

Advanced Methods and Human Cell Technologies (AMHCT)
RegBioMed Master's Course

Navigating the Reproducibility Storm with Bio-Image Analysis

Dr. Marcelo Leomil Zoccoler

Bio-Image Analysis Technology Development Group - Physics of Life (PoL) – TU Dresden

Re-using material from:

Robert Haase (Scads.AI Leipzig); Maleeha Hassan (Helmholtz AI Dresden); Johannes Soltwedel (PoL – TU Dresden);

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- Introduction to **OMERO** and **napari-omero**
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- Feature Extraction with **napari-skimage-regionprops**
- Object Classification with **napari-apoc** and **napari-clusters-plotter**
- **Exercises:**
 - **Instance Segmentation with napari-apoc**
 - **Creating a workflow with napari-omero and napari-apoc**
 - **Reproducing a workflow**
- **Discussion**



https://biapol.github.io/AMHCT_Bio_Image_Analysis_2025/intro.html

napari Installation

- napari as a Python Library
- napari as a Bundle App
- Installing Plugins

Installing napari as a Python package

napari is a Python library

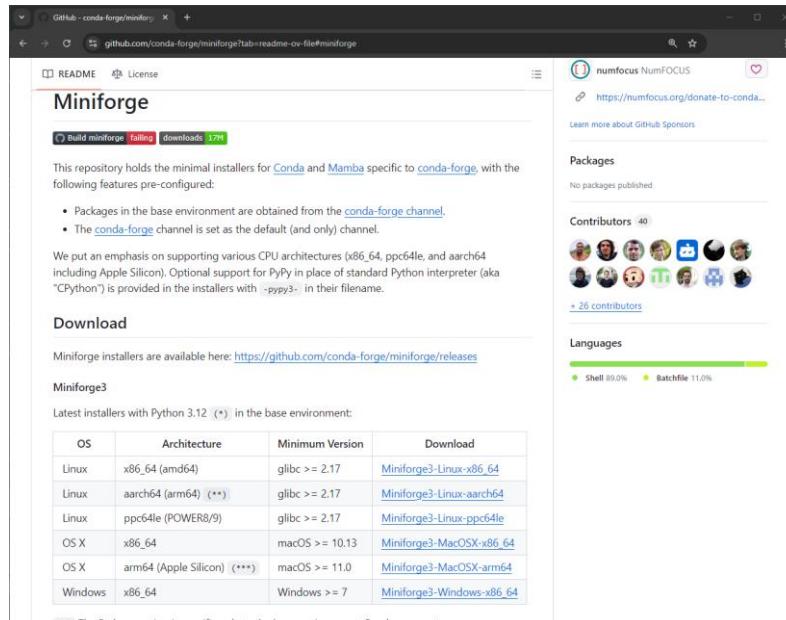
The recommended way to install napari is as a Python package

<https://napari.org/stable/tutorials/fundamentals/installation.html#install-as-python-package-recommended>

Your computer needs Python to run a Python package

- How do I install Python?

Install Miniforge!



<https://github.com/conda-forge/miniforge?tab=readme-ov-file#miniforge>

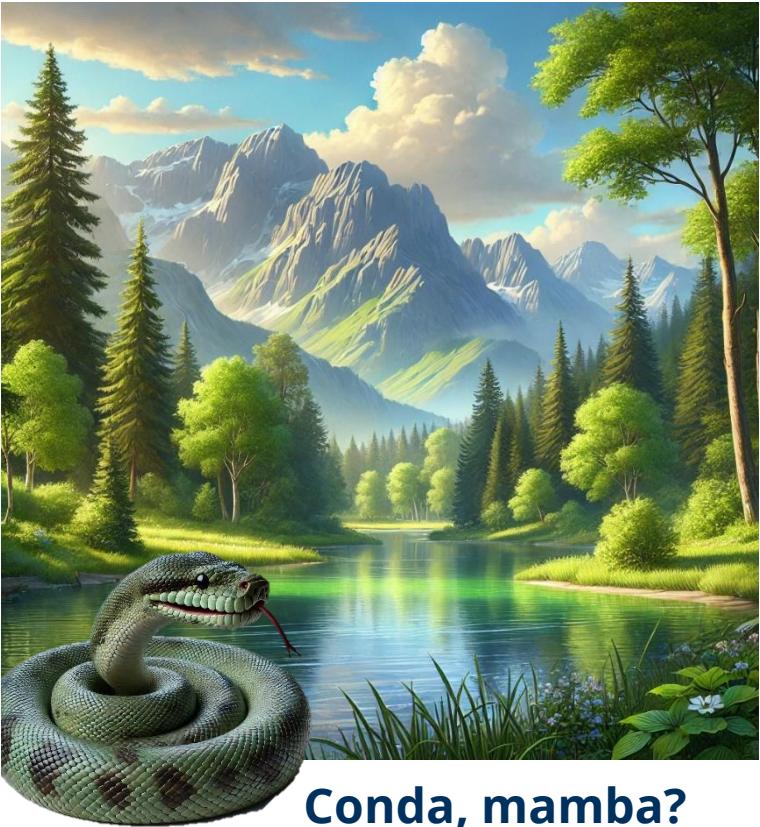
- Miniforge is a minimal installer for `conda` and `mamba` (efficient `conda` in C++)
- `conda` is an environment and a package manager
- `conda` can create Virtual Environments and install Python (and other) packages, including napari

https://hackmd.io/@talley/SJB_lObBi#Terms

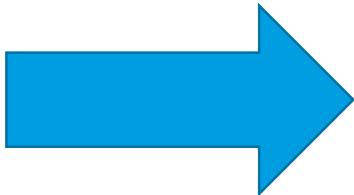
Installing napari as a Python package



Wait, environments ?



Conda, mamba?



Yes, virtual environments!

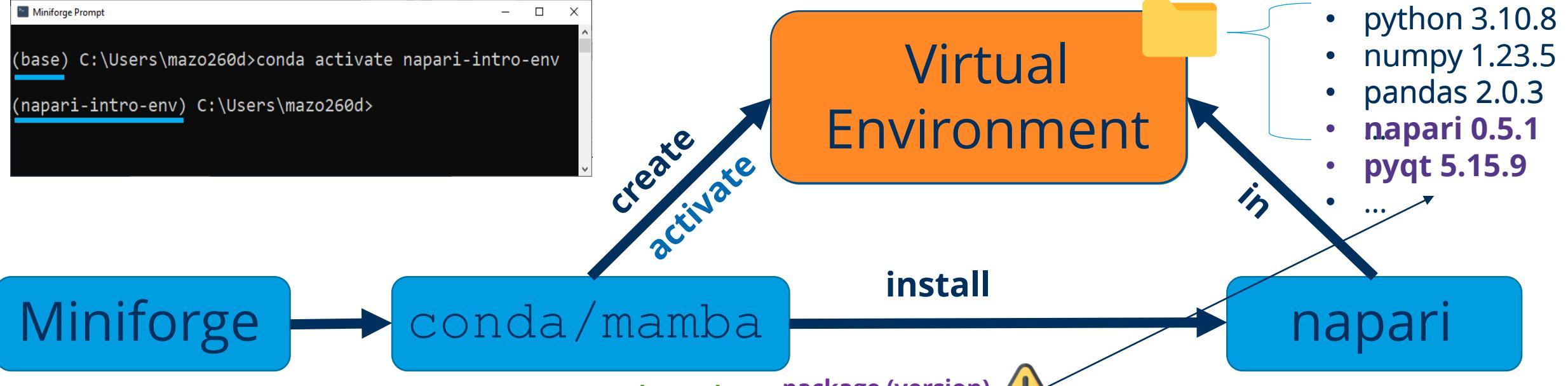


Images generated by DALL-E, developed by OpenAI.
Smiley icons from Flaticon.com

Installing napari as a Python package

Install it as a Python package in a Virtual Environment

- A virtual environment is an isolated collection of packages, settings, and an associated python interpreter



Commands:

`mamba create -y -n napari-intro-env -c conda-forge python=3.10`

`mamba activate napari-intro-env`

`mamba install -c conda-forge napari pyqt`

- **conda** checks for version compatibility before installing
- **pip** tries to install, then lets you know if something went wrong
- **pip** cannot create environments

Installing napari

Napari can also be downloaded and installed like other software

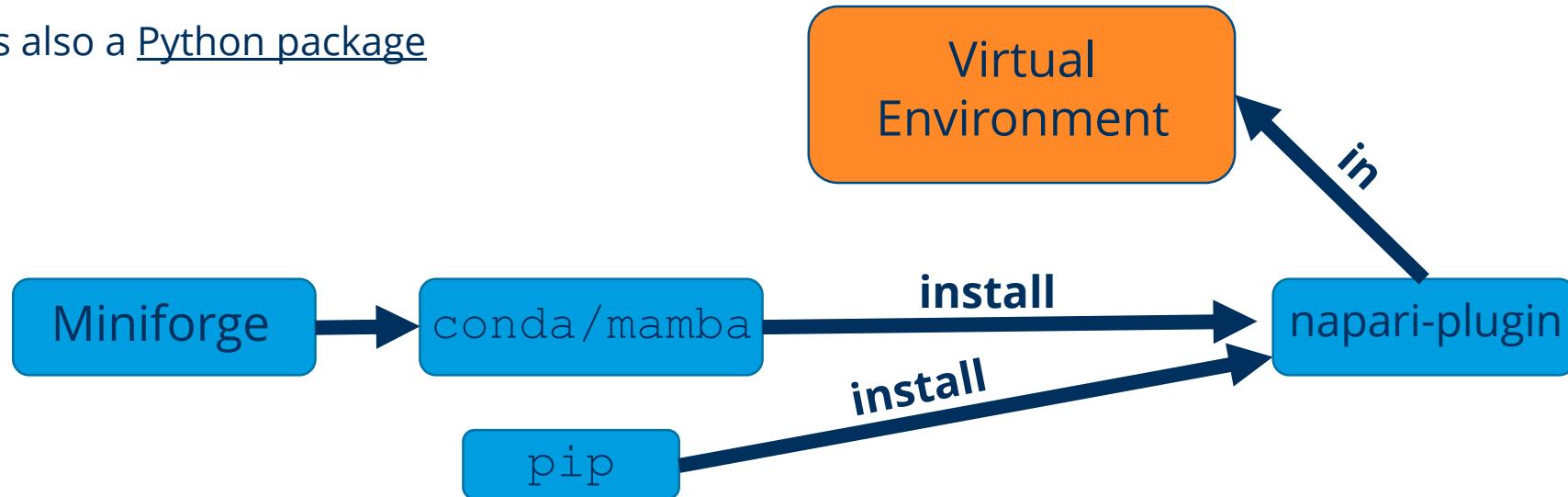
- https://napari.org/stable/tutorials/fundamentals/installation_bundle_conda.html#how-to-install-napari-as-a-bundled-app

This is more convenient, however it may be difficult to manage different plugin versions mid-long term

- In case of a dependency version mismatch, it may be necessary to uninstall and re-install the software and all the plugins again

Installing a plugin

A napari plugin is also a Python package



Commands:

`mamba activate napari-intro-env`

`mamba install napari-plugin`

`OR`

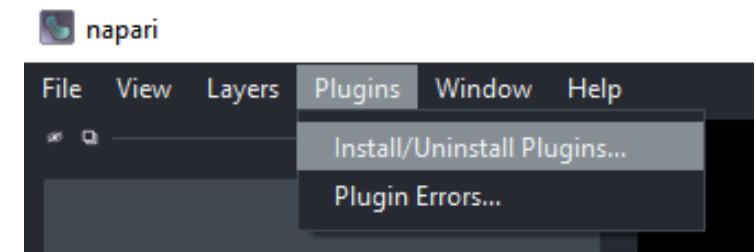
`pip install napari-plugin`

`conda install napari-plugin`



Always check plugin
installation instructions!

Via Plugins Menu:



