

Cultivating Open Training

Robert Haase

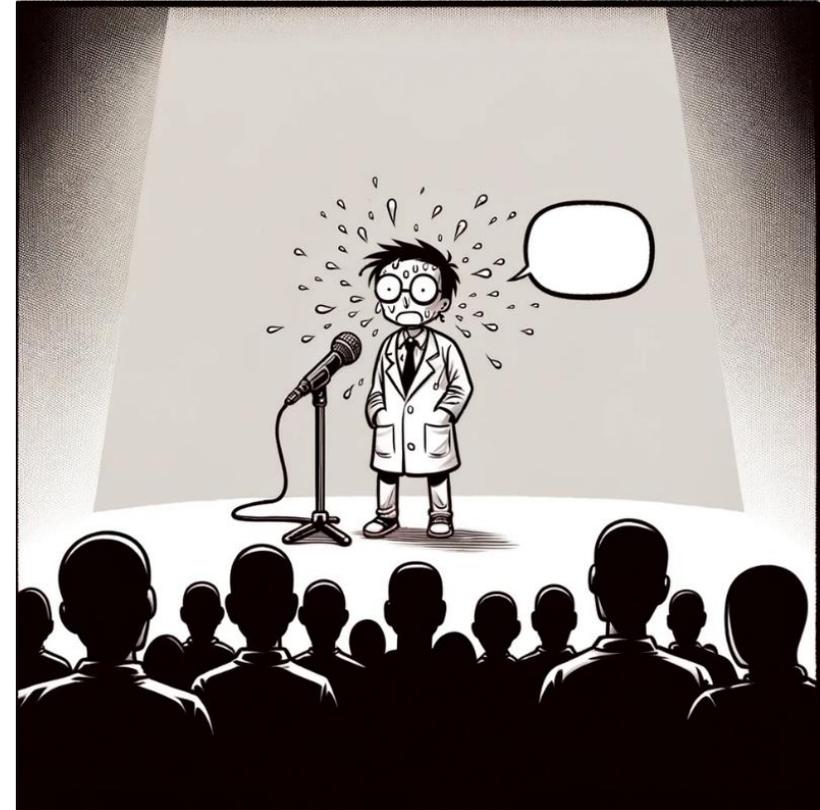


<https://doi.org/10.5281/zenodo.10816895>

Closed science

Why are some science-related materials/data/code not shared?

- Risk of being scooped
- Fear of blaming oneself (imposter syndrome)
- Lack of awareness (who is allowed to publish *my work*?)
- Assumption: it's not worth the effort.

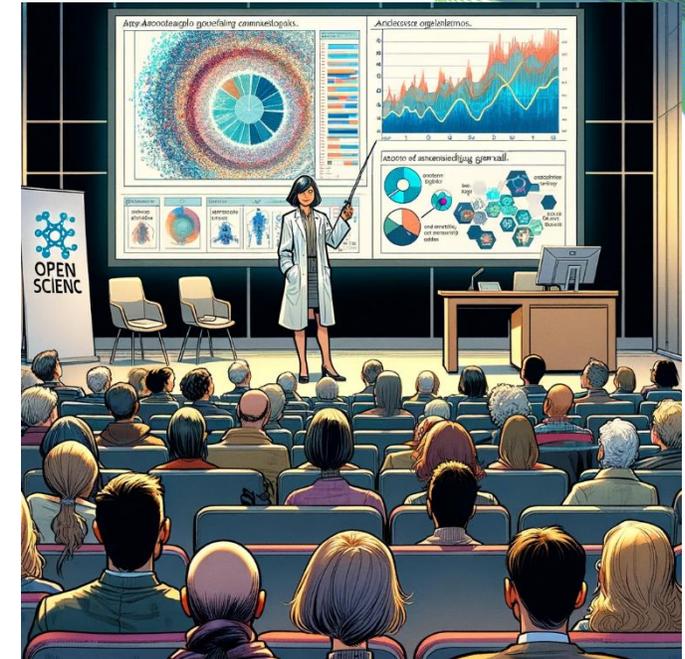


Open Science

- Research related
(hot topics)
- Often tailored towards
general audience
(science communication)
- Earliest at the time a
manuscript is published
(e.g. as preprint)

Open Training

- Routine tasks
(colder topics)
- Transfer of
domain-specific
knowledge



Am I allowed to publish my stuff?

Define responsibilities and procedures early!



"Data / materials we produce will be published under CC-BY 4.0"

"Robert will do this by end of 2025!"

DMP

- Only if procedures are defined early, everyone can follow them.
- Licenses are important when assembling materials (-> Copyright)
- Meta-data might have *higher quality* if the person responsible for publishing the data is aware of their duties.

Are we going to publish data / materials / code?

What license can we use?

Deciding by the end of the project is too late!

Where to share?

