



DRESDEN LEIPZIG

CENTER FOR SCALABLE DATA ANALYTICS  
AND ARTIFICIAL INTELLIGENCE

# Research Data Management

## Robert Haase

GEFÖRDERT VOM



Bundesministerium  
für Bildung  
und Forschung

# Recap quiz

- We write good documentation to enabling others to do an experiment. This is good for ...

Repeatability



Reproducibility



Replicability



Reliability



# Recap quiz

- “Resolution” in microscopy imaging describes

Camera  
pixel size



Screen  
pixel size



Size of  
differentiable  
objects



Objective  
magnification



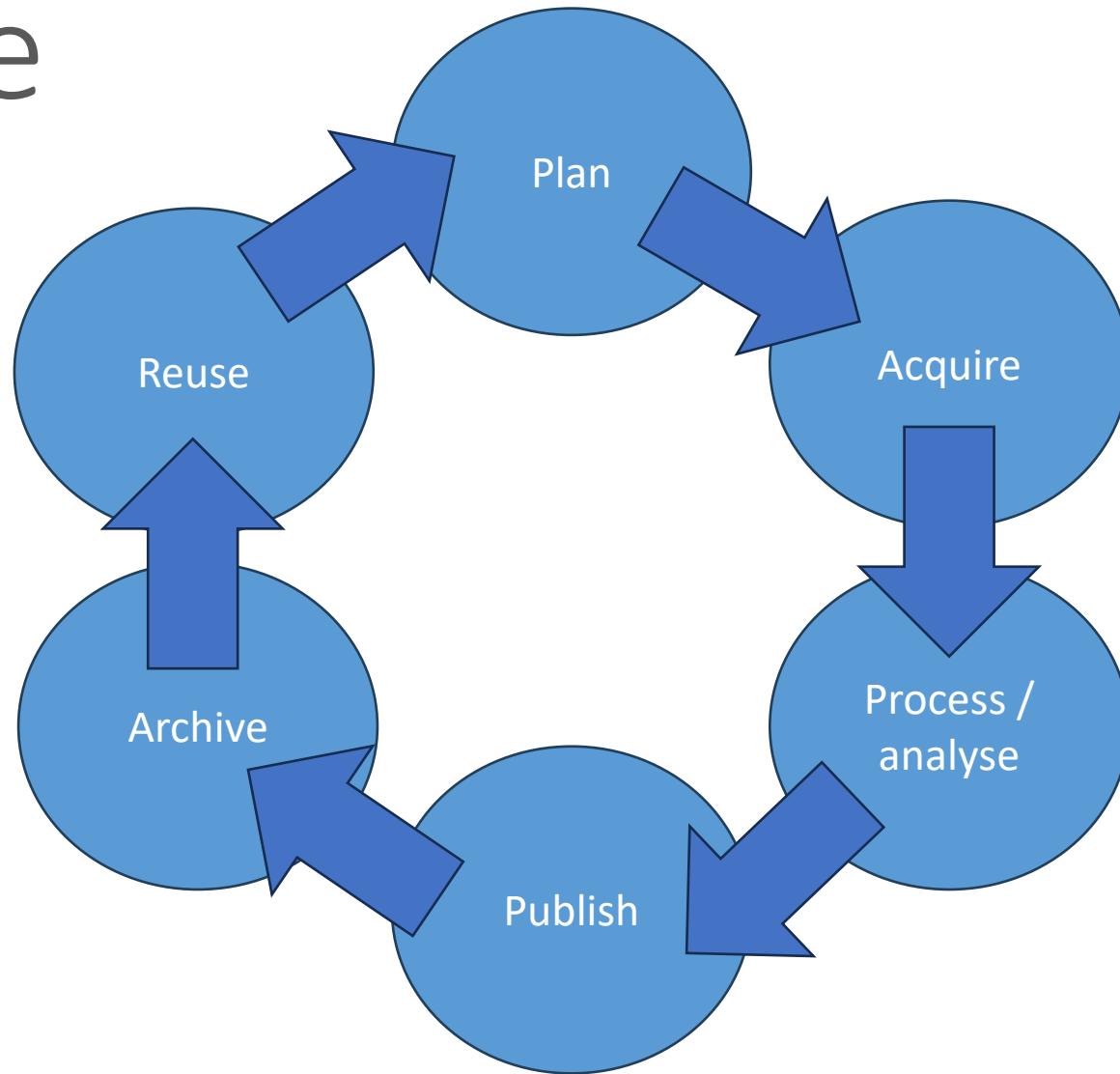
# Research Data Management (RDM)

- All activities, processes, terms, persons which have relationships with data
  - Processing
  - Storage
  - Organisation
  - Publication
  - ...
- In routine: working with data



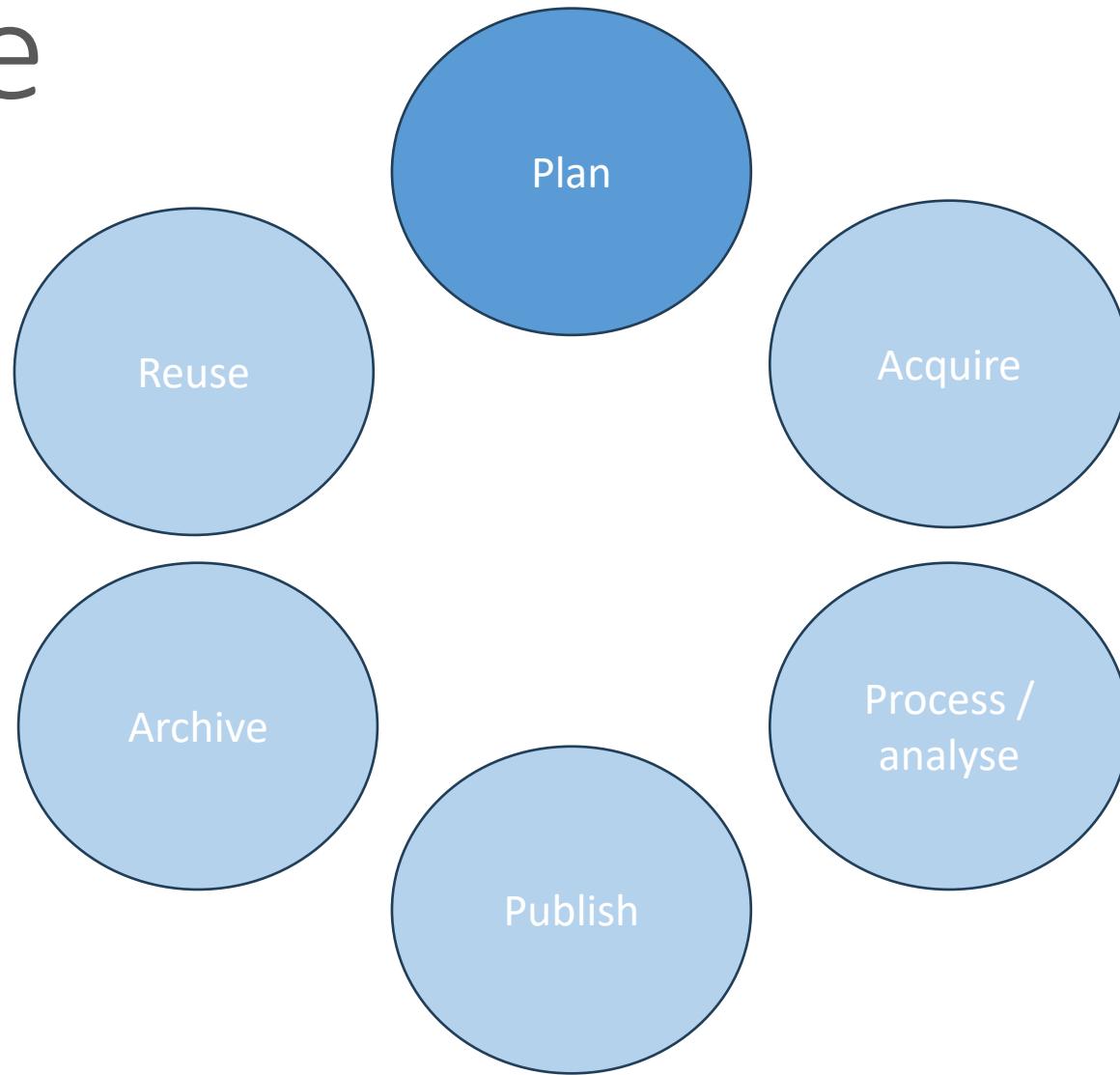
# RDM Life Cycle

- Processes are ideally cyclic



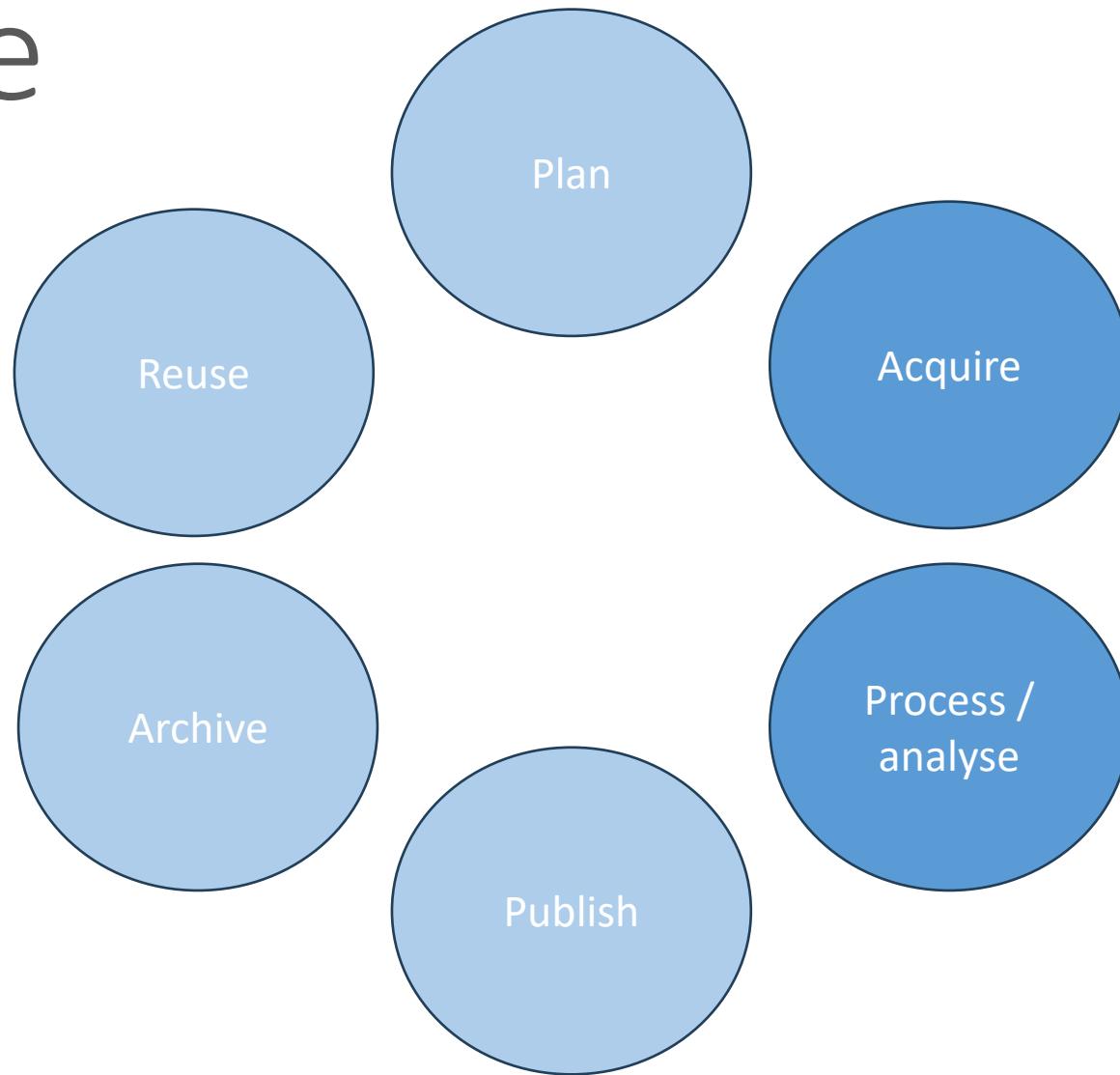
# RDM Life Cycle

- Cost
- Benefit
- Quality
- Strategic decisions



# RDM Life Cycle

- Types of data
- Terms and conditions
  - Usage rights
  - Copyright
- IT infrastructure
- Backup



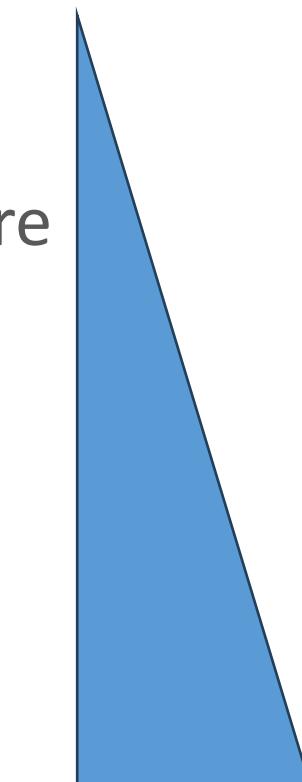
# Types of data

- Structured data
  - Tables, databases
- Unstructured data
  - Texte, emails, videos, pictures
- Semi-structured data
  - Fragebögen
  - Scientific images



# Types of data

- Openly accessible data
  - „open data“
  - „open source“ software
- Business data
- Research data
  - Hot / cold
- Personal data
- Secret data

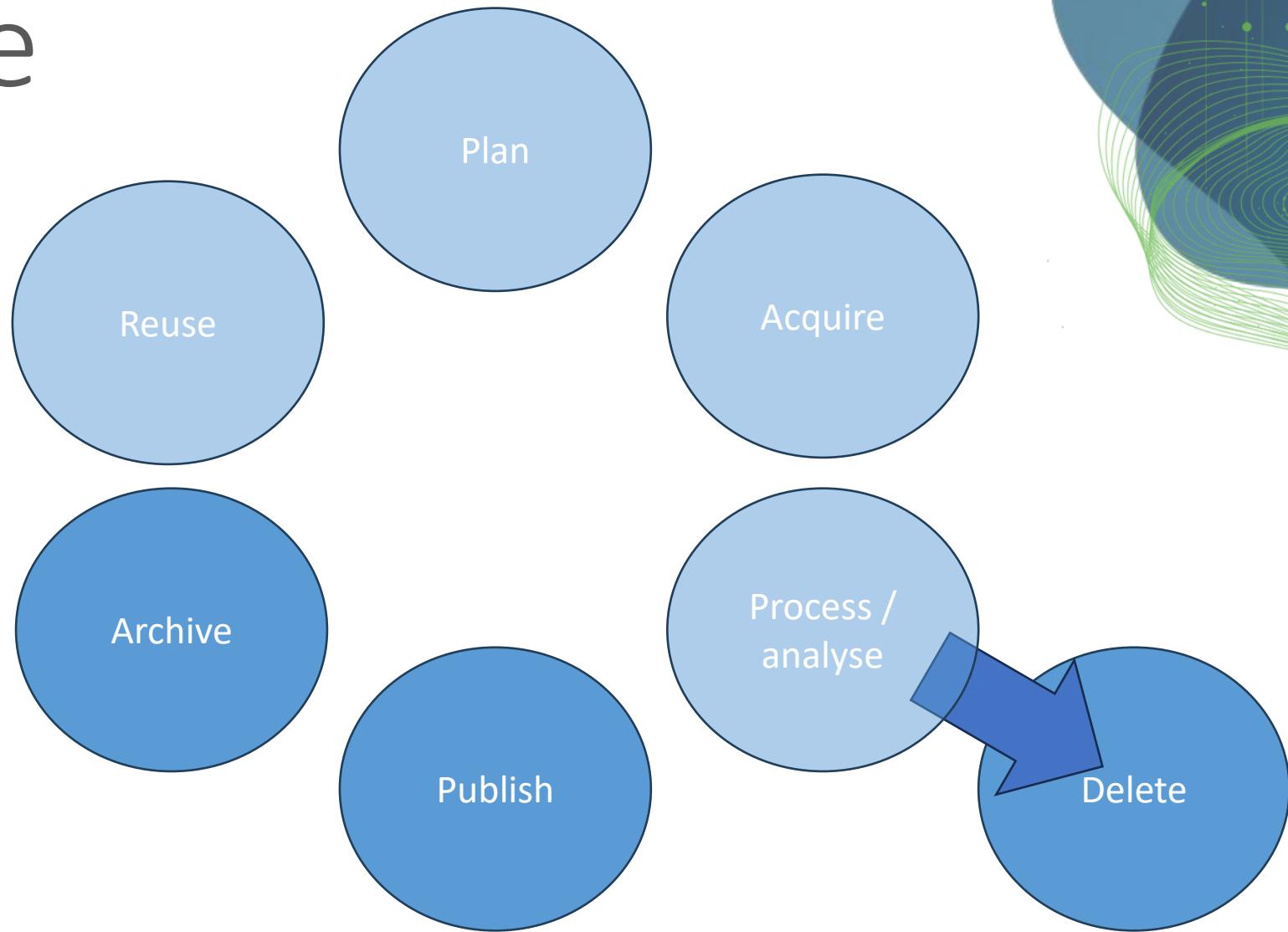


In need of  
protection  
(schutzbedürftig)



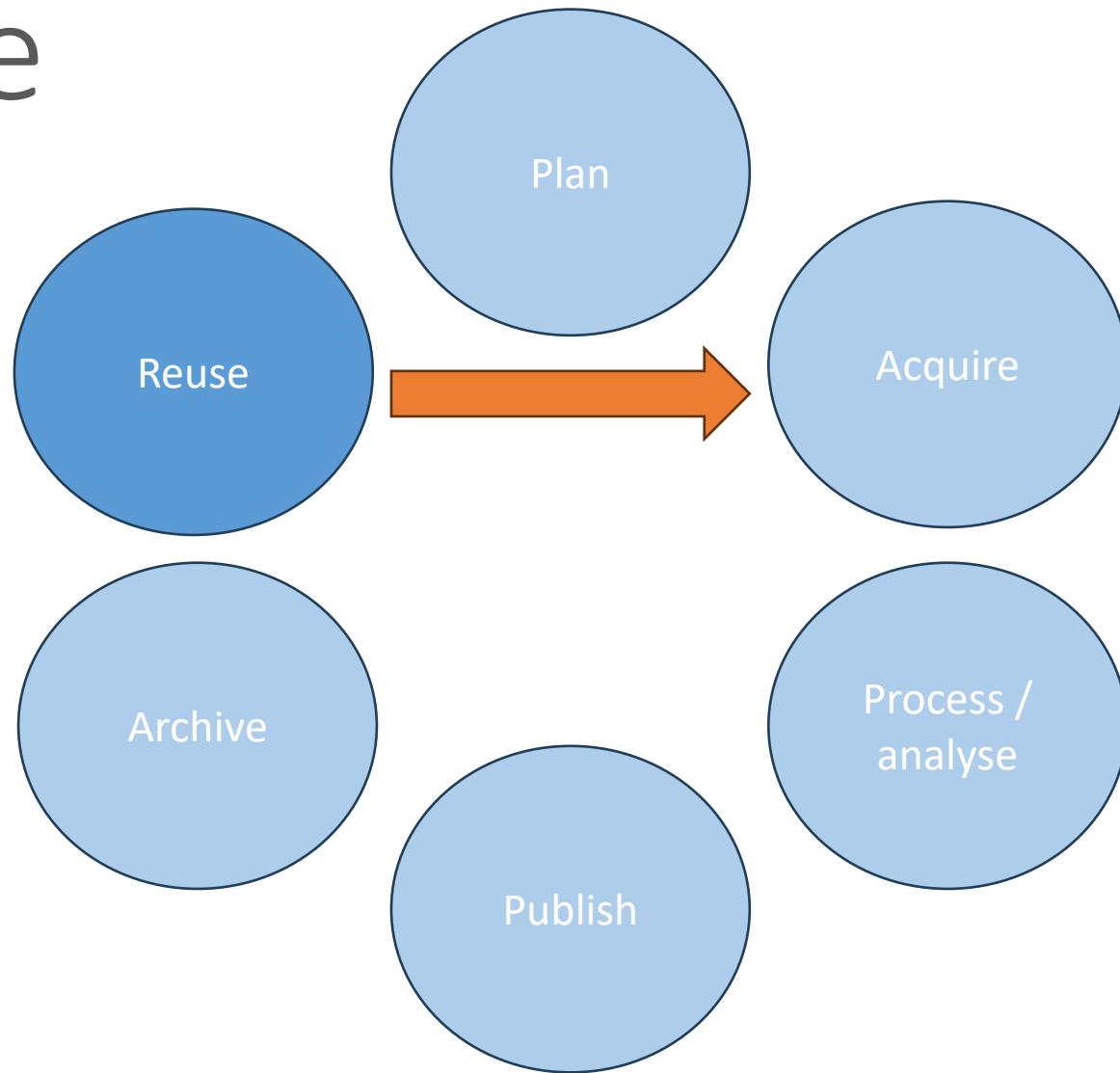
# RDM Life Cycle

- Right to publish
- Regulatory aspects
  - Research data: archive 15 years
- Authorship
- Registration (-> Findable)