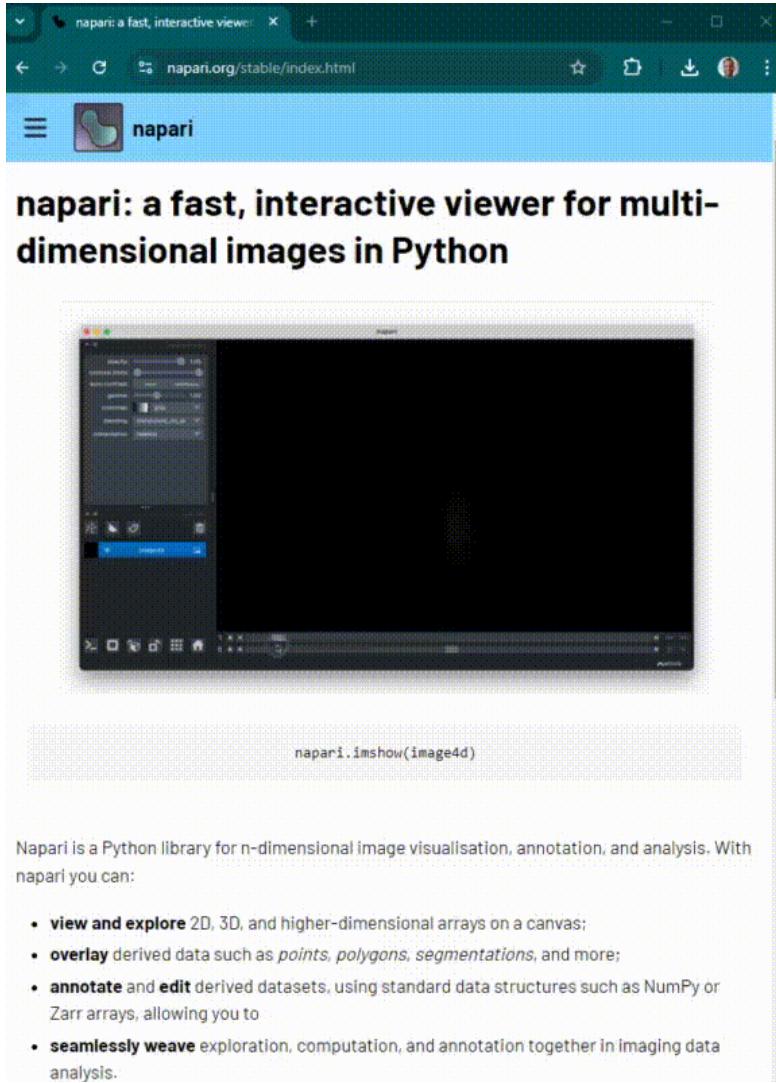
Introduction to napari

- napari Viewer
- Layer Types
- napari Plugins

Napari: 3D viewer for Python

Multi-dimensional image viewer in python

<https://napari.org/>



Napari: 3D viewer for Python



<https://napari.org/>

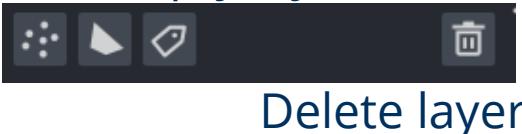
Napari user interface

Menus

View configuration / tools

```
layer.opacity = 0.5
```

Add empty layers



Delete layer

Layers

```
layer.visible = False
```

Viewer controls



Open Python Console



2D/3D view



Change axes order



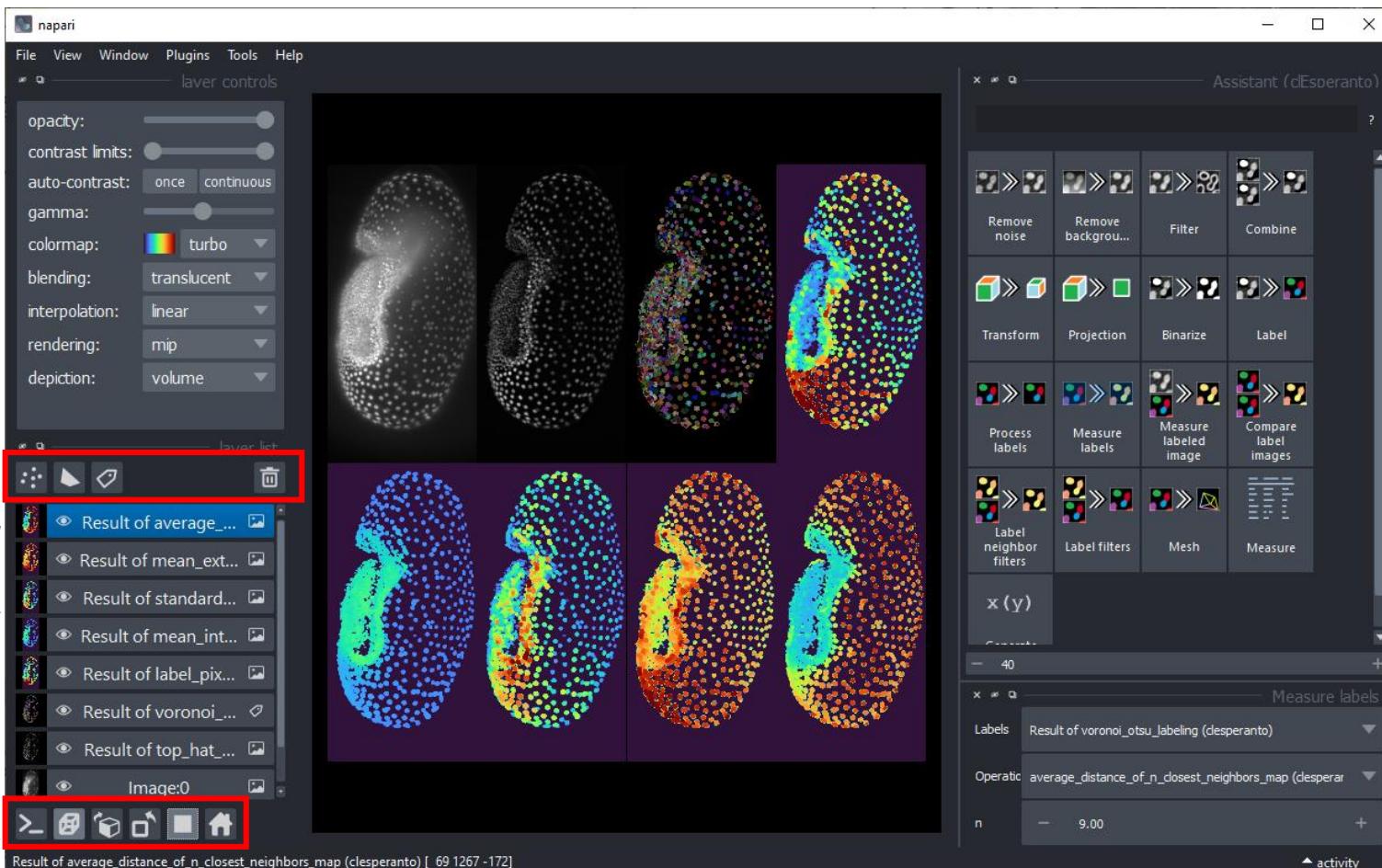
Transpose visible axes



Grid mode



Reset view

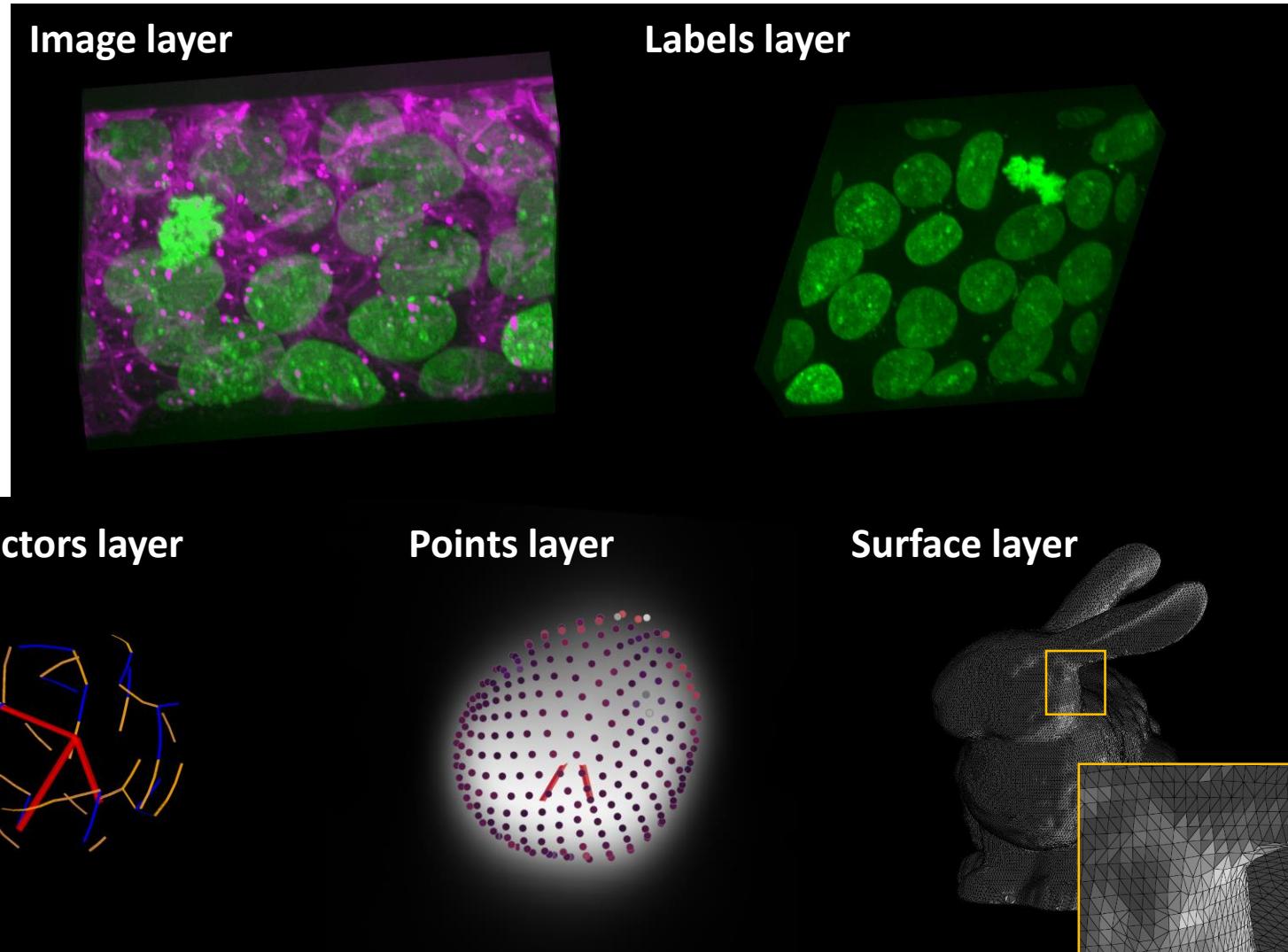


Dock widgets
(custom plugins)

Function widgets
(custom plugins)

Layer types

- **Image layer:** Can be n-dimensional grayscale data (e.g., [CTZYX])
- **Labels layer:** Similar to image layer, but contains only integer numbers (e.g., 0,1,2,3,...)
- **Points layer:** List of coordinates in space
- **Vectors layer:** Direction from point A to point B
- **Surface layer:** Mesh (Vertices, Faces, Values)
- **Tracks layer:** Follow objects through time



<https://github.com/quantumjot/arboretum> licensed under [MIT license](#)

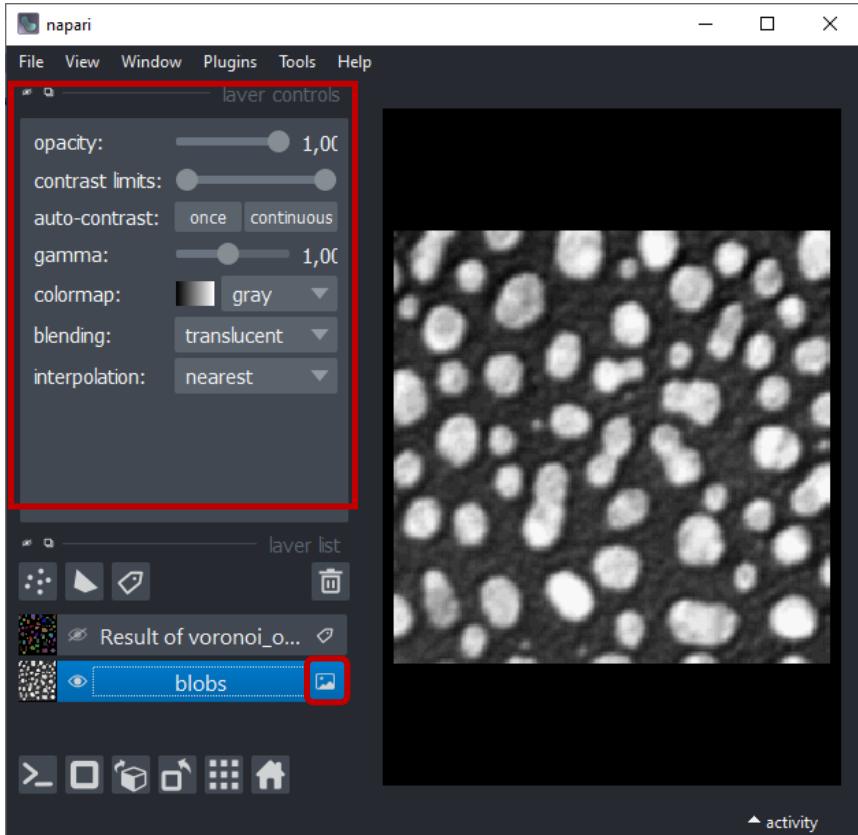
<https://github.com/campaslab/napari-stress>

<https://gitlab.kitware.com/vtk/vtk>

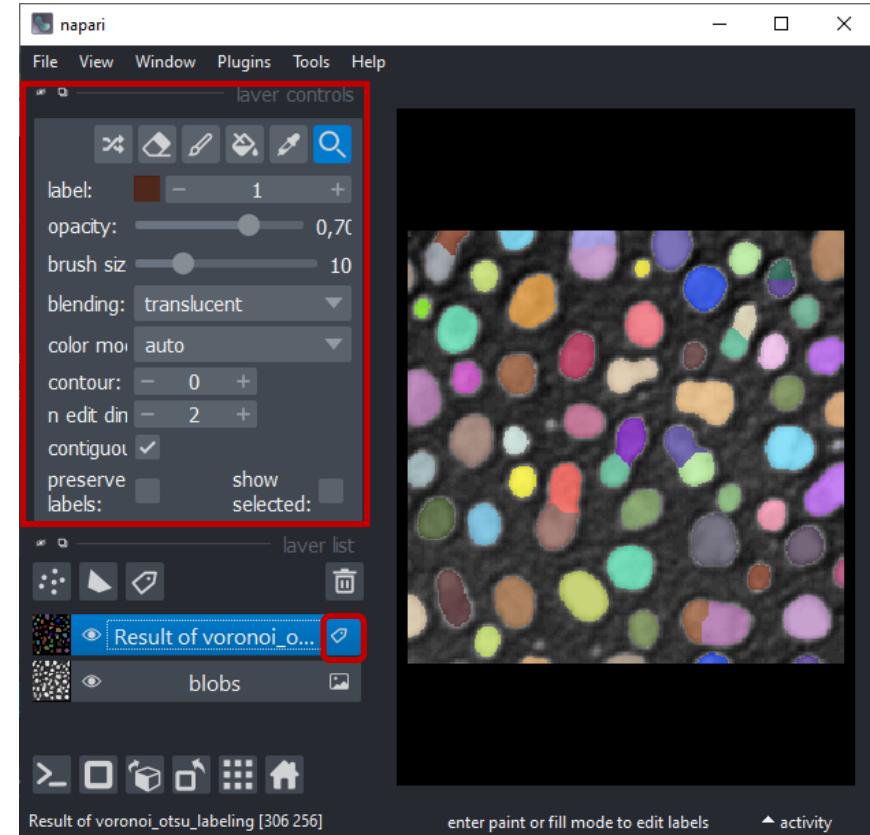
Layer types

Different layers have different tools and options

Image Layer



Labels Layer



Python image & data analysis tools are powerful!



Python scientific image computing
toolbox
<https://github.com/scikit-image>



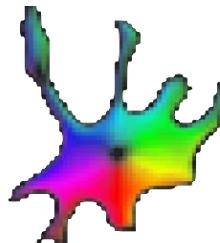
Object detection with Stardist
<https://github.com/stardist>



Python machine-learning toolbox
<https://github.com/scikit-learn>



Data visualization & exploration
<https://github.com/matplotlib>
<https://github.com/seaborn>



Cell segmentation
<https://github.com/MouseLand/cellpose>



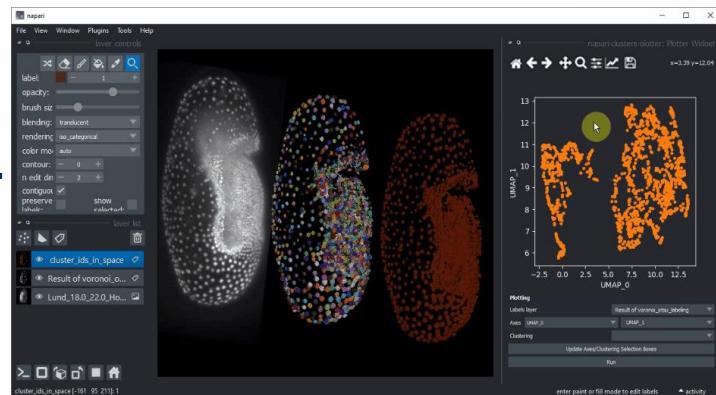
GPU-accelerated image processing
<https://github.com/cLEsperanto>

Napari



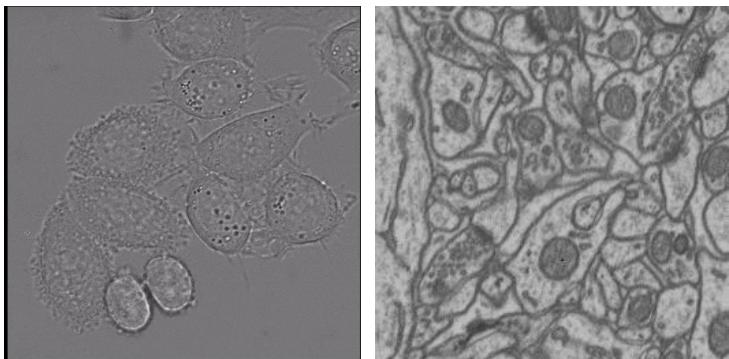
Existing functionality can
be turned into plugins!
→ Interactivity
→ Automatic GUI
generation

clusters-plotter



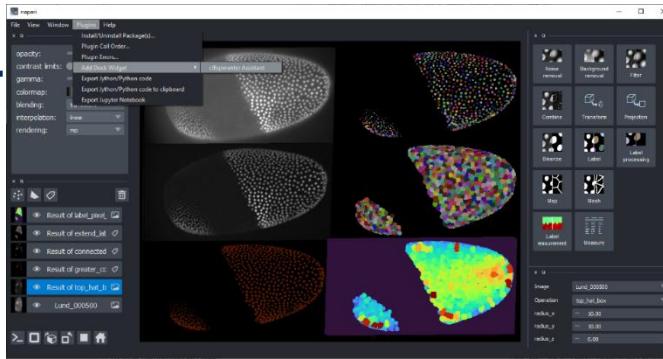
<https://github.com/BiAPoL/napari-clusters-plotter>

micro-sam



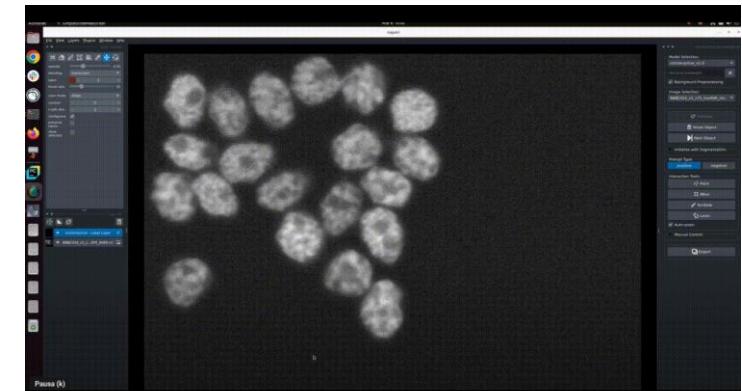
<https://github.com/computational-cell-analytics/micro-sam>

devbio-napari



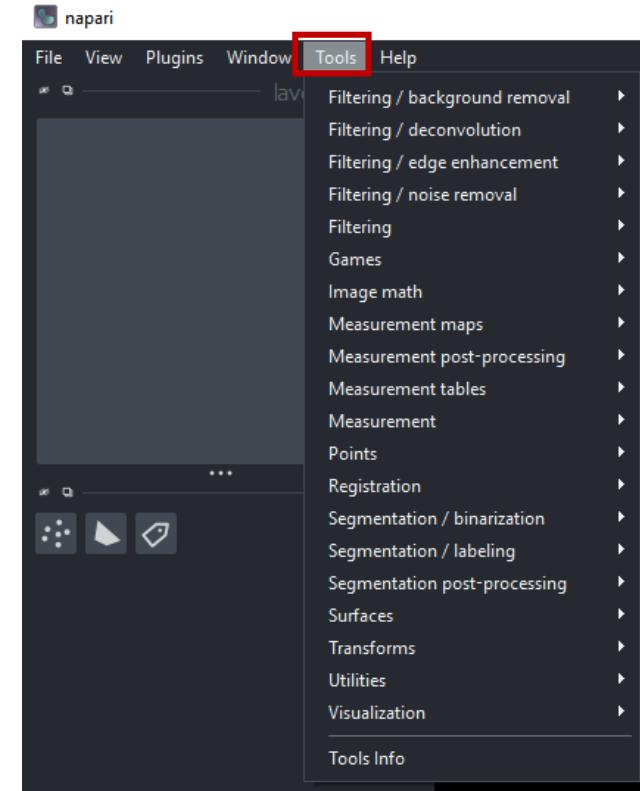
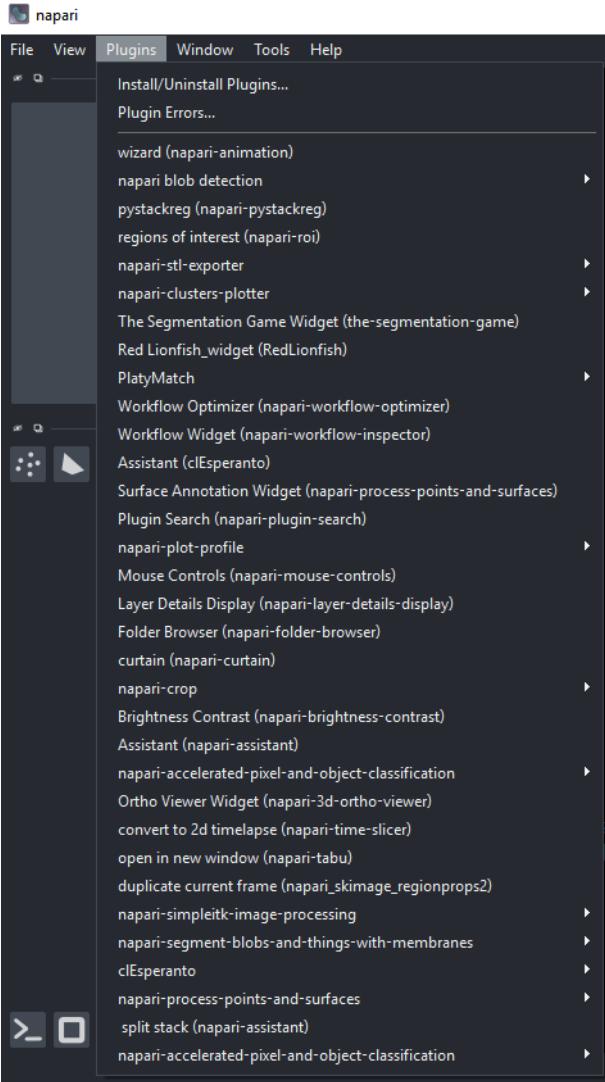
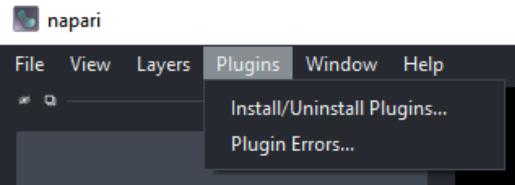
<https://github.com/haesleinhuepf/devbio-napari>

nninteractive

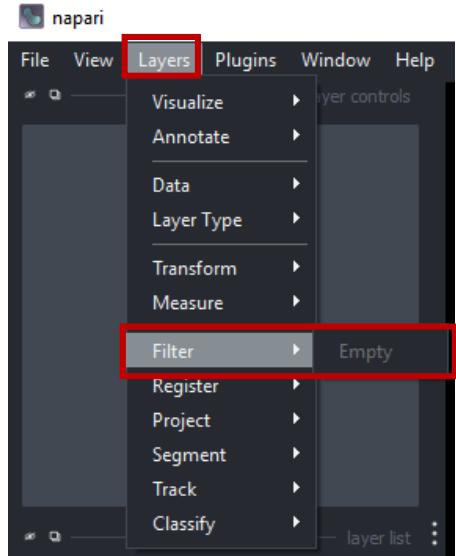


<https://github.com/MIC-DKFZ/napari-nninteractive>

Plugins and Layers Menus



devbio-napari plugin bundle



napari >= 0.5.0

Layers sub-menu items depend on plugin developers populating them

The Napari Hub

The plugin you are looking for may be near you!

Search engine for napari plugins

The screenshot shows the napari hub website at napari-hub.org. The page has a light blue header with the title 'napari hub | search' and a search bar. Below the header, there are links for 'napari hub', 'About', and 'FAQ'. The main content features a large, bold title 'Discover, install, and share napari plugins' in black text on a light blue background. A large, semi-transparent white diagonal banner across the center contains the text 'Since October 1, 2024, this version is no longer available' and 'The napari hub is transitioning to a new home at napari.org where you can continue to discover, install, and share image analysis tools with napari's growing community'. Below the banner is a search bar with the placeholder 'Search for a plugin by keyword or author'. At the bottom, there are sections for 'SORT' (with a dropdown menu) and 'Browse plugins: 227'.

napari hub | search x +

napari-hub.org/?search=cell+segmentation&sort=relevance&page=1

Search for a plugin by keyword or author

cell segmentation|

SORT

Relevance

Plugin name

Browse plugins >

Workflow step

Clear all

Workflow step: Image Segmentation

Image modality: Fluorescence microscopy

Image modality

Clear all

vollseg-napari

Irregular cell shape segmentation using VollSeg

FILTER BY REQUIREMENT

Clear all

Supported data

Varun Kapoor

...llSeg, a deep learning based 2D and 3D segmentation tool for irregular shaped cells. VollSe...