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

Github pages

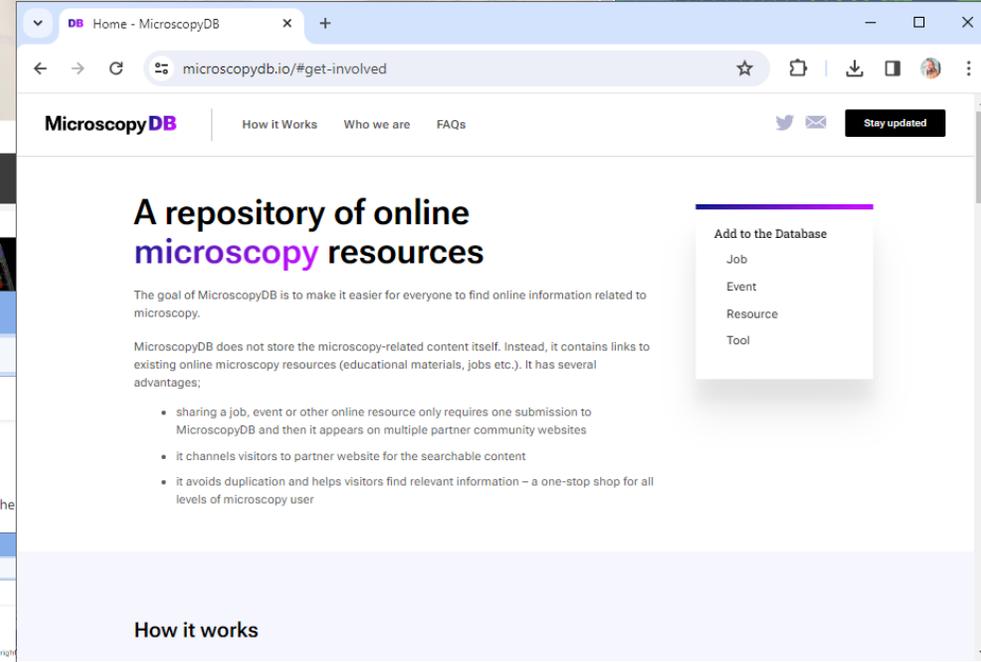
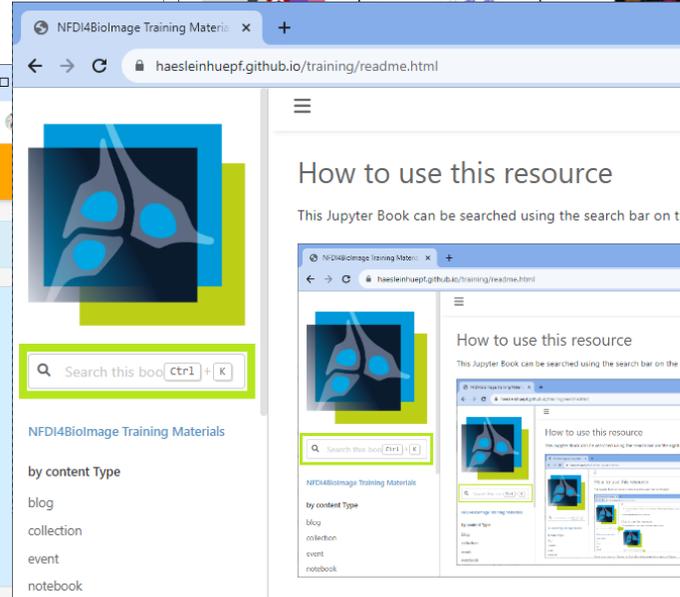
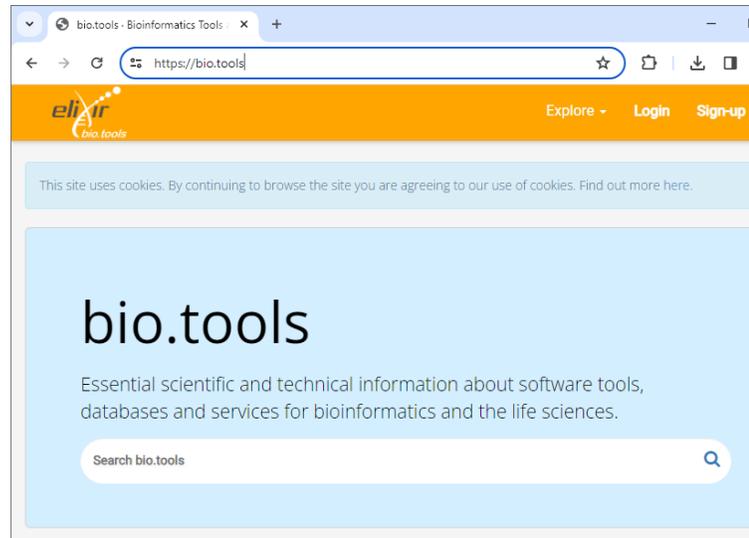
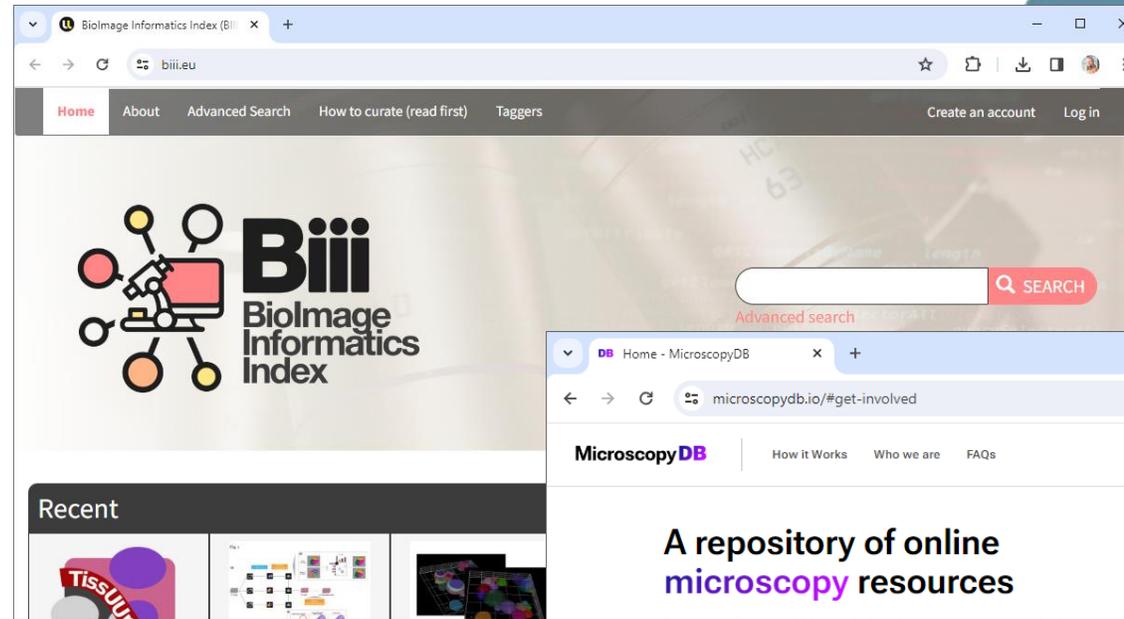