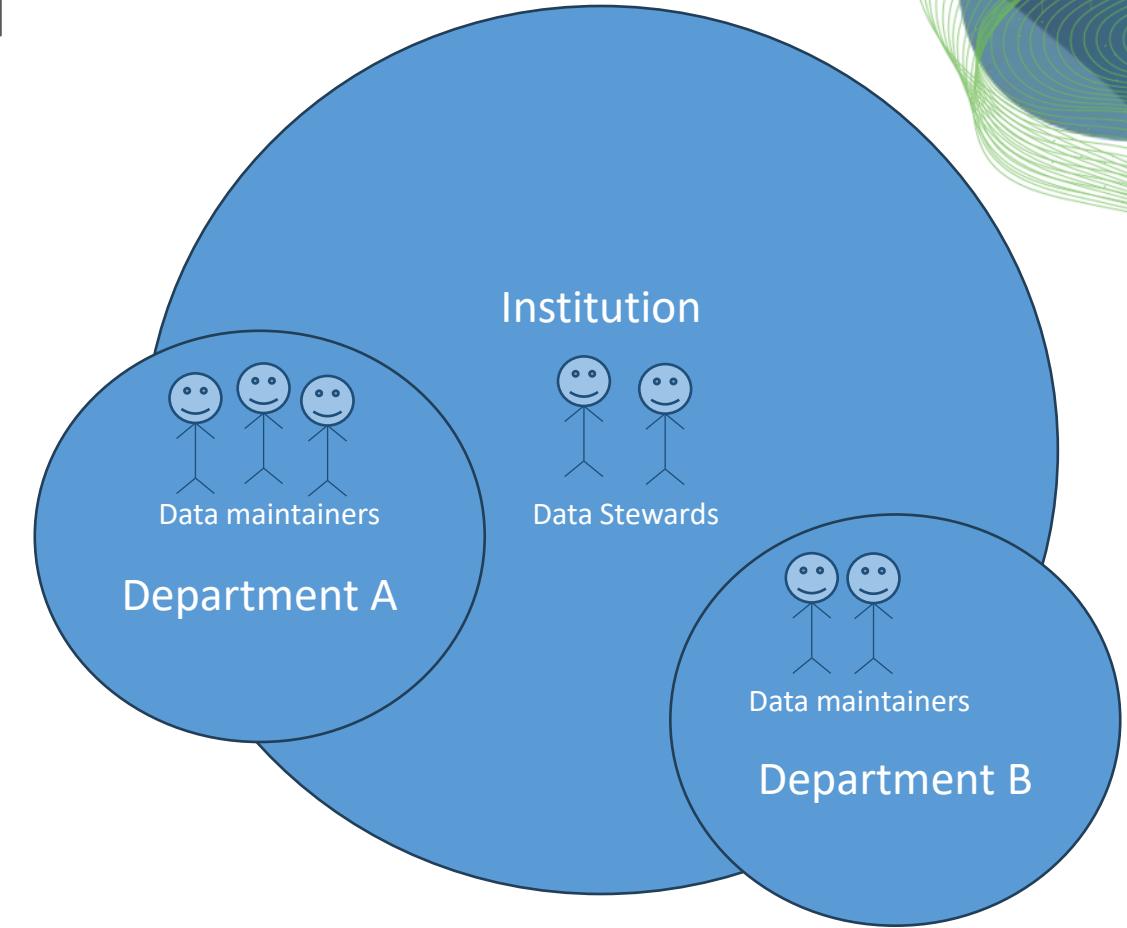
# RDM Life Cycle

- Potential future benefit
- Sustainability
- Important: **Licensing**
  - Has impact on next cycle / acquisition



# What is good RDM?

- Clearly defined responsibilities and processes (Governance)
  - Data Management Plan (DMP)
- Communication of goals, metrics, responsibilities, processes
- Dedicated personnel
  - “Data maintainers”
  - IT infrastructure maintainers
- Expert consultants
  - “Data stewards”



# • Roles != Job profiles

## Domain specialist

- Focuses on scientific question, often related to the physical world
- Requires sound insights and sustainable solutions
- Examples:
  - Biologist
  - Geologist
  - City planner

## Data analyst

- Focuses on methods for data processing / visualization
- Gains sound insights
- Examples:
  - Statistician
  - Bioinformatician
  - Data Scientist

## IT specialist

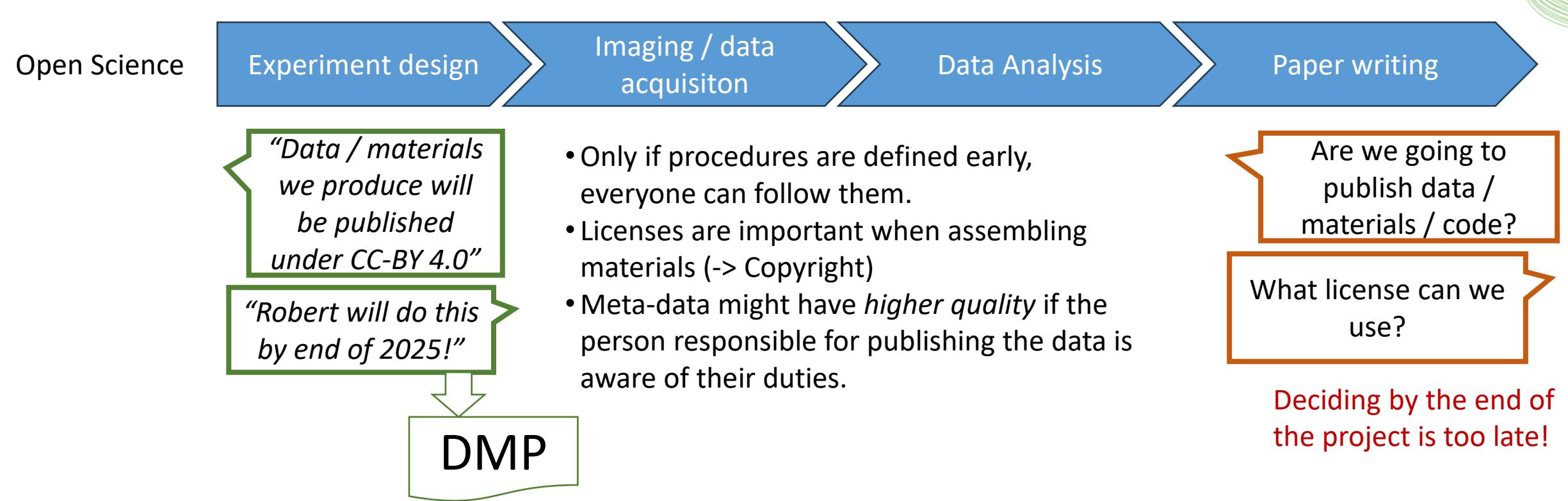
- Focuses on IT infrastructure
  - Hardware
  - Software
- Builds sustainable solutions
- Examples:
  - Computer scientist
  - IT specialist

# Data Management Plans (DMPs)

- Describes the IS-state of a data environment
  - Which data is acquired / processed?  
(content, format, amount)
  - What meta-data is collected?
  - Which quality standards are targeted?
  - How is data saved, archived, backed-up, shared, published...?
  - Who is responsible for what?
    - Roles, job-profiles
  - What does this all cost?  
(IT infrastructure + human resources)

# Data Management Plans (DMPs)

- Define responsibilities and procedures early!



# Quiz

- Regularly copying files to a remote place is ...

Archiving



Backup



# Quiz

- Data Scientists is a ...

Role



Job profile



# Quiz

- Data Steward is a ...

Role

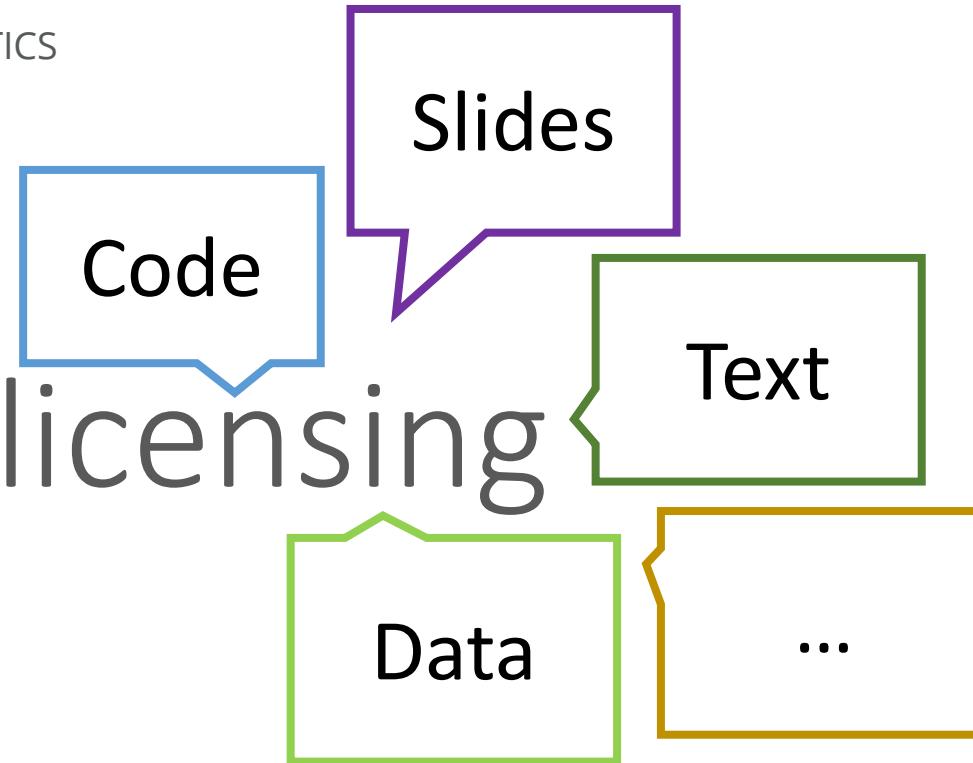


Job profile



# Sharing & licensing

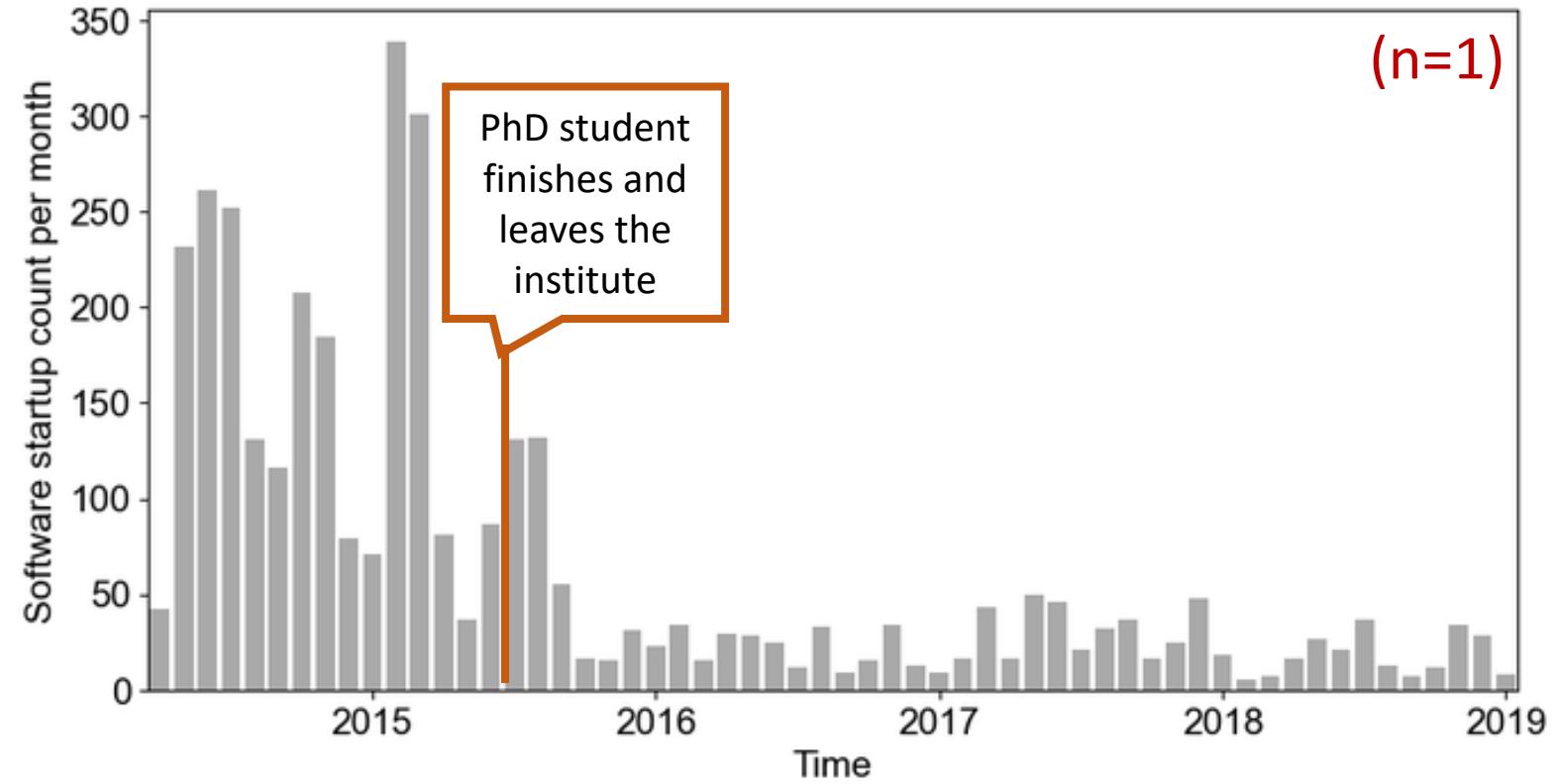
Robert Haase



Diese Maßnahme wird gefördert durch die Bundesregierung aufgrund eines Beschlusses des Deutschen Bundestages.  
Diese Maßnahme wird mitfinanziert durch Steuermittel auf der Grundlage des von den Abgeordneten des Sächsischen Landtags beschlossenen Haushaltes.

# Sustainability of my contribution to science

- What happens to research software once the PhD student leaves the institute / field?



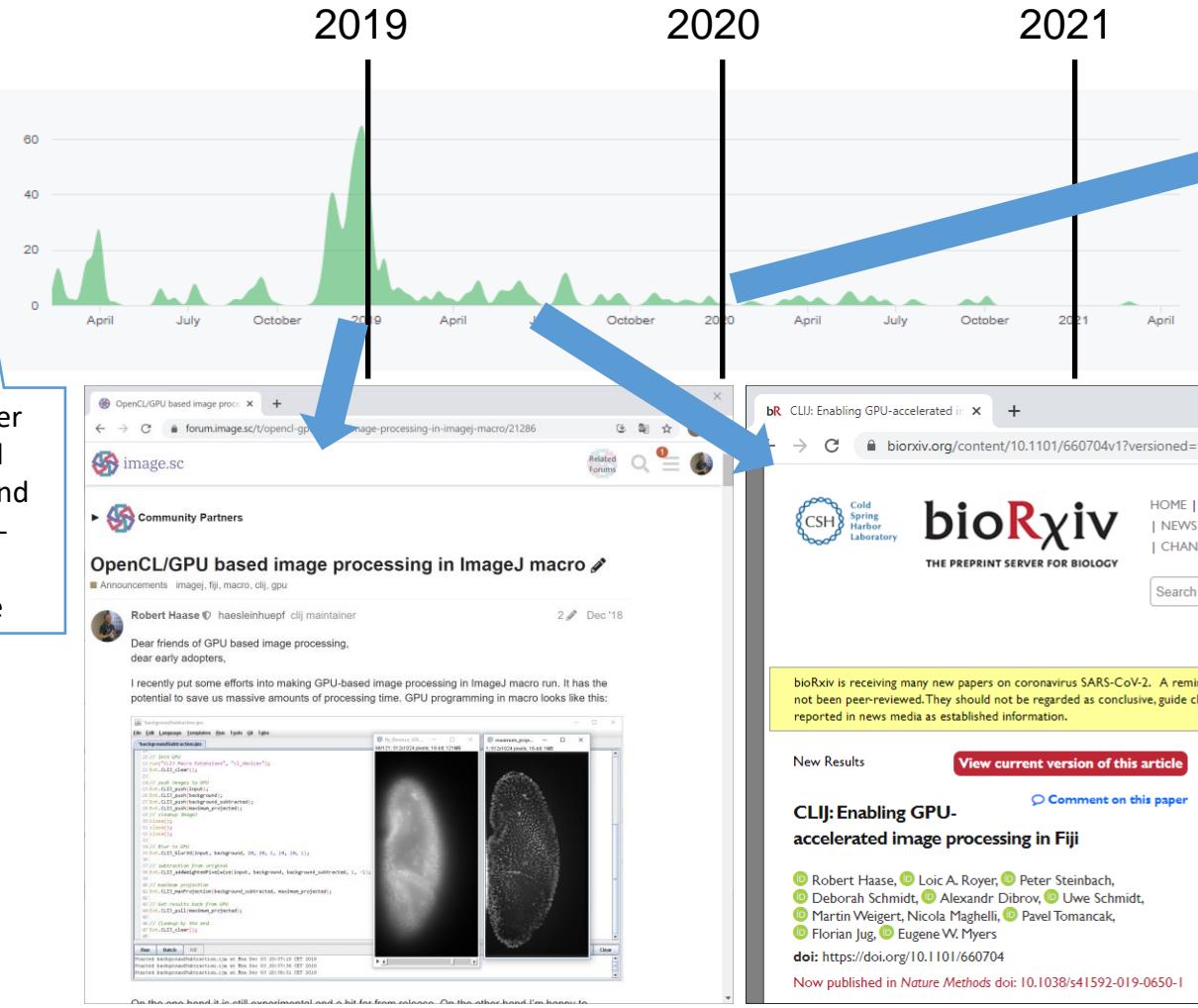
# Developing software in the open



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



Loic A. Royer  
(CZ Biohub)  
@loicaroyer



This screenshot shows the full article page for "CLIJ: GPU-accelerated image processing for everyone" published in *Nature Methods*. The page includes the journal header, author information (Robert Haase, Loic A. Royer, Peter Steinbach, Deborah Schmidt, Alexander Dibrov, Uwe Schmidt, Martin Weigert, Nicola Maghelli, Pavel Tomancak, Florian Jug, and Eugene W. Myers), the publication date (18 November 2019), and the citation details ("Nature Methods" 17, 5–6(2020) | Cite this article). A bar chart at the bottom shows citation counts for each year from 2020 to 2024, with a total of 134 citations as of March 18, 2024.

# Scientific culture

Public access to research results -> Reusability



## Guideline 13: Providing public access to research results

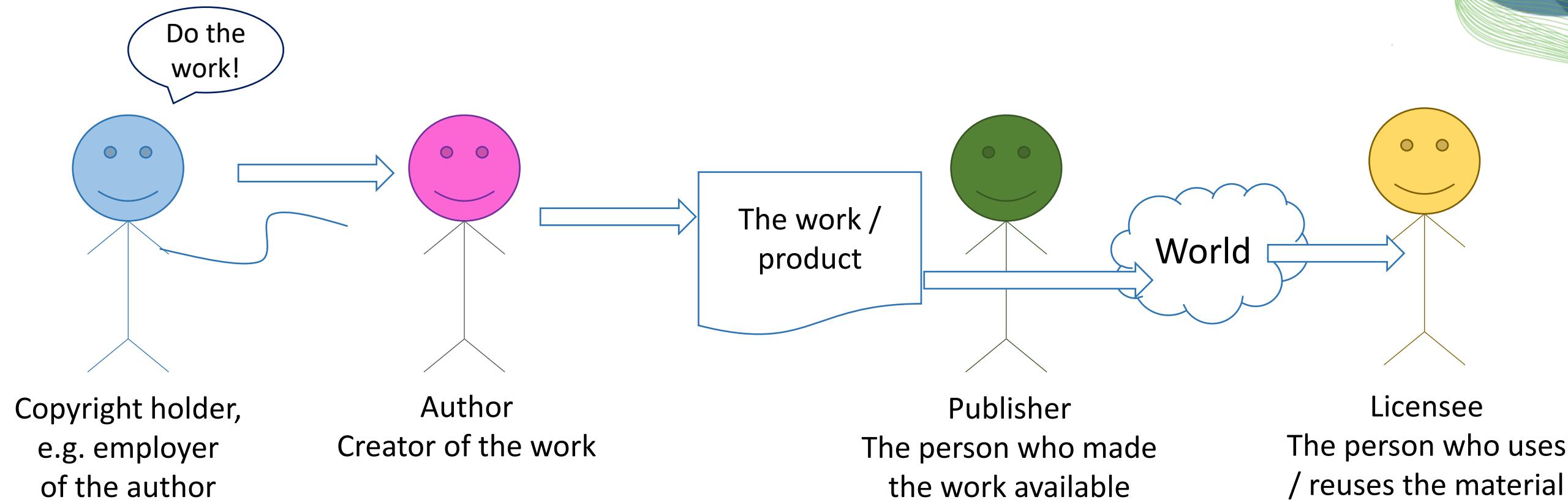
► As a rule, researchers make all results available as part of scientific/academic discourse. In specific cases, however, there may be reasons not to make results publicly available (in the narrower sense of publication, but also in a broader sense through other communication channels); this decision must not depend on third parties. Researchers decide autonomously – with due regard for the conventions of the relevant subject area – whether, how and where to disseminate their results. If it has been decided to make results available in the public domain, researchers describe them clearly and in full. Where possible and reasonable, this includes making the research data, materials and information on which the results are based, as well as the methods and software used, available and fully explaining the work processes. Software programmed by researchers themselves is made publicly available along with the source code. Researchers provide full and correct information about their own preliminary work and that of others.