Authors

Workflow step: Image Segmentation

<https://www.napari-hub.org/>

napari hub | search x + v

napari-hub.org/?search=feature+extraction&sort=relevance&page=1

Search for a plugin by keyword or author

feature extraction

feature extraction due to launch in June 2025.

Plugins: 8

Plugin name

Recently updated

Newest

FILTER BY CATEGORY [Clear all](#)

Workflow step

Image modality

FILTER BY REQUIREMENT [Clear all](#)

Supported data

Authors

napari-features

extensible, general-purpose feature extraction

version 0.1.4
release date 24 August 2021
license MIT
python version >=3.7
operating system All

Allen Goodman

... An extensible, general-purpose feature extraction plug-in for the Napari image viewer. Fe...

napari-blob-detection

Detects blobs in images

version 0.0.2
release date 22 April 2022
license BSD-3-Clause
python version >=3.8
operating system All

Andy Sweet, Chi-Li Chiu

...s to labels, users can leverage feature extraction functions that are available to labels ...

napari-skimage-regionprops

A regionprops table widget

version 0.5.3
release date 10 July 2022
license BSD-3-Clause
python version >=3.8

ed. New plugins and plugin updates will continue to be listed.



@mazoc.bsky.social



TECHNISCHE
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PoL
Physics of Life
TU Dresden



DRESDEN
concept



Inspecting plugin usage and maintenance - GitHub

The screenshot shows a GitHub repository page for 'empanada-napari'. The repository has 210 commits, with the most recent one being 'Merge pull request #34 from volume-em/empanada_v1.1.1' by 'barrybarry9' 8 months ago. A red box highlights this commit, and a red arrow points to it from the text 'Latests updates'. Another red arrow points from the text 'Documentation' to the 'Readme' link in the repository sidebar. The sidebar also lists the repository's tags, license (BSD-3-Clause), and its connection to 'volume-em/napari'. The repository has 22 stars, 3 watching, and 9 forks.

Latests updates

Documentation

File	Description	Time Ago
.github/workflows	deployment ready	3 years ago
.napari	model and data docs	3 years ago
custom_configs	allow model architecture customization	3 years ago
empanada_napari	Updated requirements.txt and Count labels module.	8 months ago
images	docs	3 years ago
.gitignore	v1.1 release	last year
LICENSE	Initial commit	4 years ago
MANIFEST.in	deployment ready	3 years ago
README.md	Updated setup.cfg and requirements.txt file to include comp...	8 months ago
pyproject.toml	code addition/deletion for project package install	last year
requirements.txt	Updated setup.cfg and requirements.txt file to include comp...	8 months ago
setup.cfg	Updated setup.cfg and requirements.txt file to include comp...	8 months ago
tox.ini	preprint citation	3 years ago

Image Data Management and Access: Napari – OMERO integration

- Demonstration: napari-OMERO plugin

Working with images in python

Open images

```
from skimage.io import imread  
  
image = imread("blobs.tif")
```

```
image
```

```
array([[ 40,  32,  24, ..., 216, 200, 200],  
       [ 56,  40,  24, ..., 232, 216, 216],  
       [ 64,  48,  24, ..., 240, 232, 232],  
       ...,  
       [ 72,  80,  80, ..., 48,  48,  48],  
       [ 80,  80,  80, ..., 48,  48,  48],  
       [ 96,  88,  80, ..., 48,  48,  48]], dtype=uint8)
```

Images are just multi-dimensional arrays or “arrays of arrays”.



https://biapol.github.io/AMHCT_Bio_Image_Analysis_2025/01_images_are_numpy_arrays.html

Opening images should, but it is not always simple

- **Paths** need attention
 - Backslashes often cause problems on Windows
OSError: [Errno 22] Invalid argument:
Add a lowercase 'r' before path to fix that: `image = imread(r'C:\data\blobs.tif')`
- **Data may be too big** for your computer
 - They would need to be opened *lazily*
- **Proprietary file formats** ('.czi', '.tif', '.nd2', '.ims', etc) may need additional packages
 - In Fiji, Bioformats usually takes care of opening many different proprietary file formats
 - In Python/napari, you may need to install:
 - <https://github.com/bioio-devs/bioio>
 - <https://github.com/AllenCellModeling/napari-aicsimageio>
- **Metadata** may be lost
 - For example, some libraries return an image with dimensions like this

What dimension is this? (1, 1, 1, 80, 520, 692, 1)

?

Tile

Z

Time

I don't know

Data Structure

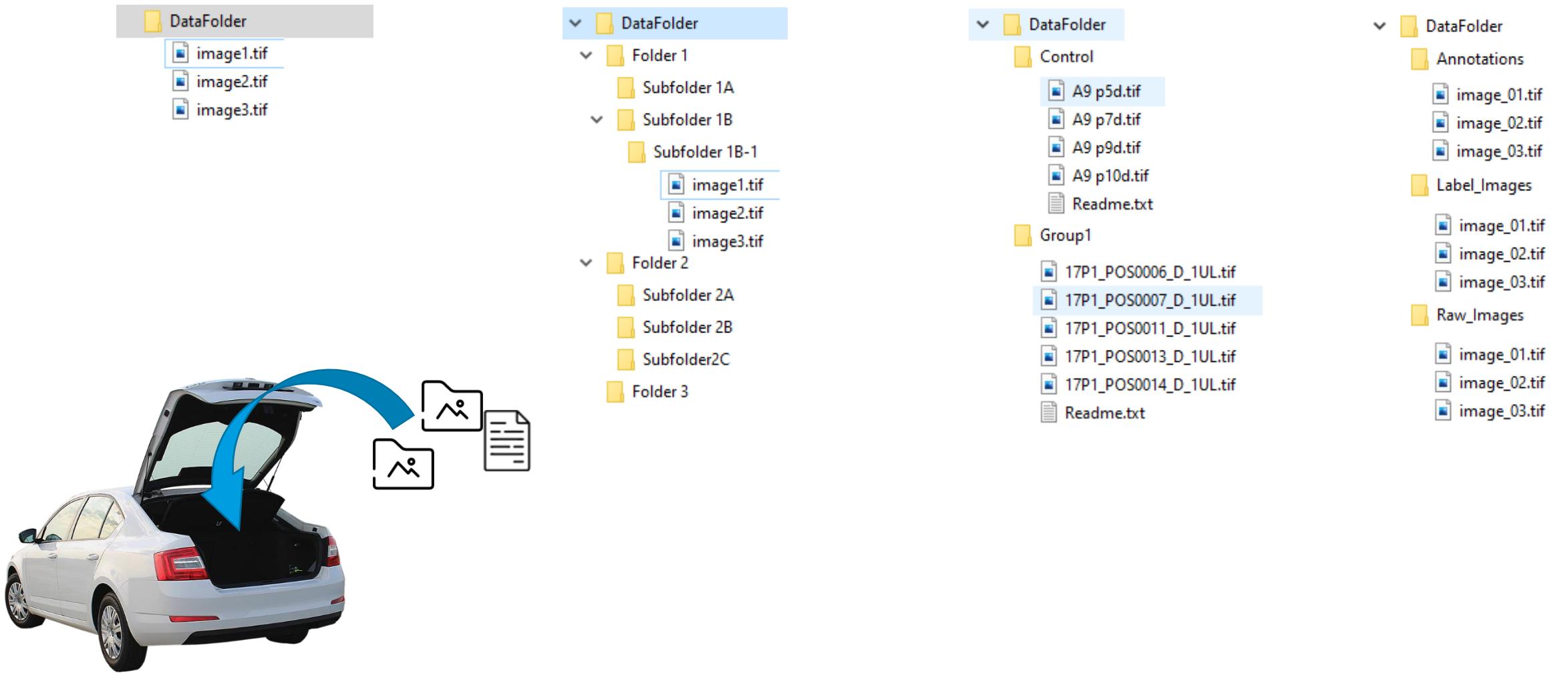


Image by [eikira](#) from [Pixabay](#) (<https://pixabay.com/photos/trunk-automobile-vehicle-luggage-1478832/>)

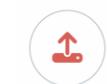
OMERO

OMERO is designed with scientists in mind



OMERO handles all your images using a secure central repository, from the microscope to [publication](#).

Using the power of Bio-Formats, OMERO supports over 140 image file formats, including all major microscope formats.



IMPORT DATA

Upload your data via the desktop app or command line, use our custom dropbox tool, or have your facility manager import it for you



ORGANIZE

View and organize your data from anywhere you have internet access



VIEW

Work with your images using the OMERO.insight desktop app, with OMERO.web in your browser, or from 3rd party software



ANALYZE

Use ImageJ, MATLAB, R, scripts and other tools to run analysis on data in OMERO and save results on the server



SHARE

Share data with collaborators or your PI using the Groups/Users permission system.



PUBLISH

Publish direct from the server via a customized website or embedded viewer

Filter by tags and more...

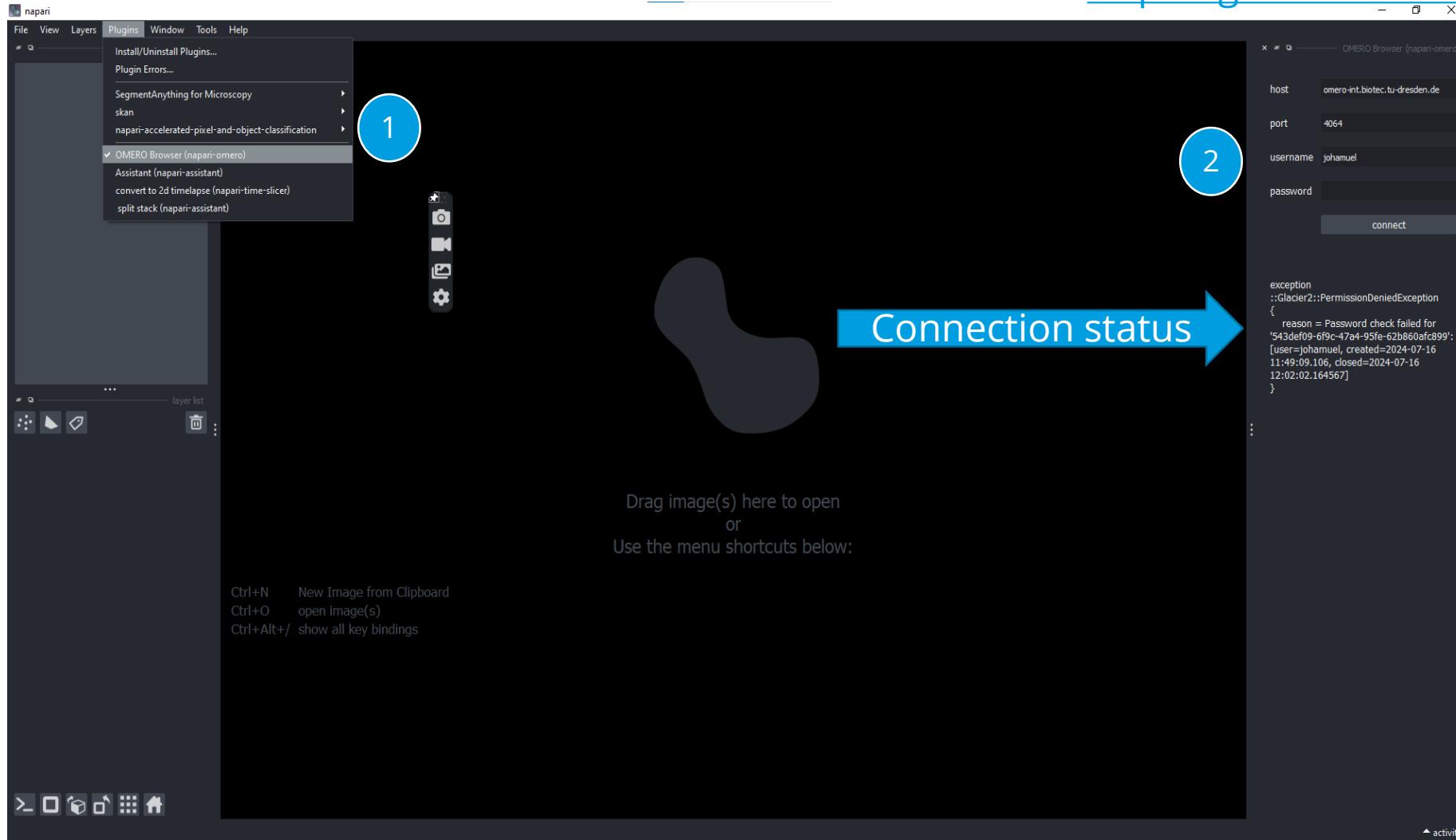
The screenshot shows the OMERO web interface. At the top, there's a navigation bar with 'OMERO', 'Data', 'History', 'Help', 'Any Value', 'Tag Search', 'Figure', 'Add', and 'Search' fields. A user profile for 'Marcelo Leomil Zoccoler' is shown. Below the navigation is a toolbar with various icons. The main area has three columns: 'Explore' (listing datasets like 'Example_DataSet 3' and 'Exercise_DataSet 2'), 'Thumbnails' (showing small versions of images), and 'Metadata' (containing fields for Dataset ID, Owner, Description, Tags, Key-Value Pairs, Attachments, and Comments). The 'Metadata' column also includes sections for 'Unique IDs' and 'Fixed 2 levels hierarchy'.

Metadatad

<https://www.openmicroscopy.org/omero/scientists/>

Napari-OMERO usage

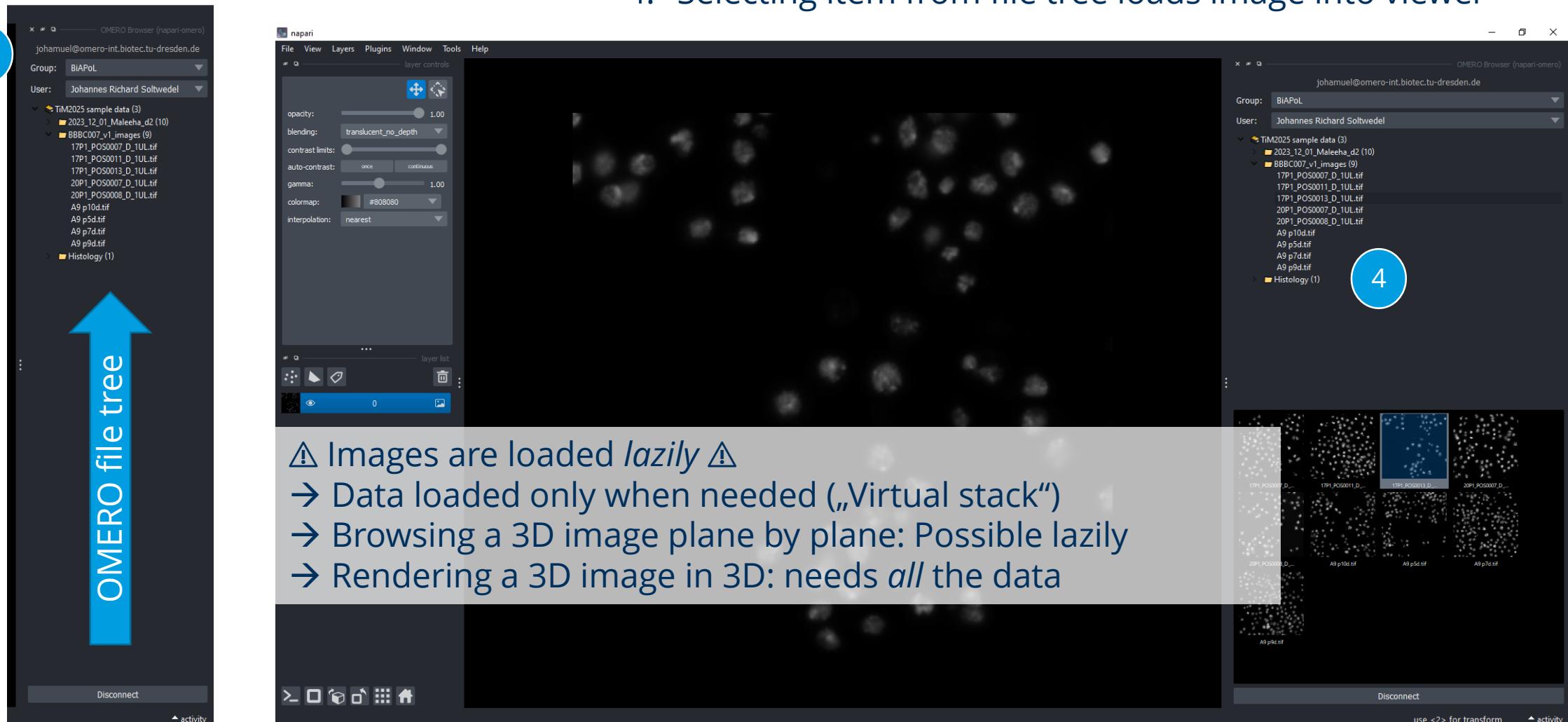
<https://github.com/tlambert03/napari-omero>



