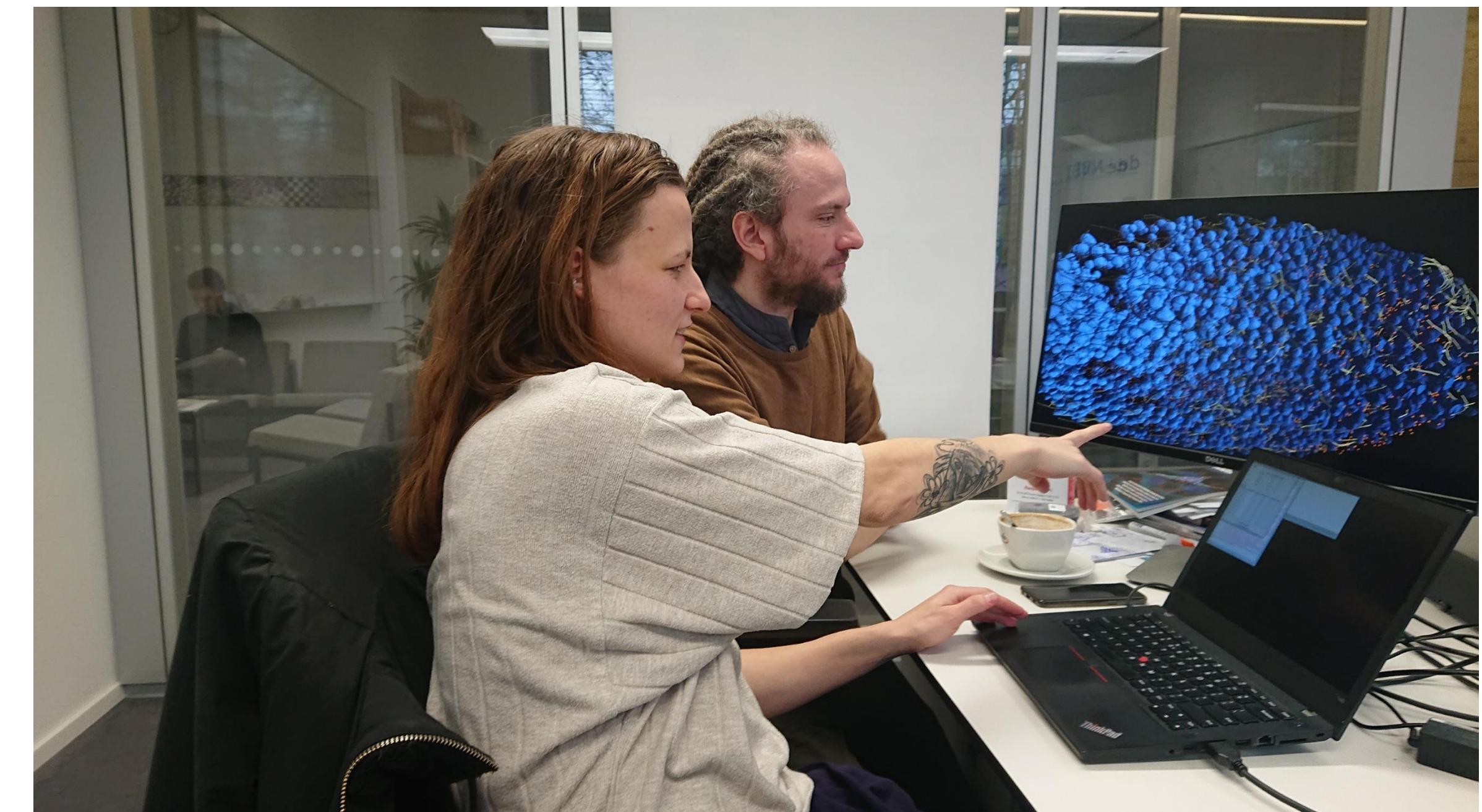
<https://image.sc>

The screenshot shows the homepage of the Image.sc Forum. At the top, there's a navigation bar with links for 'Zulip chat', 'Related Forums', a search icon, and a user profile. Below the navigation is a section titled 'Community Partners' which lists various scientific imaging projects. The list includes: All Topics, AGAVE, AICSImagelO, Aydin, BIAFLOWS, BIII, BiofilmQ, Bio-Formats, BioGlobe, Cellpose, BrainGlobe, Cytomine, DeepLabCut, Fiji, IDR, ilastik, ImageJ, Icy, JIPipe, Mars, MCMICRO, MEB, NEUBIAS, OME, OMERO, OMELiCC, OpenRIS, Orbit, Piximi, PYME, Python-Microscope, QuPath, SR-Tesseler, StarDist, starfish, and TissUUmaps. There's also a 'Dormant Partners' section with a placeholder '... Your Icon Here'. At the bottom, there are sections for 'RELATED COMMUNITIES' featuring uforum, STK, and KNIME, and a 'SPONSORED BY COBA' section with the COBA logo.

