

# FAIRy deep-learning for bioimage analysis

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Optical Cell Biology Group (Prof. Ricardo Henriques)

Instituto Gulbenkian de Ciência



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# Microscopy imaging: be ready to play

**Recommendation:** Use image processing in the loop & improve the quality of your workflow



## How can we make it accessible?

- Widefield
  - Confocal
  - SMLM
  - DIC
  - EM
- Channel unmixing
  - Image classification
  - Object detection
- Segmentation
  - Detection
  - Classification
  - Tracking
- Morphology
  - Lineages
  - Embedded features
  - Data distributions
- Statistics
  - Visualisation



- High-throughput
  - High-content
  - Multispectral
- Denoising
  - Restoration
  - Super-resolution
  - Registration



## Deep learning playground

**Open-source science (technology)**

**Reliable**

**User friendly (accessible)**

Open-source science (technology)

Reliable

User friendly (accessible)

...

2015

2017

2018

### First U-Net development



```

README.txt
This is the implementation of the u-net described in:
O. Ronneberger, Philipp Fischer, Thomas Brox:
U-Net: Convolutional Networks for Biomedical Image Segmentation.
In: Medical Image Computing and Computer-Assisted Intervention (MICCAI), 2015
http://arxiv.org/abs/1505.04597

It contains the ready trained network, the source code, the matlab
libraries of the modified caffe network, all essential third party
libraries, the matlab interface for overlaid segmentation and a
greedy tracking algorithm used for our submission for the ISBI cell
tracking challenge 2015. Everything is compiled and tested only on
Ubuntu Linux 14.04 and Matlab 2014b (64).

To apply the segmentation and the tracking to the images in
"MC-C20-037482" simply run the shell script
./segmentAndTrack.sh

The resulting segmentation masks will be written to
"MC-C20-037482".

If you do not have a CUDA-capable GPU or your GPU is smaller than
mine, edit segmentAndTrack.sh accordingly (see there for
documentation).

If you have any questions, you may contact me at
ronneber@informatik.uni-freiburg.de, but be aware that I can not
provide any support.

```

**README with description of the zip**

- C++ and Caffe binaries

O. Ronneberger & T. Brox, MICCAI 2015

### Papers with code

#### Our Mission

The mission of Papers with Code is to create a free and open resource with Machine Learning papers, code, datasets, methods and evaluation tables.

We believe in open science by NLP and astronomy.

All content is available as Wikipedia buttons!

We also open source astronomy.

```

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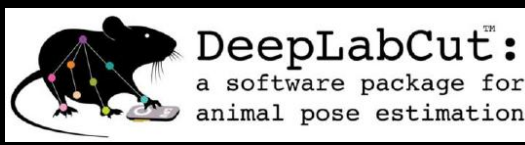
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### README with instructions for code installation and run

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2019

2020

2021

2022

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tracking challenge 2015. Everything is compiled and tested only on
Ubuntu Linux 14.04 and Matlab 2014b (64bit)

To apply the segmentation and the tracking to the images in
"MC-C20-0373481" simply run the shell script
./segmentAndTrack.sh

The resulting segmentation masks will be written to
"MC-C20-0373481_2015"

If you do not have a CUDA-capable GPU or your GPU is smaller than
mine, edit segmentAndTrack.sh accordingly (see there for
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**We believe in**  
by NLP and

**All content as Wikipedia buttons!**

**We also open**  
astronomy,

### README with instructions for code installation and run

```

=====
# README

# About
This folder contains the source code for the U-Net described in
Olaf Ronneberger, Philipp Fischer, Thomas Brox:
U-Net: Convolutional Networks for Biomedical Image Segmentation.
In: Medical Image Computing and Computer-Assisted Intervention (MICCAI), 2015
http://arxiv.org/abs/1505.04597

# Installation
1. Clone this repository
git clone https://github.com/ronneber/u-net.git
cd u-net

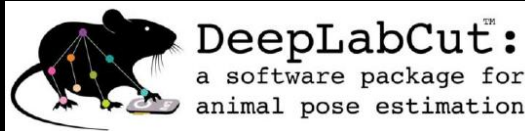
2. Set up the new environment.
See the README file for more details.

3. Run the script
./segmentAndTrack.sh

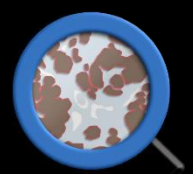
# Usage
The script will process the images in the folder 'input' and save the
segmentation masks in the folder 'output'.