1. Select Plugin from plugin menu
2. Log into BiAPoL OMERO with ZIH credentials

Napari-OMERO usage

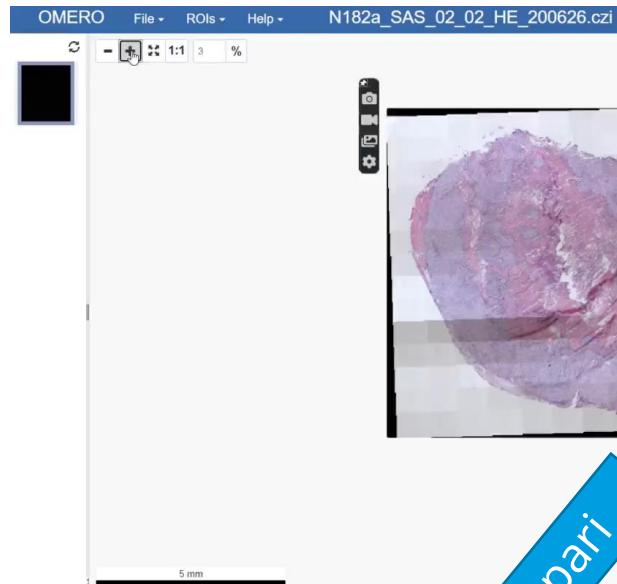
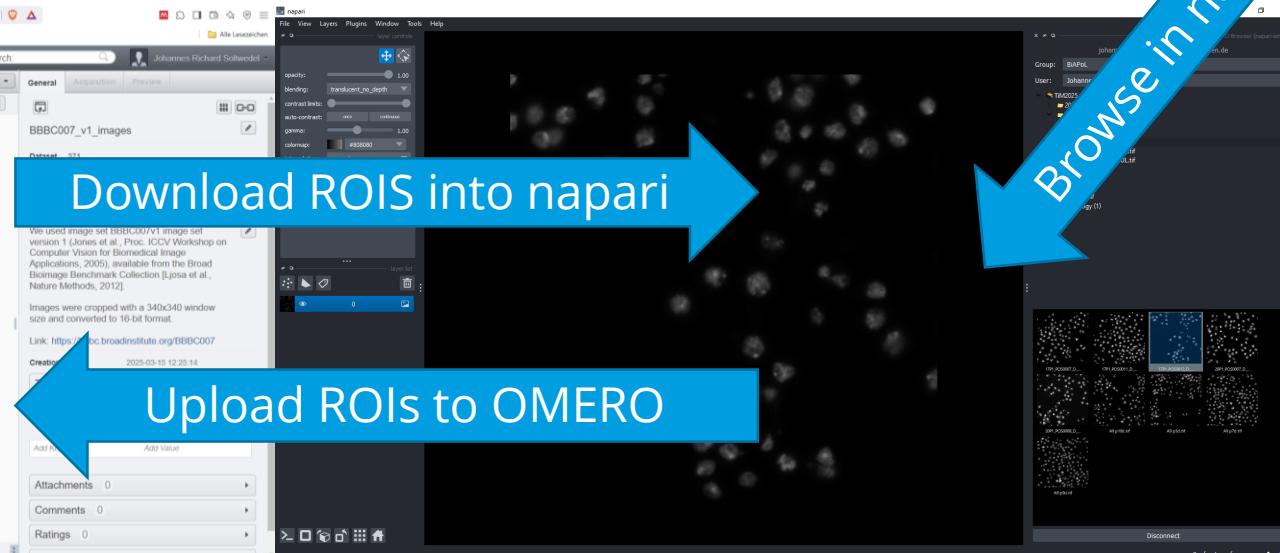
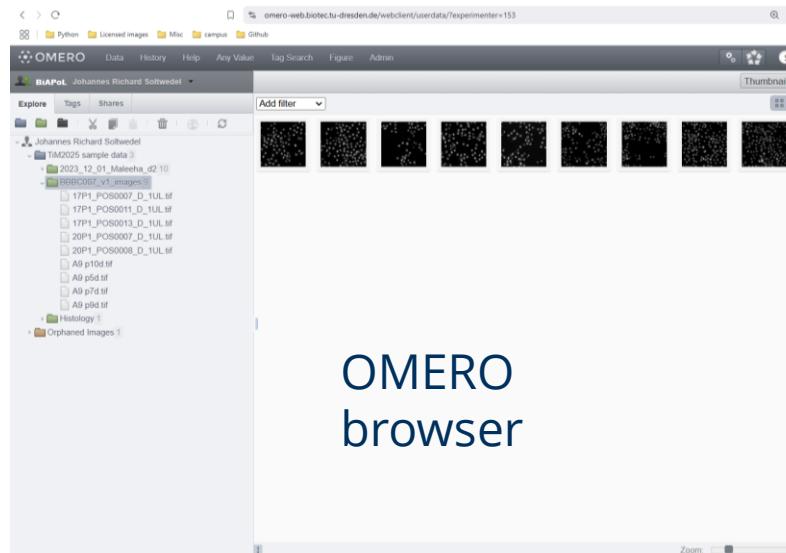
3. Select group and user
4. Selecting item from file tree loads image into viewer



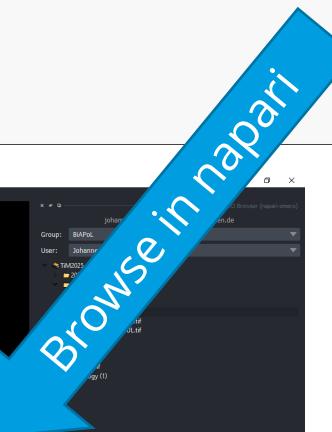
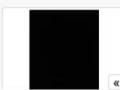
Some tips and tricks for OMERO from Python: <https://biapol.github.io/omero-tools>

Napari-OMERO usage

- ROI Upload
- Multiscale support: Browse larger-than-RAM samples (*3D limitation remains*)
- **Coming soon:**
- ROI download



Browsing multiscale data in OMERO



Segmentation and Supervised Machine Learning

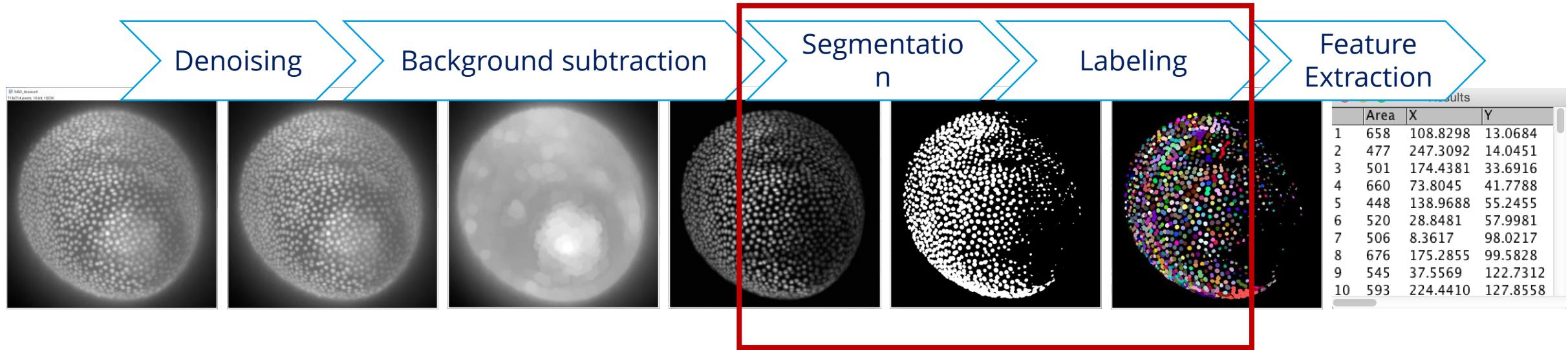
Random Forest Classifiers

- Pixel Classifier

Image Analysis Classic Workflows

Image analysis workflow is a series of processes/functions (not always linear) applied to images to achieve a certain goal (usually some measurements)

Here is a classic example:



Application: Segmentation

Aim:

Separate background from foreground

Vocabulary:

- **Segmentation:**

- **Segmentation:**
 - Assigning a meaningful *label* to each pixel
 - Segmentation is a *classification* problem

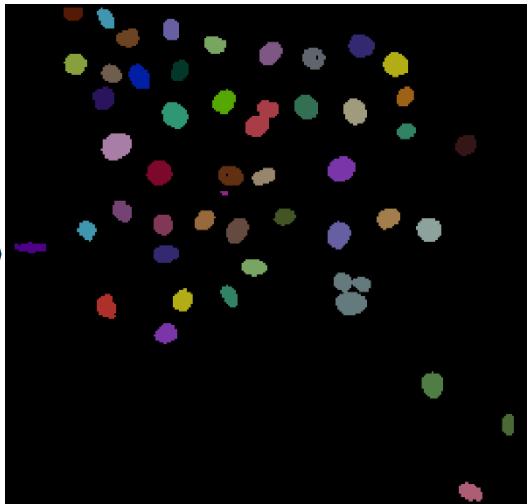
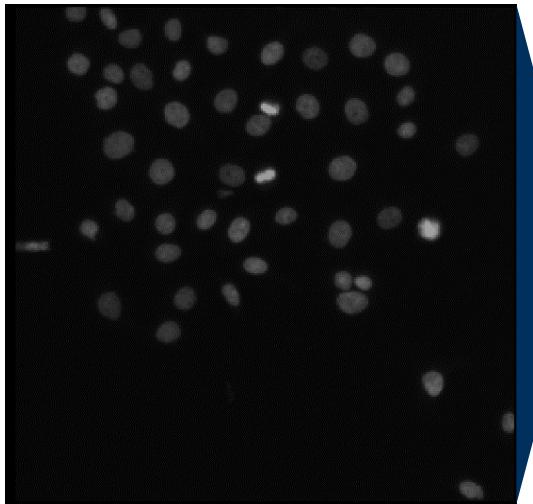
- **Semantic segmentation:**

Differentiate pixels into multiple *classes* (e.g., membrane, nucleus, cytosol, etc.)

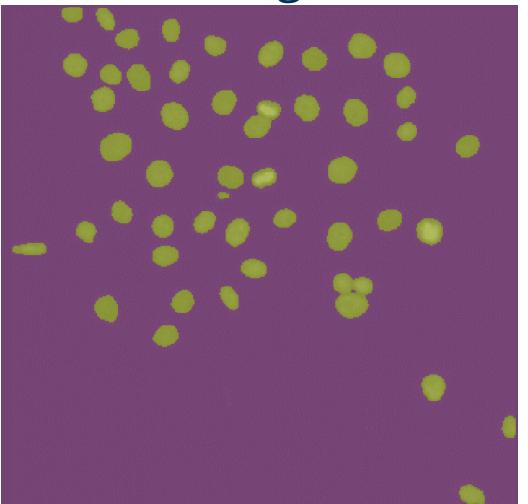
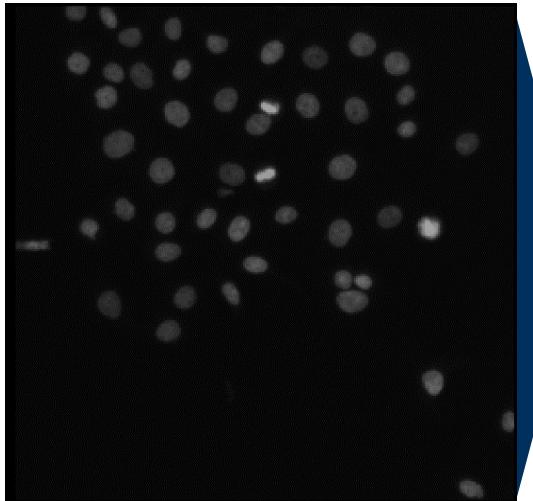
- **Instance segmentation:**

Differentiate multiple occurrences of the same class into separate instances of this class (e.g., separate *label* for each cell in image)

<https://scikit-image.org/docs/stable/api/skimage.data.html>



Instance segmentation



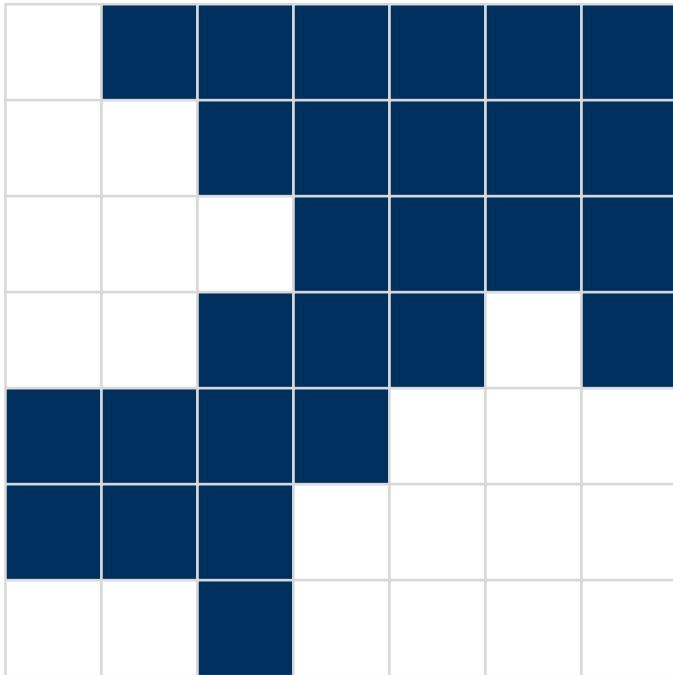
Semantic segmentation

Instance segmentation

In order to allow the computer differentiating objects, connected component analysis (CCA) is used to mark pixels belonging to different objects with different numbers

Background pixels are marked with 0.

The maximum intensity of a labelled map corresponds to the number of objects.



CCA

1	0	0	0	0	0	0
1	1	0	0	0	0	0
1	1	1	0	0	0	0
1	1	0	0	0	3	0
0	0	0	0	3	3	3
0	0	0	3	3	3	3
2	2	0	3	3	3	3

Image segmentation using thresholding

Finding the right workflow towards a good segmentation takes time

A priori, we usually don't know which information in the image is useful for a good segmentation

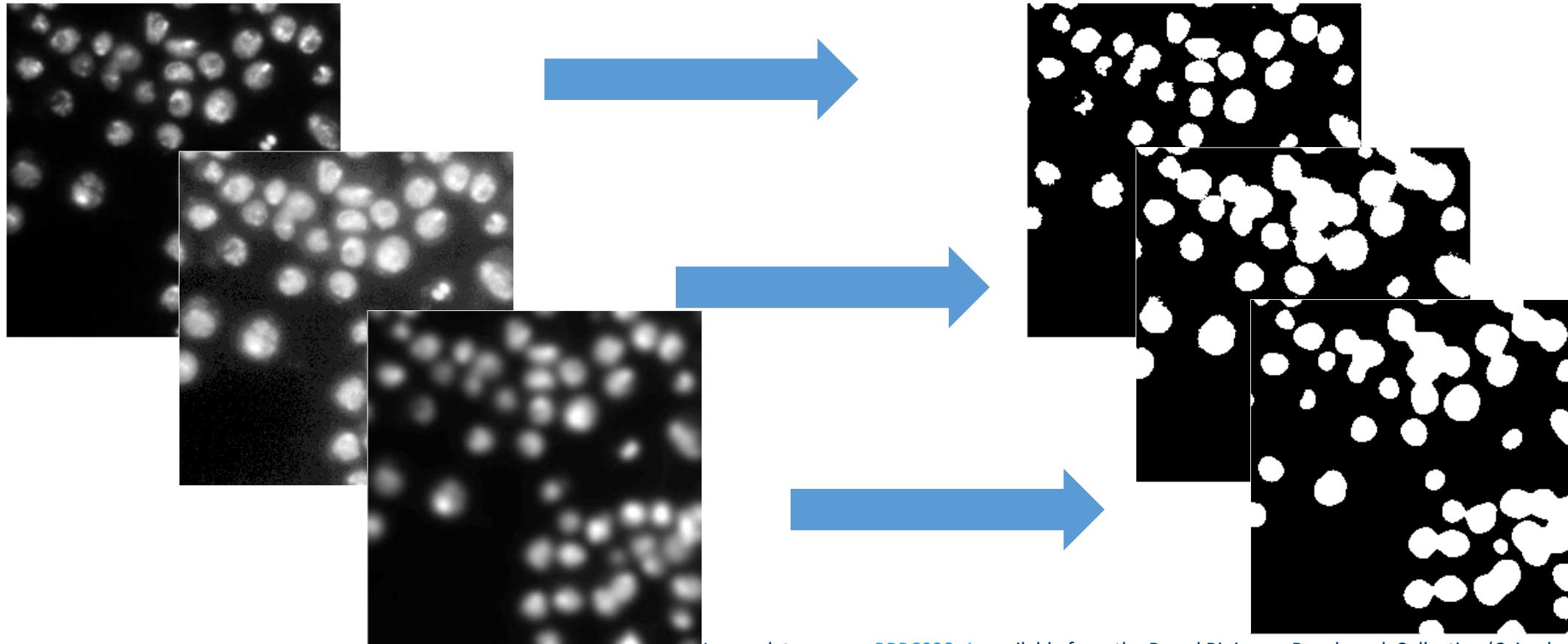


Image data source: [BBBC038v1](#), available from the Broad Bioimage Benchmark Collection (Caicedo et al., Nature Methods, 2019)

Machine learning

- A research field in computer science
- Finds more and more applications, also in life sciences.