### Explanations:

In the interest of transparency and to enable research to be referred to and reused by others, whenever possible researchers make the research data and principal materials on which a publication is based available in recognised archives and repositories in accordance with the FAIR principles (Findable, Accessible, Interoperable, Reusable). Restrictions may apply to public availability in the case of patent applications. If self-developed

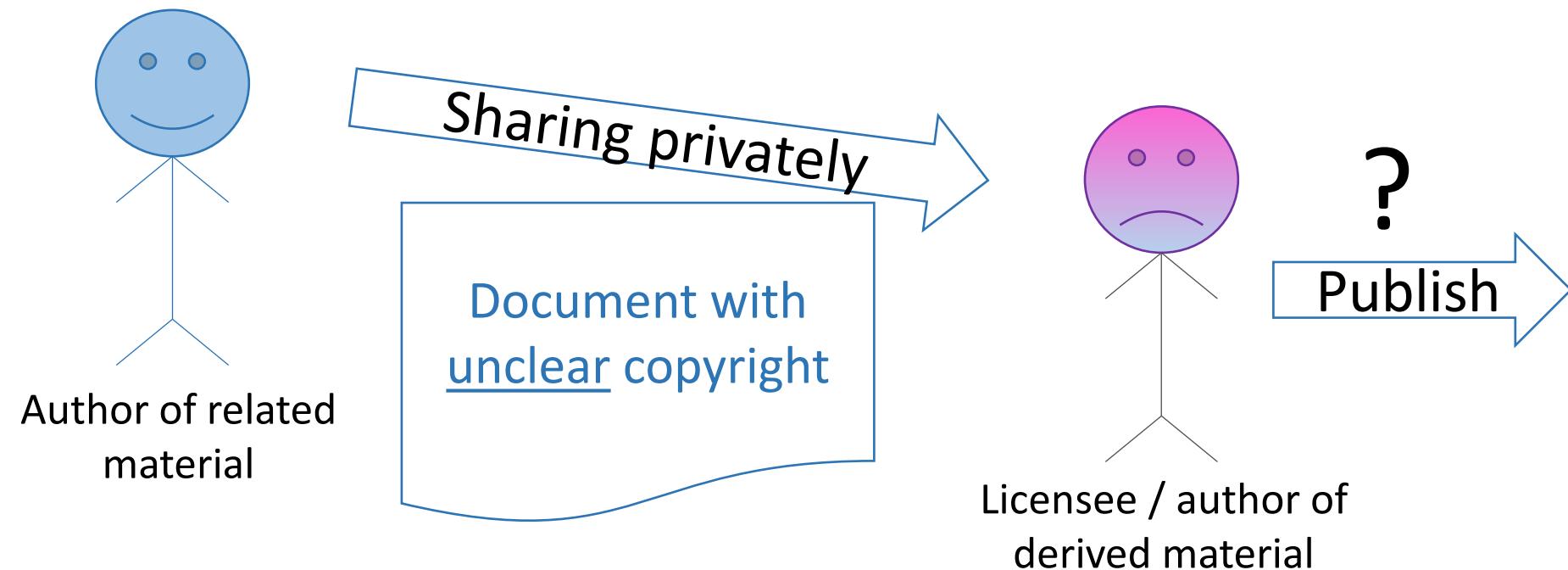
# Am I allowed to publish my stuff?

- ... it depends... on who is responsible



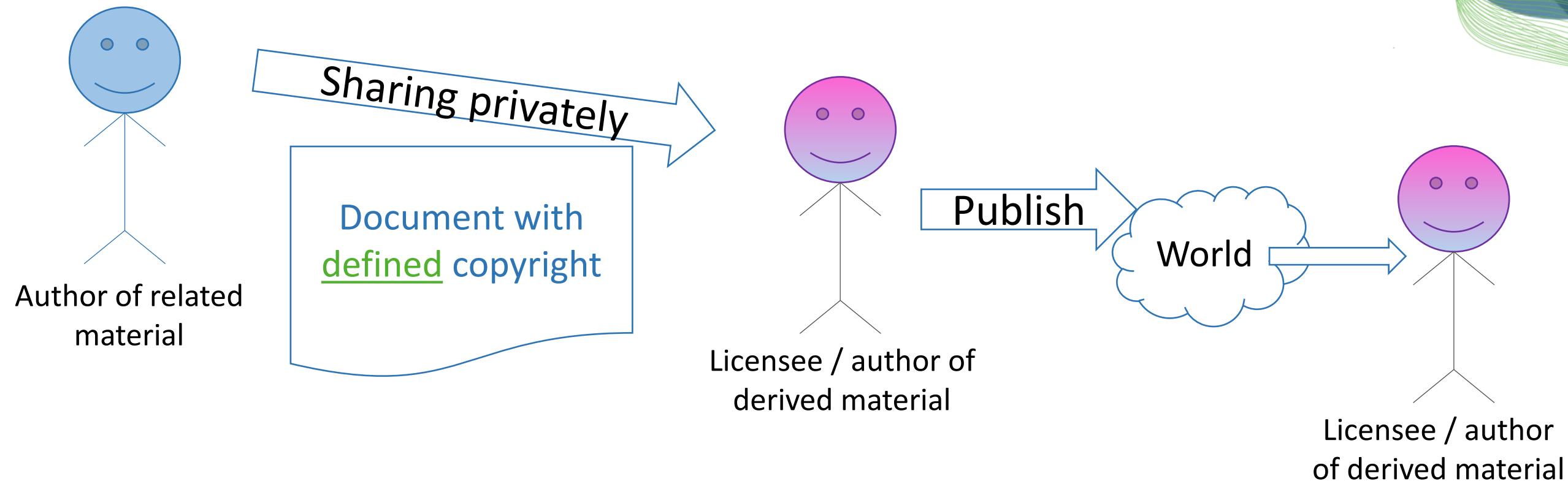
# Am I allowed to publish my stuff?

- ... it depends... on what materials served as basis



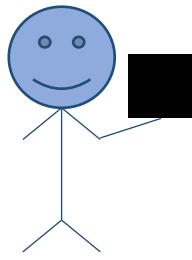
# Am I allowed to publish my stuff?

- ... it depends... on what materials served as basis



# Openness of software / projects

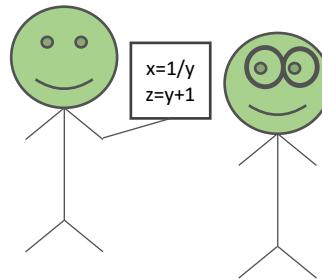
## Closed source



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

Hardware device drivers

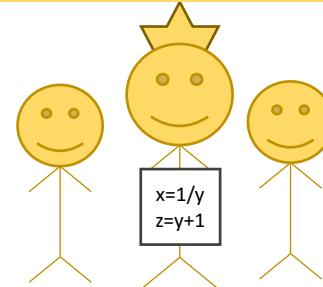
## Open source



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

Custom image analysis scripts

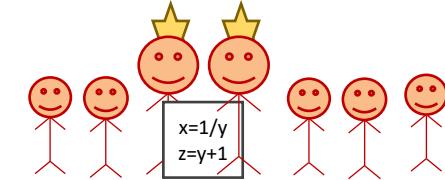
## Benevolent dictatorship



- Open to contributions
- Single maintainer, often overwhelmed
- Efficient decision making
- Bus factor ≈1

TrackMate, SNT, MorpholibJ, CLIJ

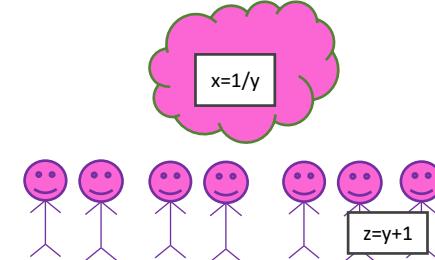
## Community driven



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

scikit-image, scipy, OpenCL

## Openly extensible



- Openly extensible; without maintainers involved
- Partially community driven

ImageJ, Python, numpy

# Quiz

- What is the role of Github in the context of publishing open-source code?

Copyright holder



Author



Publisher



Licensee



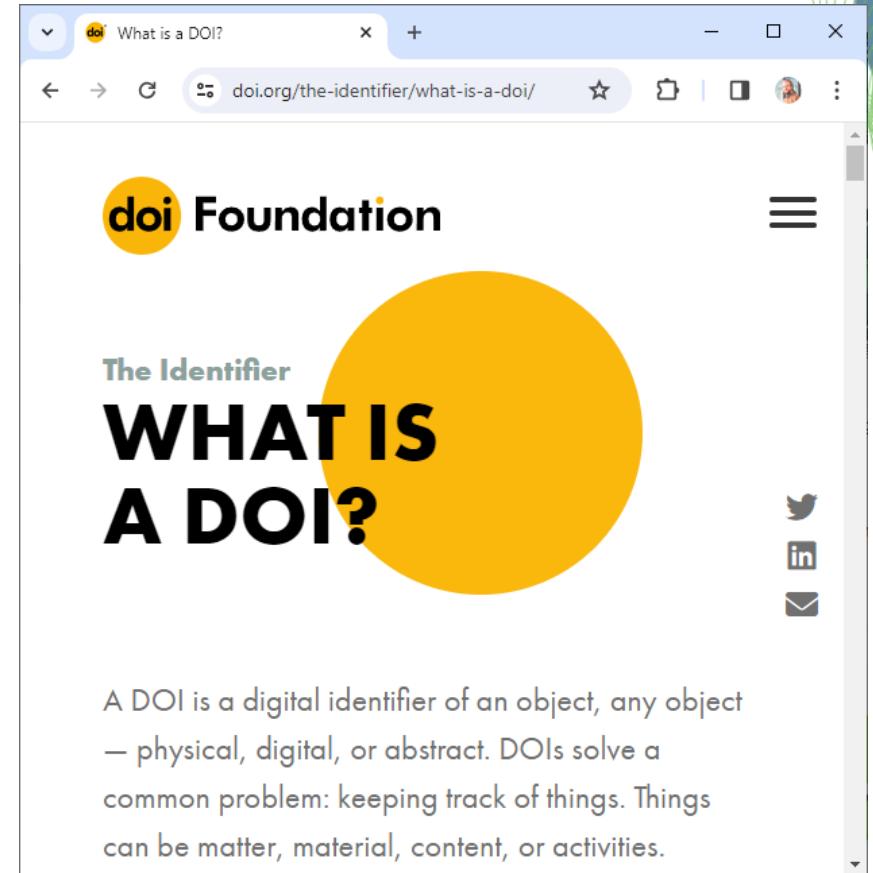
# Standard for sharing: The FAIR-principles

- Findable
- Accessible
- Interoperable
- Reusable



# The FAIR-principles

- Findable
- F1. (Meta)data are assigned a globally unique and persistent identifier
  - Universal Resource Identifier (URI)
  - Digital Object Identifier (DOI)
- F2. Data are described with rich metadata (defined by R1 below)
- F3. Metadata clearly and explicitly include the identifier of the data they describe
- F4. (Meta)data are registered or indexed in a searchable resource



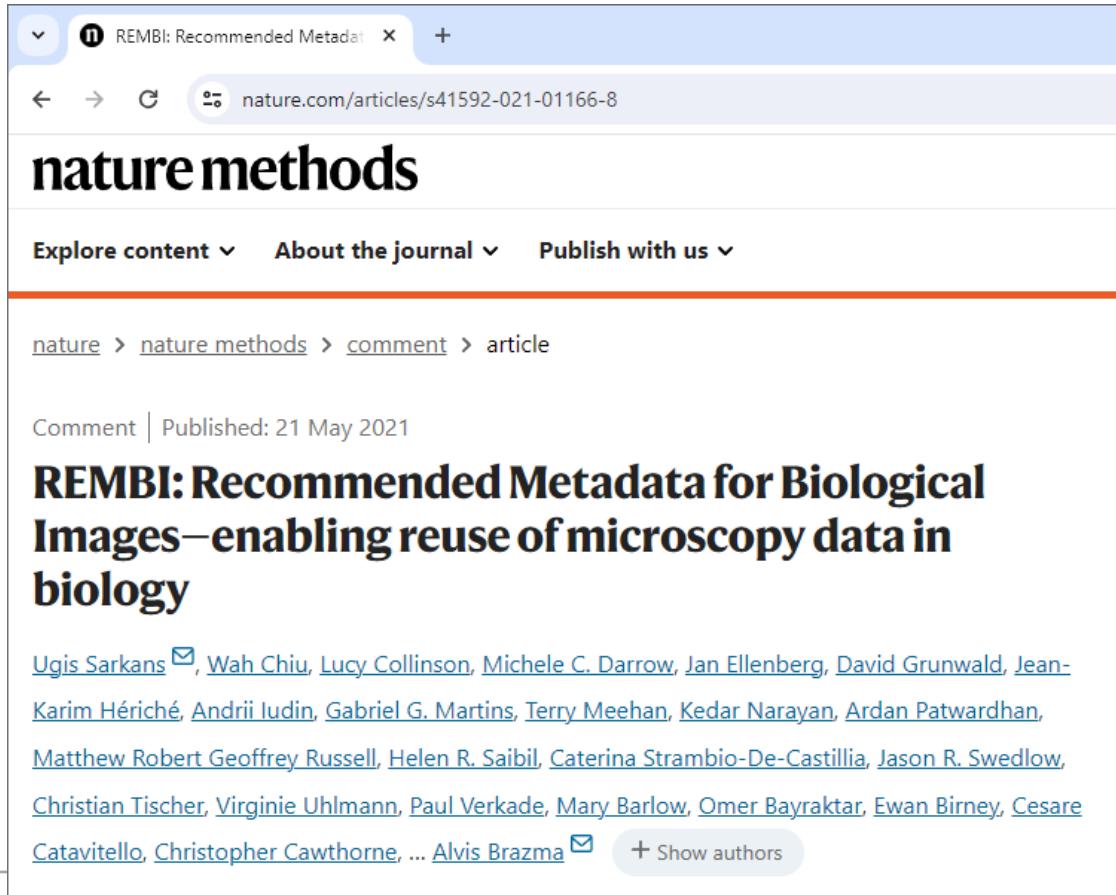
# Meta data

- Generic
  - Author
  - Usage license
  - Creation date
- Field-specific (microscopy)
  - Exposure time
  - Wavelength (colour)
  - Microscope type/vendor

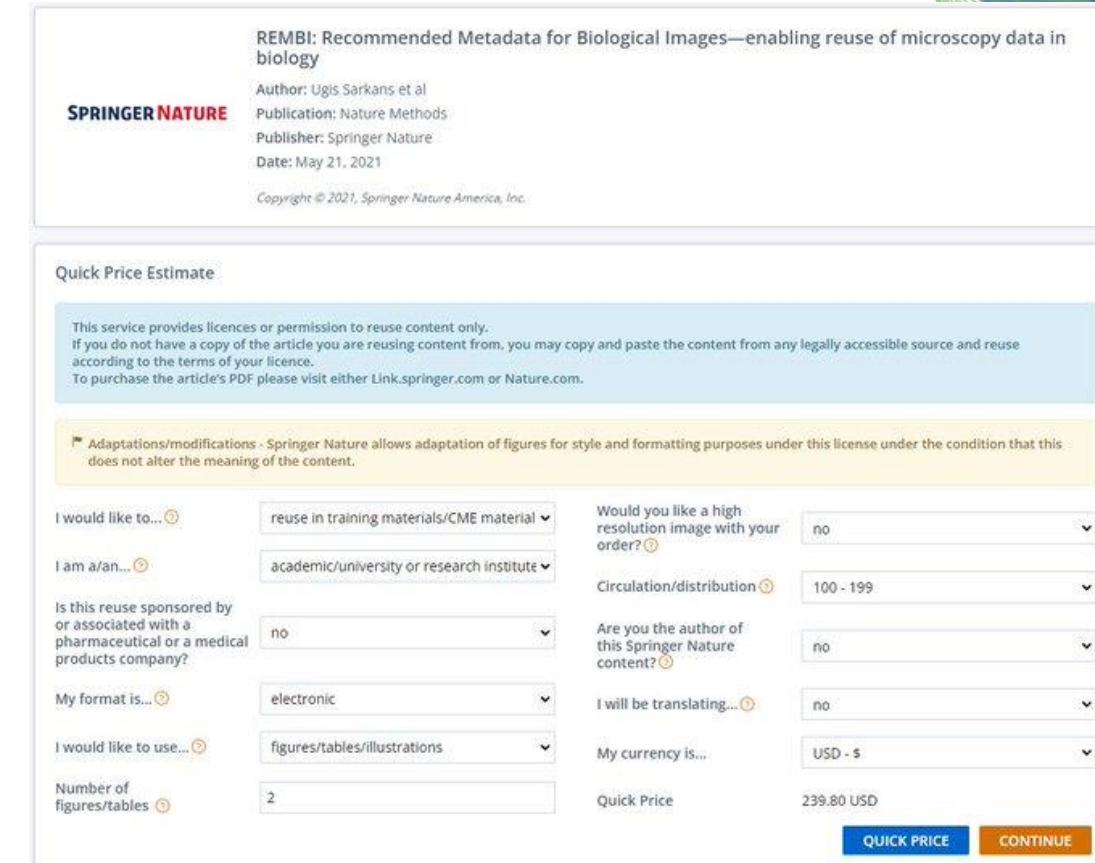
Goals:  
FAIR+  
Reproducibility

# REMBI: Recommended Metadata for Biological Images—enabling reuse of microscopy data in biology

- Read more:



A screenshot of a web browser showing the REMBI article on nature.com. The title "REMBI: Recommended Metadata for Biological Images—enabling reuse of microscopy data in biology" is displayed prominently. Below the title, a list of authors is provided, including Ugis Sarkans, Wah Chiu, Lucy Collinson, Michele C. Darrow, Jan Ellenberg, David Grunwald, Jean-Karim Hériché, Andrii Iudin, Gabriel G. Martins, Terry Meehan, Kedar Narayan, Ardan Patwardhan, Matthew Robert Geoffrey Russell, Helen R. Saibil, Caterina Strambio-De-Castillia, Jason R. Swedlow, Christian Tischer, Virginie Uhlmann, Paul Verkade, Mary Barlow, Omer Bayraktar, Ewan Birney, Cesare Catavitello, Christopher Cawthorne, and Alvis Brazma. A "Show authors" button is visible at the bottom right of the author list.



A screenshot of the REMBI article page on Springer Nature's website. The title "REMBI: Recommended Metadata for Biological Images—enabling reuse of microscopy data in biology" is shown. Below the title, the Springer Nature logo is present. To the right, there is a "Quick Price Estimate" section with fields for reuse type, organization, and other details. At the bottom right, there are "QUICK PRICE" and "CONTINUE" buttons.

# Digital Object Identifiers (DOI)

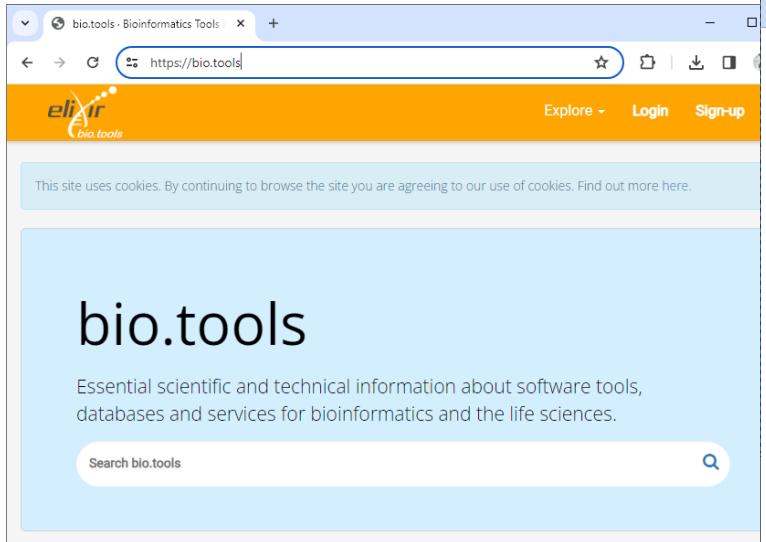
- DOIs / URIs always point at the same data
- DOIs are centrally registers, URIs not
- Unified Resource Locators (URLs) may point at different things

The screenshot shows a web browser window for the 'Straßennetz, Stadt Leipzig' dataset on the [opendata.leipzig.de](https://opendata.leipzig.de/dataset/strassennetz-stadt-leipzig) website. The page includes:

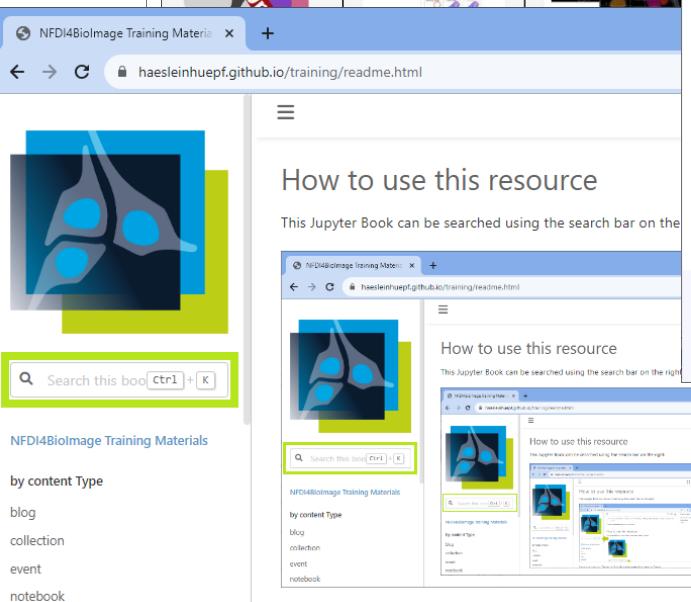
- A header with the city logo and navigation links: Datensätze, Organisationen, Kategorien, Anwendungen, Über uns, Nutzung, Hackathons.
- A breadcrumb trail: / Organisationen / Verkehrs- und Tiefbauamt / Straßennetz, Stadt Leipzig.
- A sidebar with sections for 'Verkehrs- und Tiefbauamt' and 'Sozial' (Twitter, Facebook).
- A main content area for 'Straßennetz, Stadt Leipzig' with a detailed description of the dataset.
- A section for 'Daten und Ressourcen' listing download links for CSV, GeoJSON, GeoPackage, and WFS formats.
- A table titled 'Zusätzliche Informationen' with columns 'Feld' and 'Wert'.
- A timeline table with columns 'Gemeindenname' and 'Leipzig, Stadt' (with a date of 2021-08-20), 'Ausgestellt' (with a date of 2021-08-20), and 'Aktualisiert' (with a date of 2024-01-17).
- A blue callout box pointing to the timeline table with the text: "This no DOI, no URI, it's a URL".