# License
This code is licensed under the Creative Commons Attribution-NonCommercial-ShareAlike license.

```



ALLEN INSTITUTE for CELL SCIENCE



# Community meeting the challenges for machine learning enabled bioimage analysis

- ImageJ / Fiji plugins

- CSBDeep
- Noise2Void
- DenoiSeg
- StarDist
- DeepImageJ

- Weka
- CellProfiler
- DeepCell
- Cellpose
- Google Colab\*
- ZeroCostDL4Mic
- DeepTrack
- DeepLabCut
- MONAI
- LiveCellMiner
- DeepMIB

- Ilastik
- Knime
- Icy
- Qupath

## Community making it possible

Scientific Community Image forum: <https://forum.image.sc>

NEUBIAS Academy@Home: <http://eubias.org/NEUBIAS/training-schools/neubias-academy-home/>

COBA center (Cimini & Carpenter): <https://openbioimageanalysis.org/>

iBiology: <https://www.ibiology.org/biology-online/>

BioImage Informatics Index: <https://biii.eu/>



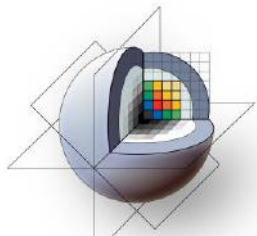
cellpose



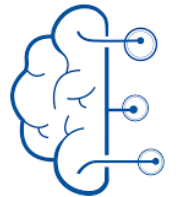
deepImageJ



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CELL SCIENCE



3DSlicer



DEEPTRACK 2.1



napari



CellProfiler™  
cell image analysis software



WEKA  
The University  
of Waikato



Open for Innovation

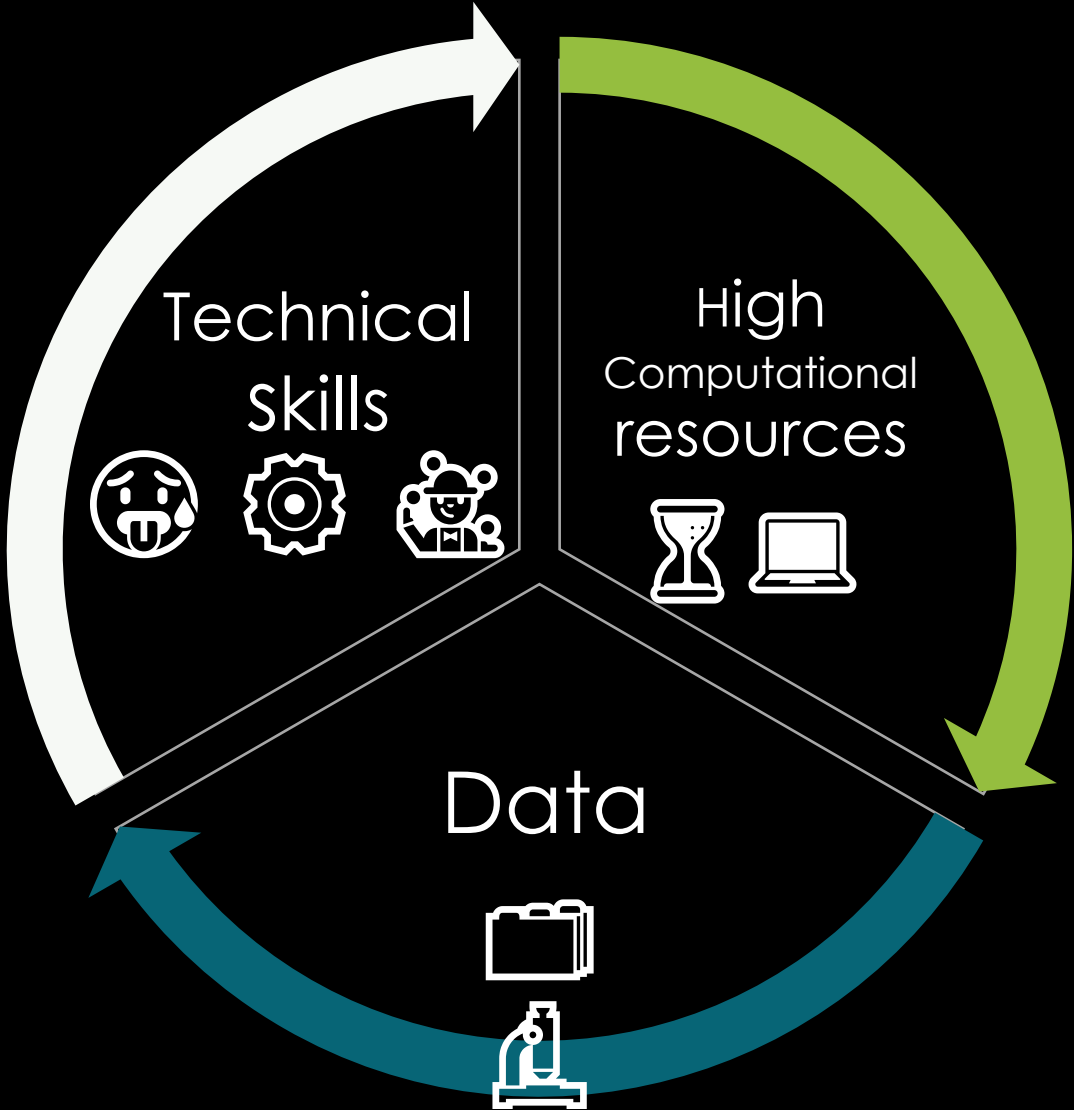
KNIME



DeepLabCut™

a software package for  
animal pose estimation

# CHALLENGES FOR ACCESSIBILITY



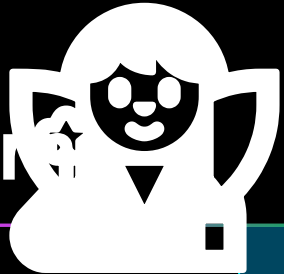
# Deep learning:

an extremely hot topic in the field 🏆

... and FAIRy\* open-source solutions, the jewel in the crown

\*Findable, Accessible, Interoperable and Reusable

## FAIRy deep-learning ecosystem



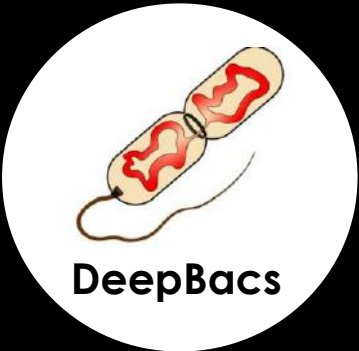
Open-source science (technology)



User friendly frameworks



Resources Computational & Data



Standards



Transfer learning

E. Gómez-de-Mariscal\*, C. García-López-de-Haro\*, et al., Nature Methods 2021  
L. von Chamier et al., Nature Communications 2021  
O. Wei\*, F. Beuttenmueler\*, E. Gómez-de-Mariscal\*, C. Pape\* et al., bioRxiv 2022

C. Spahn, E. Gómez-de-Mariscal, ..., R. Henriques, Communications Biology 2022  
I. Hidalgo-Cenalmor et al., bioRxiv 2023

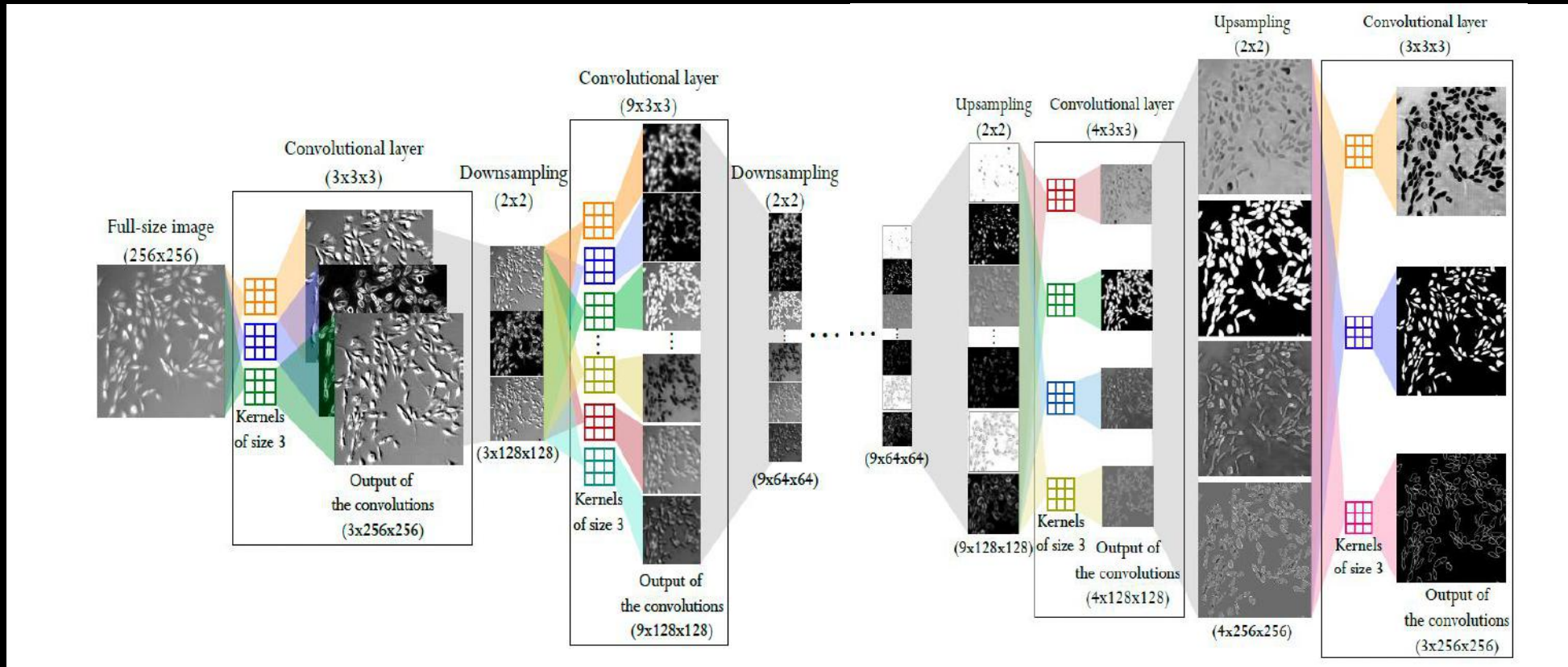


# What is a (pre)trained model?

- Architecture
- Trained Weights



Once trained, the model state is frozen and the inference consists of running a series of static operations (e.g., convolutions, downsampling)



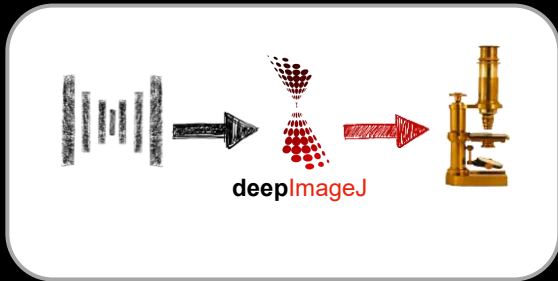
Back in 2018...



Arrate Muñoz Barrutia



Daniel Sage



ImageJ is fully equipped for scientific image  
VISUALIZATION and QUANTIFICATION



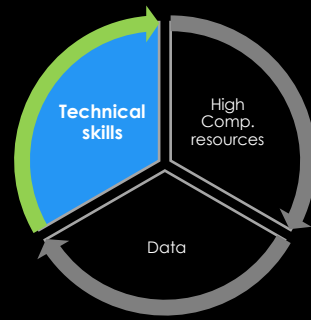
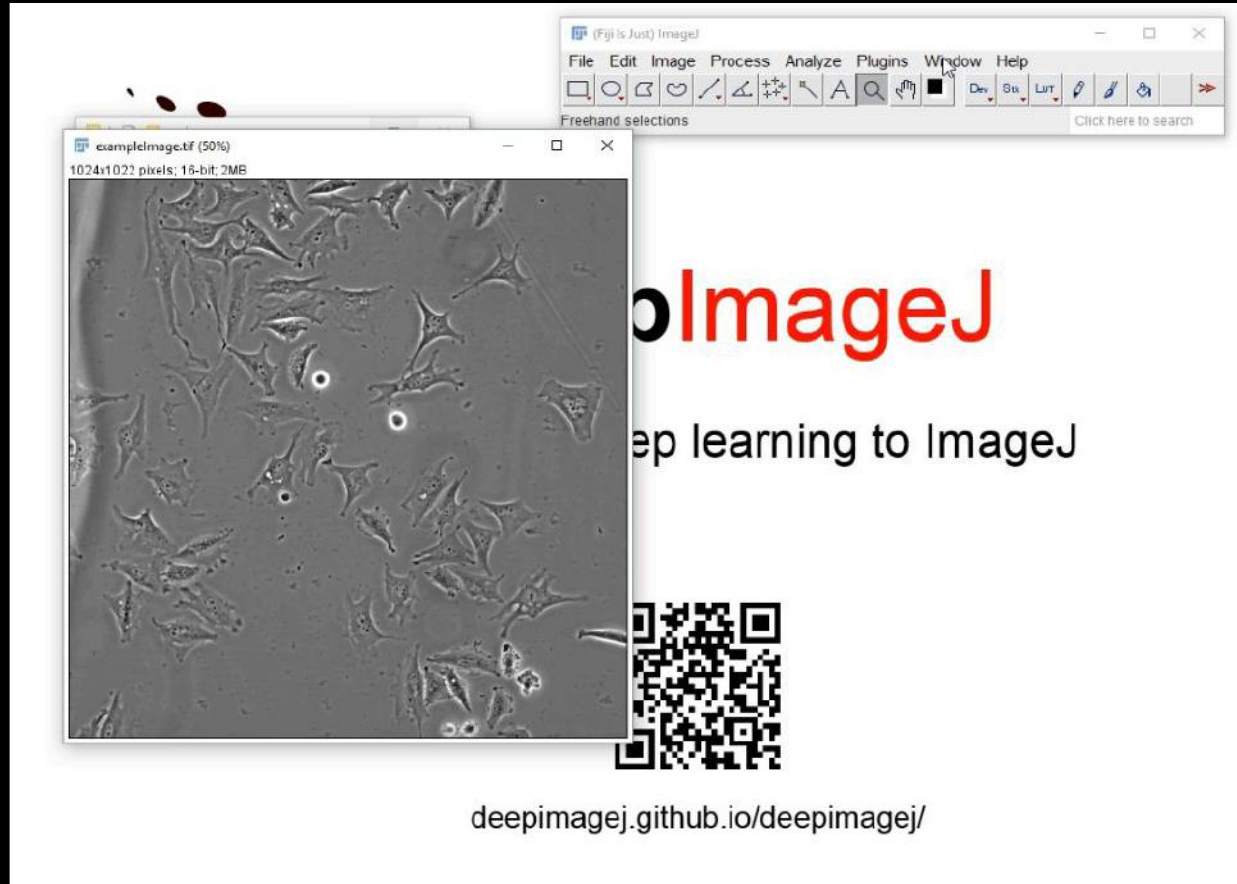
Estibaliz Gómez de Mariscal



Carlos García López de Haro



Wei Ouyang



Schneider, C. A., et al., Nature Methods, 2012  
 Rueden, C. T., et al., BMC Bioinformatics, 2017  
 Schindelin, J., et al., Nature Methods, 2012

**BRIEF COMMUNICATION** <https://doi.org/10.1038/s41592-021-01262-9> **nature methods**

**DeepImageJ: A user-friendly environment to run deep learning models in ImageJ**

Estibaliz Gómez-de-Mariscal<sup>1,5</sup>, Carlos García-López-de-Haro<sup>1,5</sup>, Wei Ouyang<sup>2</sup>, Laurène Donati<sup>3</sup>, Emma Lundberg<sup>4</sup>, Michael Unser<sup>1</sup>, Arrate Muñoz-Barrutia<sup>1,5</sup> and Daniel Sage<sup>1,5</sup>