The collage displays several digital sharing and training resources:

- ScaDS AI**: A website for the Prompt Engineering Tutorial, featuring installation instructions and a table of contents.
- GitHub**: A repository for 'Image Analysis Training Resources' with a README and code files.
- F1000Research**: A research paper titled 'Sharing and licensing material' by Robert Haase, dated June 30th 2021.
- Zenodo**: A digital object identifier (DOI) record for 'Train-the-Trainer Concept on Research Data Management', published November 4, 2020, version 3.0.
- JupyterLab**: A screenshot of a notebook interface showing code for generating images using OpenAI's API.

Indexing

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



Licensing: Permissive versus restrictive

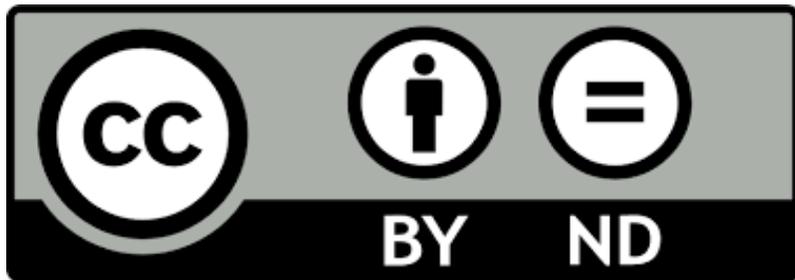
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I conclude, these are less open in a sense



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- Who knows what the ND stands for?



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“restrictive”

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I just would like to
make a point.

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doi: <https://doi.org/10.1101/2024.03.07.583909>

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Kevin J. Cutler, Carsten Stringer, Paul A. Wiggins, Joseph D. Mougous
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Now published in *Nature Methods* doi: 10.1038/s41592-022-01639-4

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Ulysse Rubens, Romain Mormont, Lassi Paavolainen, Volker Bäcker, Gino Michiels, Benjamin Pavie, Leandro A. Scholz, Martin Maška, Devrim Ünay, Graeme Ball, Renaud Hoyoux, Rémy Vandaele, Ofra Golani, Anatole Chessel, Stefan G. Stanciu, Natasa Sladoje, Perrine Paul-Gilloteaux, Raphaël Marée, Sébastien Tosi

doi: <https://doi.org/10.1101/707489>

Now published in *Patterns* doi: [10.1016/j.patter.2020.100040](https://doi.org/10.1016/j.patter.2020.100040)

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Stephen J. Cross, Jordan D.J.R. Fisher, Mark A. Jepson
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Now published in *Journal of Microscopy* doi: 10.1111/jmi.13227

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Robert Haase, Hans-Joachim Böhm, Daniel Zips & Nasreddin Abolmaali

Conference paper

1628 Accesses | 2 Citations | 3 Altmetric

Part of the [Lecture Notes in Computer Science](#) book series (LNAI, volume 7006)

Abstract

For special applications in diagnostics for oncology the analysis of imaging data from Positron Emission Tomography (PET) is obfuscated by low contrast and high noise. To deal with this issue we propose a segmentation algorithm based on Ant Colony Optimization (ACO) and evolutionary selection of ants for self reproduction. The self reproduction approach is no standard for ACO, but appears to be crucial for volume segmentation. This investigation was focused on two different ways for reproduction control and their contribution to quantity and

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Volume 116, Issue 1
January 2012

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Article Contents

- Identifying a Problem
- Limits of Agreement
- Publications
- Summing Up
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Reusing some of your pictures for teaching 2 M

Von: Martin Bland
An: Robert Haase
5. Juni 2020 22:37

You are welcome to use any of my pictures in your teaching. Thanks for asking.

Martin

On Fri, 5 Jun 2020 at 21:24, <rhaase@mpi-cbg.de> wrote:

Dear Prof. Bland,

I hope you are doing well. I'm approaching you because I'm preparing a lecture for students about Bio-statistics at the Technical University Dresden and I would like to use some pictures where you are copyright holder.

I'm referring to the photos published in this article:

<https://anesthesiology.pubs.asahq.org/article.aspx?articleid=1933992>

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Restrictive licensing is
a community-wide issue.

I presume due to lack of
awareness & training

Train the trainers!