# Indexing

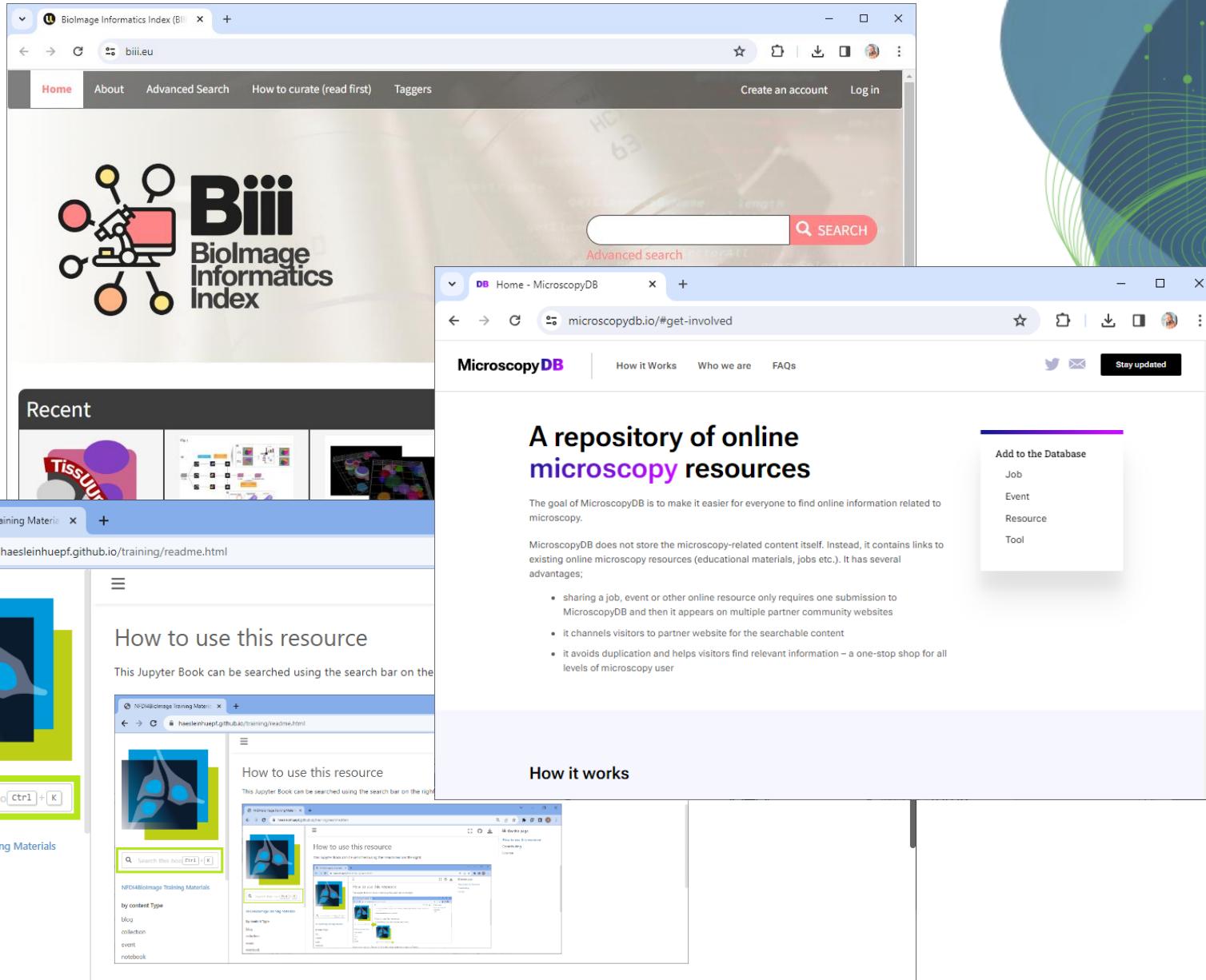
- Make sure your materials are listed in public search indices
- Do not trust google to make your stuff findable



The bio.tools homepage features the Elixir bio.tools logo at the top. Below it is a search bar and a large "bio.tools" title. A sub-header states: "Essential scientific and technical information about software tools, databases and services for bioinformatics and the life sciences." A sidebar on the right contains a search bar and a "by content Type" section with links for blog, collection, event, and notebook.



A screenshot of a Jupyter Book titled "NFDI4BioImage Training Materials". It shows a thumbnail of a brain image, a search bar with the placeholder "Search this book [ctrl + K]", and a sidebar with a "How to use this resource" section and a "by content Type" section with links for blog, collection, event, and notebook.

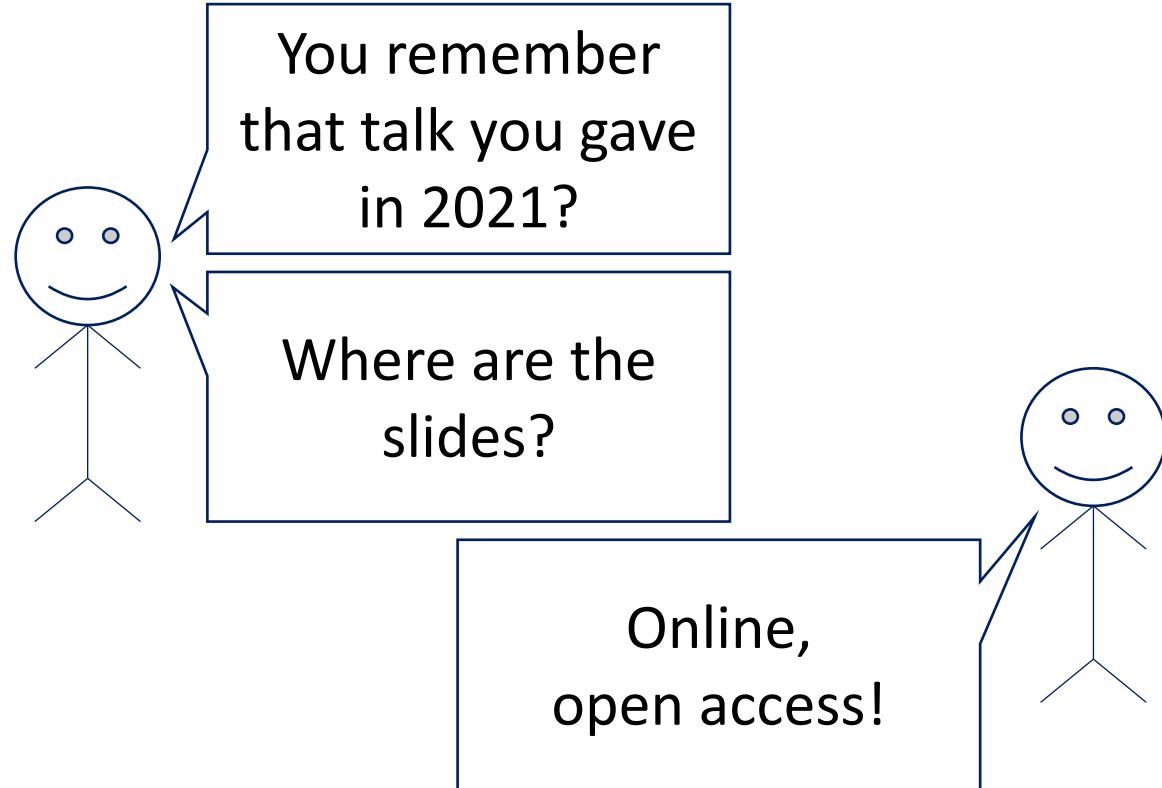


Three screenshots illustrating indexing and discoverability:

- BiiI (Biolimage Informatics Index):** Shows the BiiI logo and a search bar. The "Recent" section displays thumbnails for "Tissue" and other resources.
- MicroscopyDB:** Shows the MicroscopyDB homepage with a search bar and a "How it works" section. It highlights that MicroscopyDB is a repository of online microscopy resources.
- NFDI4BioImage Training Materials:** Shows a screenshot of the training materials page, demonstrating how the content can be indexed and searched across multiple platforms.

# Incentives: Findability

- Your *future-self* will thank you, because they will find your work



Sharing and licensing material | f1000research.com/slides/10-519

**f1000Research**

BROWSE GATEWAYS & COLLECTIONS HOW TO PUBLISH ABOUT BLOG MY RESEARCH SIGN IN

Home > Browse > Sharing and licensing material

NOT PEER REVIEWED

VIEW FULL SCREEN

DOWNLOAD 30.92 MB

SHARE CITE

PART OF THE GATEWAY

neubias - the Bioimage Analysts Network

BROWSE BY RELATED SUBJECTS

Artificial intelligence

Computer and information sciences

Electrical engineering

Sharing and licensing material  
Robert Haase  
June 30<sup>th</sup> 2021

Code Slides Text Data ...

This material is licensed by Robert Haase, PoL Dresden under the CC-BY 4.0 license <https://creativecommons.org/licenses/by/4.0/>

TECHNISCHE UNIVERSITÄT DRESDEN

# Incentives: Findability -> Visibility

- YouTube
- Github

Open & FAIR sharing  
is a PR instrument

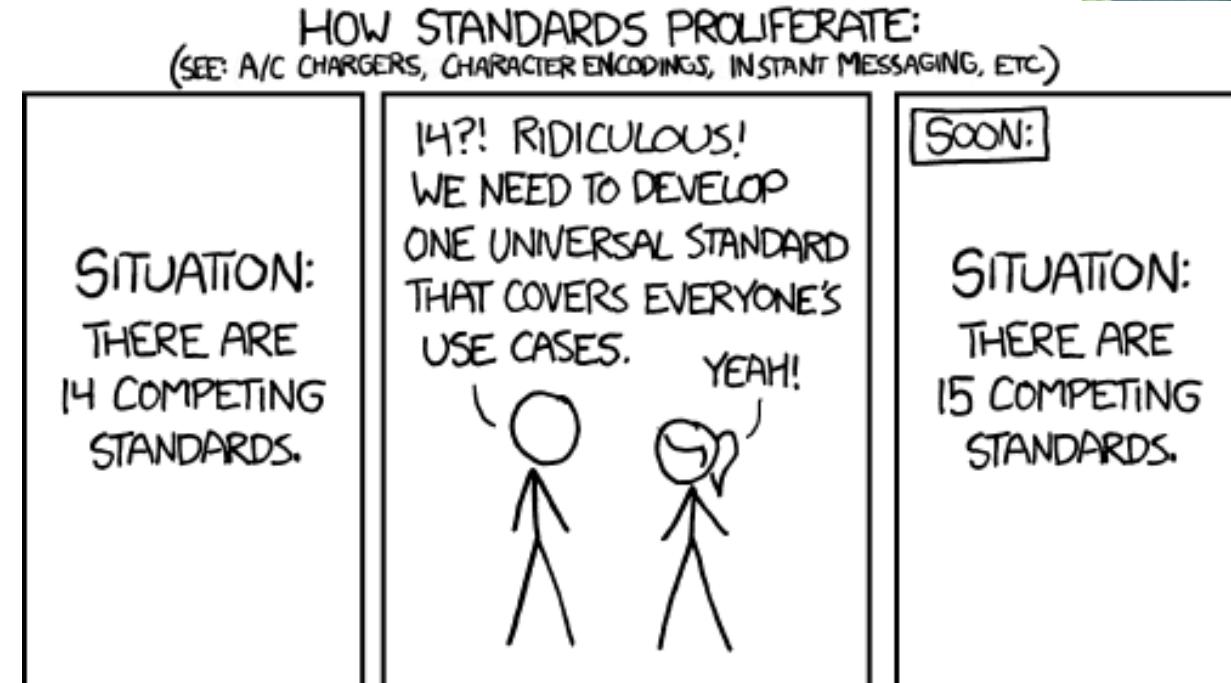
... leading to

- more software users
- new collaborations

The image displays three browser windows side-by-side. The left window shows the YouTube channel 'ScaaS-AI Living Lab' with several playlists listed under 'Created playlists'. The middle window shows the GitHub page for the 'Prompt Engineering Tutorial'. The right window shows a Jupyter Notebook titled '04\_generating\_images.ipynb' with Python code and generated images.

# The FAIR-principles

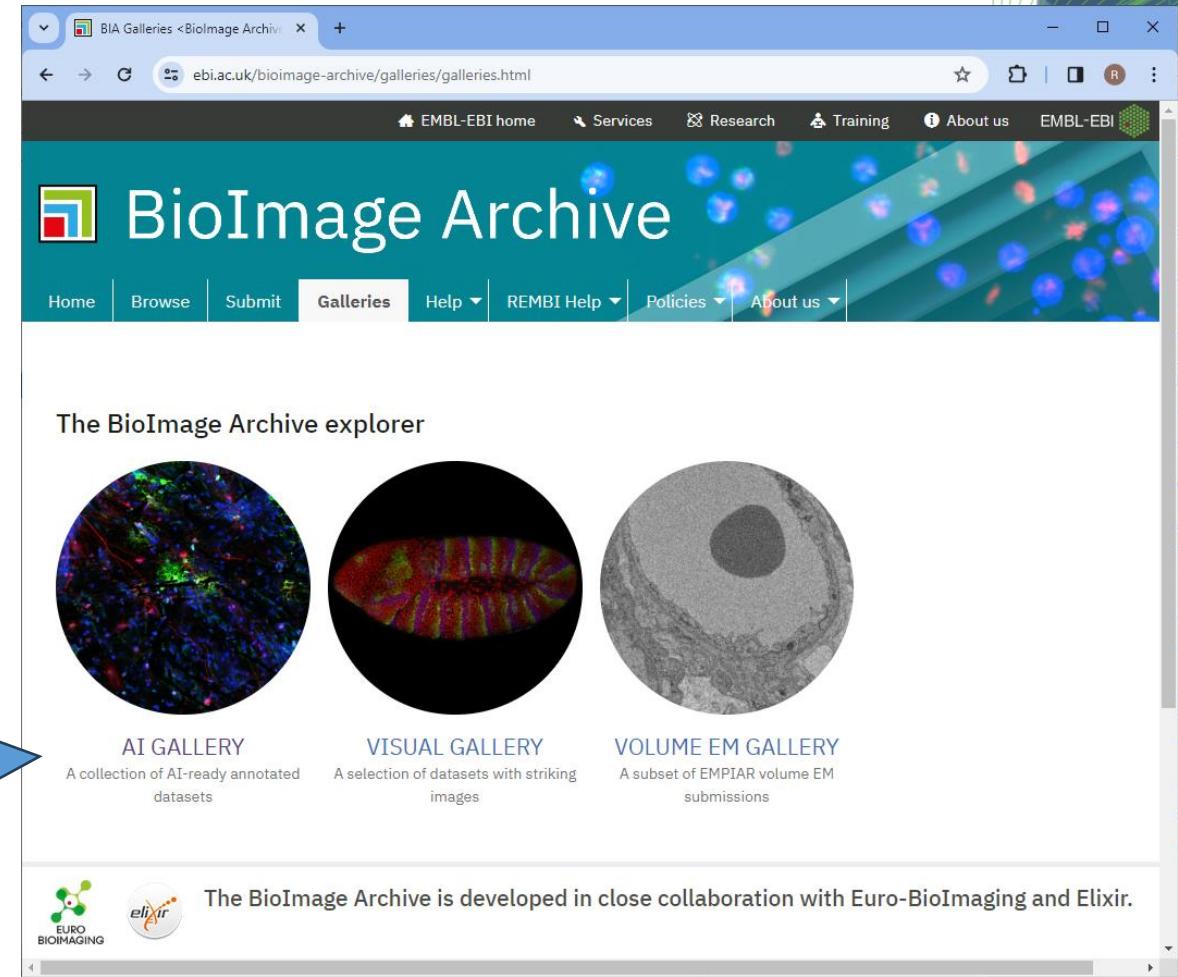
- Accessible
- A1. (Meta)data are retrievable by their identifier using a standardised communications protocol
  - A1.1 The protocol is open, free, and universally implementable
  - A1.2 The protocol allows for an authentication and authorisation procedure, where necessary
- A2. Metadata are accessible, even when the data are no longer available



# Accessibility

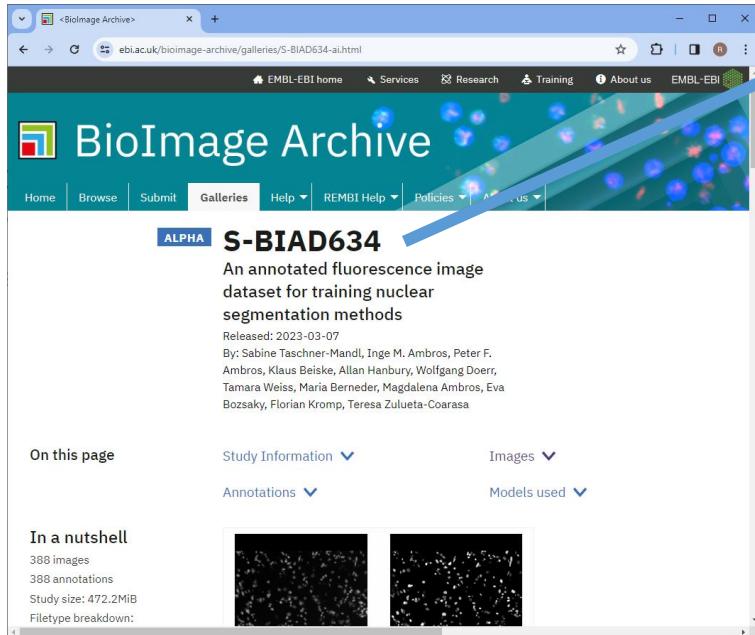
- The ability to download data, for humans and computers

Essential for AI  
developers =-)



# Accessibility

- The ability to download data, for humans and computers



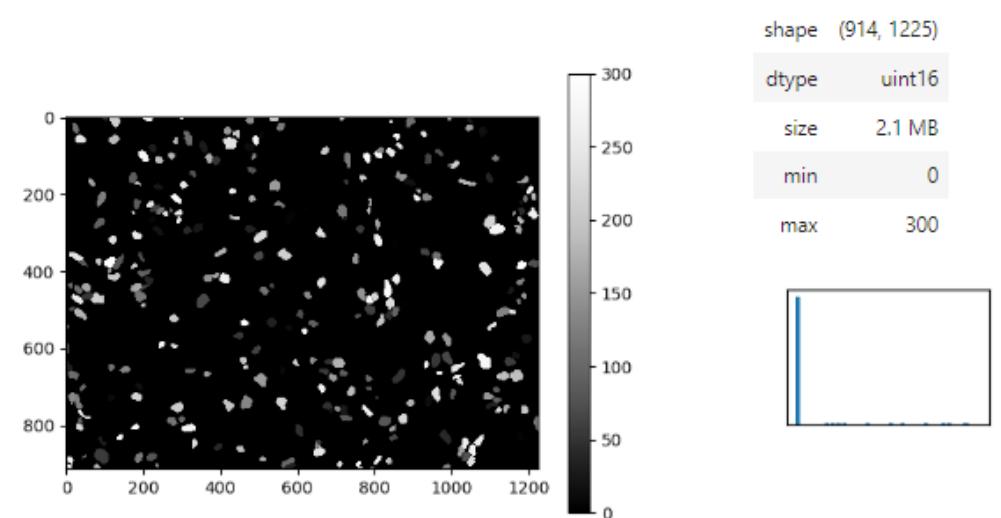
```
[1]: from bia_explorer import io, biostudies
from skimage.io import imread
import stackview

accession = 'S-BIAD634'
study = io.download_bia_study(accession)
image = study.images[0]
```

## Displaying images using stackview

```
[2]: uri = image.uri.replace("\\\\", "/")
image_data = imread(uri)
stackview.insight(image_data)
```

[2]:



# Restricted Access

- The A in FAIR does not necessarily stand for Open Access

The image shows two side-by-side screenshots of the Zenodo dataset page for the file "blobs.tif".

**Left Screenshot:** The dataset is labeled as "Restricted". A large blue arrow points from the word "Restricted" to the "Show affiliations" button. The "Files" section is highlighted with a pink background, indicating restricted access.

**Right Screenshot:** The dataset is also labeled as "Restricted". The "Edit" and "New version" buttons are visible in the top right. The "Files" section is also highlighted with a pink background, indicating restricted access.

**Common Elements:** Both screenshots show the dataset was published on March 18, 2024, with 0 views and 0 downloads. The "Versions" section shows Version v1 (10.5281/zenodo.10829230) from Mar 18, 2024. The "Cite all versions?" link is present. The "External resources" section lists "Indexed in" OpenAIRE. The URL in the address bar is <https://zenodo.org/records/10829230>.