Fully equipped for scientific image VISUALIZATION and

QUANTIFICATION

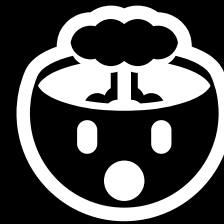
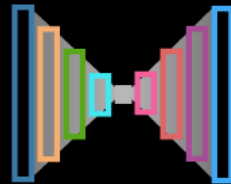


**“How can I apply it to my data?”**



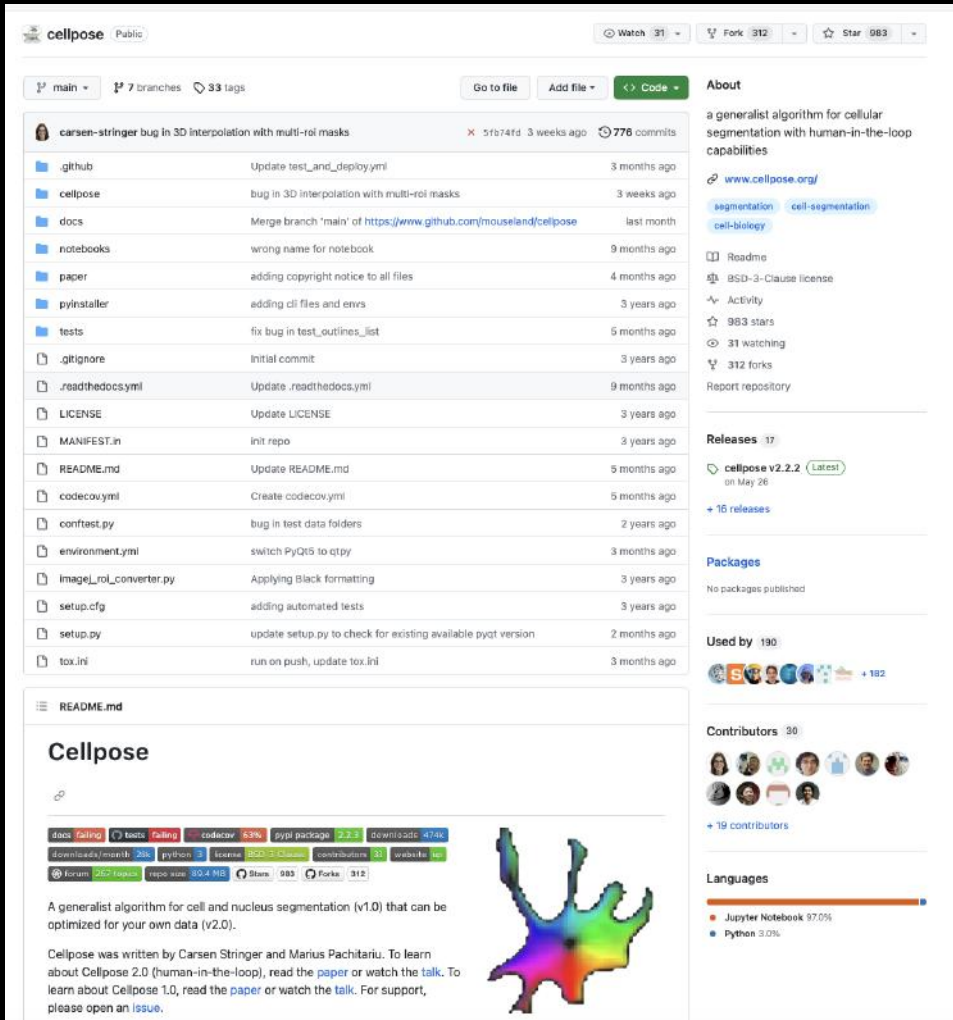
(Re-)training

Fine-tuning



# DL-based image processing is mostly about Python code

How easy could it be?



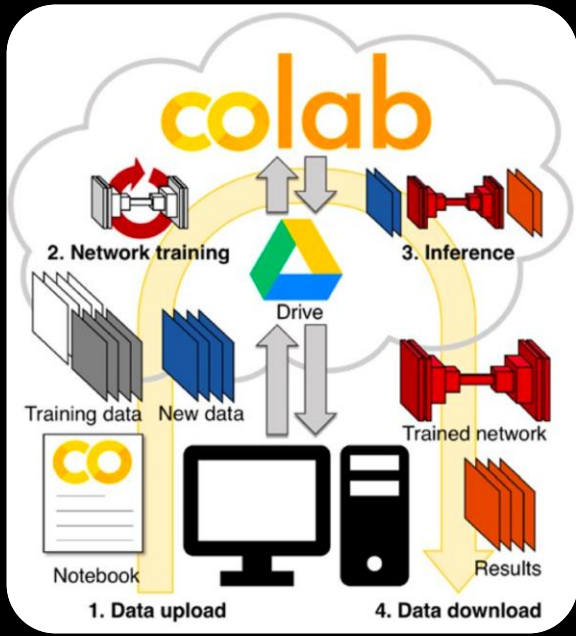
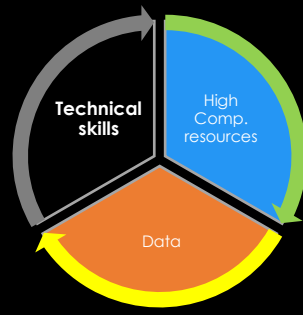
The screenshot shows the GitHub repository for Cellpose. At the top, it indicates the repository is public, with 31 watches, 312 forks, and 983 stars. The main content area lists recent commits, including updates to test files, documentation, and the README. The README section is expanded, showing the Cellpose logo and a colorful cell segmentation image. The README text describes Cellpose as a generalist algorithm for cell and nucleus segmentation, optimized for user data. It also lists various statistics such as downloads, license (BSD-3-Clause), and contributors.



There should be a way  
to make it easy



# ZeroCostDL4Mic: full user-friendly deep learning experience



Lucas von Chamier



Romain Laine



Guillaume Jacquemet



Ricardo Henriques

## Tasks and networks implemented by ZeroCostDL4Mic

<https://github.com/HenriquesLab/ZeroCostDL4Mic>

L. von Chamier et al., Nat Comms 2021

Unified user-friendly interface

→ No coding



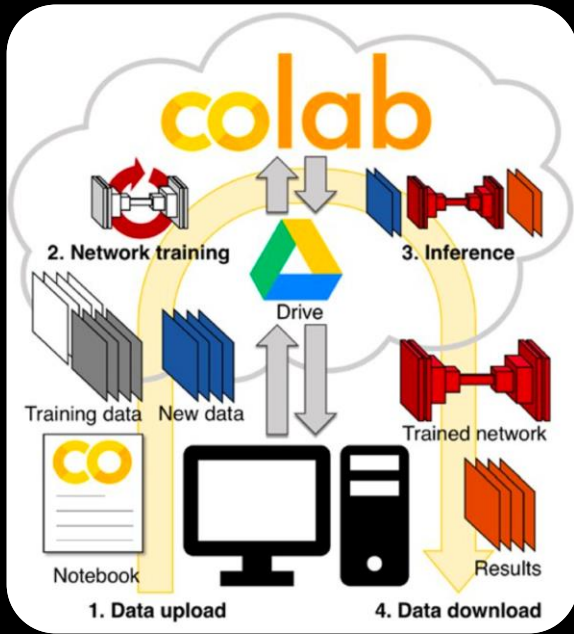
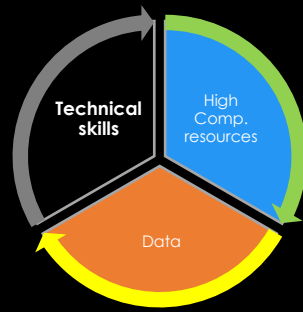
 Open in Colab

FREE GPU service





# ZeroCostDL4Mic: full user-friendly deep learning experience



L. von Chamier et al., Nat Comms 2021

Unified user-friendly interface  
→ No coding



 Open in Colab

FREE GPU service



Lucas von Chamier



Romain Laine





Guillaume Jacquemet



Ricardo Henriques

Directly open the notebooks  
from the documentation

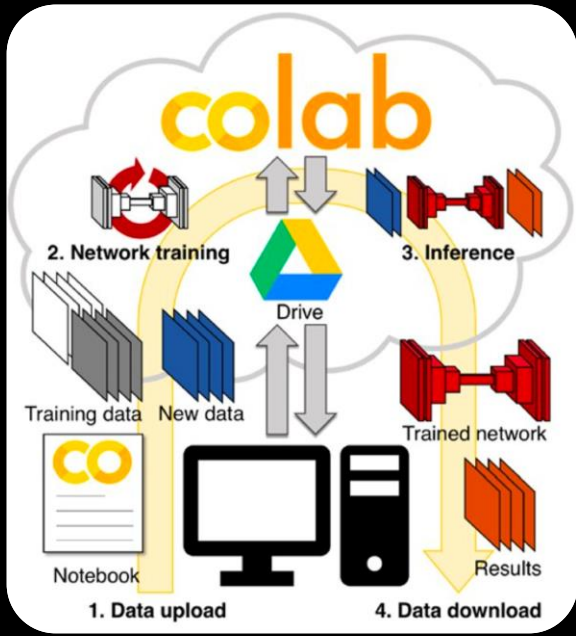
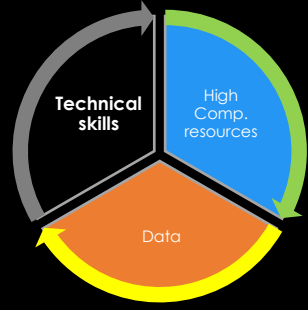
Segmentation networks						
Network	Paper(s)	Tasks	Status	Last test	Link to example training and test dataset	Direct link to the notebook in Colab
U-Net (2D)	<a href="#">here and here</a>	Binary segmentation	Fully supported	27/07/23  working (IH)	<a href="#">here</a>	<a href="#">Open in Colab</a>
U-Net (3D)	<a href="#">here</a>	Binary segmentation	Fully supported	27/07/23  working (IH)	<a href="#">EPFL dataset</a>	<a href="#">Open in Colab</a>
U-Net (2D) multilabel	<a href="#">here and here</a>	Semantic segmentation	Under beta-testing	16/07/23  working (IH)	<a href="#">here</a>	<a href="#">Open in Colab</a>
DenoSeg	<a href="#">here</a>	Joint denoising and binary segmentation	Fully supported	 broken (no GPU) (GJ)	<a href="#">Available soon</a>	<a href="#">Open in Colab</a>
StarDist (2D)	<a href="#">here and here</a>	Instance segmentation	Fully supported	10/05/23  working (EGM)	<a href="#">here</a>	<a href="#">Open in Colab</a>