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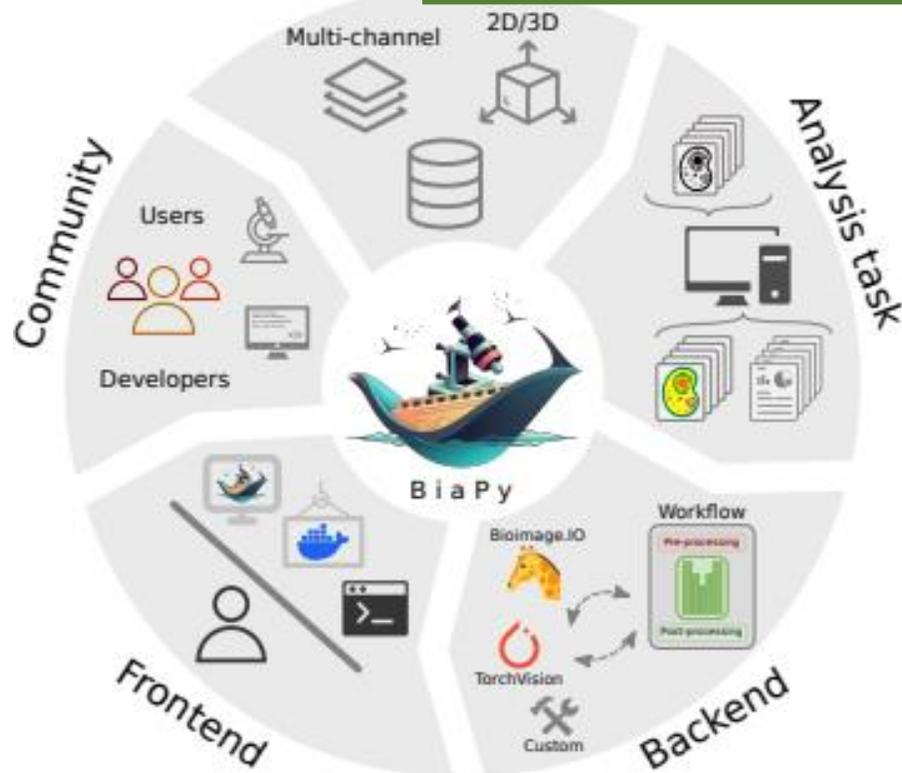
Bad for the progress of science

In particular in the context of training

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DOI: <https://doi.org/10.1101/2024.02.03.576026>

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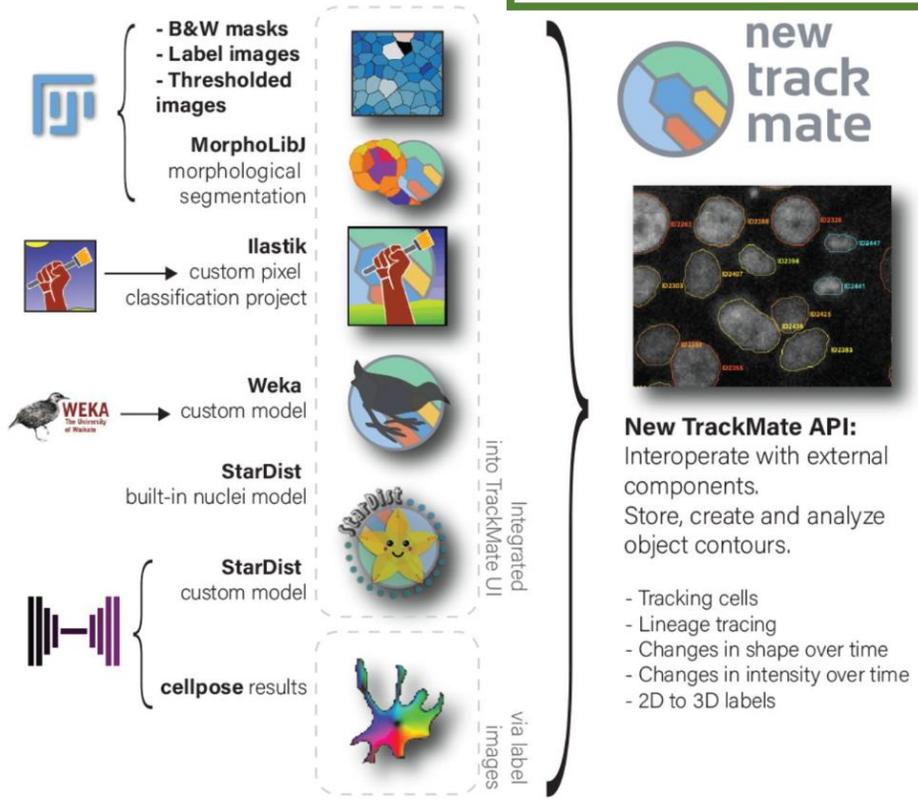
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Bringing TrackMate into the era of machine-learning and deep-learning

Dmitry Ershov, Minh-Son Phan, Joanna W. Pylvänäinen, Stéphane U. Rigaud, Laure Le Blanc, Arthur Charles-Orszag, James R.W. Conway, Romain F. Laine, Nathan H. Roy, Daria Bonazzi, Guillaume Duménil, Guillaume Jacquemet, Jean-Yves Tinevez