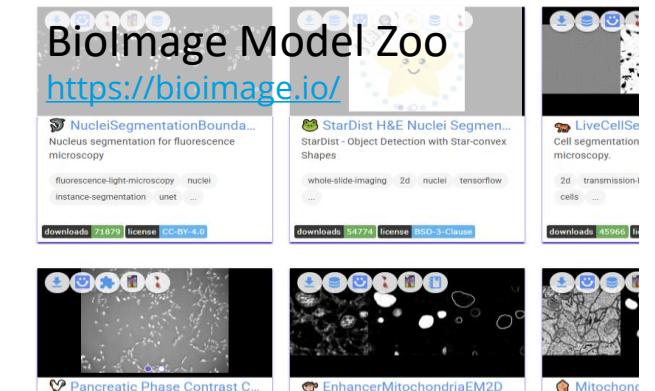
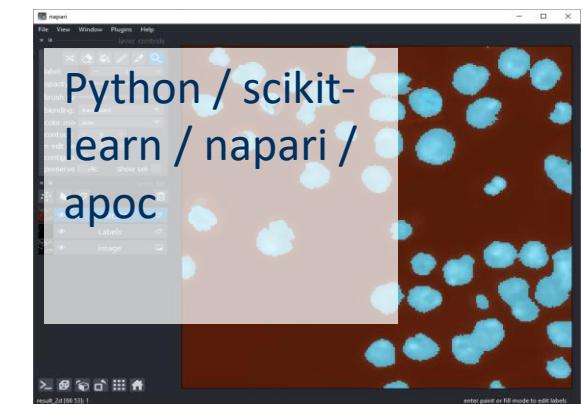
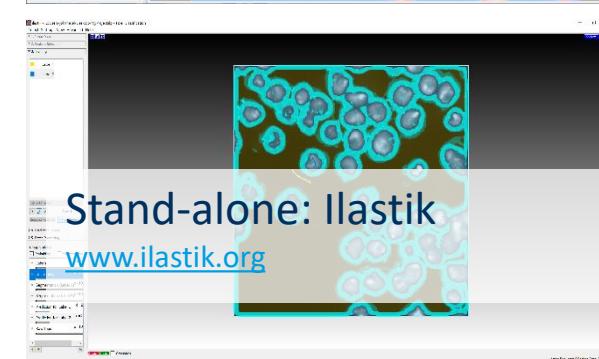
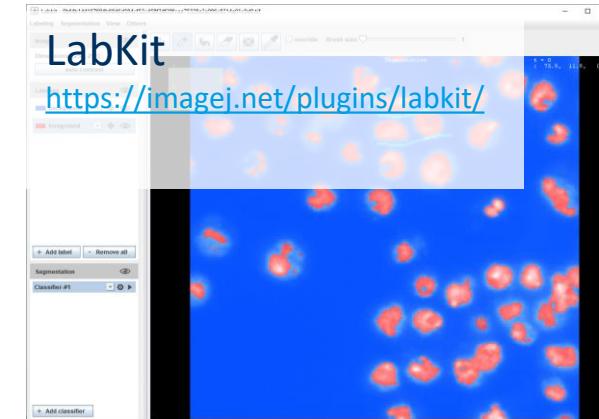
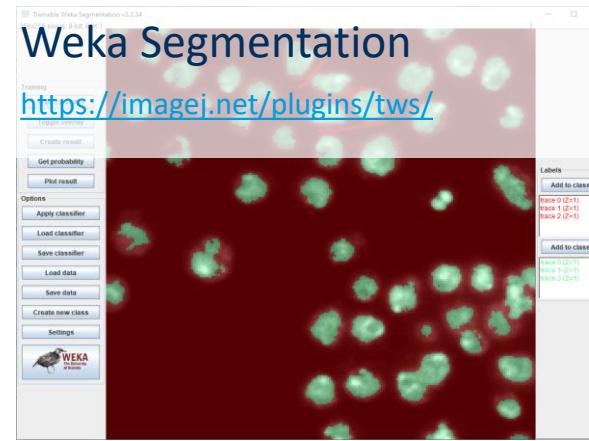
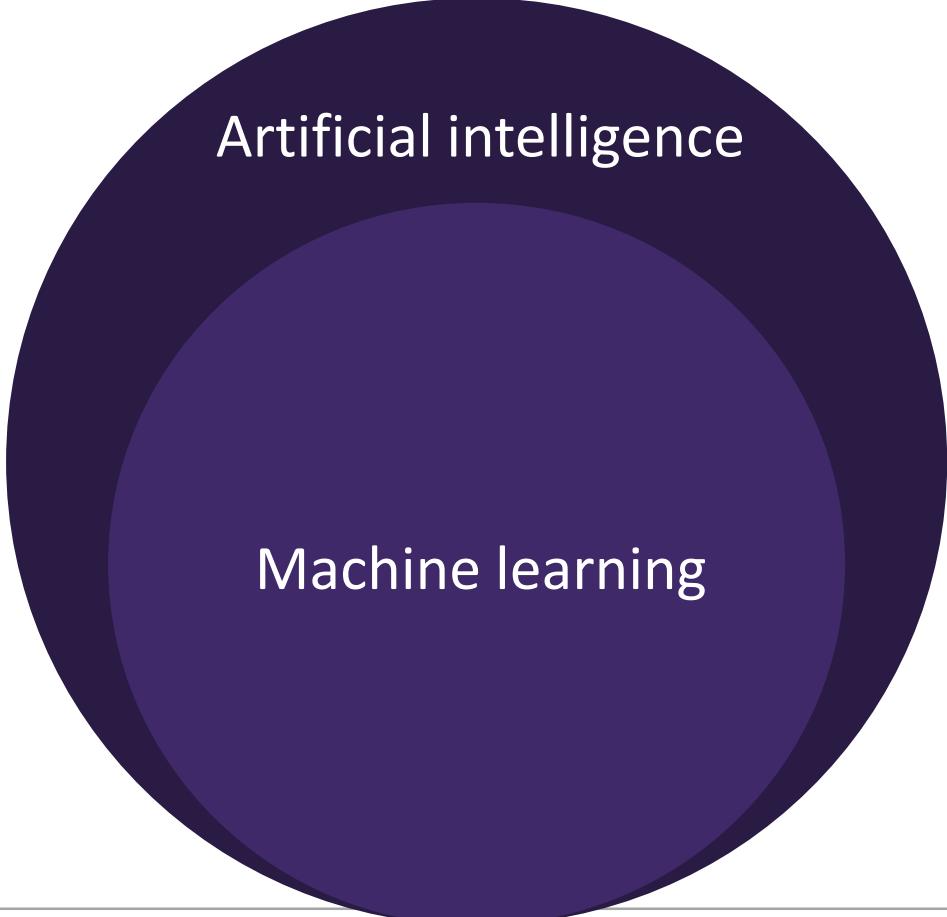
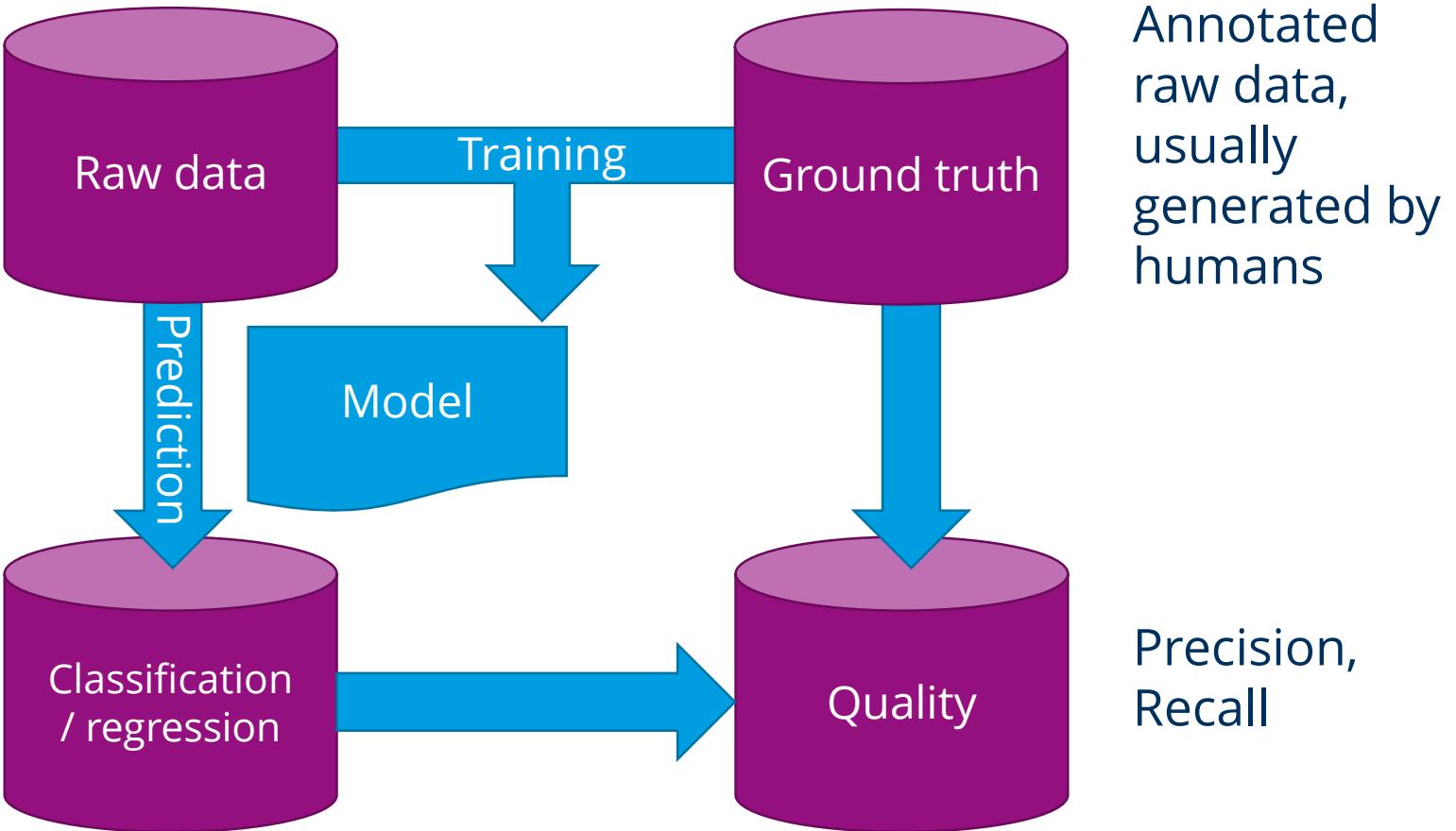
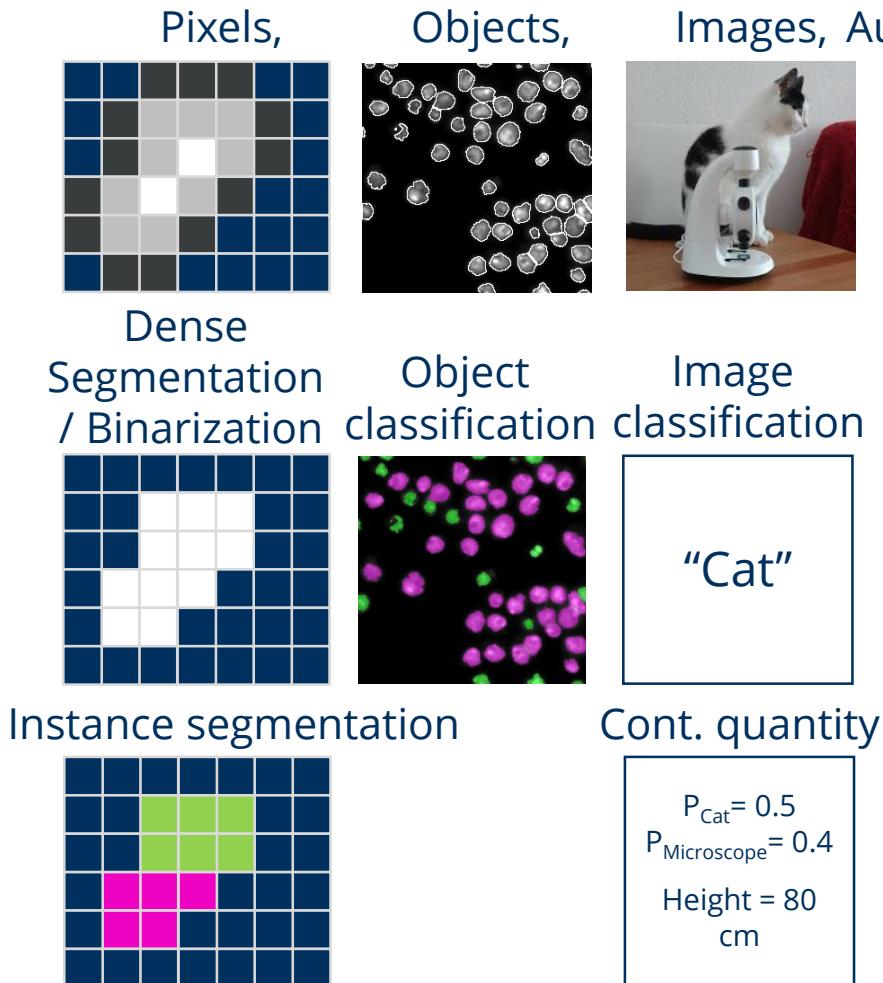


Image data source: [BBBC038v1](#), available from the Broad Bioimage Benchmark Collection (Caicedo et al., Nature Methods, 2019)

Machine learning

Automatic construction of predictive models from given data



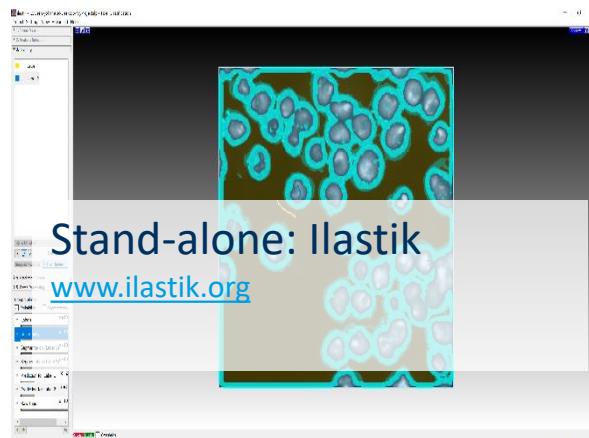
Segmentation: Latest developments

1970s-2010: Filtering,
thresholding

A Threshold Selection Method
from Gray-Level Histograms
NOBUYUKI OTSU

Abstract—A nonparametric and unsupervised method of automatic threshold selection for picture segmentation is presented. An optimal threshold is selected by the discriminant criterion, namely, so as to maximize the separability of the resultant classes in gray levels. The procedure is very simple, utilizing only the zeroth- and the first-order cumulative moments of the gray-level histogram. It is straightforward to extend the method to multithreshold problems. Several experimental results are also presented to support the validity of the method.

2010s: Random
forests et al.



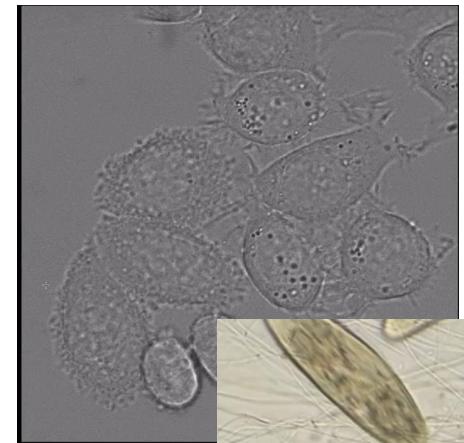
Deep
learning

2015: UNet
2018: Stardist



Foundational
models

2023: Segment
anything (SAM)
2024: SAM 2



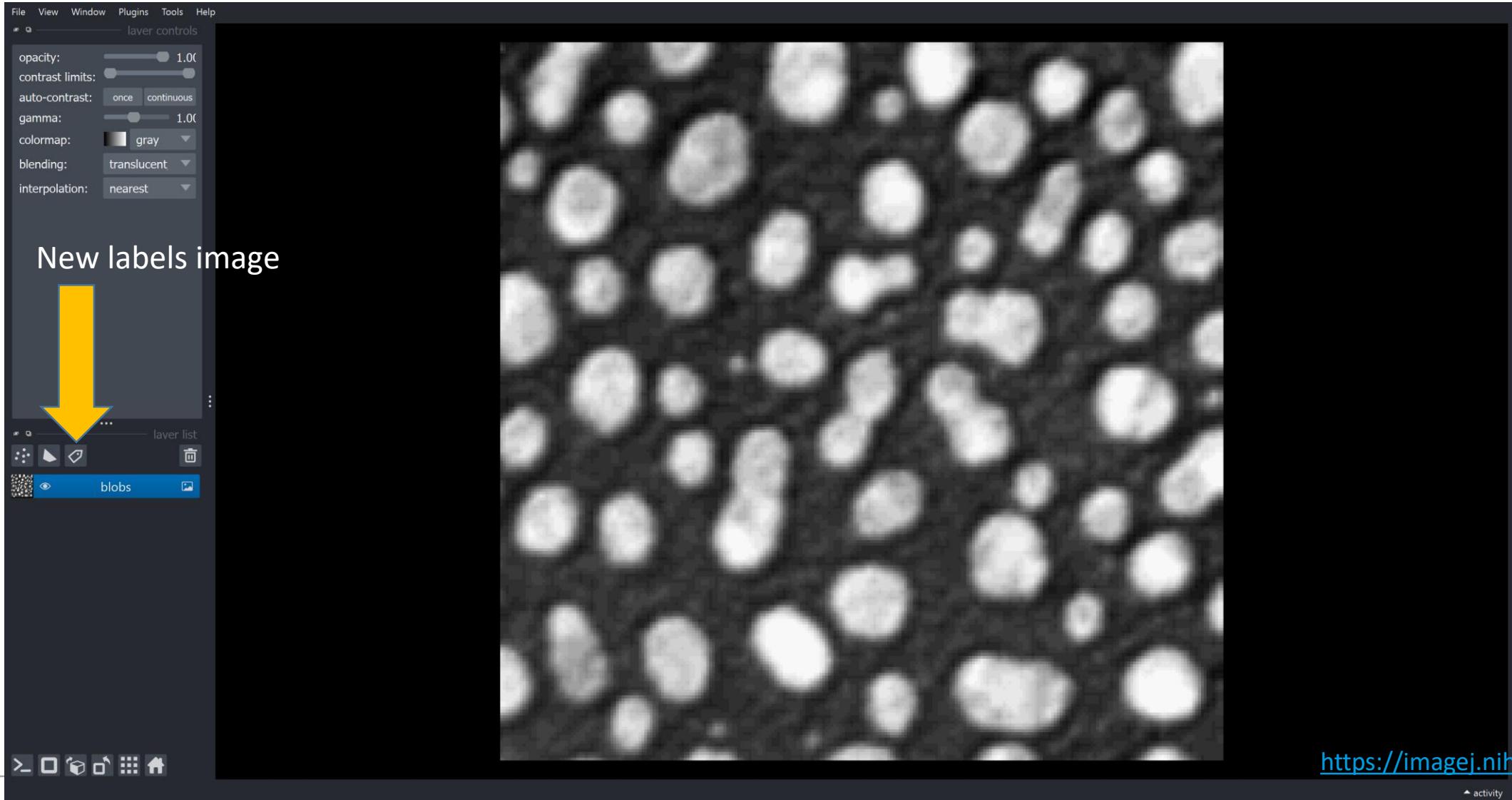
Computational demand

Segmentation and Supervised Machine Learning in napari

Random Forest Classifiers

- Pixel Classifier
- **napari-apoc plugin**

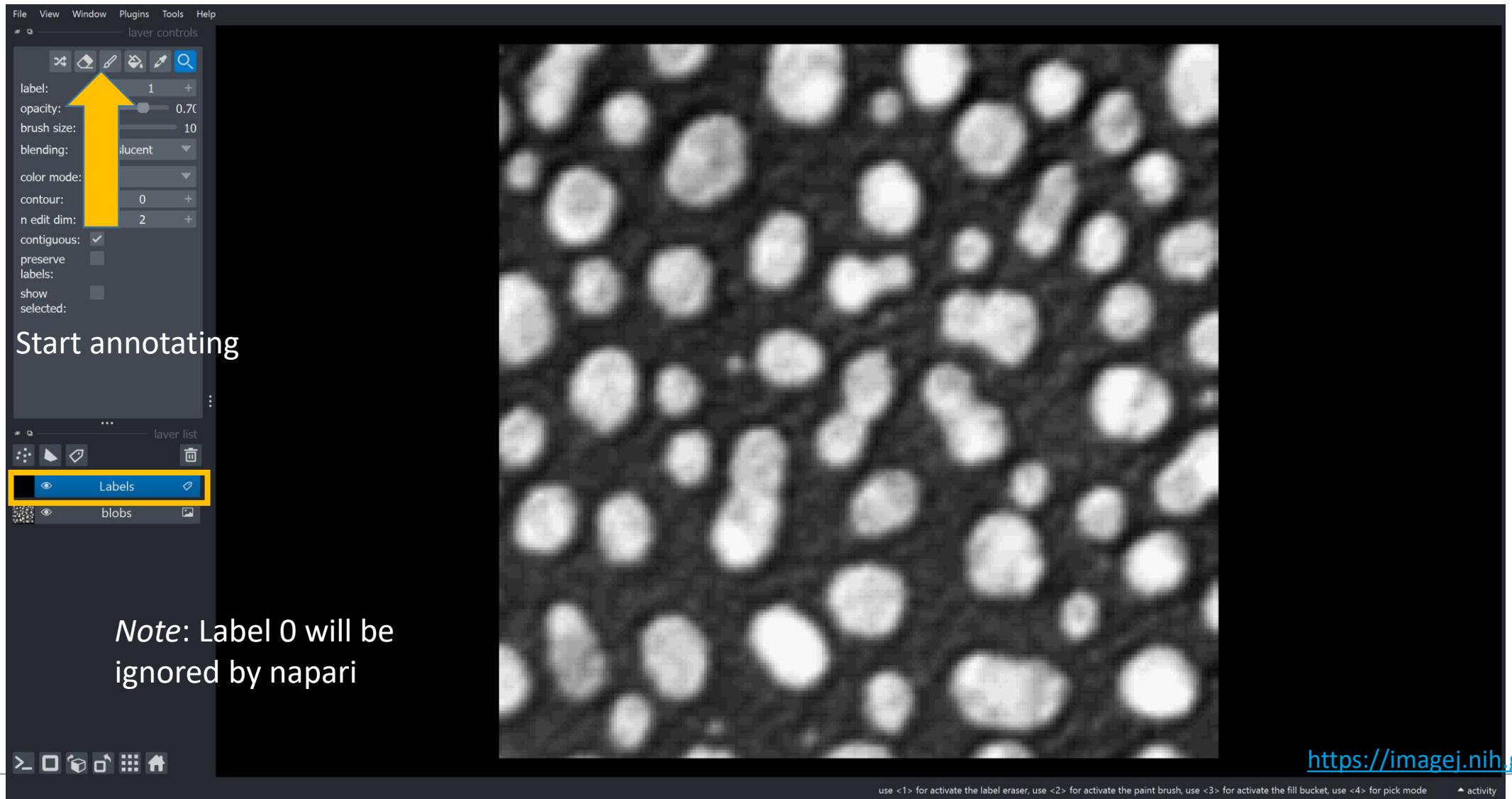
In napari: annotation



<https://imagej.nih.gov/ij/images/>

▲ activity

In napari: annotation



In napari: annotation

The screenshot shows the napari software interface. On the left is a toolbar with various tools for annotation, including a brush, eraser, and selection tools. A panel on the far left lists settings for the current layer: label (set to 2), opacity (0.70), brush size (1), blending (translucent), color mode (auto), contour (0), n edit dim (2), contiguous (checked), preserve labels, and show selected. Below these are buttons for layer controls and a layer list containing 'Labels' and 'blobs'. At the bottom are standard window control buttons.