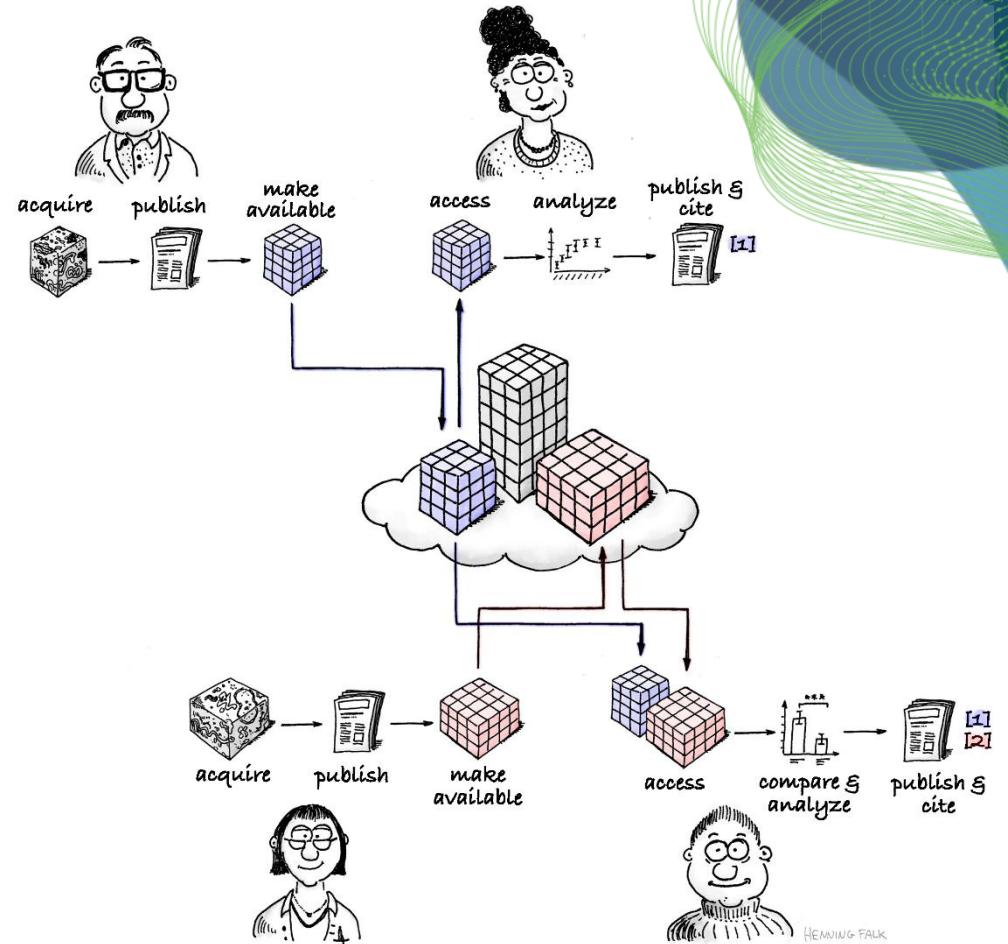
# The FAIR-principles

- Interoperable
  - I1. (Meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
  - I2. (Meta)data use vocabularies that follow FAIR principles
  - I3. (Meta)data include qualified references to other (meta)data



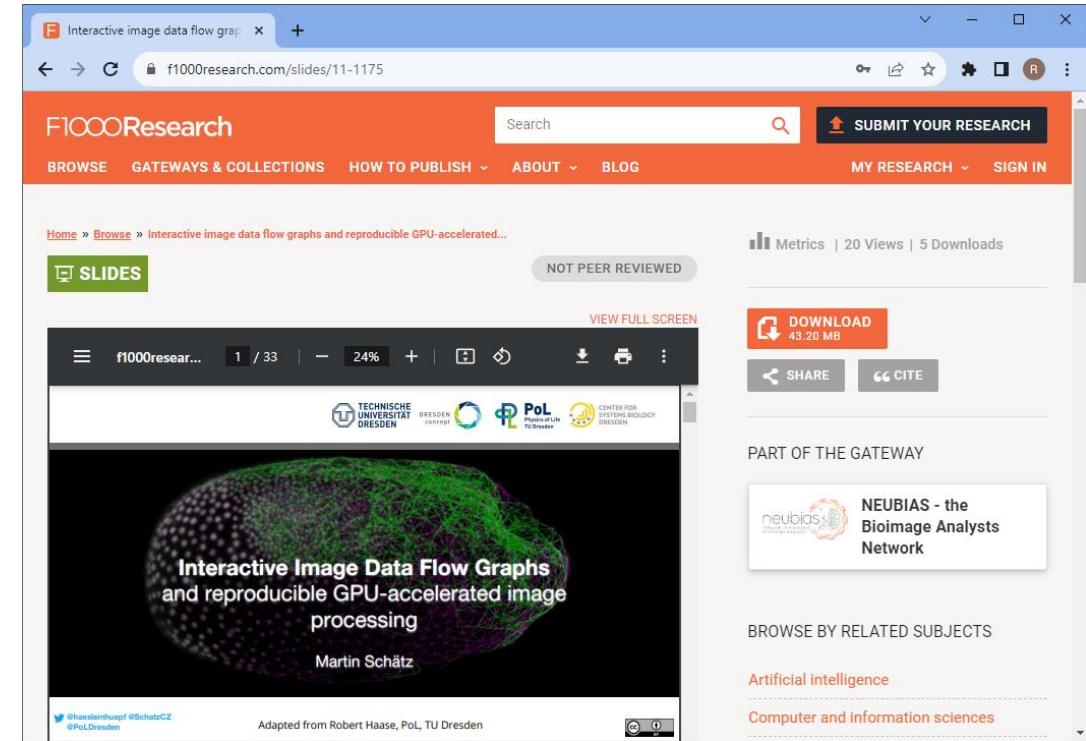
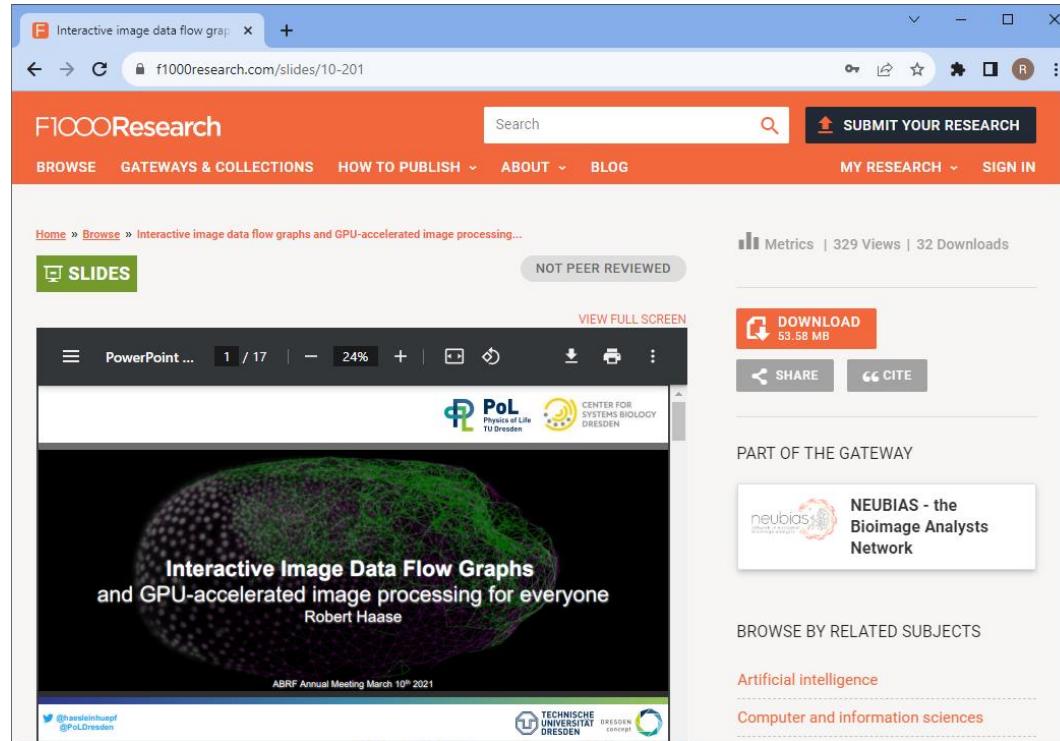
# The FAIR-principles

- Reusable
  - R1. (Meta)data are richly described with a plurality of accurate and relevant attributes
  - R1.1. (Meta)data are released with a clear and accessible data usage license
  - R1.2. (Meta)data are associated with detailed provenance
  - R1.3. (Meta)data meet domain-relevant community standards



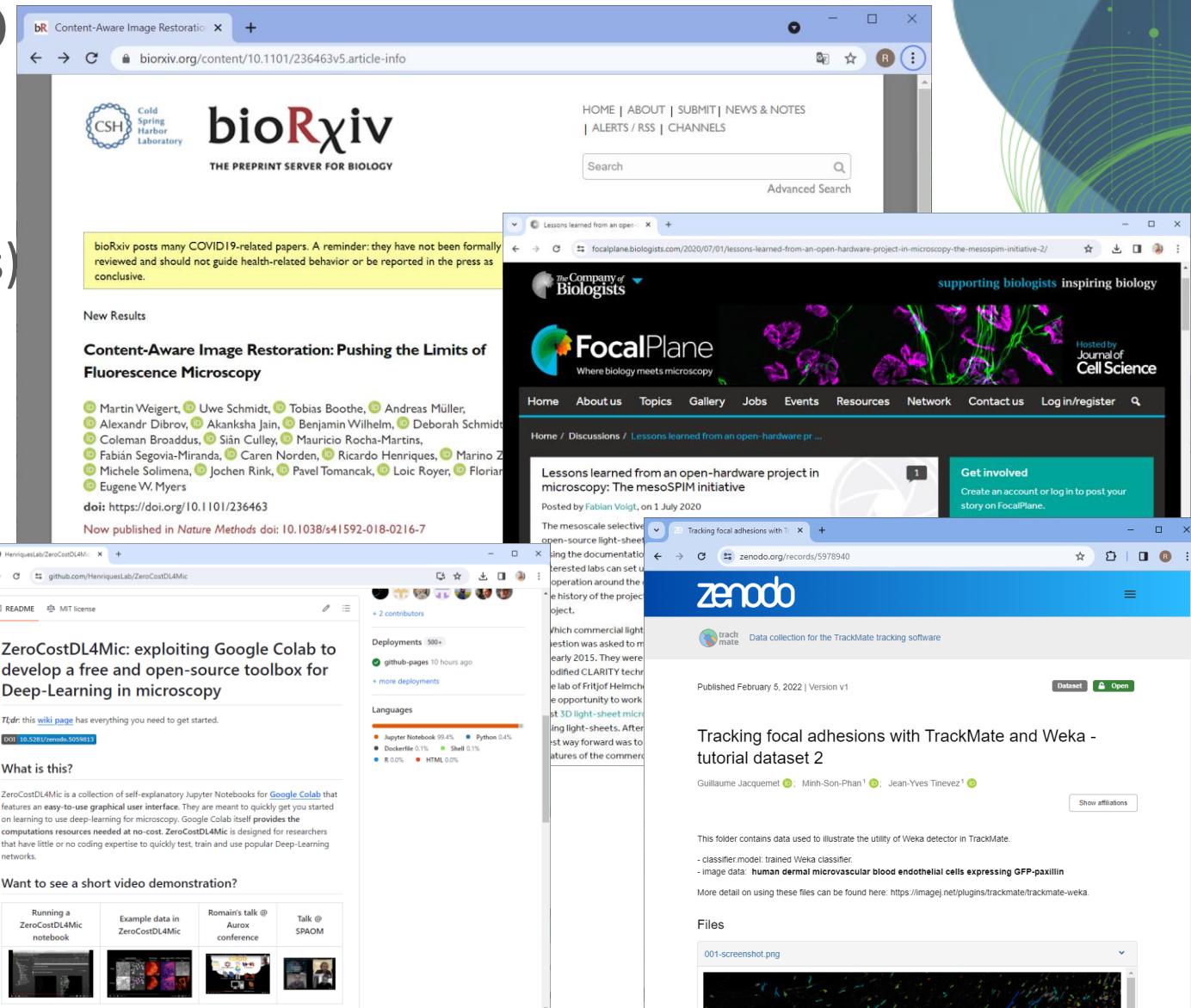
# Incentives: Reusability

- Open Access -> Others teach how to use your tools & methods



# Where to share?

- Open science related content
  - bioRxiv (manuscripts, no reviews)
  - Figshare
  - F1000
  - Bioimage Archive (data)
  - Github (code)
  - Zenodo
  - Focalplane
  - Institutional servers  
(if there is no alternative)



# Quiz

- Where might open source code be most *visible*?

Git server of the  
university



Zenodo.org



Github.com



Group / institute /  
personal website



# A short excursion...

- Published 2 weeks ago:

Claim to  
outperform current  
state of the art.

The screenshot shows the nature methods website with the following details:  
- Title: The multimodality cell segmentation challenge: toward universal solutions  
- Authors: Jun Ma, Ronald Xie, Shamini Ayyadhury, Cheng Ge, Anubha Gupta, Ritu Gupta, Song Gu, Yao Zhang, Gihun Lee, Joonkee Kim, Wei Lou, Haofeng Li, Eric Upschulte, Timo Dickscheid, José Guilherme de Almeida, Yixin Wang, Lin Han, Xin Yang, Marco Labagnara, Vojislav Gligorovski, Maxime Scheder, Sahand Jamal Rahi, Carly Kempster, Alice Pollitt, Bo Wang (with a '+ Show authors' link)  
- Date: Published: 26 March 2024  
- Metrics: 7645 Accesses | 19 Altmetric | Metrics  
- Additional content: You have full access to this article via Universitätsbibliothek Leipzig, Download PDF, Associated content (Creating a universal cell segmentation algorithm), and Nature Methods | Research Briefing | 01 Apr 2024

“The T1 algorithms achieved a median F1 score of 89.7% (IQR 36.7–82.4%), surpassing the KIT-GE, Cellpose-pretrain, Cellpose-scratch, Omnipose-pretrain and Omnipose-scratch by 49.9%, 24.4%, 35.4%, 58.9% and 48.7%, respectively.”

# A short excursion...

- “However my initial testing of the winning entry [mediar 8](#) reveals errors (which are typical without tuning) when applied to recent data posted [here 6](#) for which cellpose produced a (subjectively) good result.”

►  Community Partners

## Thoughts on the latest SOTA Segmentation algorithms

Blog Posts segmentation, cellpose, deep-learning, paper-review

---

 Brian Northan  bnorthan Community Forum Team member 2  13d

Curious what people think about the latest paper on DL Segmentation that can be found [here](#) 45

It's behind a paywall but some of the figures are available publicly. In particular I am trying to understand this figure as it does not really reconcile with my practical experience. The F1 scores for cellpose seem really low.

# A short excursion...

- Published on Sunday:  
(by the CellPose authors)
- “In fact, Mediar directly copied our codebase for implementing the Cellpose framework without modification”

The image shows a screenshot of a bioRxiv preprint page. At the top left is the CSHL logo and the bioRxiv logo with the tagline "THE PREPRINT SERVER FOR BIOLOGY". To the right is a "Follow this preprint" button with a bell icon. Below the header, the title "Transformers do not outperform Cellpose" is displayed, along with the authors' names, Carsten Stringer and Marius Pachitariu, and the DOI: <https://doi.org/10.1101/2024.04.06.587952>. A note states that this is a preprint and has not been certified by peer review. Below the title are social media sharing icons and a preview PDF link. A navigation bar at the bottom includes "Abstract", "Info/History", "Metrics", and "Preview PDF". The main content area starts with an "Abstract" section, followed by a "Competing Interest Statement" and a "Copyright" notice.

New Results Follow this preprint

**Transformers do not outperform Cellpose**

Carsten Stringer, Marius Pachitariu  
doi: <https://doi.org/10.1101/2024.04.06.587952>

This article is a preprint and has not been certified by peer review [what does this mean?].

0 0 0 0 0 126

**Abstract** Info/History Metrics Preview PDF

**Abstract**

In a recent publication, Ma et al (2024) claim that a transformer-based cellular segmentation method called Mediar - which won a Neurips challenge - outperforms Cellpose (0.897 vs 0.543 median F1 score). Here we show that this result was obtained by artificially impairing Cellpose in multiple ways. When we removed these impairments, Cellpose outperformed Mediar (0.861 vs 0.826 median F1 score on the updated test set). To further investigate the performance of transformers for cellular segmentation, we replaced the Cellpose backbone with a transformer. The transformer-Cellpose model also did not outperform the standard Cellpose (0.848 median F1 test score). Our results suggest that transformers do not advance the state-of-the-art in cellular segmentation.

**Competing Interest Statement**

The authors have declared no competing interest.

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# A short excursion...

- Professional discussion about Copyright:

Please retain the Cellpose copyright as required by the BSD-3 license #17

**Closed** marius10p opened this issue last week · 7 comments

marius10p commented last week

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In addition, we ask that you include this copyright statement at the top of your file:

Copyright © 2022 Howard Hughes Medical Institute, Authored by Carsen Stringer and Marius Pachitariu.

Thank you.

Assignees  
Lee-Gihun  
joonkeekim

Labels  
**documentation**

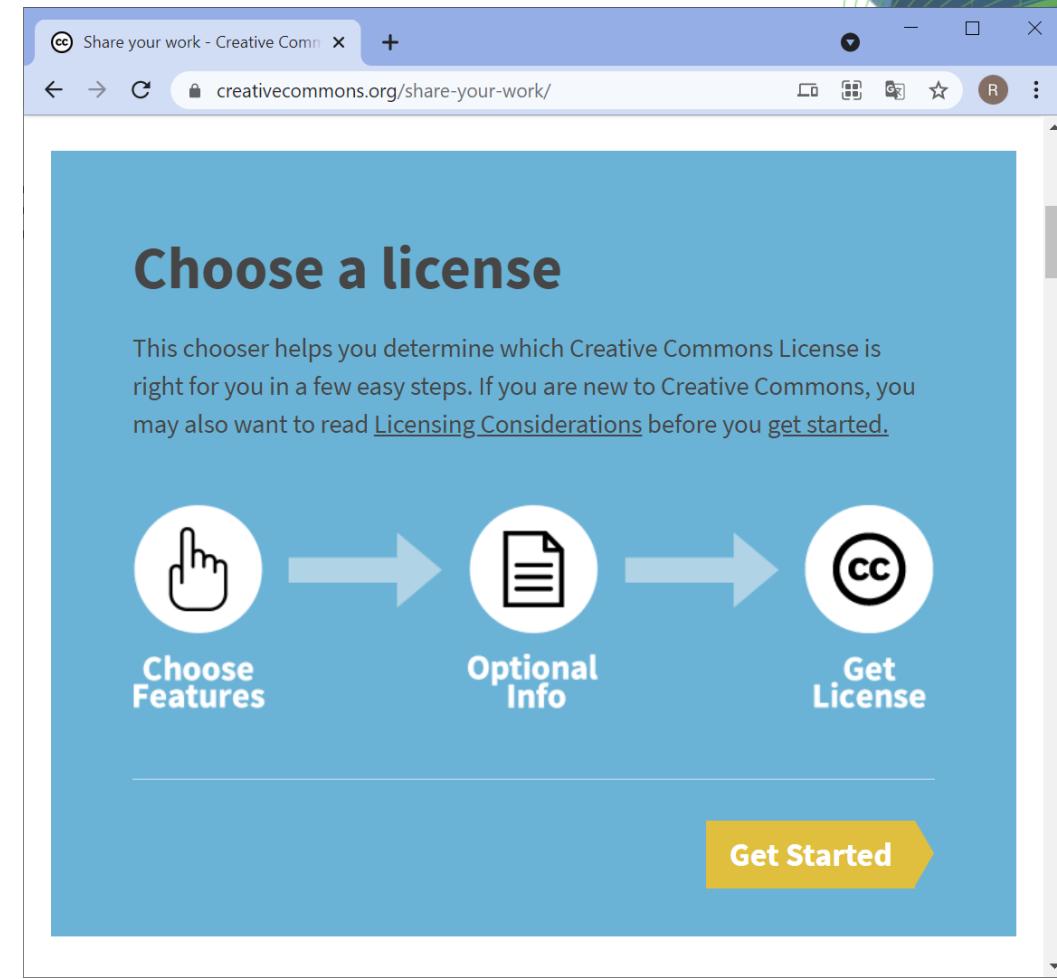
Projects  
None yet

Milestone  
No milestone

Development

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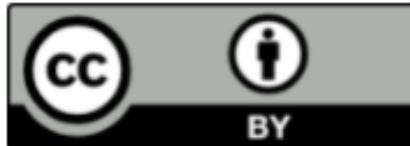


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## Example



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# Quiz

- May I use one of the Figures from this preprint?
- May I download and redistribute this preprint to students of a course for free?