StarDist (3D)	<a href="#">here and here</a>	Instance segmentation	Fully supported	07/10/22  working (GJ)	<a href="#">from Stardist github</a>	<a href="#">Open in Colab</a>
Cellose (2D and 3D)	<a href="#">here</a>	Instance segmentation (Cells or Nuclei)	Fully supported	05/09/23  working (IH)	<a href="#">Coming soon!</a>	<a href="#">Open in Colab</a>
SplineDist (2D)	<a href="#">here</a>	Instance segmentation	Fully supported	07/10/22  working (GJ)	<a href="#">here</a>	<a href="#">Open in Colab</a>
EmbedSeg (2D)	<a href="#">here</a>	Instance segmentation	Under beta-testing	01/07/23  working (ARI)	<a href="#">here</a>	<a href="#">Open in Colab</a>
MaskRCNN (2D)	<a href="#">here</a>	Instance segmentation	Under beta-testing		<a href="#">Coming soon!</a>	<a href="#">Open in Colab</a>
Interactive Segmentation - Kalbu (2D)	<a href="#">here</a>	Interactive instance segmentation	Under beta-testing		<a href="#">Coming soon!</a>	<a href="#">Open in Colab</a>

Denoising and image restoration networks						
Network	Paper(s)	Tasks	Status	Last test	Link to example training and test dataset	Direct link to the notebook in Colab
Noise2Void (2D)	<a href="#">here</a>	Self-supervised denoising	Fully supported	14/07/23  working (IH)	<a href="#">here or here</a>	<a href="#">Open in Colab</a>
Noise2Void (3D)	<a href="#">here</a>	Self-supervised denoising	Fully supported	14/07/23  working (IH)	<a href="#">here</a>	<a href="#">Open in Colab</a>



# ZeroCostDL4Mic: full user-friendly deep learning experience



Lucas von Chamier



Romain Laine



Streamlined deep learning for microbiology



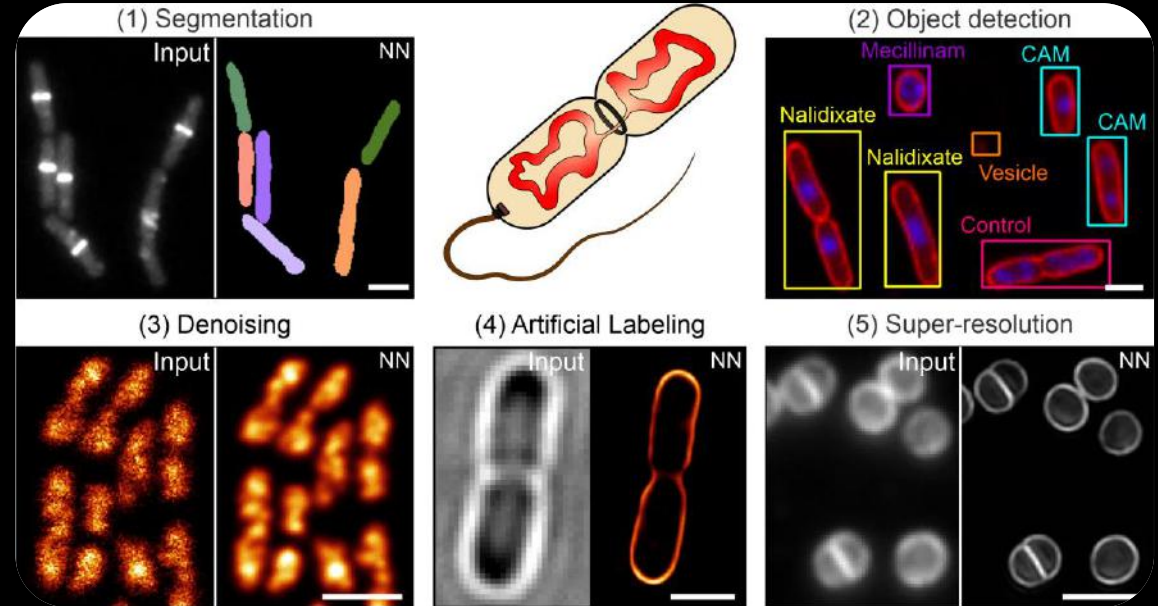
Christoph Spahn



Guillaume Jacquemet



Ricardo Henriques



C. Spahn et al., Communications Biology 2022

Unified user-friendly interface  
→ No coding



Open in Colab

FREE GPU service

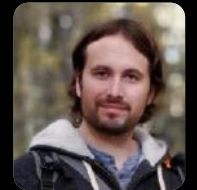




# DL4MicEverywhere: Deep learning for microscopy made flexible, shareable, and reproducible



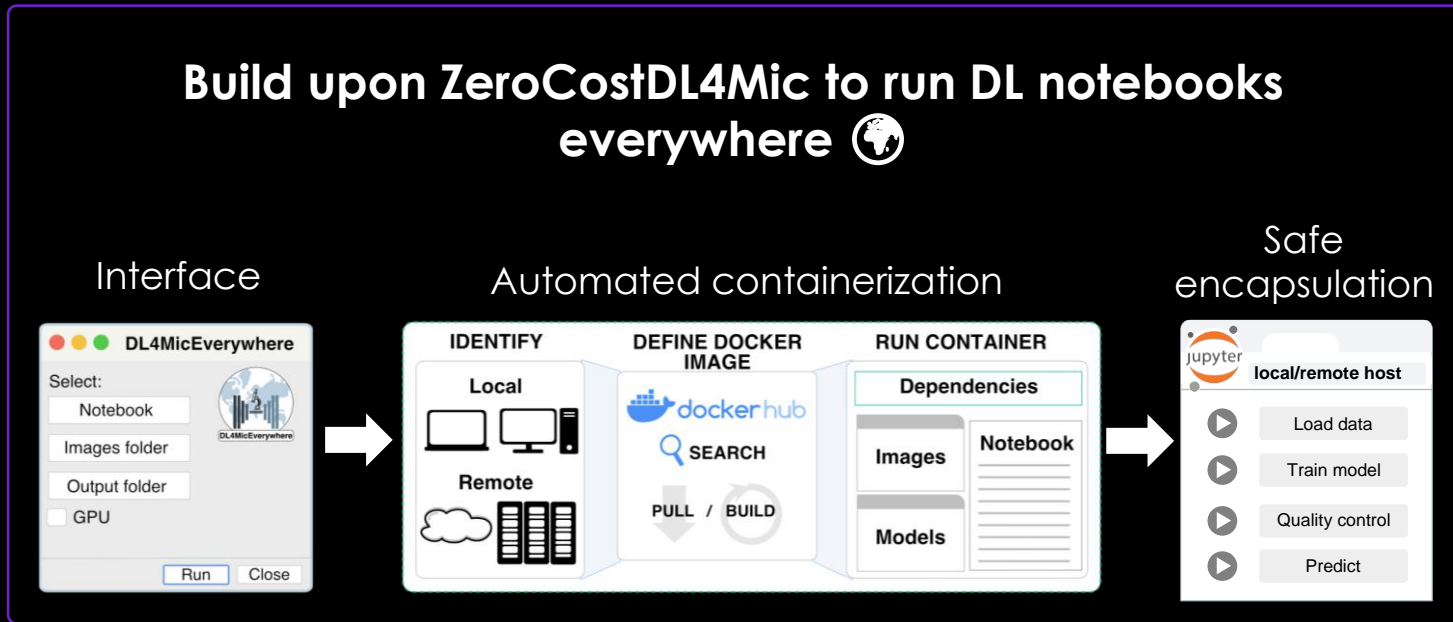
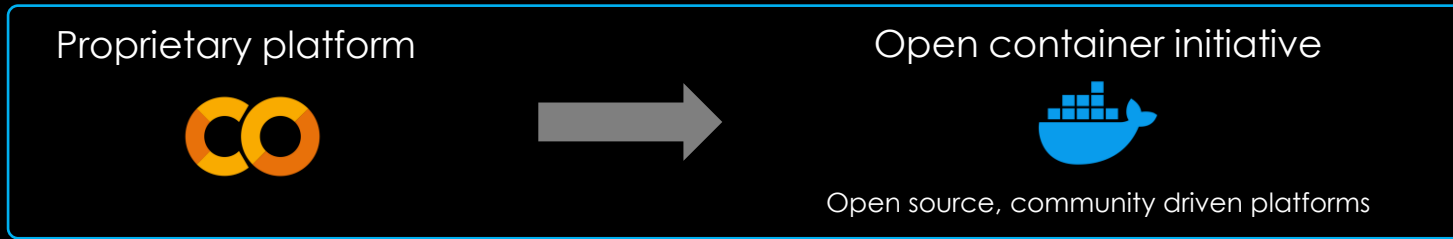
I. Hidalgo-Cenalmor



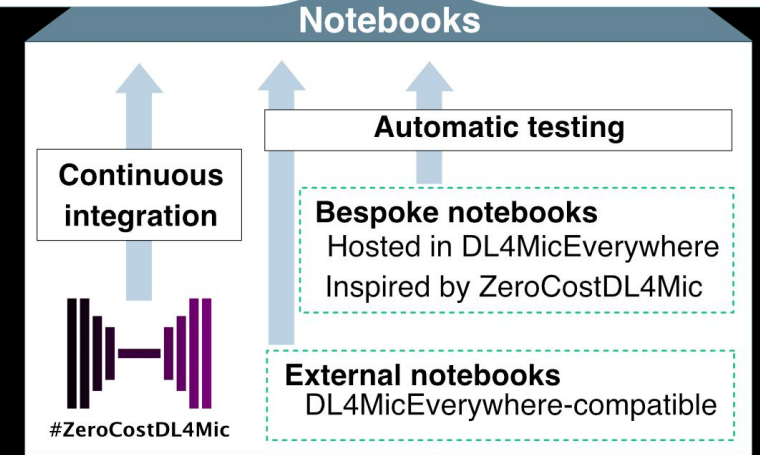
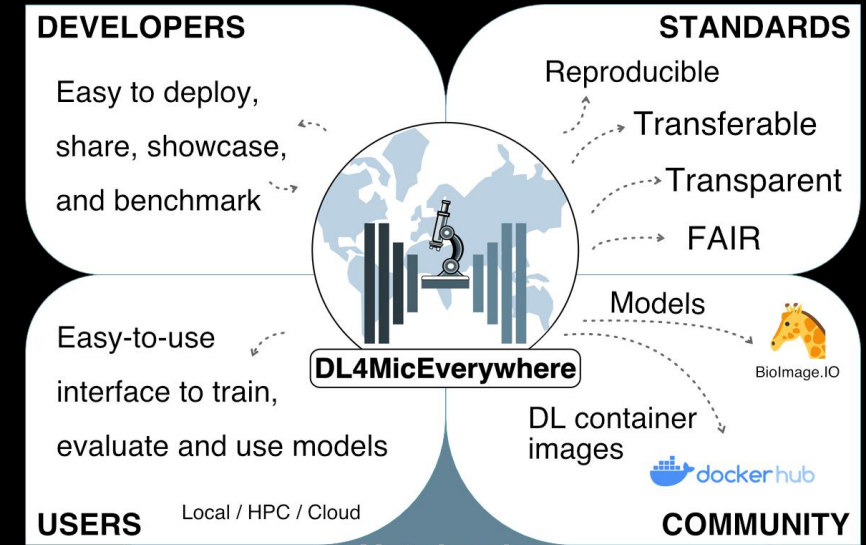
G. Jacquemet



R. Henriques



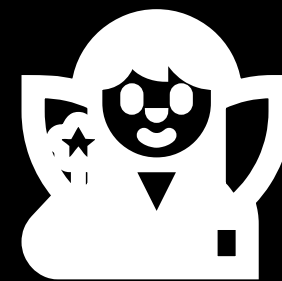
[github.com/HenriquesLab/DL4MicEverywhere/](https://github.com/HenriquesLab/DL4MicEverywhere/)







# FAIRy deep-learning

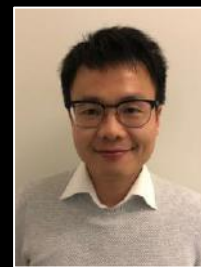


Findable, Accessible, **Interoperable** and Reusable



# BiImage Model Zoo

## Advanced AI models in one-click



Wei Ouyang



Florian Jug



Anna Kreshuk



# FAIRy deep-learning (Findable, Accessible, Interoperable, Reproducible)

**Search and explore the model collection**

**Dataset**

- Link to dataset
- Acquisition & task description, help

**Jupyter notebook**

- Open notebook
- Training & task description, help

**Applications**

- Run
- Interaction with biimage.io content

**Model card**

Trained model for microtubule reconstruction

Download Share DOI License Dataset Notebook

Test run the model

Input Output

Documentation, training data, help... Tests passed