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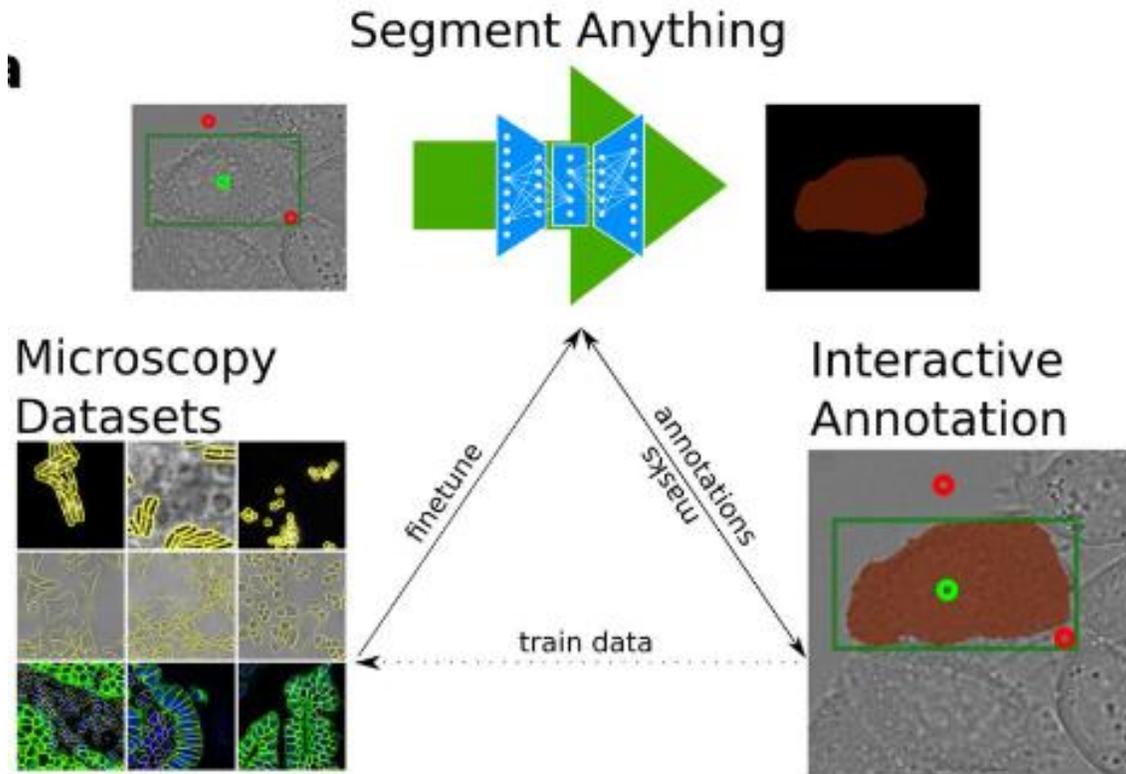
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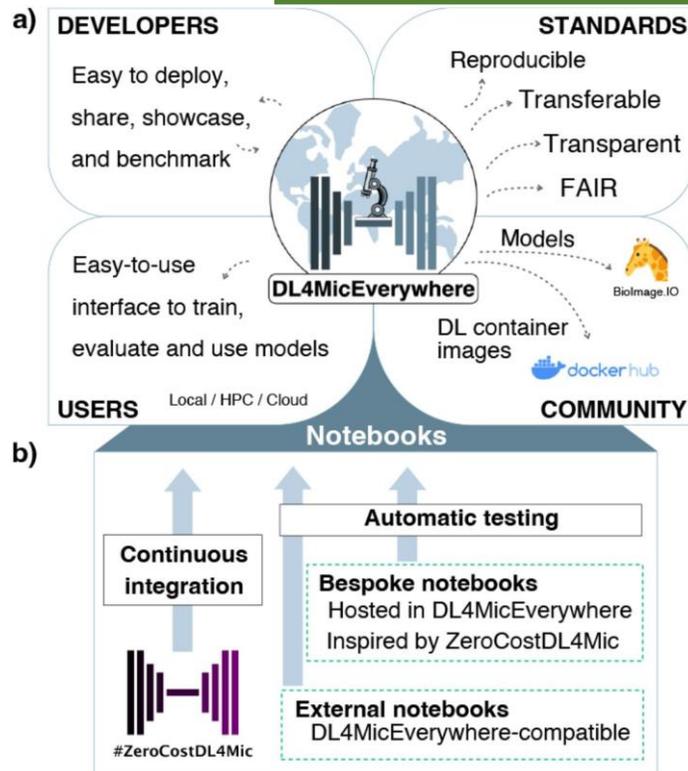


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DL4MicEverywhere: Deep learning for microscopy made flexible, shareable, and reproducible