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Yes



No



Yes

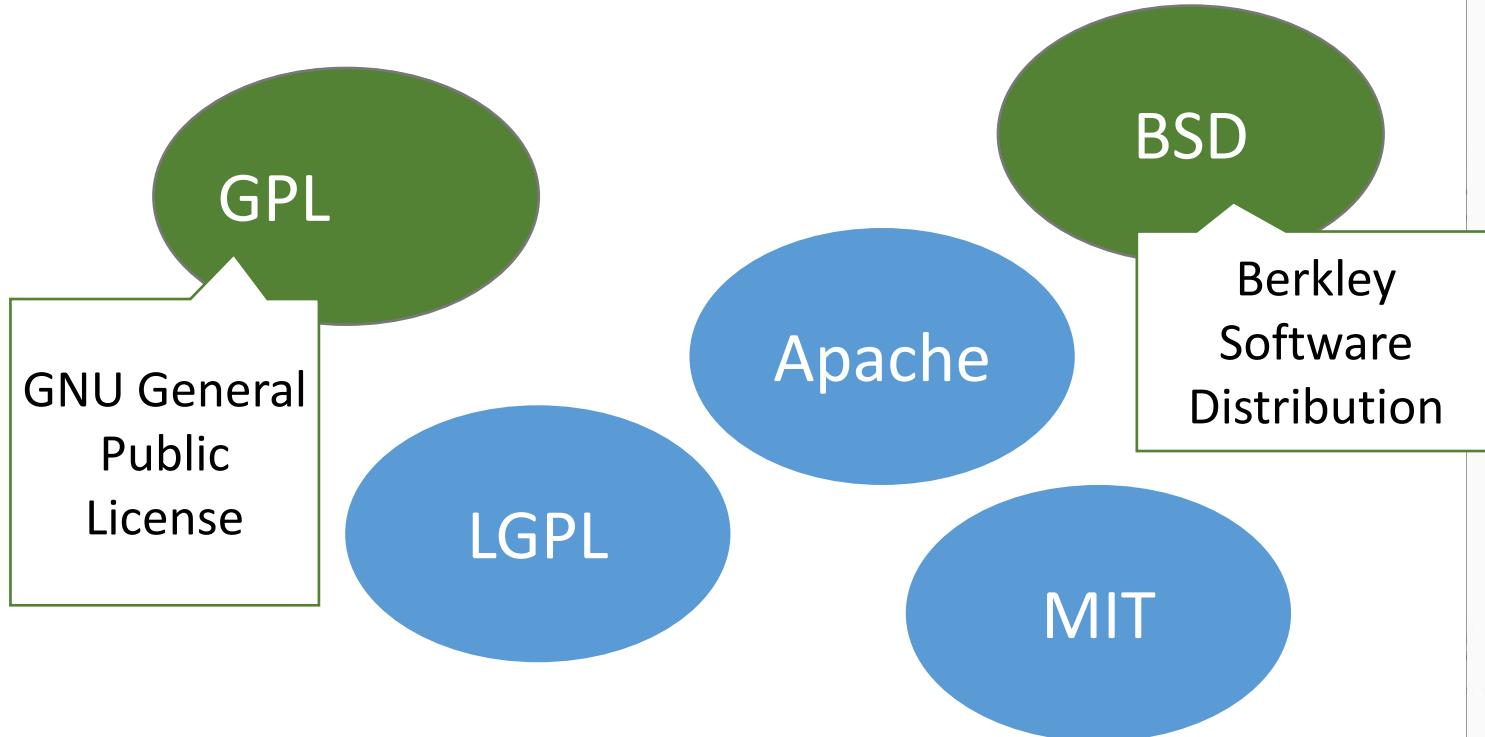


No



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In the software world, other licenses are more popular, historically grown.



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Which of the following best describes your situation?

I need to work in a community.

I want it simple and permissive.

I care about sharing improvements.

What if none of these work for me?

My project isn't software.

I want more choices.

I don't want to choose a license.

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# Quiz

Can I build a commercial product on the basis of GPL-licensed code?

Yes



No



Do I have to release the code openly for this commercial product?

Yes



No



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  - You can reuse our stuff, but only if you ...
    - License your work with the same license we do
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    - Make no money with derivatives of our work
  - Examples: **GPL, CC-BY-SA, CC-BY-NC, CC-BY-ND**
- Permissive licensing:
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I conclude,  
these are  
*less open* in  
a sense



# Quiz

May I reuse code  
from this repository  
in my own BSD-  
licensed work?

Yes



No



The screenshot shows a GitHub repository page for 'cnr-isti-vclab/meshlab'. The 'Code' tab is selected, displaying a list of commits. The repository is described as 'The open source mesh processing system'. It has 150 watchers, 686 forks, and 3.3k stars. The code tab shows the main branch with 3 branches and 40 tags. A recent commit by alemuntoni is shown: 'bugfix while loading exif info' (commit 2672c14, 22 days ago). Other commits include fixing missing windeployqt in windows workflows, various typos in documentation, and adding gltf samples. The repository is associated with several topics: point-cloud, mesh, mesh-generation, 3d-printing, 3d-scanning, 3d, 3d-reconstruction, 3d-models, mesh-processing, mesh-editing, mesh-simplification, and triangle-mesh. The repository also includes a Readme, a GPL-3.0 license, 3.3k stars, 150 watching, and 686 forks.

Commit	Message	Date
alemuntoni bugfix while loading exif info	fix missing windeployqt in windows workflows	22 days ago
.github	fix missing windeployqt in windows workflows	5 months ago
docs	Fix various typos	8 months ago
resources	icon on windows folder	5 months ago
sample	add gltf samples	16 months ago
scripts	deploy all plugins in macos script	4 months ago
src	bugfix while loading exif info	22 days ago
textures	moved textures folder outside distrib	3 years ago
unsupported	remove "vertex color noise" filter	12 months ago
.aitianore	move build and install dirs on macos outside src	5 months ago

# Quiz

May I reuse code  
from this repository  
in my own GPL-  
licensed work?

Yes



No



A screenshot of a web browser displaying the GitHub repository page for "napari/napari". The repository is described as "napari: a fast, interactive, multi-dimensional image viewer for python". The "Code" tab is selected, showing a list of recent commits:

Author	Commit Message	Time Ago
Czaki	set selection color for QListView item. (#5202)	15 hours ago
	feat: add codespace (#4599)	4 months ago
	Move docs to separate repo (#5216)	5 days ago
	Drop python 3.7 (#4063)	8 months ago
	Move docs to separate repo (#5216)	5 days ago
	set selection color for QListView item. (#5202)	15 hours ago
	Split out builtins into another top-level module (#4706)	3 months ago
	Re-add README screenshot (#5220)	4 days ago
	Update some strings to be translated, some to be igno...	last month
	Add event.debugging tool (#3802)	10 months ago



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# Software environments

Robert Haase

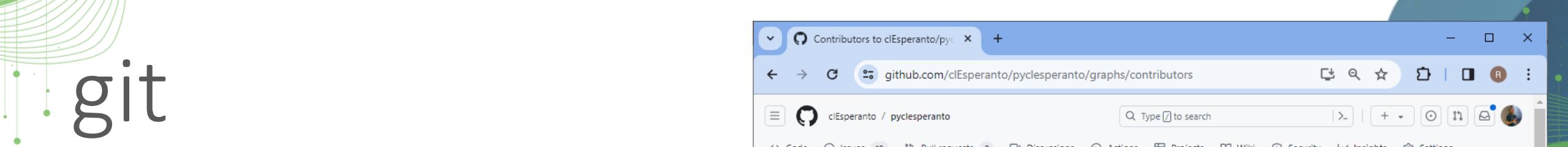
GEFÖRDERT VOM



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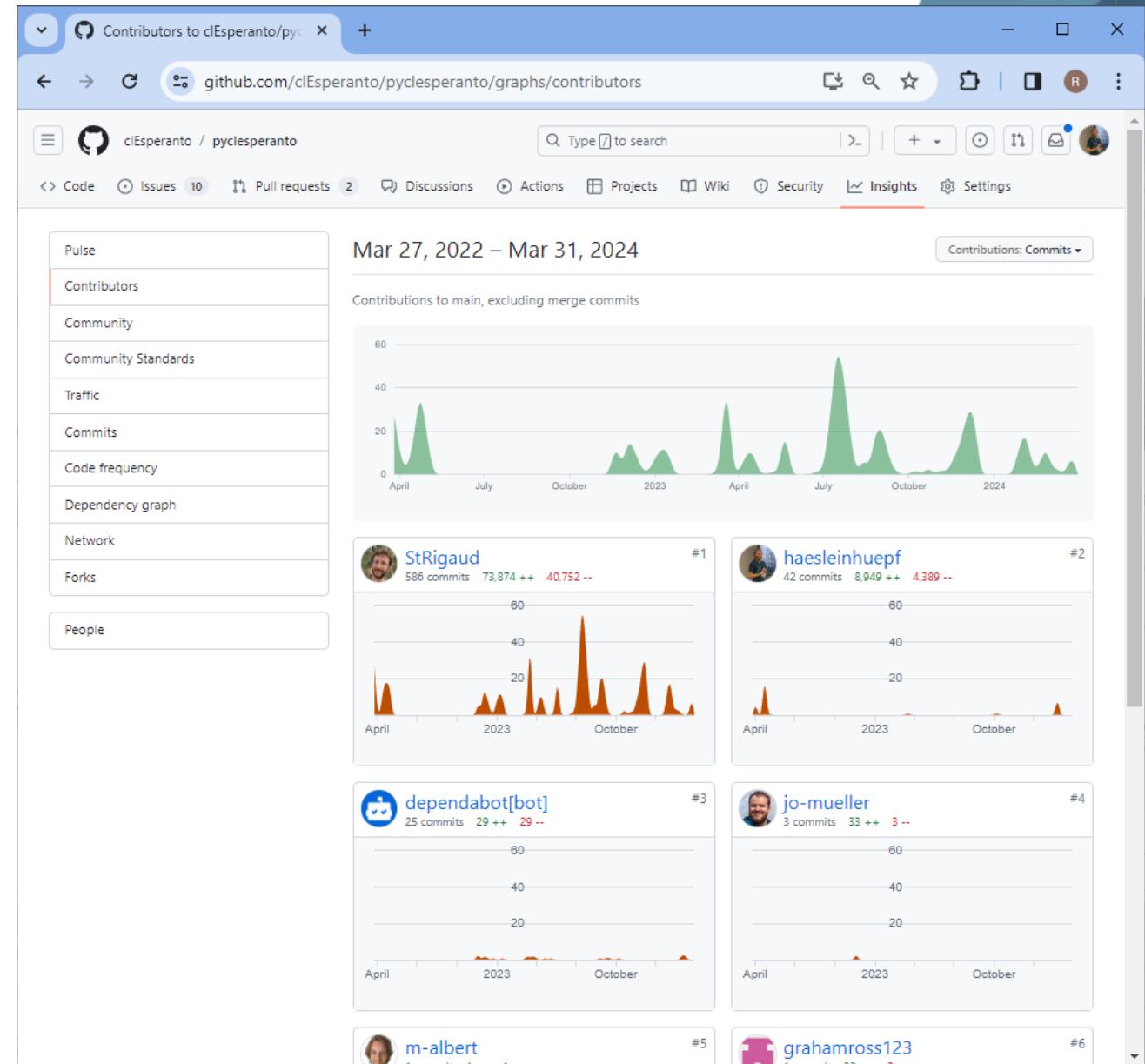


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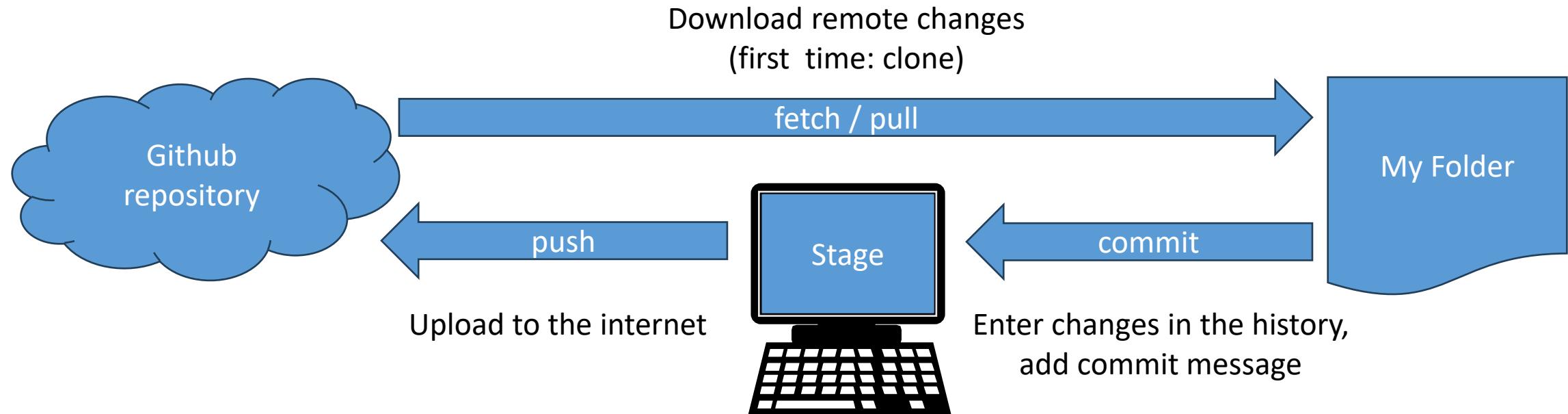
# git

- Version control is key element of data scientist's toolbox
- Distributed file system with sophisticated logging mechanisms
- Control about what becomes part of a repository and what not



# git

- Git makes file modifications a more active / involved process (making people think about)



# git

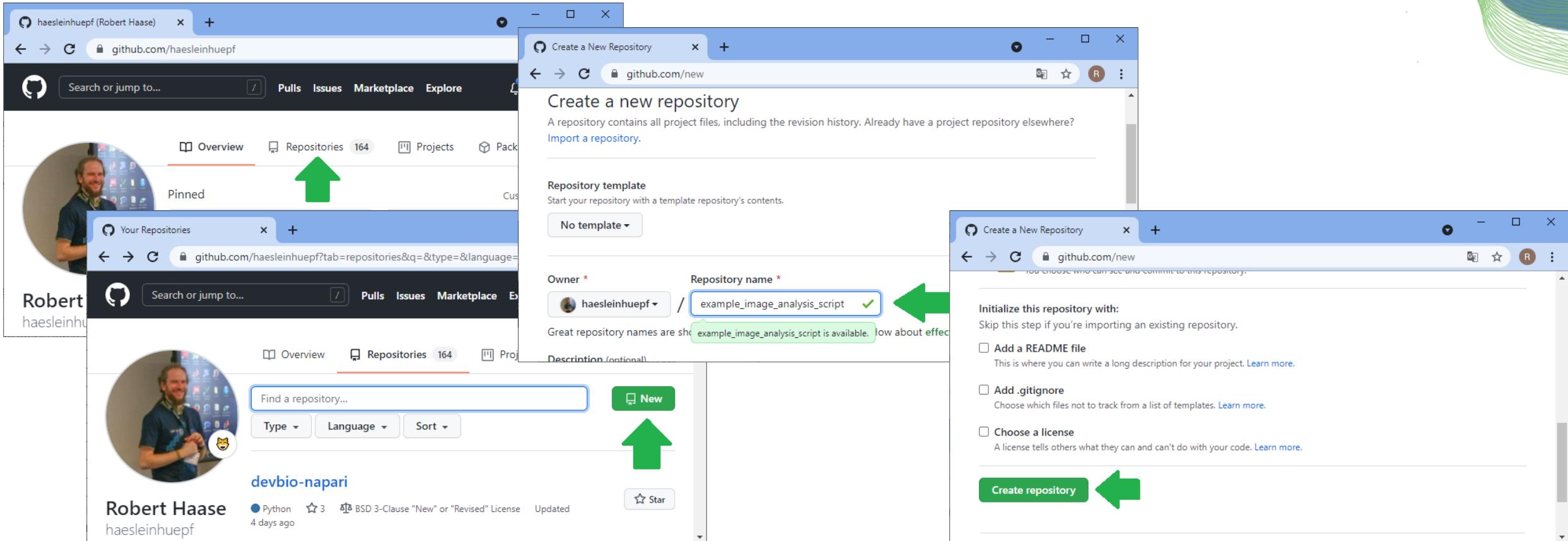
- Who wrote this code
- when and
- why?

The screenshot shows two GitHub browser windows side-by-side. The left window displays the commit history for the repository `haesleinhuepf/example_image_analysis_script`. It lists several commits, with the commit titled "bugfix: threshold\_otsu" highlighted by an orange arrow. The right window shows a detailed view of the changes made in that specific commit, specifically the file `my_library.py`. The diff view highlights the addition of the `threshold_otsu` function and its subsequent use in the script.

```
diff --git a/my_library.py b/my_library.py
index 3e31f1..65c074 100644
--- a/my_library.py
+++ b/my_library.py
@@ -6,7 +6,8 @@ def segment_image(image):
 6   6     blurred = gaussian(image, sigma=2)
 7   7
 8   8     # binarize the image
 9 - 9     binary = threshold_otsu(blurred)
 9 + 9     threshold = threshold_otsu(blurred)
10 + 10    binary = blurred > threshold
11   11
12   12     # label connected components
13   13     result = label(binary)
```

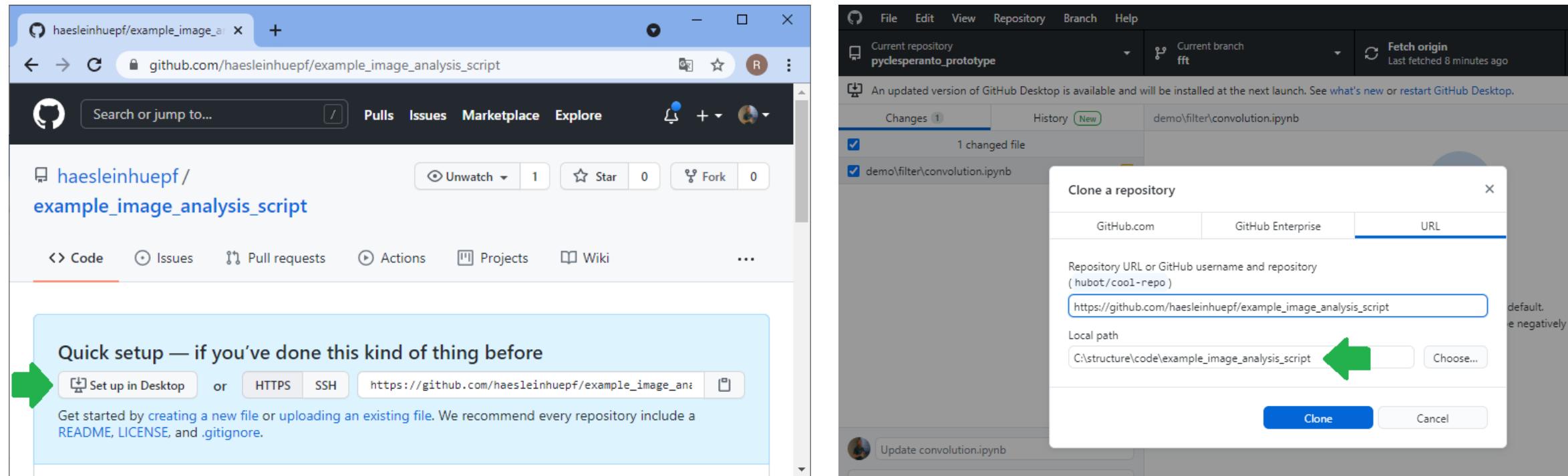
# github – creating repositories

- Add a new, empty repository



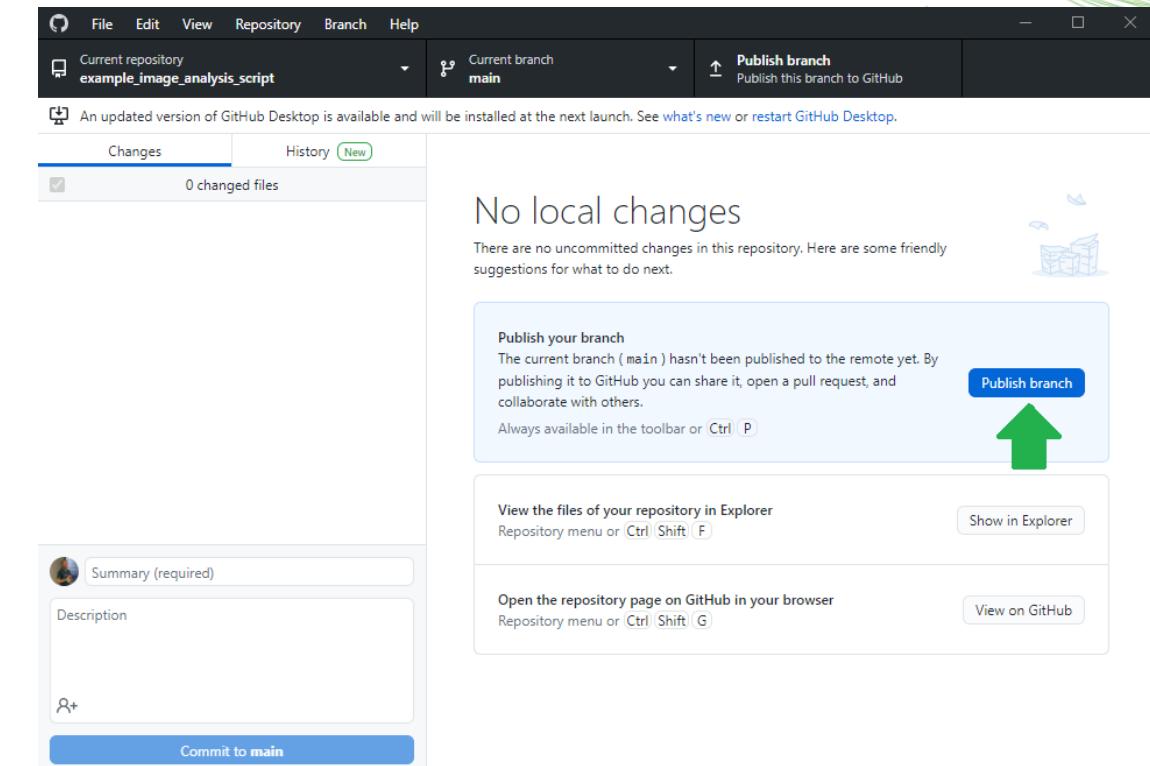
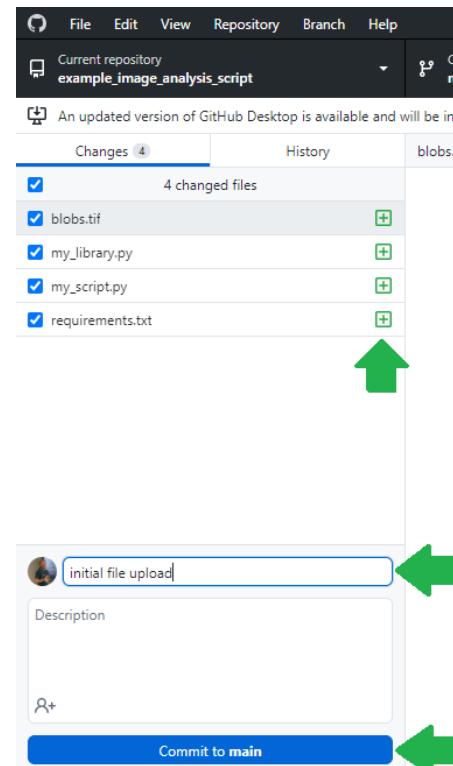
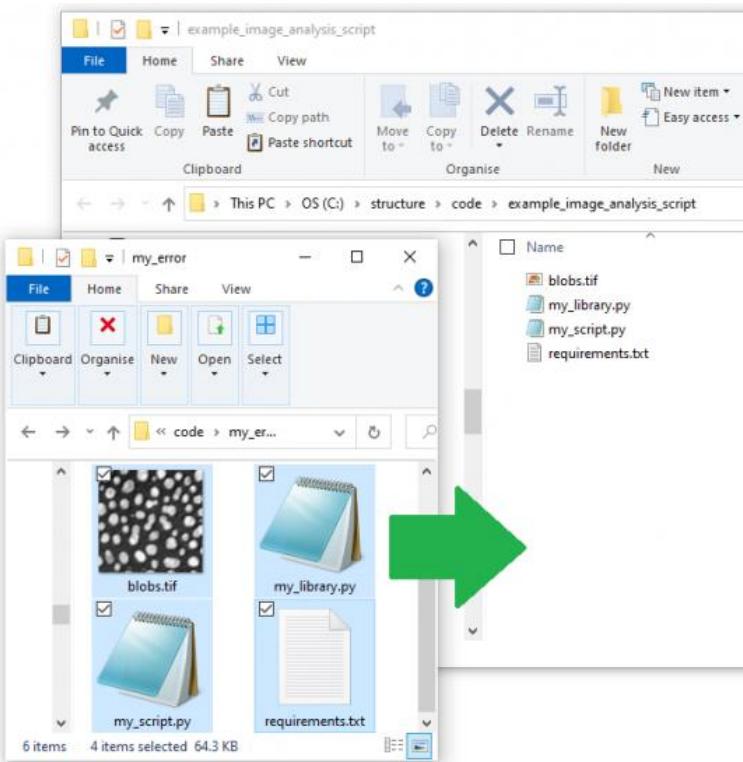
# github – clone repositories