## The trained model

B. Sutilist bacteria segmentation - Widefield microscopy - 2D UNet

10.5281/zenodo.7261974

placid-llama

Contributor: Estibaliz Gómez de Mariscal

zerocostdl4mic deepimage segmentation unet semantic-segmentation cells fluorescence-light-microscopy bacillus-subtilis deepbase 2d tensorflow microbiology bacteria

This trained 2D U-Net model segments the contour, foreground and background of Bacillus Subtilis bac...  
 • Fine tune the model with your data\*  
 • <https://github.com/HenriquesLab/ZeroCostDL4Mic/wiki/BiImage-Model-Zoo>

Spahn C., et al., Comm Biology 2022

## The training data

B. Sutilist bacteria segmentation - Widefield microscopy - 2D UNet

Training Data

Multi-label U-Net training dataset (Bacillus subtilis...  
 Paired bright field images and segmented binary masks of the E...

Test Summary

This model can be used in:

It has been tested with: bioimageio deepimage litstik

How to cite

- Falk et al. Nature Methods 2019 [doi]
- Ronneberger et al. arXiv in 2015 [doi]
- Lucas von Chamier et al. bioRxiv 2020 [doi]

Direct contact with the developer

## The notebook

U-Net (2D) multi-label segmentation - ZeroCostDL4Mic

fluorescence image semantic segmentation (multi-label)

boundary cytoplasm

1 μm

B. Sutilist bacteria segmentation - Widefield microscopy - 2D UNet

egomez commented 19 hours ago Contributor

I see. This is a problem for Java consumers as they need to know the names of the input and output layers.

egomez commented 10 hours ago Contributor

Hi @brave

I'm trying to update this model but the webpage does not allow me. See issue here [biimage.io/biimage.opf42](https://biimage.io/biimage.opf42)

Seems to be working now

@brave I'm hoping I have updated the model. It will take some time to open the PR but the problem should be solved now. If you find yet another problem, we open the issue again!

Write Preview

Sign in to comment

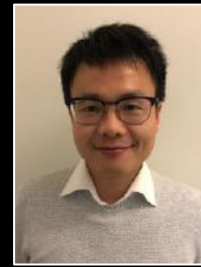
Helping with Markdown is supported

Sign in with GitHub



# BiImage Model Zoo

Advanced AI models in one-click



Wei Ouyang



Florian Jug



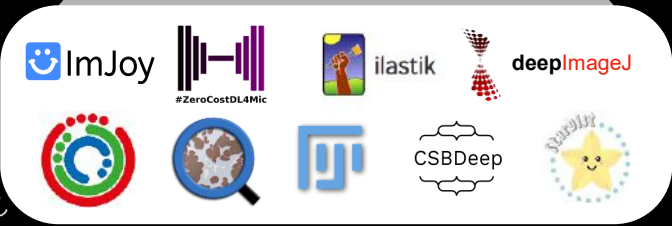
Anna Kreshuk



## Interoperability: From the community for the community



Universal deep learning model format



**Consumer: deepImageJ**

segment nuclei in new data

**Consumer: QuPath**

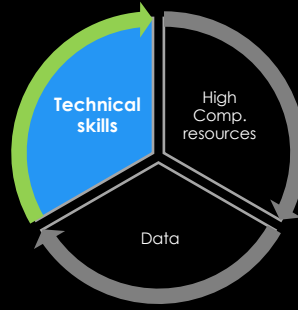
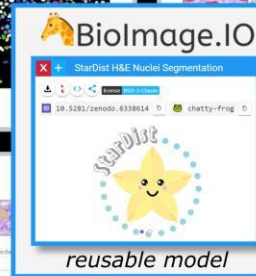
segment, curate, quantify

programmatic use in notebook

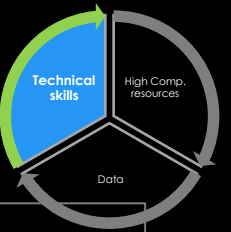
Consumer: **ZeroCostDL4Mic**

programmatic use in python

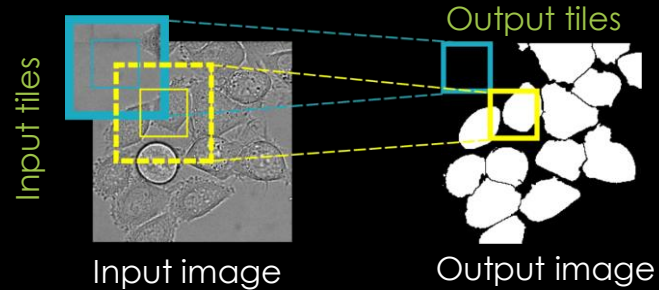
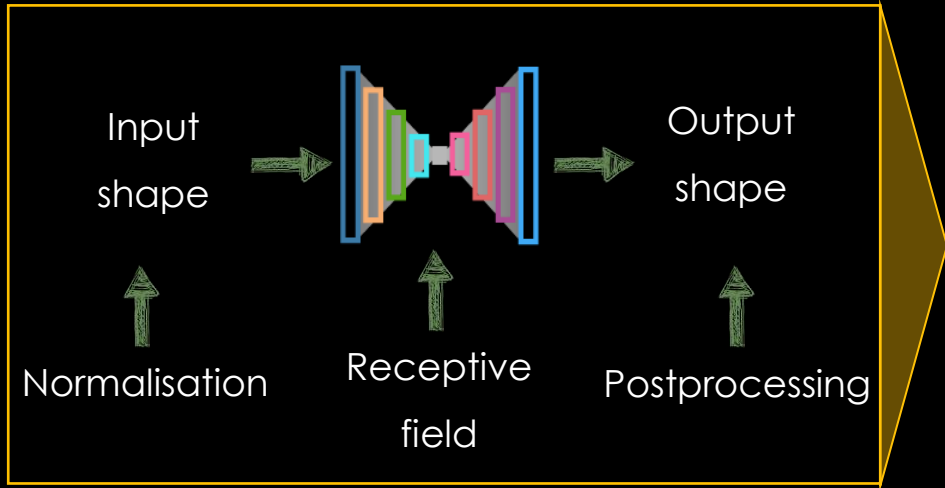
Consumer: **stardist python**



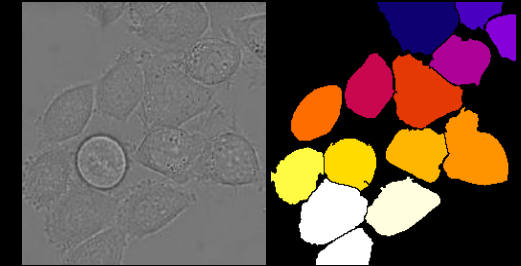
# Bringing **standards** to the FAIRy deep learning ecosystem



## Model metadata



## Models tailored for bioimage analysis



Input example    Output example

### Metadata

Shape: 256 x 256 pixels

Pixel size: 0.19  $\mu\text{m}$  x 0.19  $\mu\text{m}$

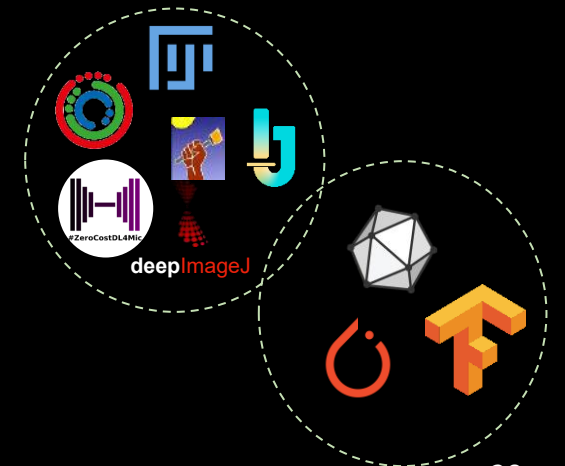
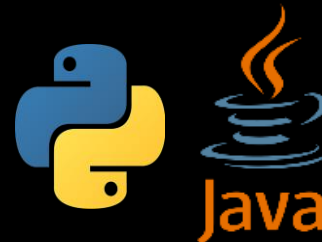
```