Tips for annotations:

- Use **small brush size**: Pixels next to each other do not give much additional information to the classifier
- Annotate only pixels the class of which (e.g., background, foreground, etc) is **unambiguous** to you
- **Annotate few pixels**: If you already annotated 100k pixels, annotating 100 more will not change the result – annotating few pixels allows you to **tune the result**

On the right, there are three panels showing examples of cell segmentation. The top panel shows a cell with a blue outline labeled 'good'. The middle panel shows a cell with a blue outline and some internal red outlines, labeled 'Not so good'. The bottom panel shows a cell with a complex multi-colored outline (blue, green, red) labeled 'bad'.

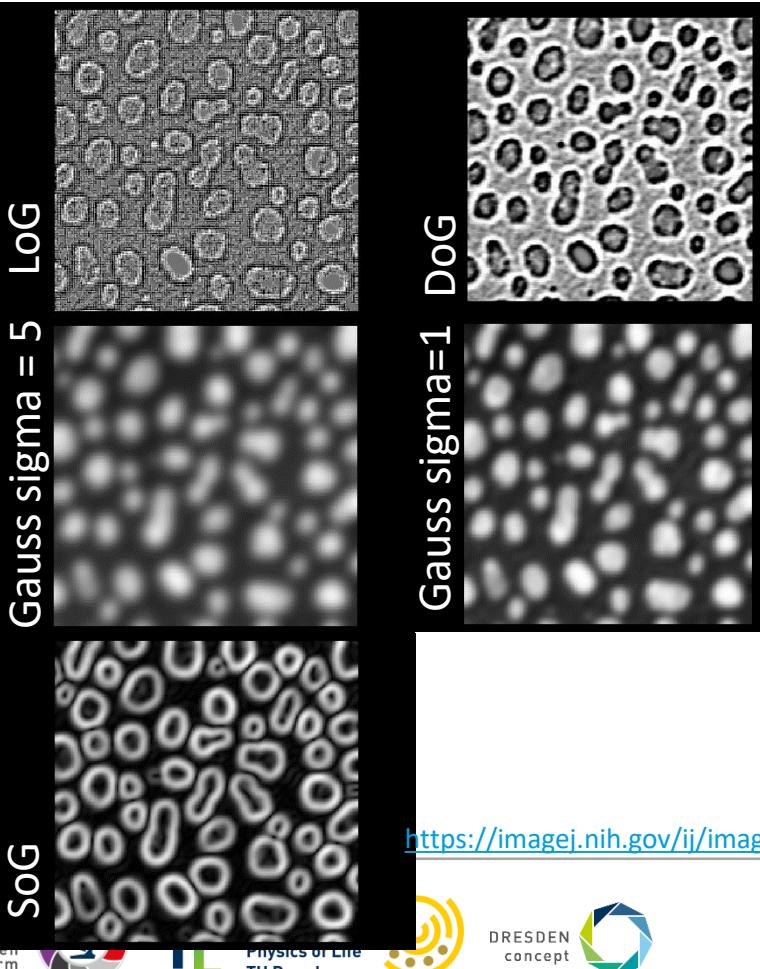
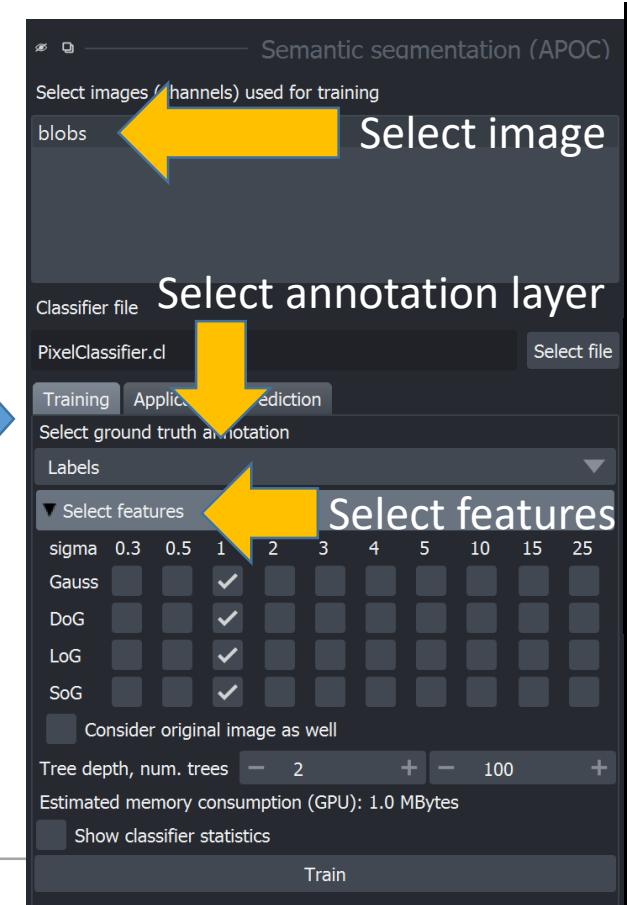
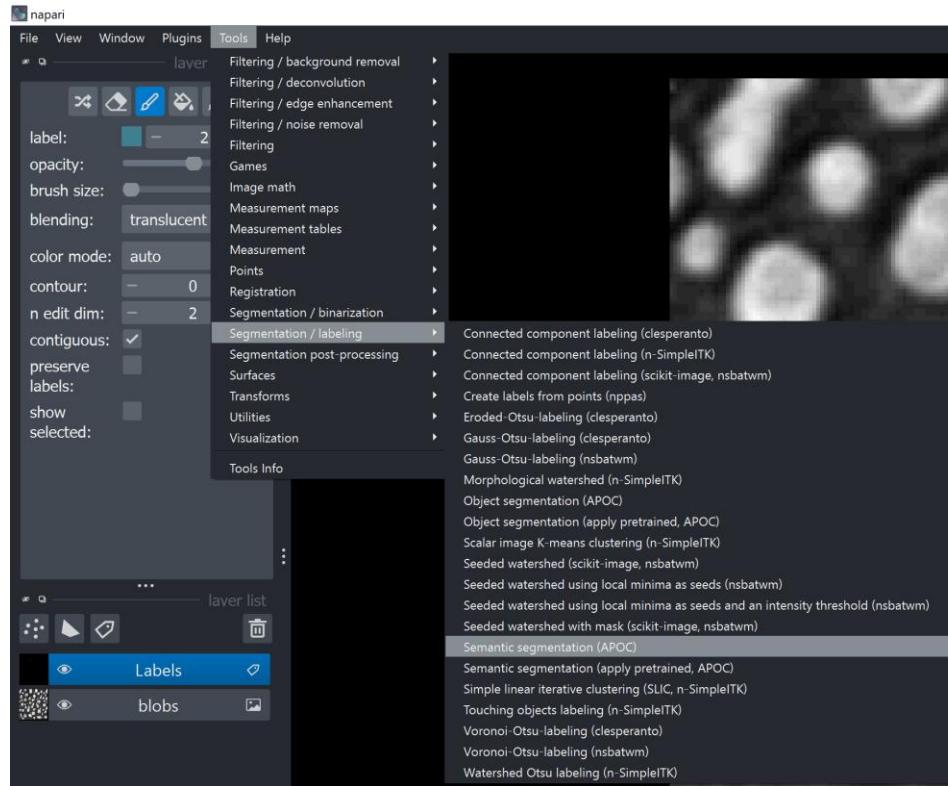
<https://imagej.nih.gov/ij/images/>

In napari: Semantic segmentation (training)

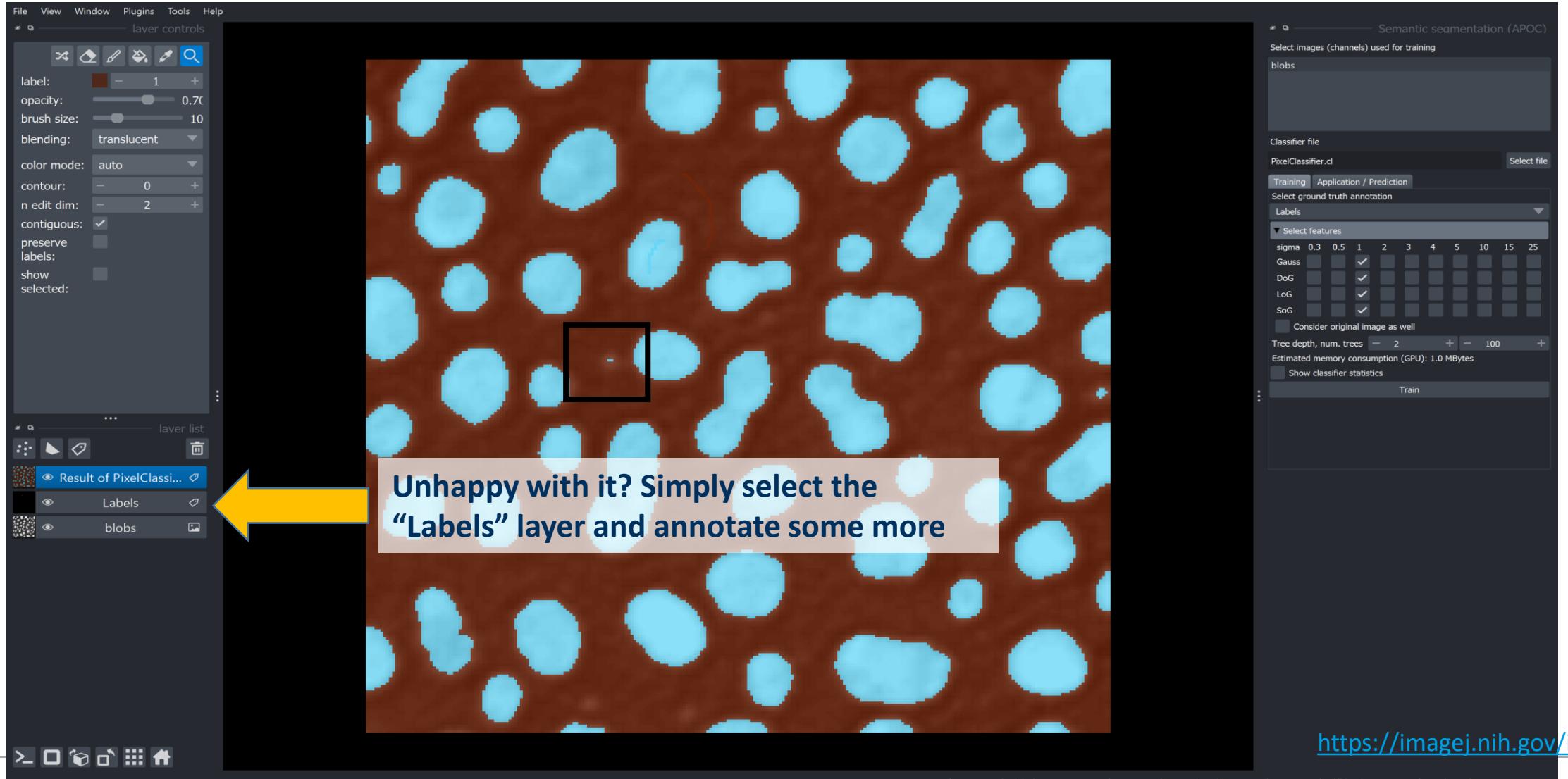
Two options:

Semantic segmentation: Predict class of every pixel according to annotation

Object segmentation: Assumes that class “1” refers to background – applies connected component analysis to other class



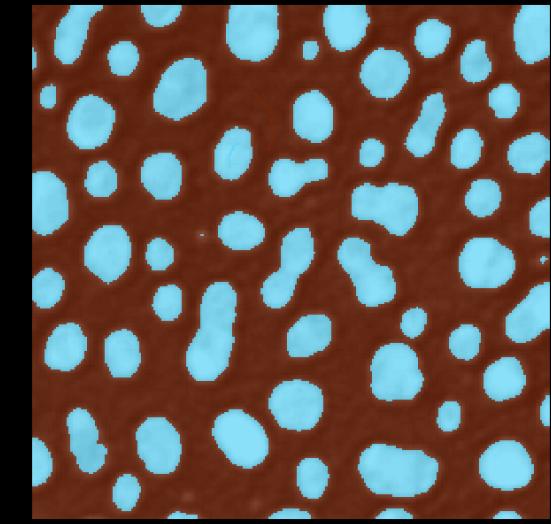
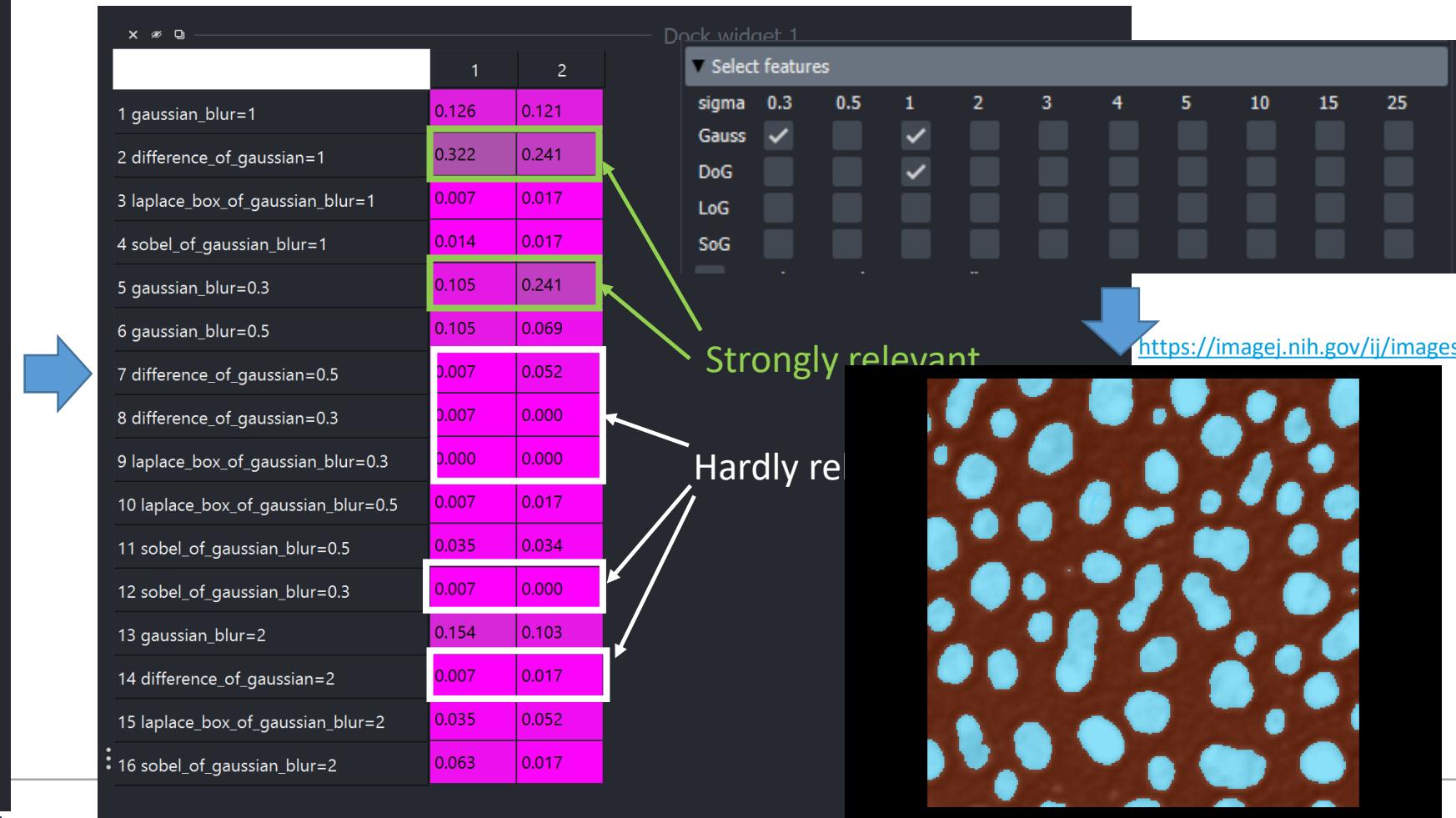
In napari: Semantic segmentation (training)



Semantic segmentation: Choosing the right features

Why not just do this?

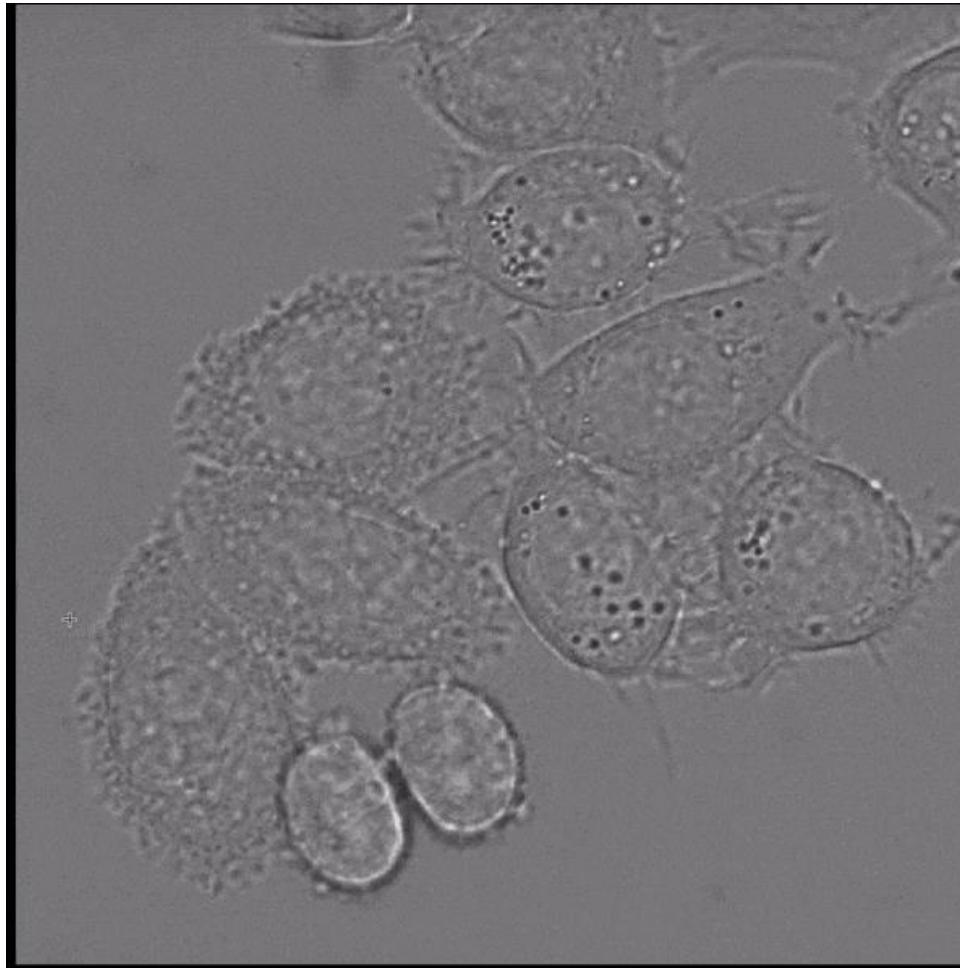
- Not all features are equally relevant!
- Calculating the features takes time and computation resources!