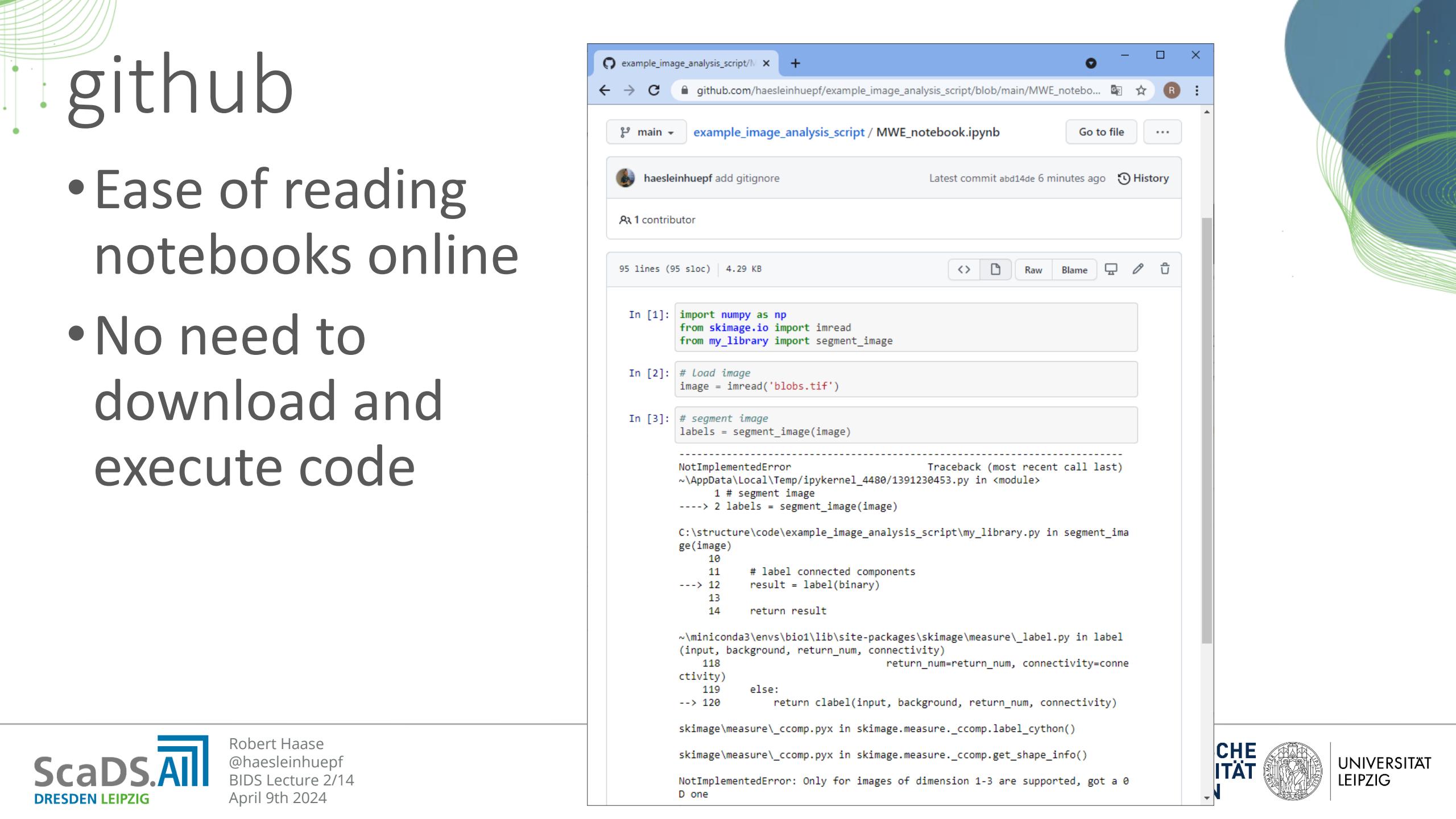
- git clone <https://github.com/organization/repository>
- Or: Use the Github Desktop app



# github - uploading

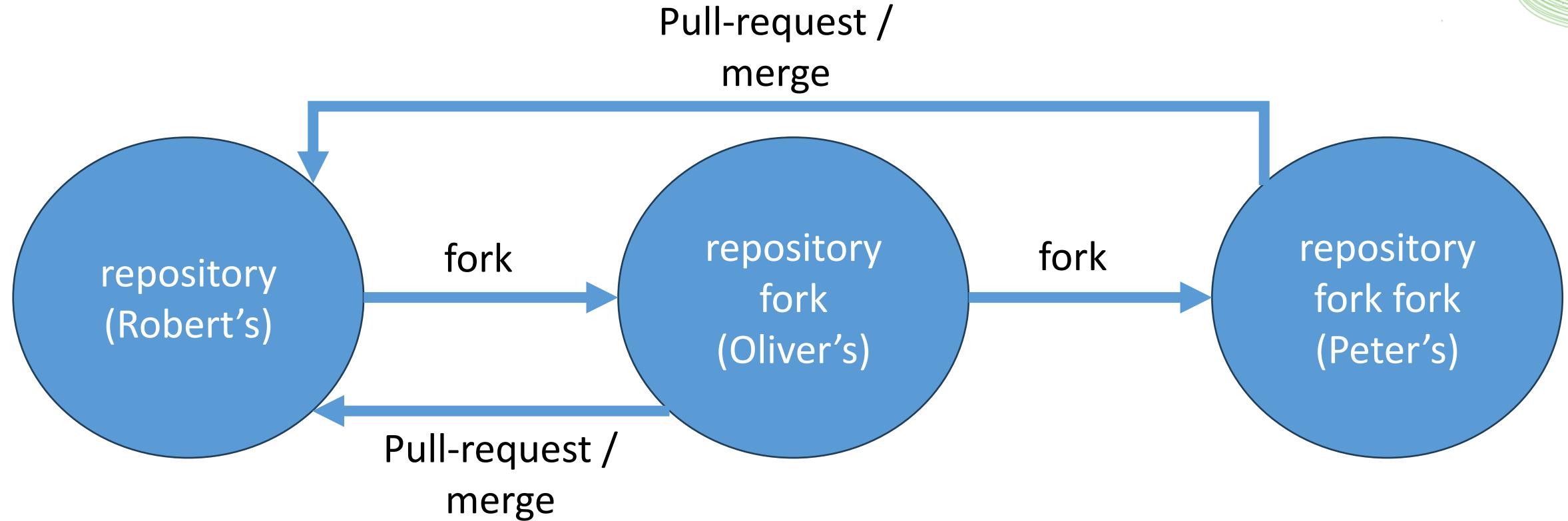
- git [add], commit, push





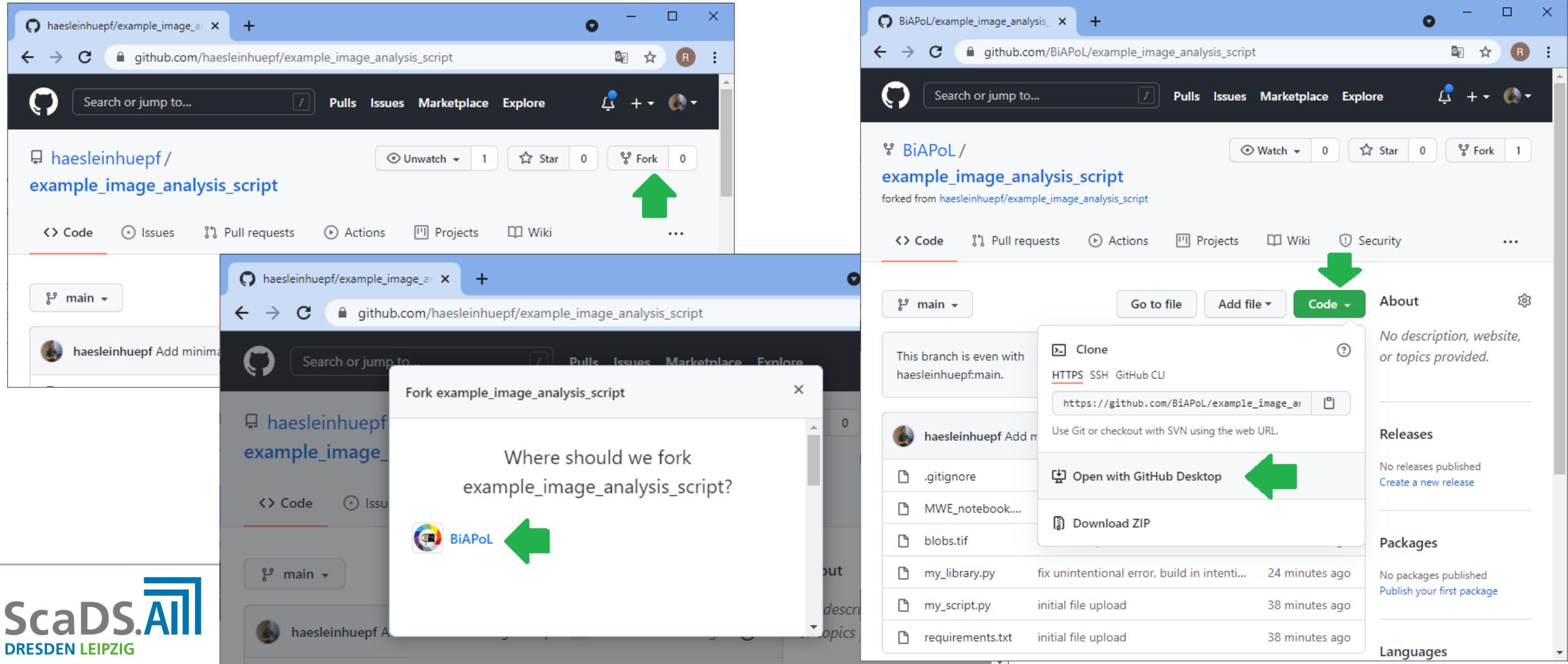
# git - forking

- Making a copy where we have edit rights



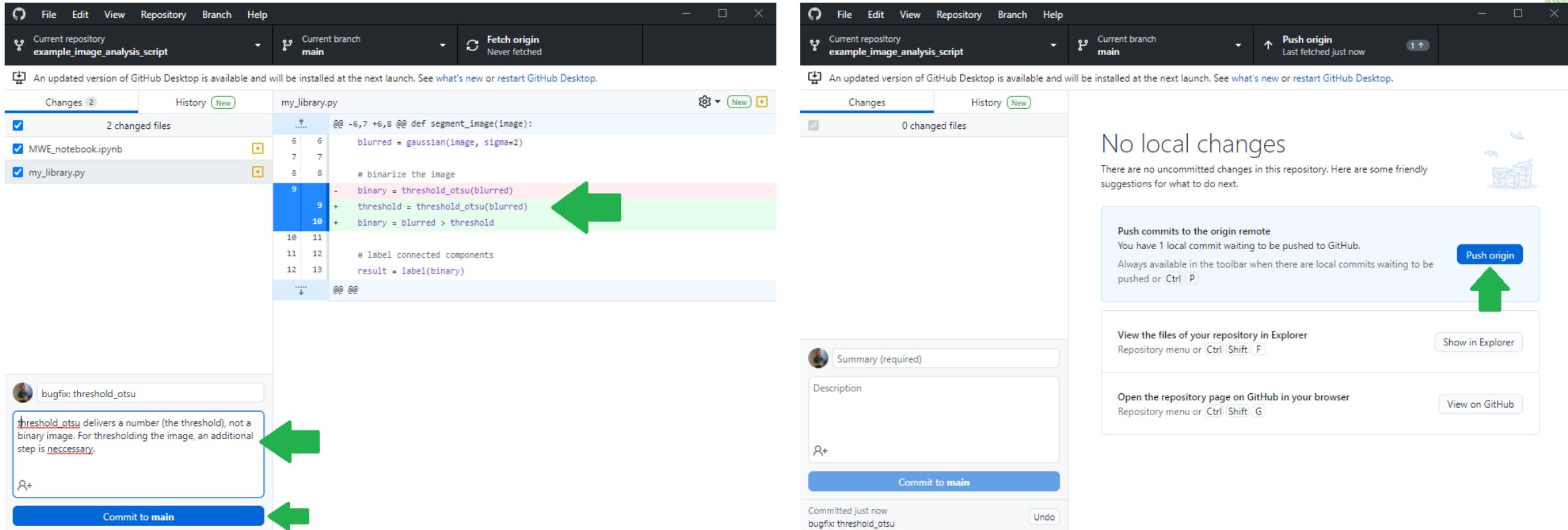
# github - forking

- Making a copy where we have edit rights



# github – uploading (again)

- After fixing a bug, we upload the changes to our fork



# Github – pull requests

- Contribute to open-source projects

The image consists of two side-by-side screenshots of GitHub repositories.

**Left Screenshot (BiAPoL repository):**

- The URL is [github.com/BiAPoL/example\\_image\\_analysis\\_script](https://github.com/BiAPoL/example_image_analysis_script).
- The repository name is **BiAPoL / example\_image\_analysis\_script**, forked from [haesleinhuepf/example\\_image\\_analysis\\_script](#).
- The main branch is **main**.
- A green arrow points to the **Open pull request** button at the bottom of the commit list.

**Right Screenshot (haesleinhuepf repository):**

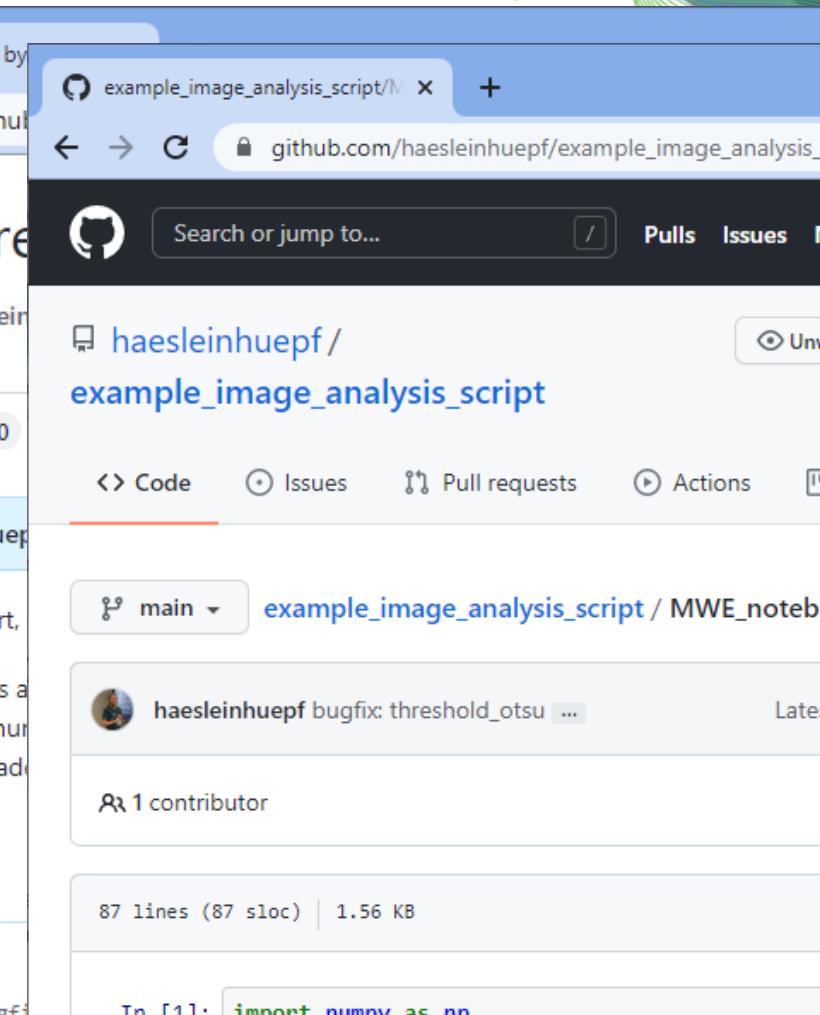
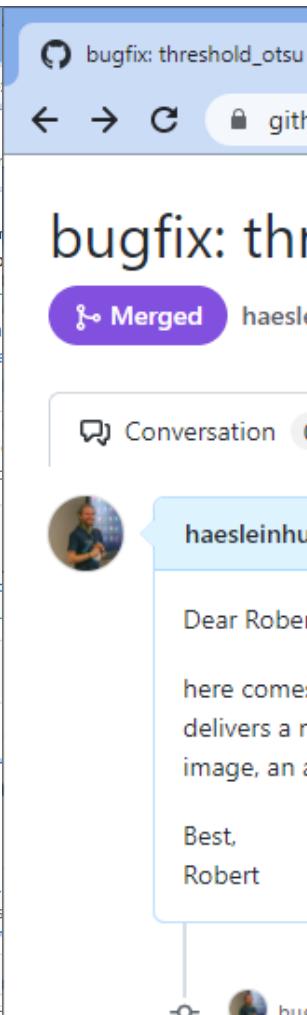
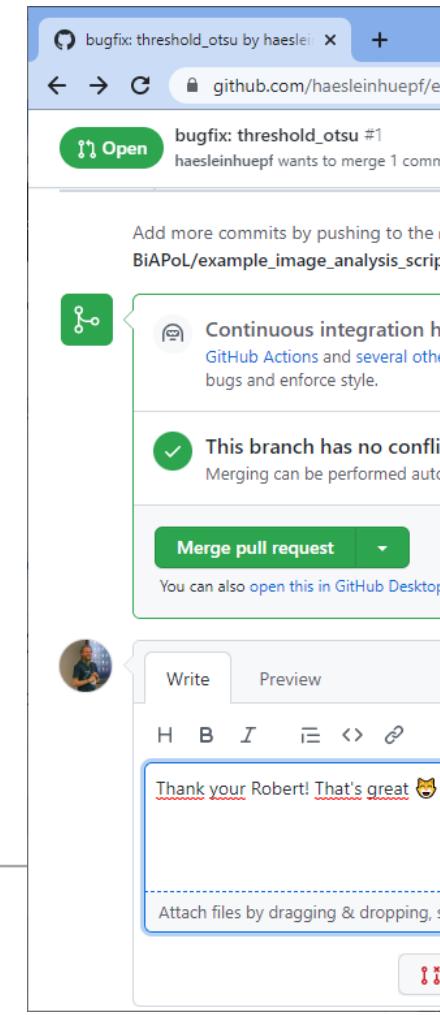
- The URL is [github.com/haesleinhuepf/example\\_image\\_analysis\\_script/compare/main...BiAPoL%2Fmain](https://github.com/haesleinhuepf/example_image_analysis_script/compare/main...BiAPoL%2Fmain).
- The repository name is **haesleinhuepf / example\_image\_analysis\_script**.
- The base repository is **base repository: haesleinhuepf/example\_image...** and the head repository is **head repository: BiAPoL/example\_image\_analys...**.
- A green arrow points to the **Create pull request** button at the bottom of the pull request creation form.