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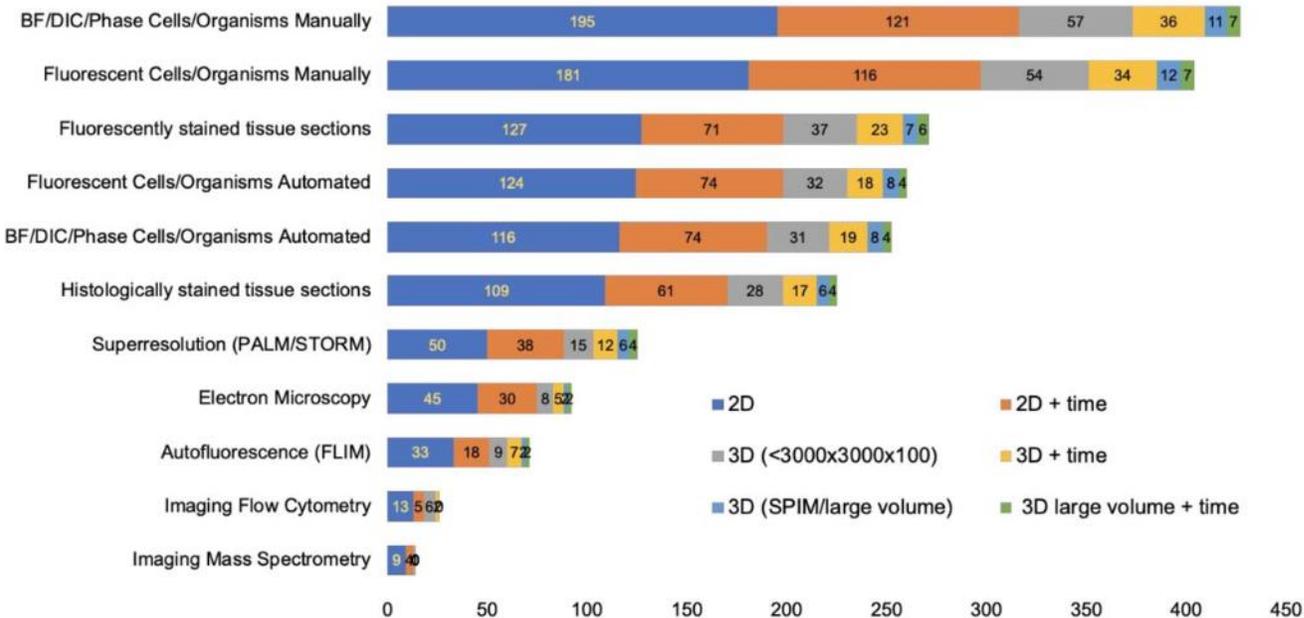
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What kinds of images do you commonly want to analyze?



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2020 BioImage Analysis Survey: Community experiences and needs for the future

Nasim Jamali, Ellen TA Dobson, Kevin W. Eliceiri, Anne E. Carpenter, Beth A. Cimini

doi: <https://doi.org/10.1101/2021.08.16.456498>

Now published in *Biological Imaging* doi: [10.1017/S2633903X21000039](https://doi.org/10.1017/S2633903X21000039)

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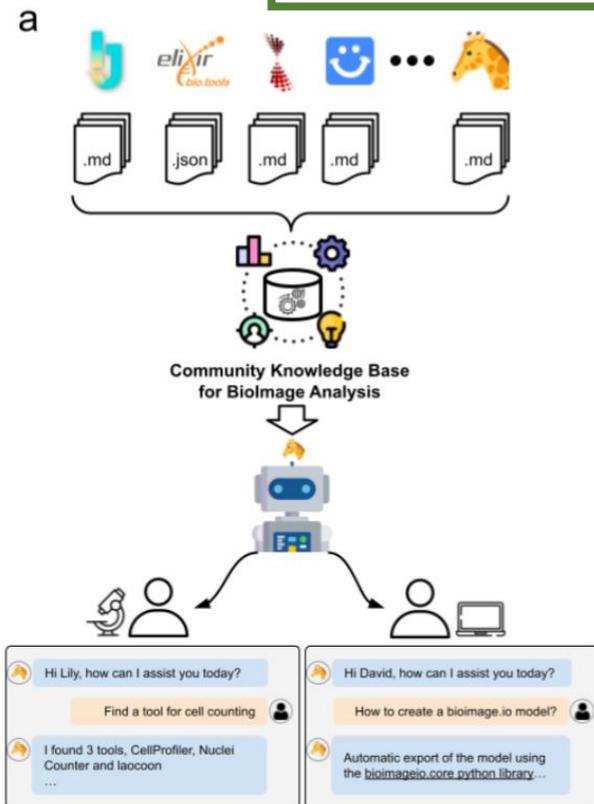
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Biolmage.IO

Published December 5, 2023 | Version v2

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Biolmage.IO Chatbot: A Personalized Assistant for Biolmage Analysis Augmented by Community Knowledge Base

Lei, Wanlu^{1,2}; Fuster-Barceló, Caterina^{3,4}; Muñoz-Barrutia, Arrate^{3,4}; Ouyang, Wei¹

Version v2 Dec 5, 2023
Version 0.1.0 Oct 23, 2023

Additional details

Identifiers DOI 10.48550/arXiv.2310.18351

Related works Is identical to Publication: 10.48550/arXiv.2310.18351 (DOI)

Funding Horizon Europe research and innovation programme 101057970 European Commission

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Bruno M. Saraiva, Inês M. Cunha, António D. Brito, Gautier Follain, Raquel Portela, Robert Haase, Pedro M. Pereira, Guillaume Jacquemet, Ricardo Henriques

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Example

Look at this great figure! It's taken from M. Hartley et al.

The screenshot shows the BioImage Archive interface. At the top, there is a search bar with the text "Search BioImages" and "Examples: brain, cap40". Below the search bar, there are navigation links: Home, Browse, Submit, About us, and Feedback. The main content area displays the title "The glucosylceramide synthase inhibitor PDMP causes lyso-somal lipid accumulation and mTOR inactivation" by Pia Hartwig and Doris Höglinger. The accession number is S-BIAD144. A description follows: "We investigated subcellular sphingolipid distribution using a functionalized sphingosine analogue (pacSph) by confocal microscopy in control, PDMP and NB-DNJ (Miglustat) treated WT and SGPL1 knock-out cells". Below the description, there is a "Data files" section with a table of results.