Project-specific questions



[biapol@groups.tu-dresden.de](mailto:biapol@groups.tu-dresden.de)  
[scicomp@mpicbg.de](mailto:scicomp@mpicbg.de)



# Related publications

F1000Research

BROWSE GATEWAYS & COLLECTIONS HOW TO PUBLISH ABOUT BLOG

Home » Browse » Developing open-source software for bioimage analysis: opportunities...

OPINION ARTICLE

Developing open-source software for bioimage analysis: opportunities and challenges [version 1; peer review: 2 approved]

✉ Florian Levet  <sup>1,2</sup>, Anne E. Carpenter  <sup>3</sup>, Kevin W. Eliceiri  <sup>4</sup>, Anna Kreshuk  <sup>5</sup>, Peter Bankhead  <sup>6</sup>, Robert Haase  <sup>7</sup>

+ Author details

This article is included in the NEUBIAS - the Bio

This article is included in the Bioinformatics ga

This article is included in the Research on Rese

 ALL METRICS

1683 VIEWS  
223 DOWNLOADS

TOTAL VIEWS 1,085



**PERSPECTIVE article**

Front. Bioinform., 14 April 2022 | <https://doi.org/10.3389/fbinf.2022.889755>

**Meeting in the Middle: Towards Successful Multidisciplinary Bioimage Analysis Collaboration**

Anjalie Schlaeppli<sup>1,2\*</sup>, Wilson Adams<sup>3,4†</sup>, Robert Haase<sup>5†</sup>, Jan Huisken<sup>1,6†</sup>, Ryan B. MacDonald<sup>7†</sup>, Kevin W. Eliceiri<sup>1,8†</sup> and Elisabeth C. Kugler<sup>7\*</sup>

<sup>1</sup>Morgridge Institute for Research, Madison, WI, United States  
<sup>2</sup>BioImaging and Optics Platform, École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland  
<sup>3</sup>Department of Biomedical Engineering, Vanderbilt University, Nashville, TN, United States  
<sup>4</sup>Department of Pharmacology, Vanderbilt University, Nashville, TN, United States  
<sup>5</sup>DFG Cluster of Excellence "Physics of Life", Germany and Center for Systems Biology Dresden, TU Dresden, Dresden, Germany  
<sup>6</sup>Department of Biology and Psychology, Georg-August-University Göttingen, Göttingen, Germany  
<sup>7</sup>Faculty of Brain Sciences, Institute of Ophthalmology, University College London, London, United Kingdom  
<sup>8</sup>Center for Quantitative Cell Imaging, University of Wisconsin-Madison, Madison, WI, United States

Cornell University

arXiv > q-bio > arXiv:2110.13951

Quantitative Biology > Other Quantitative Biology

[Submitted on 26 Oct 2021]

**Open microscopy in the life sciences: Quo Vadis?**

Johannes Hohlbein, Benedict Diederich, Barbora Marsikova, Emmanuel G. Reynaud, Seamus Holden, Wiebke Jahr, Robert Haase, Kirti Prakash

This allows observing cellular features and objects with sub-micron resolution. Such, light microscopy has been playing a fundamental role in the life sciences for over a hundred years. Fueled by the availability of mass-produced electronic components, openly shared documentation and building instructions, open-source software, rapid prototyping and 3D printing, and the enthusiasm of contributors, the concept of open microscopy has been gaining incredible momentum. From sophisticated tools to an expanding user base. Here, we will first introduce open science and open microscopy before highlighting recent progress in open microscopy. We argue that the availability of well-designed software solutions targeting broad user groups or even non-experts is relevant to cope with the increasing complexity of cutting-edge microscopy. We will then extensively discuss the current and future challenges.

Cornell University

arXiv > q-bio > arXiv:2204.07547

Quantitative Biology > Quantitative Methods

[Submitted on 15 Apr 2022]