format_version: 0.4.0
id: 10.5281/zenodo.7261374/7688040
inputs:
  - name: base
    data_ranges:
      - 0.0
      - 255.0
    data_type: uint8
    label: input
  preprocessing:
    - name: XPC
      max_percentile: 99.8
      min_percentile: 1
      mode: per_sample
      name: scale_range
    shapes:
      - 1
      - 512
      - 512
      - 1
    licenses: MET
    links:
      - deepimage/DeepImageJ
      - lejay/BioImageIO-Parser
      - zenodo/dataset_converter_2d_multilabel_deepiac
      - 11astik/11astik
      - zenodo/noreobak_u-net_2d_multilabel_zenocostlabmic
    maintainers:
      - github_user: asgomeza
    name: Estibaliz Gómez de Mariscal
    name: 8_Santisteban_Bacterias Segmentation - Watershed microscopy - JD Iker
    outputs:
      - name: base
    data_range:
      - -inf
      - inf
    data_type: float32
    name: output
    shapes:
      offset:
        - 0.0
        - 0.0
          
```

Common  
resource  
specifications

## Quick AI feature integrations

Python and Java utilities



- W. Ouyang\*, F. Beuttenmueller\*, E Gómez-de-Mariscal\*, C. Pape\*, et al., bioRxiv 2022
- C. García-López-de-Haro, JDLL: A library to run Deep Learning models on Java bioimage informatics platforms, 2023

# Support reproducibility



### Model fine tuning

U-Net\_3D\_ZeroCostDL4Mic\_BioImageModelZoo\_export.ipynb

Archivo Editar Ver Insertar Entorno de ejecución Herramientas Ayuda No se pueden guardar cambios

Indice

- U-Net (3D)
- How to use this notebook?
- 0. Before getting started
- 1. Install 3D U-Net dependencies
  - 1.1. Install key dependencies
  - 1.2. Restart your runtime
  - 1.3. Load key dependencies
- 2. Complete the Colab session
  - 2.1. Check for GPU access
  - 2.2. Mount Google Drive
- 3. Select your parameters and paths
  - 3.1. Choosing parameters**
  - 3.2. Data augmentation
- 4. Train the network
  - 4.1. Show model and start training
  - 4.2. Download your model from Google Drive
- 5. Evaluate your model
  - 5.1. Inspecting loss function
  - 5.2. Error mapping and quality metrics

Checkpointing parameters