Name	Size	Section	staining	cells	labelling	treatment	Channel 1	Channel 2	timepoint
experimentA_11_WT_Miglustat.czi	1.6 MB	Study Component	click chemistry and IF	WT	pacSph	50 µM NB-DNJ (Miglustat)	pacSph	Lamp1	continuous labelling
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experimentA_13_SGPL1_PDMP.czi	1.6 MB	Study Component	click chemistry and IF	SGPL1 ^{-/-}	pacSph	20 µM PDMP	pacSph	Lamp1	continuous labelling

The screenshot shows the bioRxiv preprint server interface. The article title is "The Biolmage Archive - building a home for life-sciences microscopy data" by Matthew Hartley, Gerard J. Kleywegt, Ardan Patwardhan, Ugis Sarkans, Jason R. Swedlow, and Alvis Brazma. The DOI is https://doi.org/10.1101/2021.12.17.473169. The article is published in the Journal of Molecular Biology with DOI 10.1016/j.jmb.2022.167505. The article information section shows the DOI, history (February 11, 2022), and article versions (Version 1 (December 21, 2021 - 20:06) and Version 2 (the most recent version)). The copyright notice states: "The copyright holder has placed this preprint in the Public Domain. It is no longer restricted by copyright. Anyone can legally share, reuse, remix, or adapt this material for any purpose without crediting the original authors." The subject area is Bioinformatics.

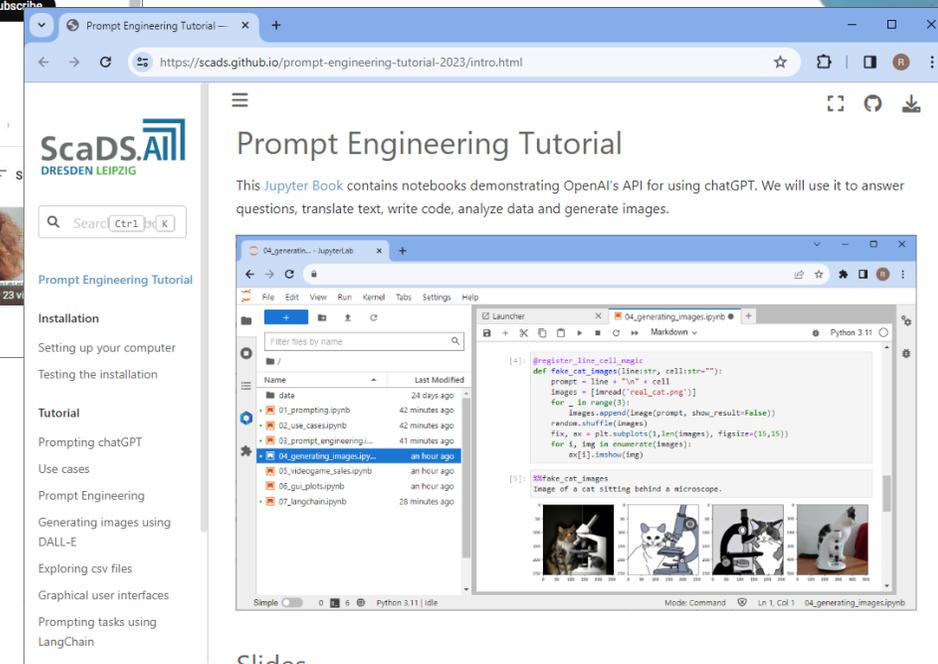
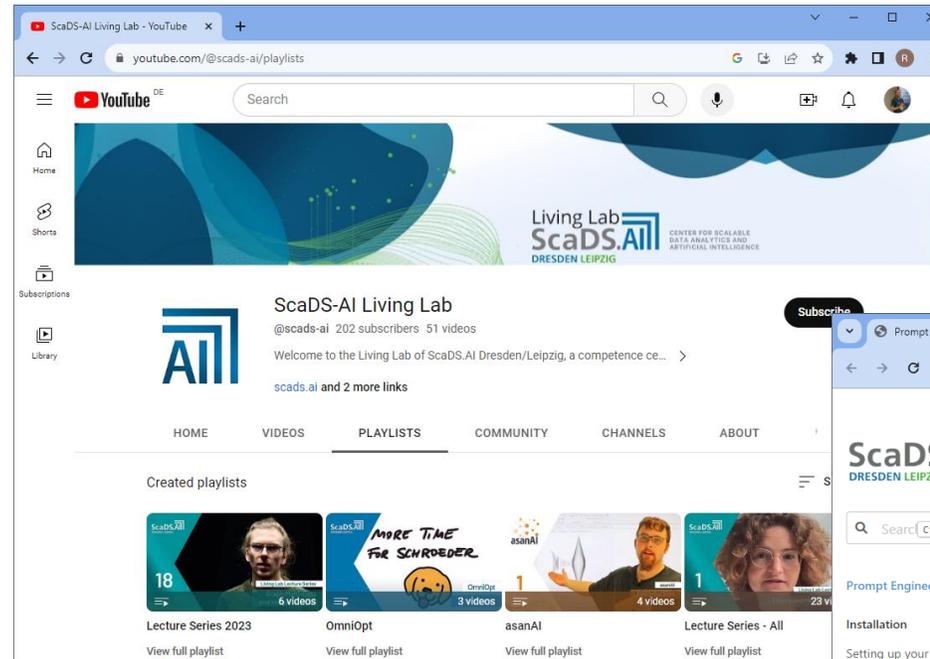
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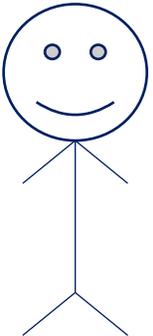
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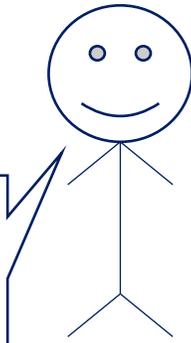
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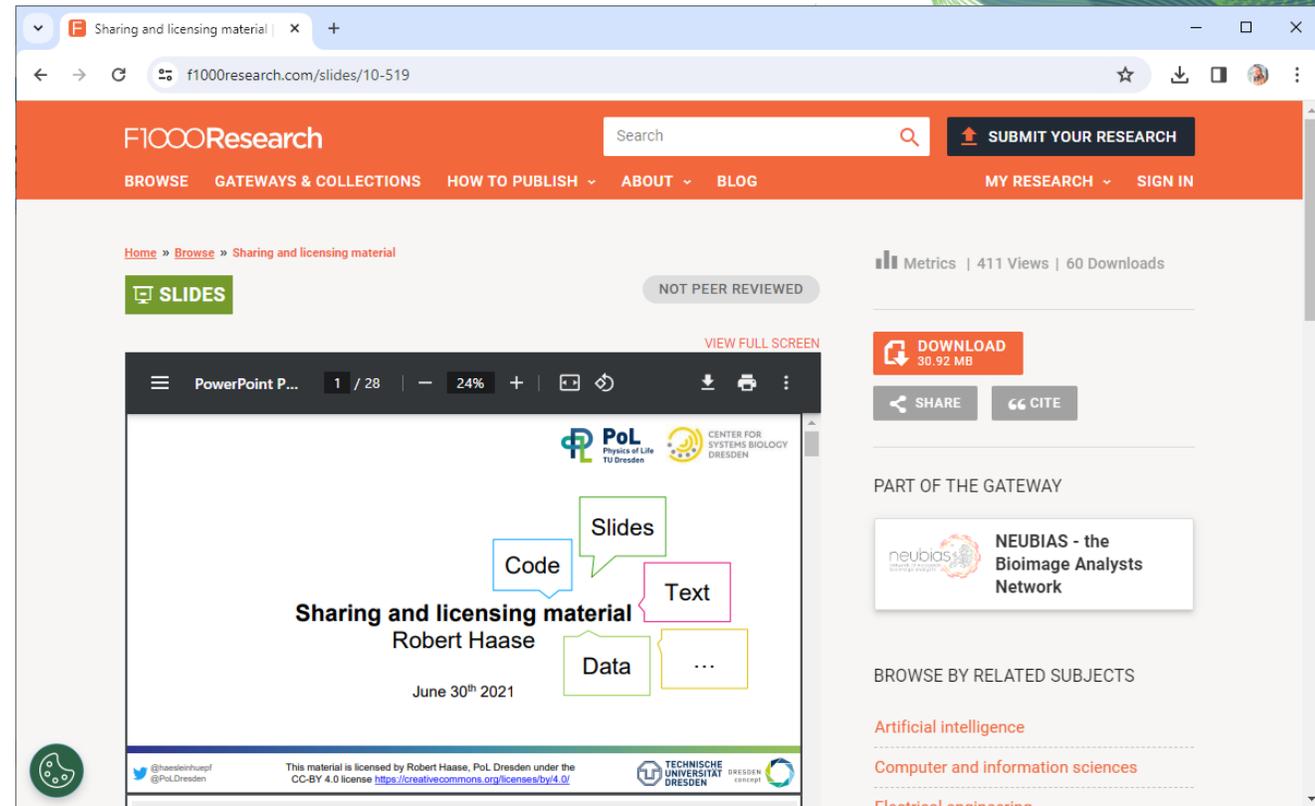