**A Hitchhiker's Guide through the Bio-image Analysis Software Universe**

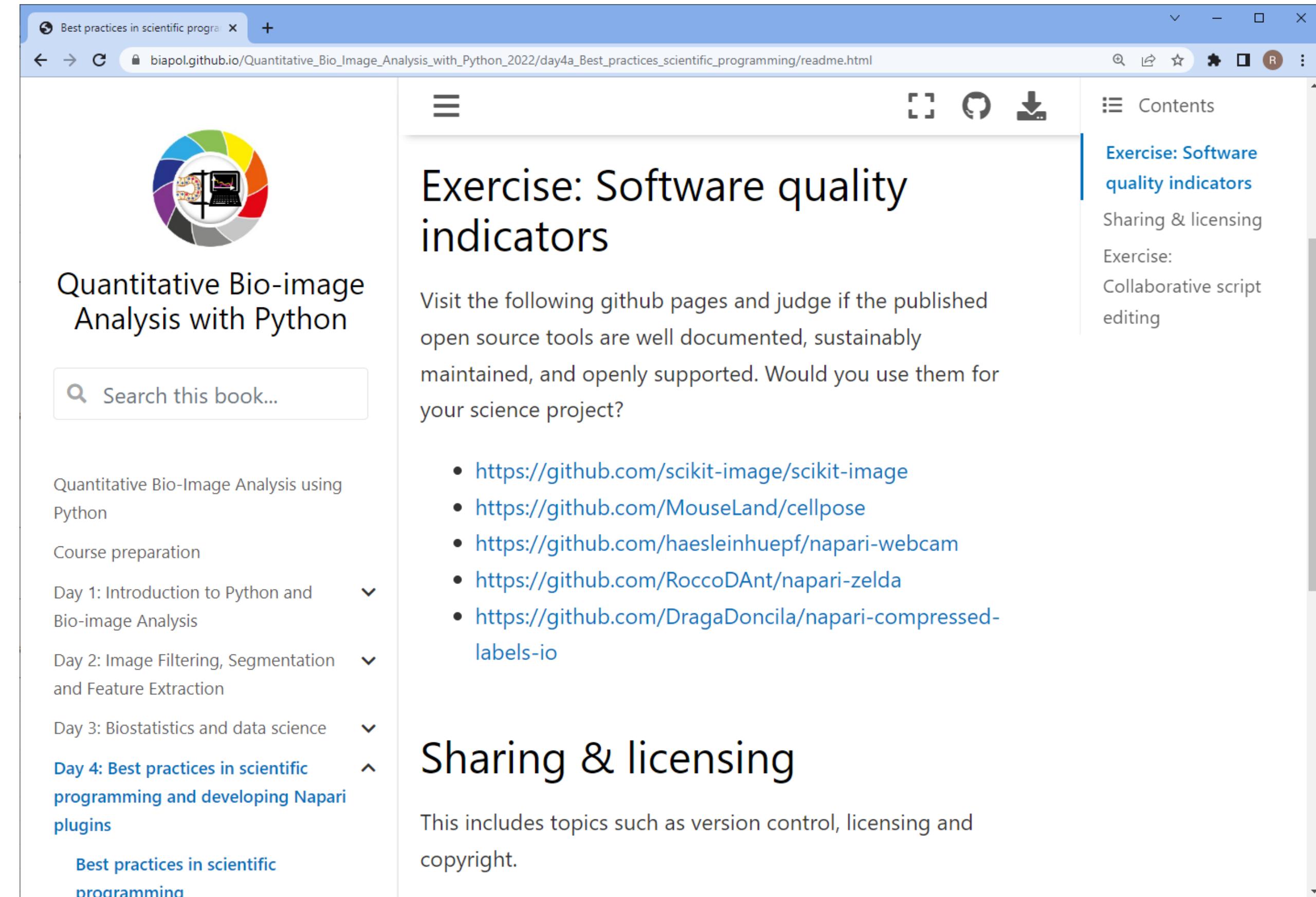
Robert Haase, Elnaz Fazeli, David Legland, Michael Doube, Siân Culley, Ilya Belevich, Eija Jokitalo, Martin Schorb, Anna Klemm, Christian Tischer

Modern research in the life sciences is unthinkable without computational methods for extracting, quantifying and visualizing information derived from biological microscopy imaging data. In the past decade, we observed a dramatic increase in available software packages for these purposes. As it is increasingly difficult to keep track of the number of available image analysis platforms, tool collections, components and emerging technologies, we provide a conservative overview of software we use in daily routine and give insights into emerging new tools. We give guidance on which aspects to consider when choosing the right platform, including aspects such as image data type, skills of the team, infrastructure and community at the institute and availability of time and budget.

<https://www.frontiersin.org/articles/10.3389/fbinf.2022.889755/full>  
<https://f1000research.com/articles/10-302>  
<https://arxiv.org/abs/2110.13951>  
<https://arxiv.org/abs/2204.07547>

# Exercise / discussion

Would you use those libraries?



Best practices in scientific programming

biapol.github.io/Quantitative\_Bio\_Image\_Analysis\_with\_Python\_2022/day4a\_Best\_practices\_scientific\_programming/readme.html

## Exercise: Software quality indicators

Visit the following github pages and judge if the published open source tools are well documented, sustainably maintained, and openly supported. Would you use them for your science project?

- <https://github.com/scikit-image/scikit-image>
- <https://github.com/MouseLand/cellpose>
- <https://github.com/haesleinhuepf/napari-webcam>
- <https://github.com/RoccoDAnt/napari-zelda>
- <https://github.com/DragaDoncila/napari-compressed-labels-io>

## Sharing & licensing

This includes topics such as version control, licensing and copyright.

Contents

- Exercise: Software quality indicators
- Sharing & licensing
- Exercise: Collaborative script editing