Segmentation and Supervised Machine Learning in napari

- Demonstration: Micro-sam plugin

Micro-sam



<https://github.com/computational-cell-analytics/micro-sam>

Feature Extraction

- napari-skimage-regionprops

Feature extraction

- A feature is a countable or measurable property of an image or object.
- Goal of feature extraction is finding a minimal set of features to describe an object well enough to differentiate it from other objects.

- **Intensity based**

- Mean intensity
- Standard deviation
- Total intensity
- Textures

- **Shape based /spatial**

- Area / Volume
- Roundness
- Solidity
- Circularity / Sphericity
- Elongation
- Centroid
- Bounding box

- **Spatio-temporal**

- Displacement,
- Speed,
- Acceleration

- **Others**

- Overlap
- Colocalization
- Neighborhood

- **Mixed features**

- Center of mass
- Local minima / maxima

Further reading:

<https://focalplane.biologists.com/2023/05/03/feature-extraction-in-napari/>

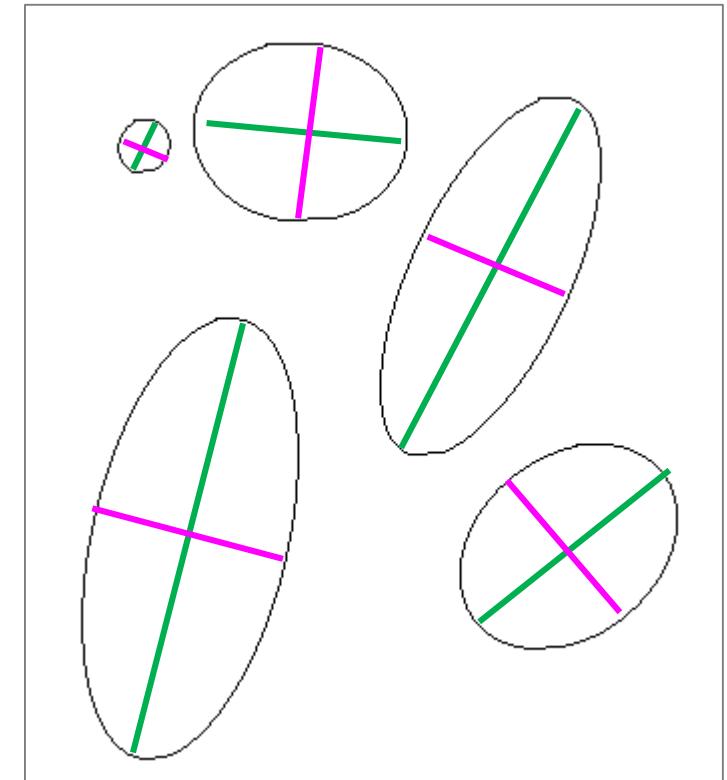
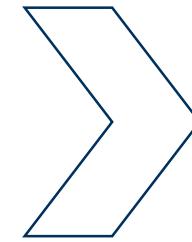
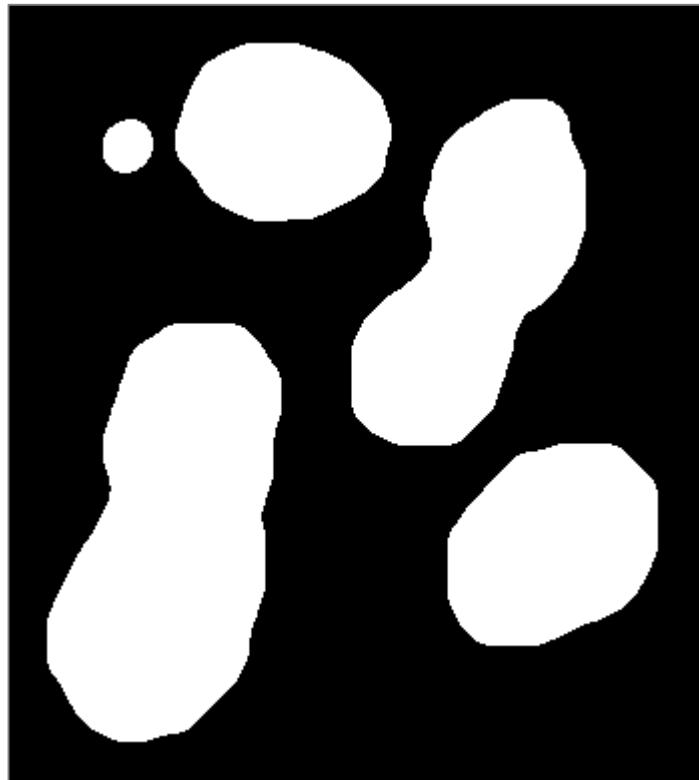
Fit ellipse

For every object, find the optimal ellipse simplifying the object.

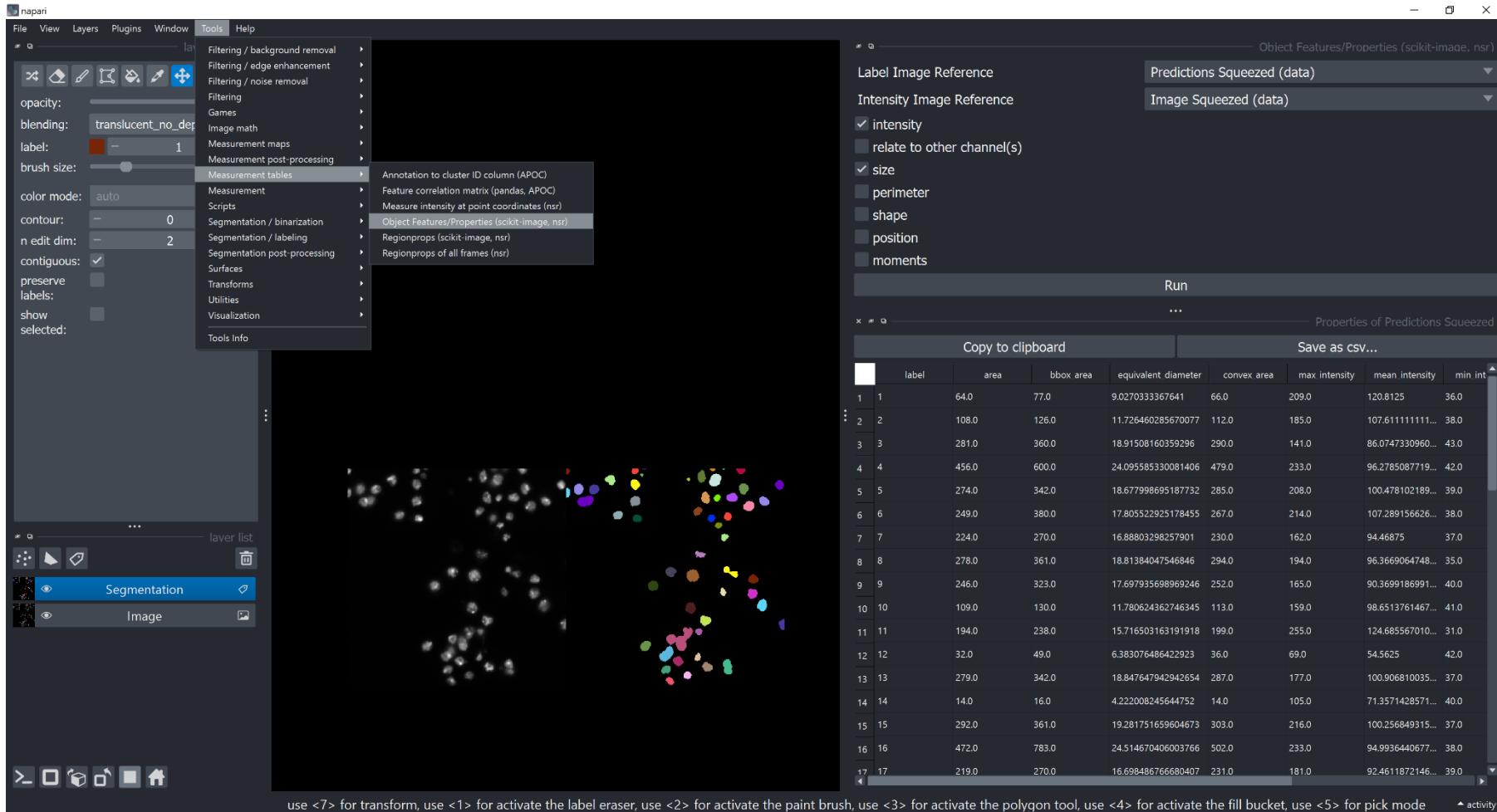
Major axis ... long diameter

Minor axis ... short diameter

Major and minor axis are
perpendicular to each other



napari-skimage-regionprops



<https://github.com/haesleinhuepf/napari-skimage-regionprops>

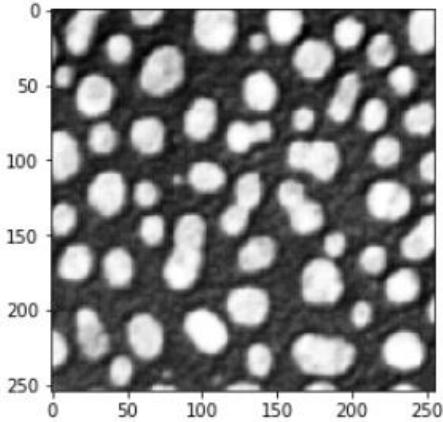
Object Classification and Supervised Machine Learning in napari

Random Forest Classifiers

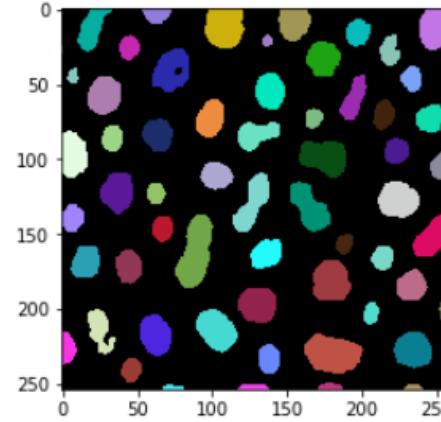
- Object Classifier
- napari-apoc plugin

Object classification

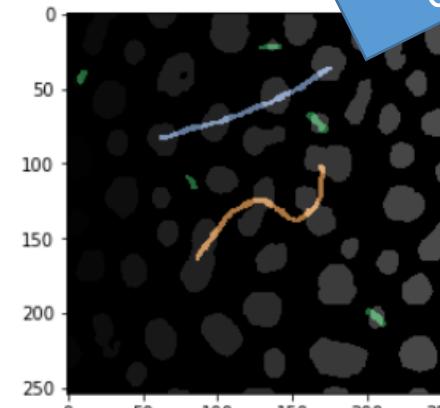
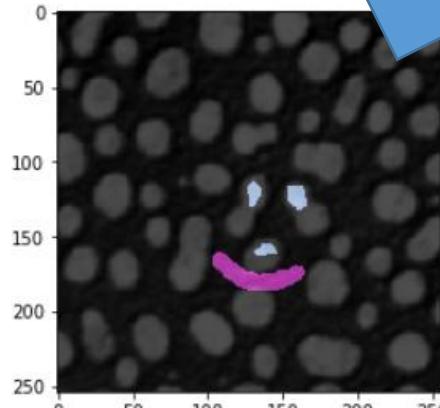
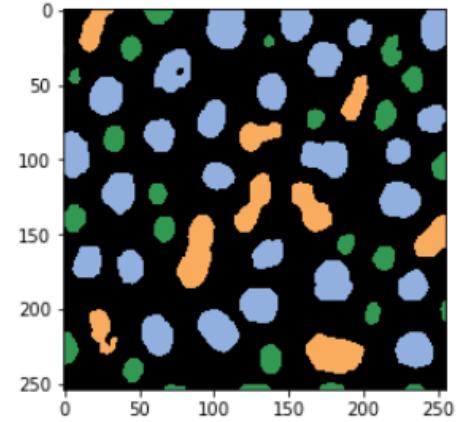
- Object classification is a task that can be applied to an existing instance segmentation in order to identify a particular group of objects