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The screenshot shows a slide presentation on the F1000Research website. The slide title is "Interactive Image Data Flow Graphs and GPU-accelerated image processing for everyone" by Robert Haase. The slide content includes a 3D visualization of a cell with a network of green and purple lines. The slide is part of a 17-slide presentation. The website interface shows a search bar, navigation menu, and a "SUBMIT YOUR RESEARCH" button. The slide is marked as "NOT PEER REVIEWED". The metrics for this slide are 329 Views and 32 Downloads. The slide is part of the NEUBIAS - the Bioimage Analysts Network. The slide is also part of the Gateway. The slide is related to Artificial intelligence and Computer and information sciences.

The screenshot shows a slide presentation on the F1000Research website. The slide title is "Interactive Image Data Flow Graphs and reproducible GPU-accelerated image processing" by Martin Schätz. The slide content includes a 3D visualization of a cell with a network of green and purple lines. The slide is part of a 33-slide presentation. The website interface shows a search bar, navigation menu, and a "SUBMIT YOUR RESEARCH" button. The slide is marked as "NOT PEER REVIEWED". The metrics for this slide are 20 Views and 5 Downloads. The slide is part of the NEUBIAS - the Bioimage Analysts Network. The slide is also part of the Gateway. The slide is related to Artificial intelligence and Computer and information sciences.



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Communities & platforms

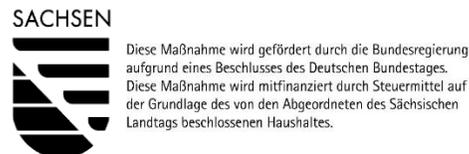


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