```
checkpointing_period: 1
```

If chosen only the best checkpoint is saved, otherwise a checkpoint is saved every checkpoint\_period epochs:

```
save_best_only: 
```

Resume training

Choose if training was interrupted:

```
resume_training: 
```

Transfer learning

For transfer learning, do not select resume\_training and specify a checkpoint\_path below.

-If the model is already downloaded or is locally available, please specify the path to the .h5 file.

```
-To use a model from the BioImage Model Zoo, write the model ID. For example: 10.5281/zenodo.5749843
```

```
pretrained_model_choice: bioimageio_model
```

```
checkpoint_path: "Insertar text aquí"
```

```
model_id: "10.5281/zenodo.5749843"
```

5.4. Export your model into the BioImage Model Zoo format

This section exports the model into the [BioImage Model Zoo](#) format so it can be used directly with deepimagej or Ilastik. The new files will be stored in the model folder specified at the beginning of Section 5.

Once the cell is executed, you will find a new zip file with the name specified in `trained_model_name`, [bioimage.io](#) model.

To use it with deepimagej, download it and install it using DeepImageJ `Install Model > Install from a local file`.

To try the model in imagej, go to `Plugins > DeepImageJ > DeepImageJ.Run`, choose this model from the list and click on `Test Model`.

More information at <https://deepimagej.github.io/deepimagej/>

Introduce the information to document your model:

```
trained_model_name: "Insertar text aquí"
```

```
trained_model_authors: ["Author 1 name, Author 2 name"]
```

```
trained_model_authors_affiliations: ["Author affiliation, Author 2 affiliation"]
```

```
trained_model_descriptions: "Description of the model"
```

```
trained_model_license: "MIT"
```

Include information about training data (optional):

```
include_training_data: 
```

- If it is published in the BioImage Model Zoo, please, provide the ID

```
data_train_bioimage_model_zoo: 
```

```
training_data_id: "Insertar text aquí"
```

- If not, please provide the URL, tot ha data and a short description

```
training_data_source: "insertar text aquí"
```

```
training_data_descriptions: "insertar text aquí"
```

Choose if you want to threshold the network output and if you want to use the best threshold calculated before.