# Github – pull requests

- Reviewer perspective

A screenshot of a GitHub pull request page. The title is "bugfix: threshold\_otsu #1". It shows a diff of the file "my\_library.py". The diff highlights changes from line 9 to 10. The commit message is "haesleinhuepf wants to merge 1 commit into haesleinhuepf:main from BiAPoL:main". The "Files changed" section shows 2 files with +13 and -20 changes. A green arrow points to the "Review changes" button.

```
diff --git a/my_library.py b/my_library.py
--- a/my_library.py
+++ b/my_library.py
@@ -6,7 +6,8 @@ def segment_image(image):
 6   6     blurred = gaussian(image, sigma=2)
 7   7
 8   8     # binarize the image
 9 - 9     binary = threshold_otsu(blurred)
 10 + 9     threshold = threshold_otsu(blurred)
 11 + 10    binary = blurred > threshold
 12   11
 13   12     # label connected components
 14     result = label(binary)
```



# Github – pull requests

- Reviewer perspective

The screenshot shows a GitHub pull request page for a repository named "example\_image\_analysis\_script". The pull request is titled "bugfix: threshold\_otsu #1" and has been merged. The commit message is "bugfix: threshold\_otsu ...". A review comment from "haesleinhuepf" says:

Dear Robert,  
here comes a bug fix for your image segmentation function. `threshold_otsu` delivers a number (the threshold), not a binary image. For thresholding the image, an additional step is necessary.  
Best,  
Robert

Below the comment, another review comment from "haesleinhuepf" says:

Thank your Robert! That's great 😊

On the right side of the page, there are sections for "Reviewers", "Assignees", "Labels", "Projects", "Milestone", and "Linked issues".

The screenshot shows a GitHub repository page for "haesleinhuepf/example\_image\_analysis\_script". The repository has 1 pull request, 0 issues, 1 action, 1 project, and 1 wiki. The pull request is titled "bugfix: threshold\_otsu ..." and was merged 17 minutes ago. The commit message is "bugfix: threshold\_otsu ...". The repository has 1 contributor.

On the right side, there is a Jupyter notebook named "MWE\_notebook.ipynb" with the following code and output:

```
In [1]: import numpy as np
from skimage.io import imread
from my_library import segment_image

In [2]: # Load image
image = imread('blobs.tif')

In [3]: # segment image
labels = segment_image(image)

In [4]: # count objects
number_of_objects = labels.max()
print('Number of objects', number_of_objects)

Number of objects 61
```

A green box highlights the text "Problem solved :-)".

# Github

- If this was too fast...

The screenshot shows a web browser window displaying a blog post from the FocalPlane website. The header features the FocalPlane logo and the text "Where biology meets microscopy". Below the header is a navigation bar with links to Home, About us, Topics, Gallery, Jobs, Events, Resources, Network, Contact us, and Log in/register. A search icon is also present. The main content area shows a breadcrumb trail: Home / How to / Collaborative bio-image analysis script ... The title of the post is "Collaborative bio-image analysis script editing with git". It was posted by Robert Haase on 4 September 2021. The post begins with a TL;DR summary: "I'm a computer scientist who often collaborates with biologists on bio-image analysis scripts. We are using more and more git, a version control program, for working on code collaboratively. When using git, we speak about repositories, commits and pushing to the origin. We also make forks, send pull-requests and merge code. This blog post explains these terms and demonstrates how a typical collaborative bio-image analysis scripting project looks like." The text continues with a personal anecdote about writing a script that counts cells and needing help from experts.

The screenshot shows a web browser window displaying a GitHub profile page for the user "haesleinhuepf". The profile page includes a bio image of a smiling man, a pinned item, and sections for Overview, Repositories (164), Projects, and Packages. A green arrow points upwards towards the "Repositories" tab, indicating where to click to demonstrate how to share code on GitHub.

# Quiz

It's ok to reuse this code if ...

haesleinhuepf / **imagej-run-async** Public

**Code** Issues Pull requests Actions Projects Wiki Security Insights Settings

master 1 branch 0 tags Go to file Add file Code

haesleinhuepf initial version 2f8c334 on 23 Jun 2019 1 commit

src/main/java/net/haeslein... initial version 3 years ago

.gitignore initial version 3 years ago

pom.xml initial version 3 years ago

Help people interested in this repository understand your project by adding a README. Add a README

About No description, website, or topics provided.

0 stars 1 watching 0 forks

Releases No releases published Create a new release



Mention author



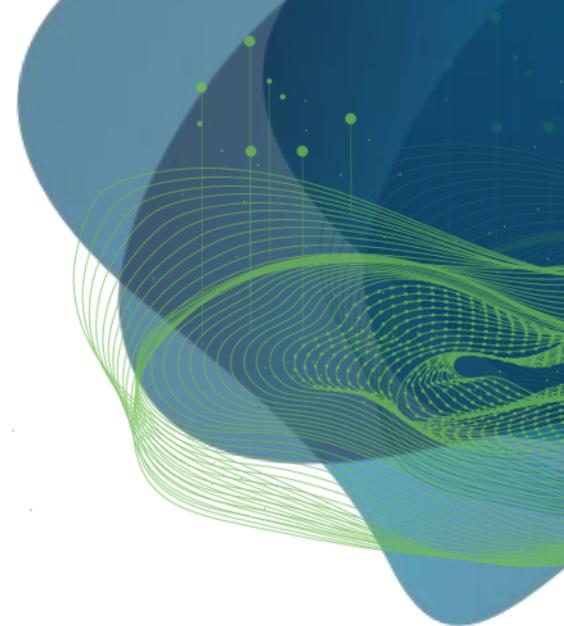
Ask the authors



Link to the license



Copy the copyright statement



# Exercises

# Robert Haase

GEFÖRDERT VOM



Bundesministerium  
für Bildung  
und Forschung



Diese Maßnahme wird gefördert durch die Bundesregierung aufgrund eines Beschlusses des Deutschen Bundestages.  
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# Exercises

Training resources for Students at Uni Leipzig who want to dive into bio-image data science with Python. The material will develop between April and July 2024

CC-BY-4.0 license  
1 star 0 forks 2 watching 1 Branch 0 Tags Activity Public repository

haesleinhuepf added first exercise

01a\_setting\_up\_local\_environment added first exercise

01b\_setting\_up\_sc\_ulei\_environment added first exercise

01c\_testing\_environment added first exercise

.gitignore added first exercise

LICENSE-CC-BY The Beginning

README.md added first exercise

## Bio-image Data Science

This repository contains training resources for Students at Uni Leipzig who want to dive into bio-image data science with Python. The material will develop between April and July 2024 and shared here in this github repository.

### Teaching Goal

Students learn the full workflow of common bio-image data science projects to a degree that they can execute a scientific data analysis project in this context on their own. They will be familiar with common bio-image analysis algorithms and workflows, how to choose them according to a scientific goal, and how to measure quality of derived results. Attending the lecture and executing the practicals qualifies the students to work as bio-image data scientist in the pharmaceutical industry or basic biological research.

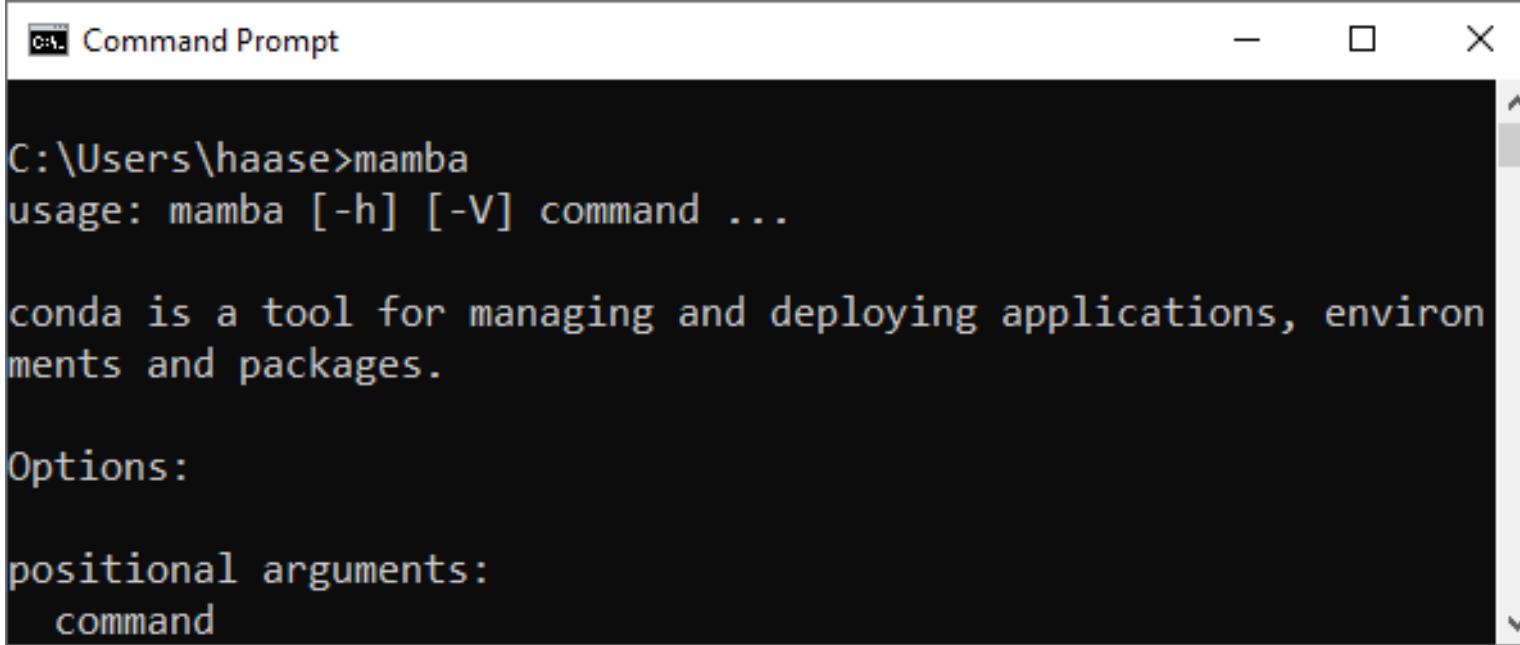
### Course contents

- Introduction to Bio-image Data Science (Apr 2nd 2024)
  - Basics of microscopy
  - Introduction to Bio-image Analysis
  - Exercises:
    - Setting up a local environment
    - Setting up Jupyter Hub at Scientific Computing / Leipzig University
    - Execute the trailer notebook



# Exercise (recap)

- Make sure mamba is installed on your computer  
(see instructions from last week)



A screenshot of a Windows Command Prompt window titled "Command Prompt". The window shows the following text output:

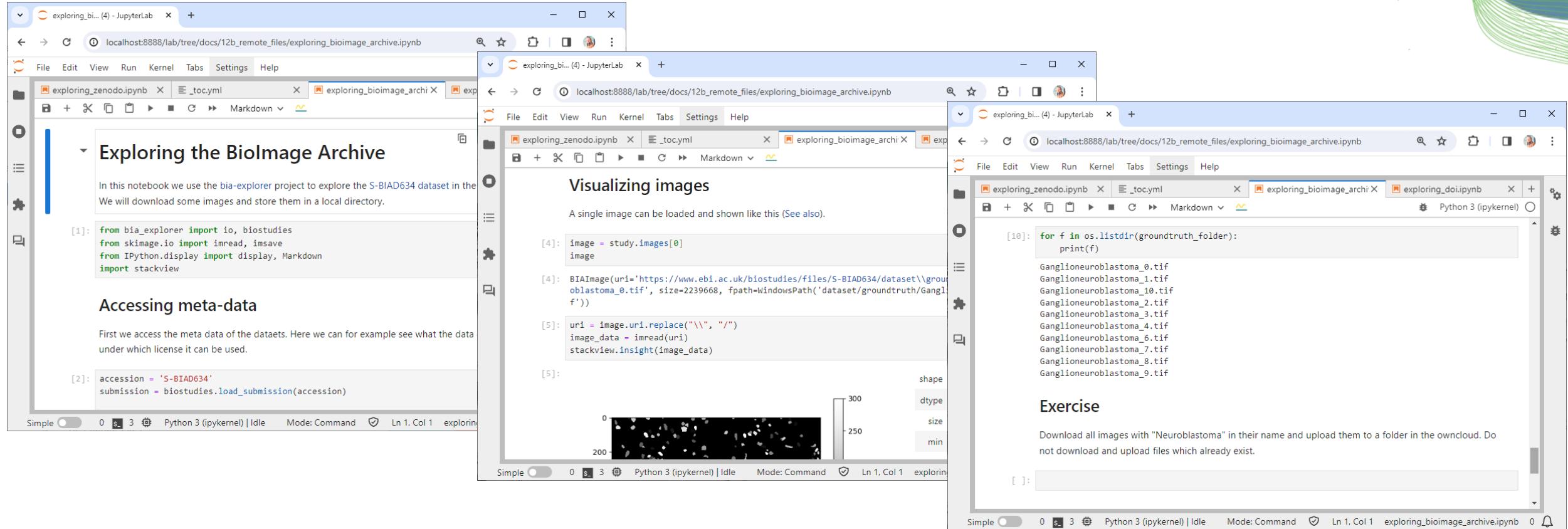
```
C:\Users\haase>mamba
usage: mamba [-h] [-V] command ...
conda is a tool for managing and deploying applications, environments and packages.

Options:

positional arguments:
    command
```

# Exercise (BioImage Archive)

- Download a dataset from the BioImage Archive



The image shows three side-by-side JupyterLab interfaces, each displaying a different notebook related to exploring the BioImage Archive.

- Left Notebook:** Titled "Exploring the BioImage Archive". It contains code to import necessary libraries and download the S-BIAD634 dataset. A section titled "Accessing meta-data" shows how to retrieve submission information for the dataset.
- Middle Notebook:** Titled "Visualizing images". It demonstrates how to load and display images from the dataset. A code cell shows how to replace file separators and use stackview to visualize a stack of images. An image visualization is shown with axes ranging from 0 to 300.
- Right Notebook:** Titled "Exercise". It shows a code cell listing files in a groundtruth folder, which includes various .tif files for Ganglioneuroblastoma. It also contains instructions for an exercise: "Download all images with "Neuroblastoma" in their name and upload them to a folder in the owncloud. Do not download and upload files which already exist."

# Exercise (nextcloud)

- Register at Speicherwolke @ Uni Leipzig,
- Upload the images from the BioImage Archive to a folder in the Speicherwolke.

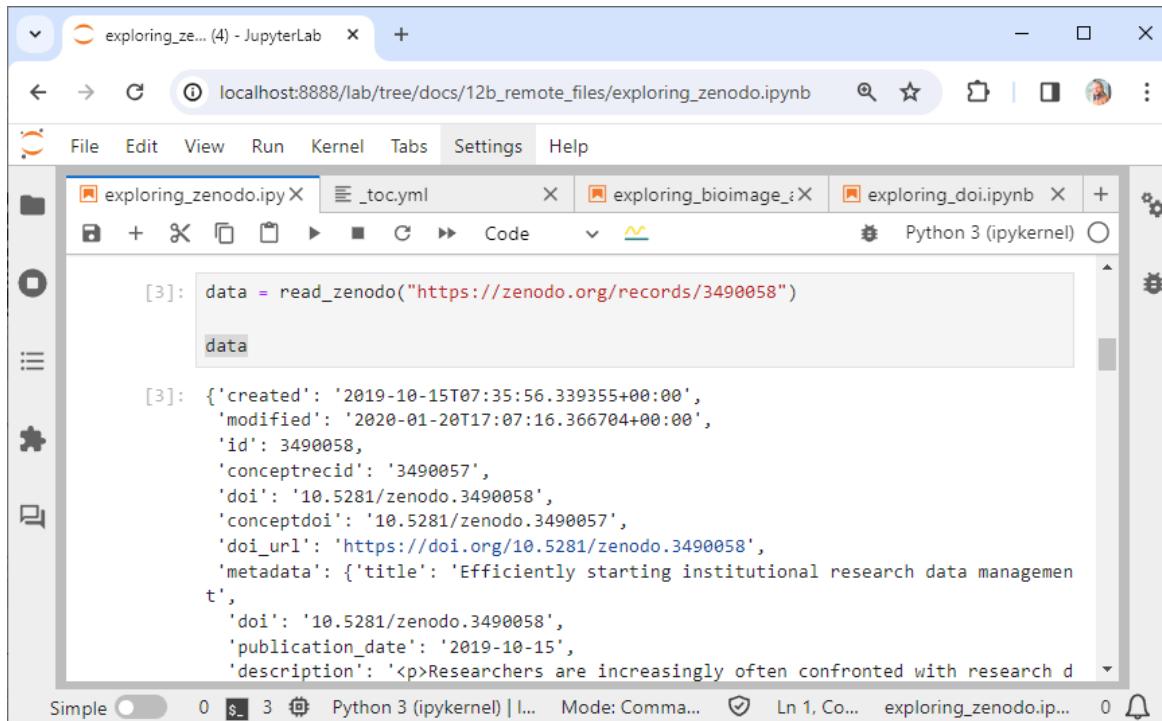
The screenshot shows the Universit t Leipzig website with a blue header. Below it, there's a section for 'EIGENER CLOUD-SPEICHER (SPEICHERWOLKE)'. It includes a brief description of the service, mentioning its purpose for storing files and synchronizing them across devices. A 'Servicebeschreibung' link is also present.

The screenshot shows the BioImage Archive website with a blue header. It displays a dataset titled 'S-BIAD634', described as an annotated fluorescence image dataset for training nuclear segmentation methods. It includes links for 'Study Information', 'Annotations', 'Images', and 'Models used'. Below this, there's a summary section 'In a nutshell' with details like '388 images' and '388 annotations'.

The screenshot shows the Speicherwolke NextCloud interface with a blue header. It displays a file list in a table format. The table includes columns for Name, Size, and Modified. It lists several files and folders: 'groundtruth' (0 KB, modified a minute ago), 'images' (0 KB, modified a minute ago), 'blobs.tif' (23 KB, modified a year ago), and 'blobs\_labels.tif' (254 KB, modified 22 minutes ago). There are also sections for 'Recent', 'Favorites', 'Shares', 'Group folders', 'Shared to Circles', 'Deleted files', and 'Files settings'.

# Exercise (Zenodo and DOI)

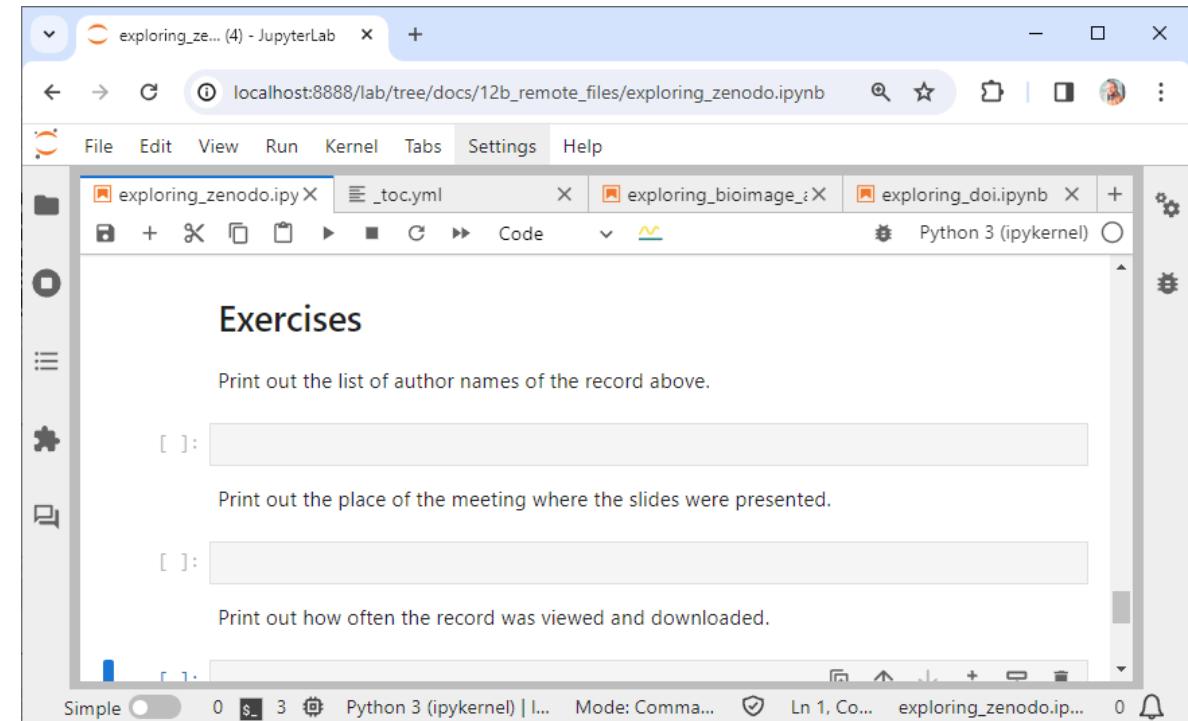
- Explore the DOI and Zenodo APIs to find out the author of online records



The screenshot shows a JupyterLab interface with two tabs open: "exploring\_zenodo.ipynb" and "exploring\_doi.ipynb". The code cell contains the following Python code:

```
[3]: data = read_zendoo("https://zenodo.org/records/3490058")
data
```

The output cell displays the JSON data of the Zenodo record, which includes fields like 'created', 'modified', 'id', 'doi', and 'description'.



The screenshot shows a JupyterLab interface with two tabs open: "exploring\_zenodo.ipynb" and "exploring\_doi.ipynb". The main area contains the following text:

## Exercises

Print out the list of author names of the record above.

```
[ ]:
```

Print out the place of the meeting where the slides were presented.

```
[ ]:
```

Print out how often the record was viewed and downloaded.

```
[ ]:
```

# Exercise

- Clone the training materials repository
- Fix the typo on this page, send a pull-request