```
apply_threshold: 
```

```
use_the_best_average_threshold: 
```

```
not please input:
```

```
whold: 210
```

note the voxel size (pixel size for each Z-slice and the distance between Z-slices) (in microns) of the image provided as an example of the model process:

```
Pixel Size: 1
```

```
ZF slices: 1
```



## New model contribution

### GUI for model management

BioImageIO Model Manager

napari

Validate a model

Models folder: /home/om/bioimageio-models Change

Filters: Filter by id... Filter by tag...

Downloaded models:

Model Name	Author	Version
Neuron Segmentation in 2D EM (Membrane)	creative-panda	5906839
HPA Nucleus Segmentation (DPNUnet)	conscientious-seashell	6538911
StarDist H&E Nuclei Segmentation	chatty-frog	6338615

Available models:

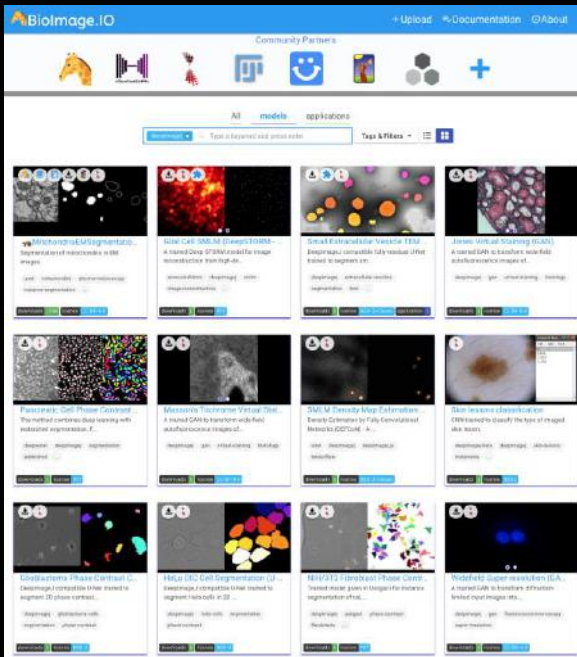
Model Name	Author	Version
StarDist H&E Nuclei Segmentation	chatty-frog	6338615
StarDist Fluorescence Nuclei Segmentation	fearless-crab	6348085
PlatynereisEMnucleiSegmentationBoundaryModel	organized-badger	6028098
PlatynereisEMcellsSegmentationBoundaryModel	willing-hedgehog	6647695



# Boost data annotation

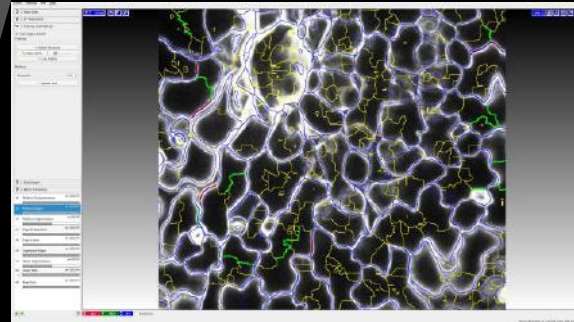


Download a pretrained model

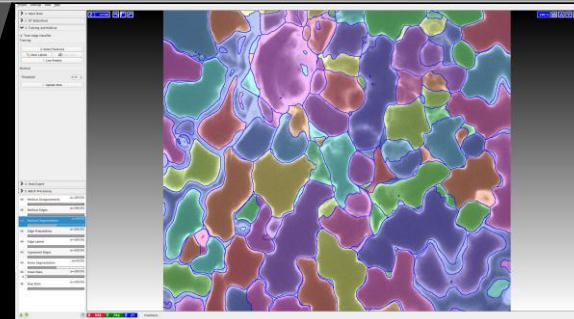


Speed up data annotation

Process an image

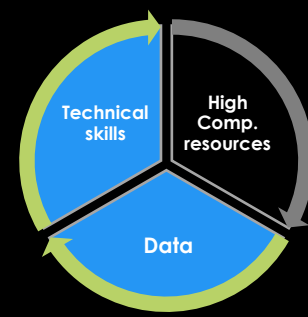


Curate the results

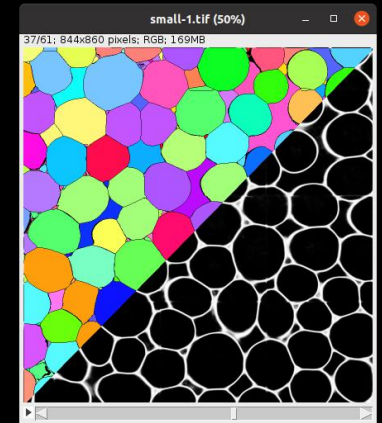


New training data

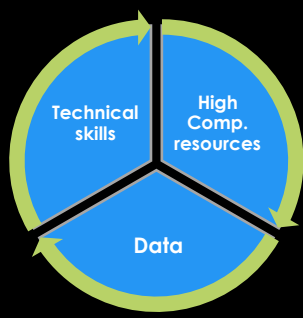
Fine tuning



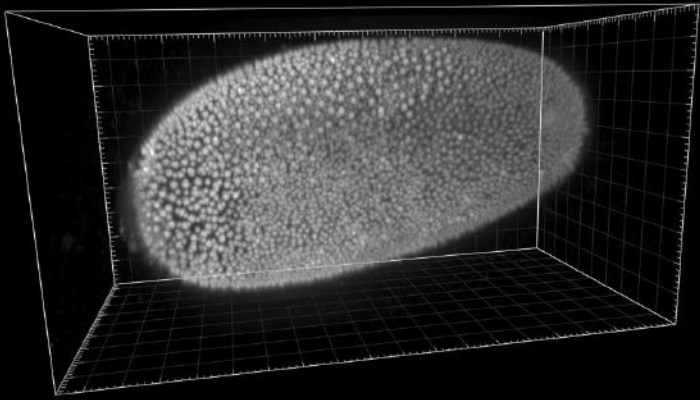
Analyze



# The potential of pre-trained models and interoperability



## Time lapse movies of 3D volumes

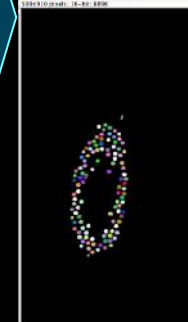


Considerations when annotating data

~300 GB of data

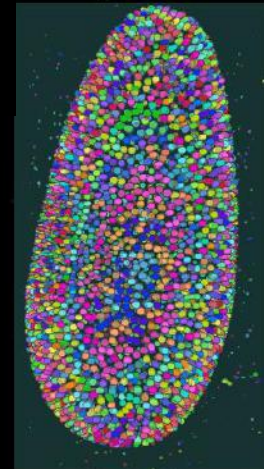
> 300 (3D) nuclei per time frame

## 2D PARTIAL Annotations (Cell Tracking Challenge) + pre-trained model

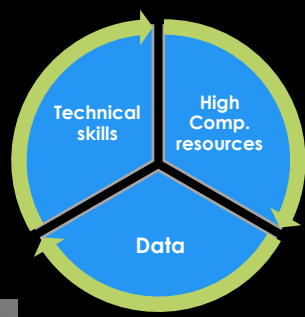


## Reconstruct 3D nuclei

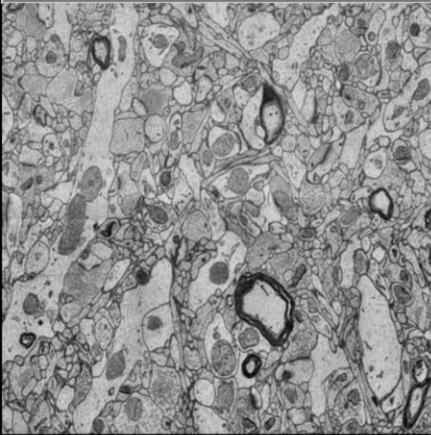
DL segmentation + 3D connected components



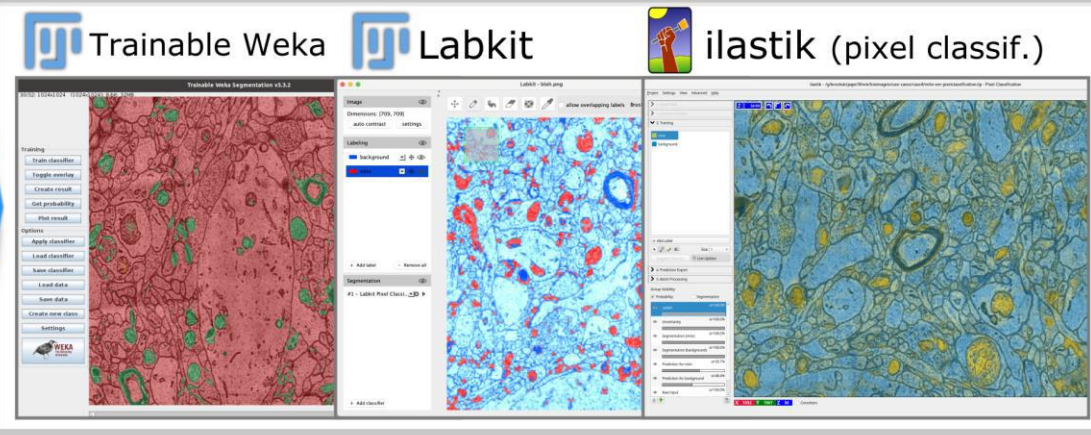
# The potential of pre-trained models: domain adaptation



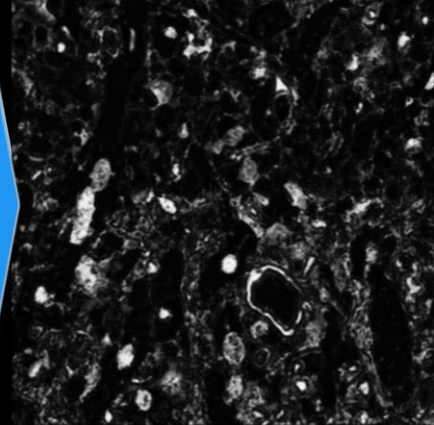
raw data



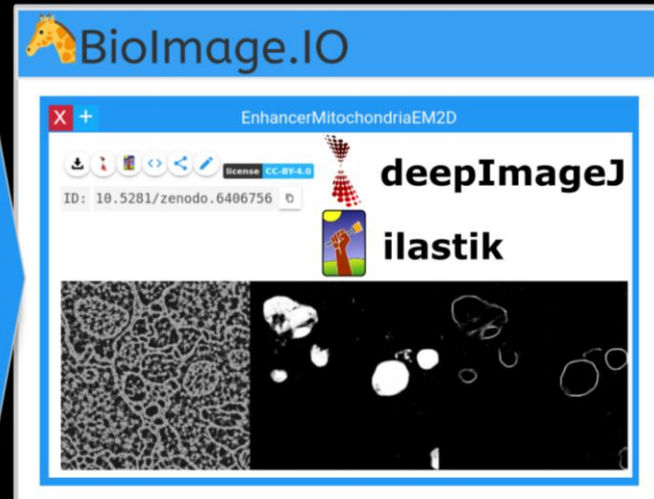
train and apply favorite pixel classifier



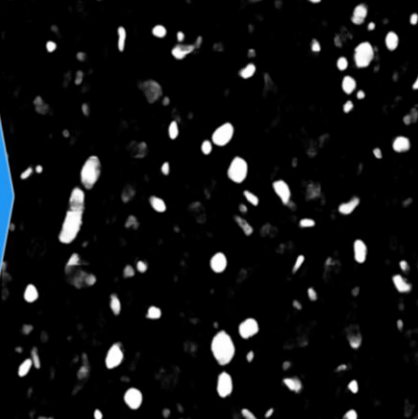
pixel classification



Download a trained enhancer model from the BiImage Model Zoo

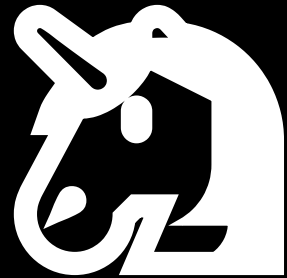


enhanced results





What's the vibe in the  
community?



# INFRASTRUCTURE FOR LIFE SCIENCES



10 PARTNERS 8 COUNTRIES

3 YEARS 4M EUROS

## AI4Life

AI MODELS AND METHODS FOR THE LIFE SCIENCES



### Community Partners



ImJoy

ilastik

HPA

### Project Partners



LIFE SCIENCE COMMUNITY

SOFTWARE

AI MODELS

STANDARDS

AI METHODS

COMPUTER SCIENCE COMMUNITY

# What's the vibe?

## Tech-in-the-lab

Seeking for an empowered life-sciences community



# What's the vibe?

## Tech-in-the-lab

- Seeking for an empowered life-sciences community
- Data analysis on the loop
- Optimised integration of DL into imaging

## Computer Scientists: Awareness of reusability to speed up

- Benchmarking
- Scientific breakthrough

Vladimir Ulman      Martin Maska

Organizers and Contacts

Member	Institution
Michael Kowalek, Ph.D., Segmental in Benchmarking Coordinator	Center for Biomedical Image Analysis, Masaryk University
Alimuddin Khan, Ph.D.	Caltech
Edith Weisberg, Ph.D.	UNSW
Arantza Muñoz-Barrutia, Ph.D.	Universidad Carlos III de Madrid
Paul F. Jäger, Ph.D.	CBG

nature methods

Analysis <https://doi.org/10.1038/s41592-023-01879-y>

### The Cell Tracking Challenge: 10 years of objective benchmarking

Received: 5 August 2022  
Accepted: 13 April 2023  
Published online: 18 May 2023

Check for updates

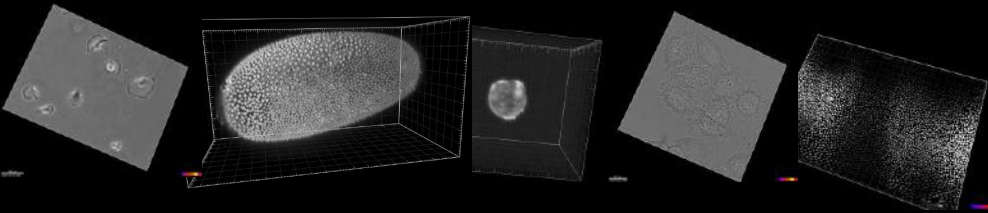
Martin Maška<sup>1</sup>, Vladimir Ulman<sup>1,2</sup>, Pablo Delgado-Rodriguez<sup>3,4</sup>, Estibaliz Gómez-de-Mariscal<sup>3,4,5</sup>, Tereza Nečasová<sup>1</sup>, Fidel A. Guerrero Peña<sup>6,7</sup>, Tsang Ing Ren<sup>8</sup>, Elliot M. Meyerowitz<sup>9</sup>, Tim Scherr<sup>9</sup>, Katharina Löffler<sup>9</sup>, Ralf Mikut<sup>9</sup>, Tianqi Guo<sup>10</sup>, Yin Wang<sup>10</sup>, Jan P. Allebach<sup>10</sup>, Rina Bao<sup>10,12</sup>, Noor M. Al-Shakarji<sup>12</sup>, Gani Rahmon<sup>12</sup>, Imad Eddine Toubal<sup>12</sup>, Kannappan Palaniappan<sup>12</sup>, Filip Lux<sup>1</sup>, Petr Matula<sup>1</sup>, Ko Sugawara<sup>13,14</sup>, Klas E. G. Magnusson<sup>15</sup>, Layton Aho<sup>16</sup>, Andrew R. Cohen<sup>16</sup>, Assaf Arbelle<sup>17</sup>, Tal Ben-Haim<sup>17</sup>, Tammy Riklin Raviv<sup>17</sup>, Fabian Isensee<sup>18,19</sup>, Paul F. Jäger<sup>18,20</sup>, Klaus H. Maier-Hein<sup>18,21</sup>, Yanming Zhu<sup>22,23</sup>, Cristina Ederra<sup>24</sup>, Ainhoa Urbiola<sup>24</sup>, Erik Meijering<sup>22</sup>, Alexandre Cunha<sup>7</sup>, Arrate Muñoz-Barrutia<sup>3,4</sup>, Michal Kozubek<sup>1,25,26</sup> & Carlos Ortiz-de-Solórzano<sup>24,25</sup>

V. Ulman & M. Maska et al., Nat Methods 2017

2021: Reusability guidelines (optional)

ISBI 2022: 11 participants

- All top performing methods
- 100% followed reusability guidelines



# What's the vibe?

## Tech-in-the-lab

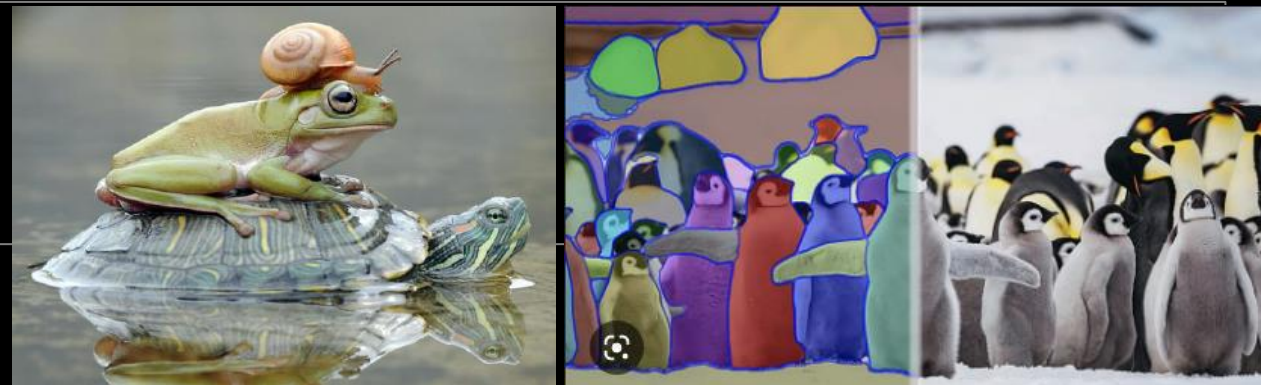
- Seeking for an empowered life-sciences community
- Data analysis on the loop
- Optimised integration of DL into imaging

## Computer Scientists: Awareness of reusability to speed up

- Benchmarking
- Scientific breakthrough

## Scientists & researchers: Automatically guided analysis

- Embedding non-digested scientific knowledge  
(sparse information)





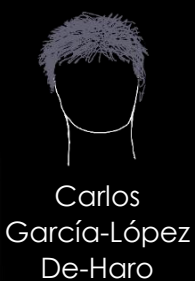
deepImageJ team

uc3m

Universidad Carlos III de Madrid

EPFL

EPFL Center for Imaging



Carlos García-López De-Haro



Lucía Moya



Wei Ouyang



Arrate Muñoz Barrutia

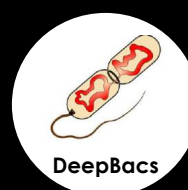


Daniel Sage

Donati, Laurène, EPFL

Unser, Michael, EPFL

Lundberg, Emma, ScilifeLab, KTH



Prof. R. Henriques



G. Jacquemet



R.F. Laine



C. Spahn



P.M. Pereira



### Biolmage Model Zoo



- Pengo, Thomas, University of Minnesota
- M. Gordaliza, Pedro, UC3M
- Yair Rivenson, UCLA
- Hongda, Wang, UCLA
- Tosi, Sébastien, IRB Barcelona

- Eglinger, Jan, FMI Basel
- Reuden, Curtis LOCI Lab
- Schmidt, Deborah, MDC
- Olivo-Marin, Jean-Christophe, Institut Pasteur
- Tivenez, Jean-Yves, Institut Pasteur

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