Object
segmentation



Object
classification

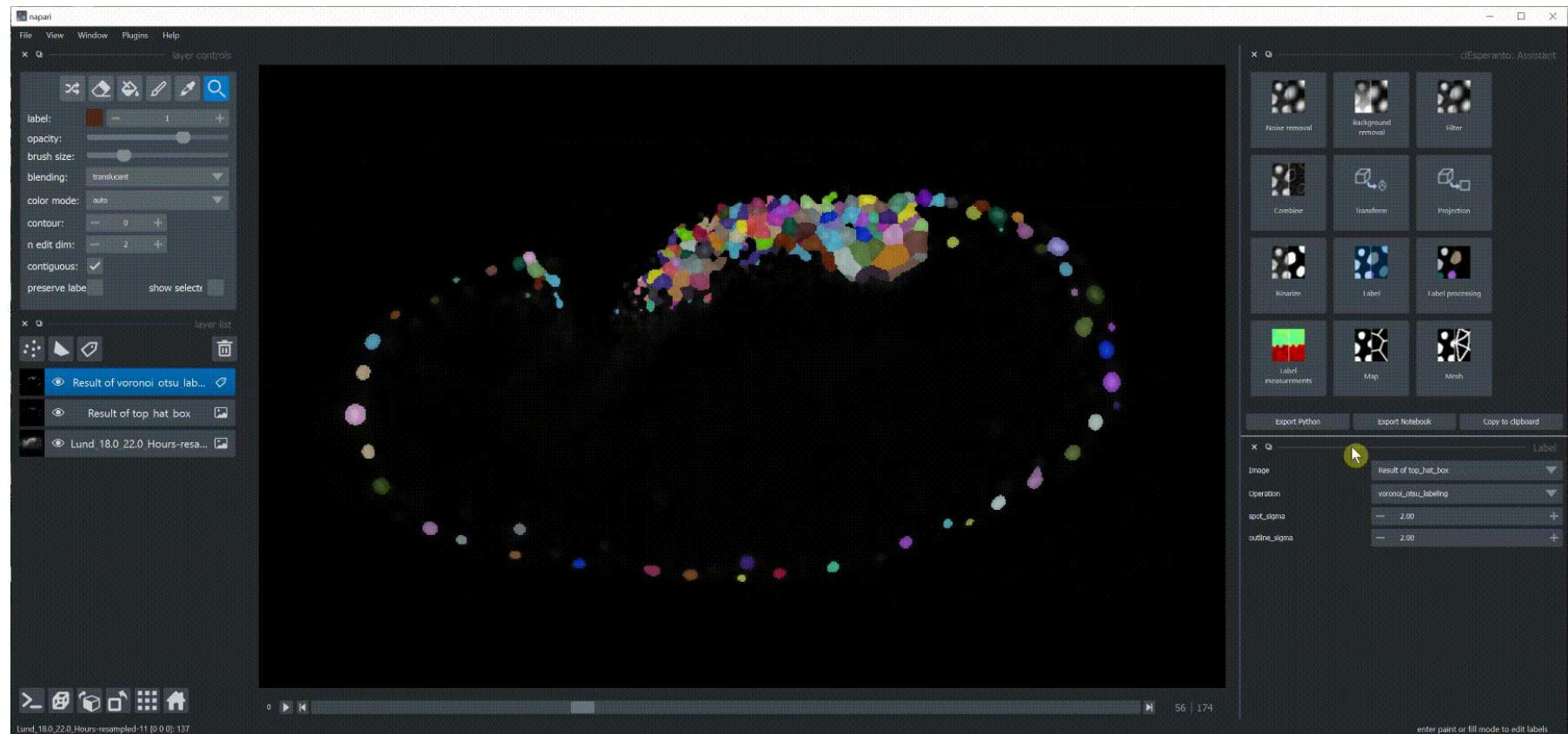


<https://imagej.nih.gov/ij/images/>

Object classification

Random Forest Classifiers based on

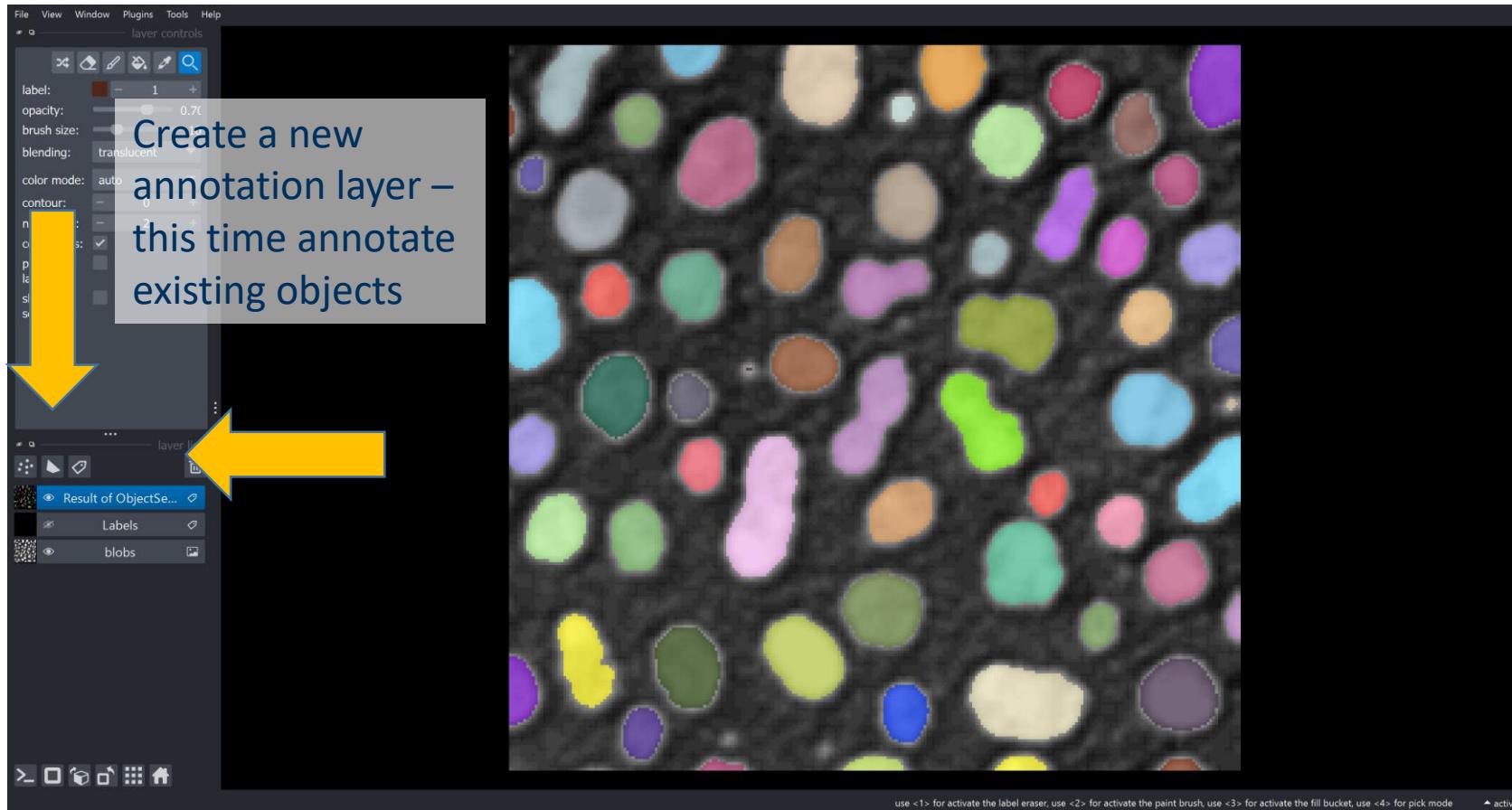
- scikit-learn and
- clesperanto



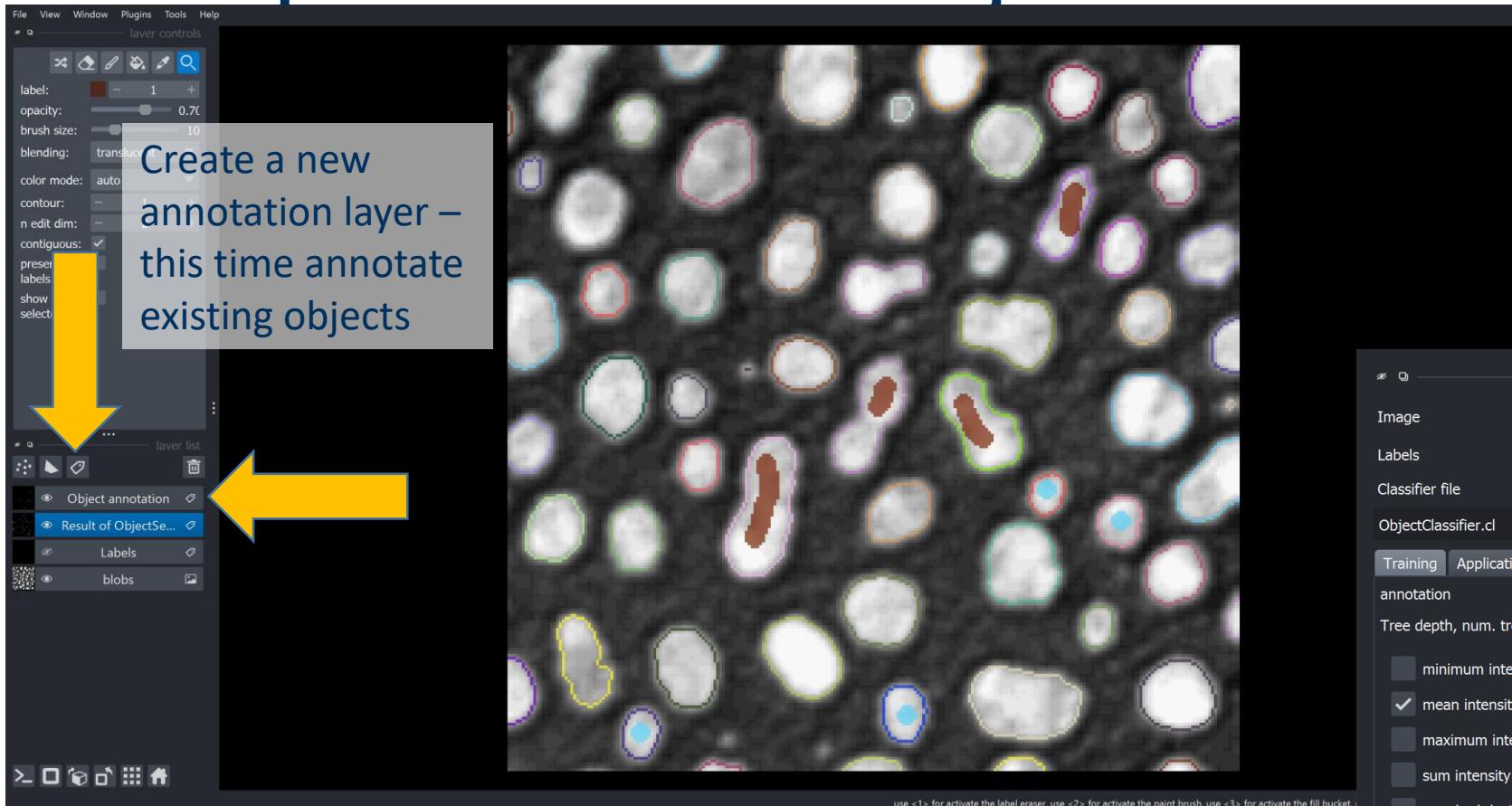
<https://github.com/haesleinhuepf/napari-accelerated-pixel-and-object-classification>

Image data source: Daniela Vorkel, Myers lab, MPI-CBG/CSBD

In napari: annotation



In napari: annotation and object classification

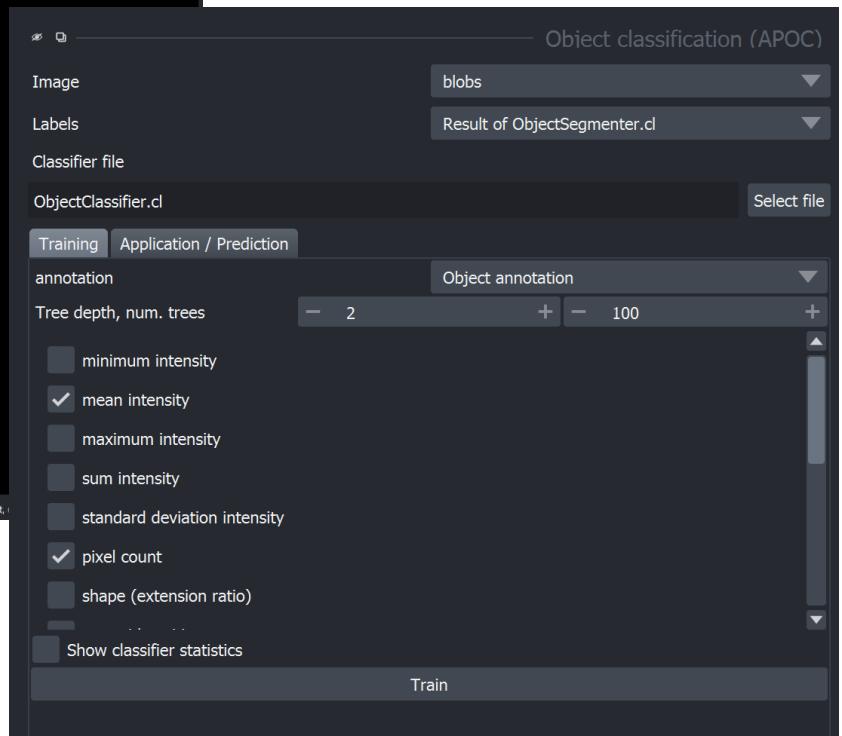


Telling different classes of objects apart requires:

- An **annotation** for some example objects
- **Features** for each objects upon which to make a prediction

<https://imagej.nih.gov/ij/images/>

Tools ->
Segmentation post-processing ->
Object Classification (APOC)

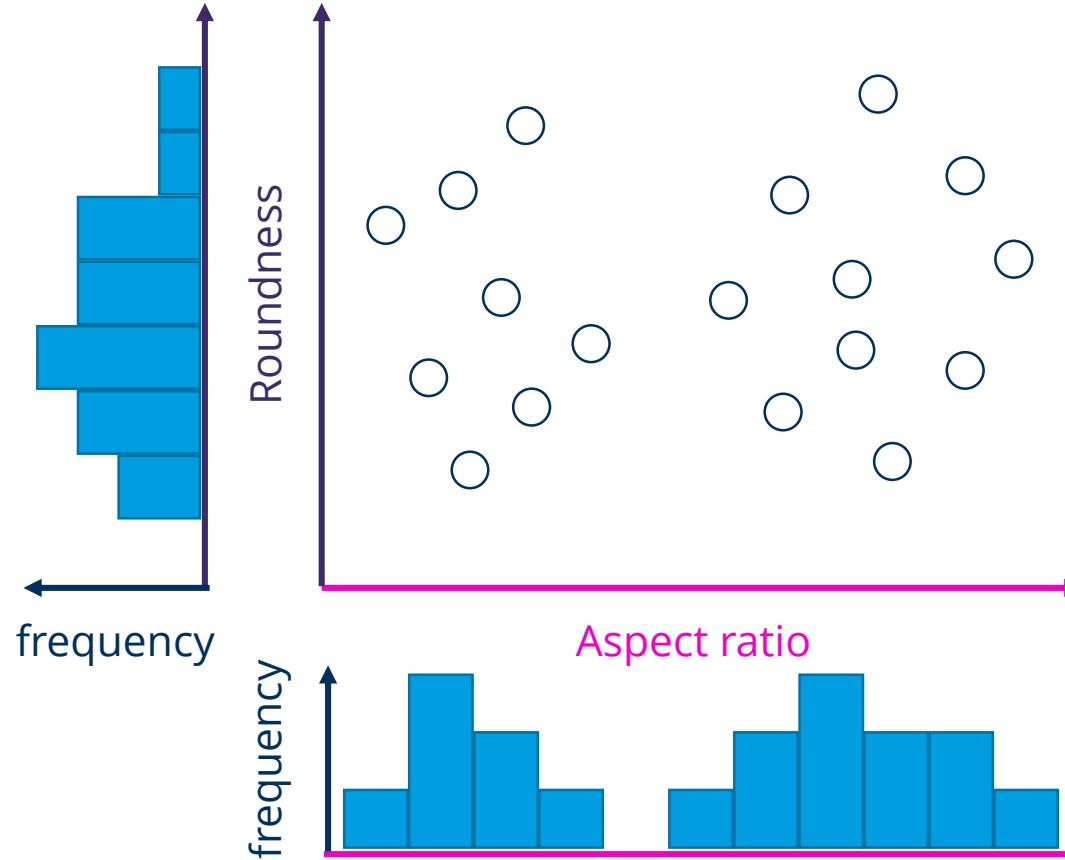


Object Classification and Unsupervised Machine Learning

- Dimensionality Reduction
- Clustering
- napari-clusters-plotter plugin

Unsupervised machine learning

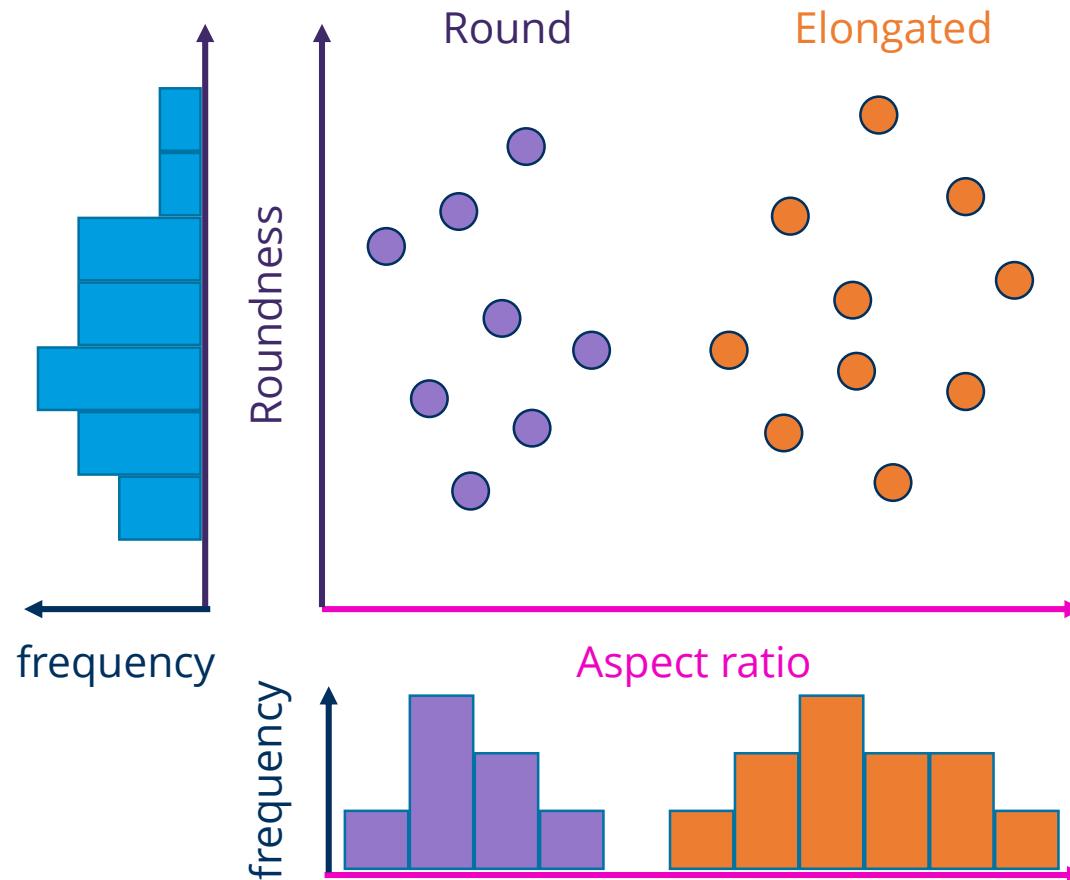
If you don't provide ground truth, the algorithm is *unsupervised*.



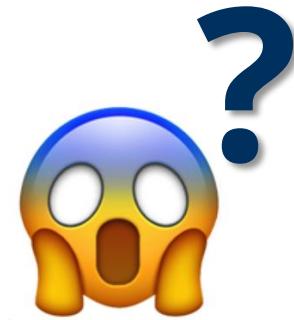
Unsupervised machine learning

If you don't provide ground truth, the algorithm is unsupervised.

Nevertheless, algorithms can tell us something about the data



- Mean intensity
- Standard deviation
- Total intensity
- Textures
- Area / Volume
- Roundness
- Solidity
- Circularity / Sphericity
- Elongation
- Centroid
- Bounding box
- ...



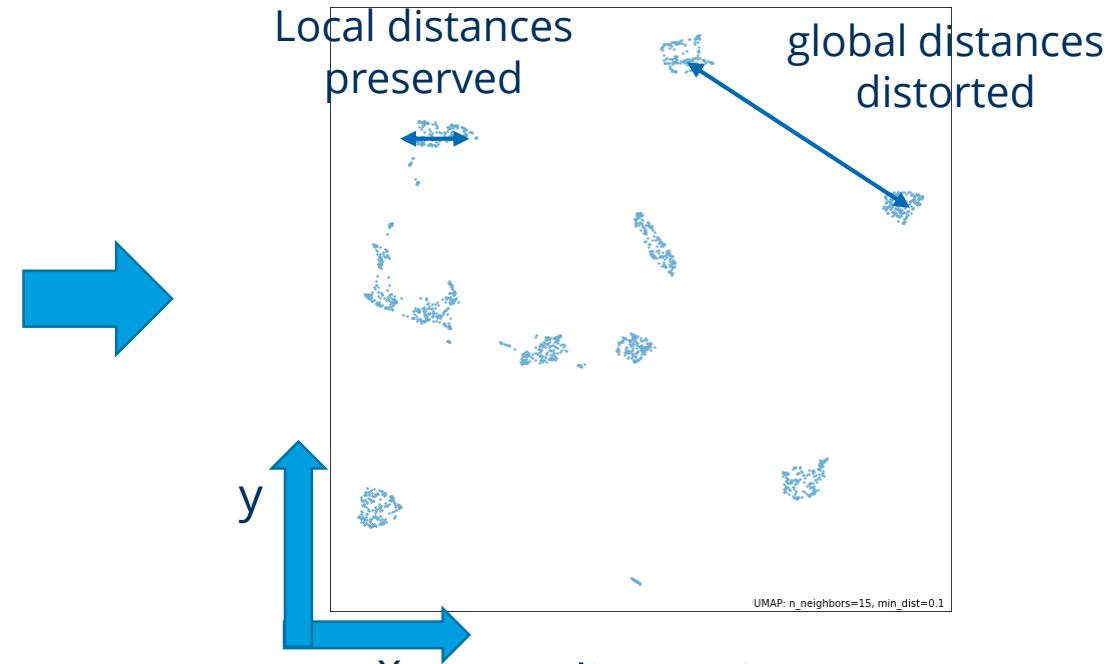
Dimensionality reduction

Challenge: Find a representation (embedding) of your data that represents the data in fewer dimensions

Preserve local distances at the expense of global distortions

		x	y	z	...								
	label	area	bbox_area	convex_area	equivalent_diameter	max_intensity	mean_intensity	min_intensity	solidity	extent	eret_diameter_ma	local_centroid-0	l...
1	1	3379	13949	5120	18.61786412639...	613.0	345.617963894...	259.0	0.6599609375	0....	37.3496987939662	15.77952056821...	18...
2	2	2319	7448	3491	16.4223022924...	421.0	297.8434670116...	240.0	0....	0....	38.65229618017...	4....	12...
3	3	2304	14415	4281	16.38681751812...	456.0	300.8298611111...	245.0	0....	0....	34.1906419455...	17.73828125	13...
4	4	3278	13804	5139	18.43048549951...	467.0	316.1446003660...	249.0	0....	0....	34.84250278036...	15.52287980475...	10...
5	5	1501	3315	1681	14.20563625190...	458.0	302.147235176549	236.0	0....	0....	17.97220075561...	6....	6...
6	6	2341	6061	2714	16.47407088948...	594.0	355.4446817599...	261.0	0....	0....	30.67572330035...	16.54250320375...	6...
7	7	1725	3584	1940	14.87979081163...	568.0	343.7866666666...	257.0	0....	0....	17.72004514666...	7.80463768115942	7...
8	8	1502	3840	1753	14.20879025650...	431.0	290.0659121171...	235.0	0....	0....	18.57417562100...	8....	6...
9	9	1602	4080	1894	14.51737058294...	475.0	297.8008739076...	241.0	0....	0....	18.70828693386...	8....	8...
10	10	1395	3600	1624	13.86304166283...	424.0	304.8494623655...	247.0	0....	0.3875	17.60681686165...	7....	7...
11	11	609	1100	697	10.51654029260...	323.0	274.2528735632...	241.0	0....	0....	13.45362404707...	3....	4...
12	12	1686	3757	1894	14.76679738567...	460.0	303.8303677342...	240.0	0....	0....	17.97220075561...	9....	7...
13	13	2157	5184	2531	16.03062694504...	576.0	339.990264255911	270.0	0....	0....	19.54482028569...	8....	8...
14	14	863	2340	1032	11.81237949737...	327.0	272.4449594438...	237.0	0....	0....	16.0312195418814	6....	5...

Many dimensions

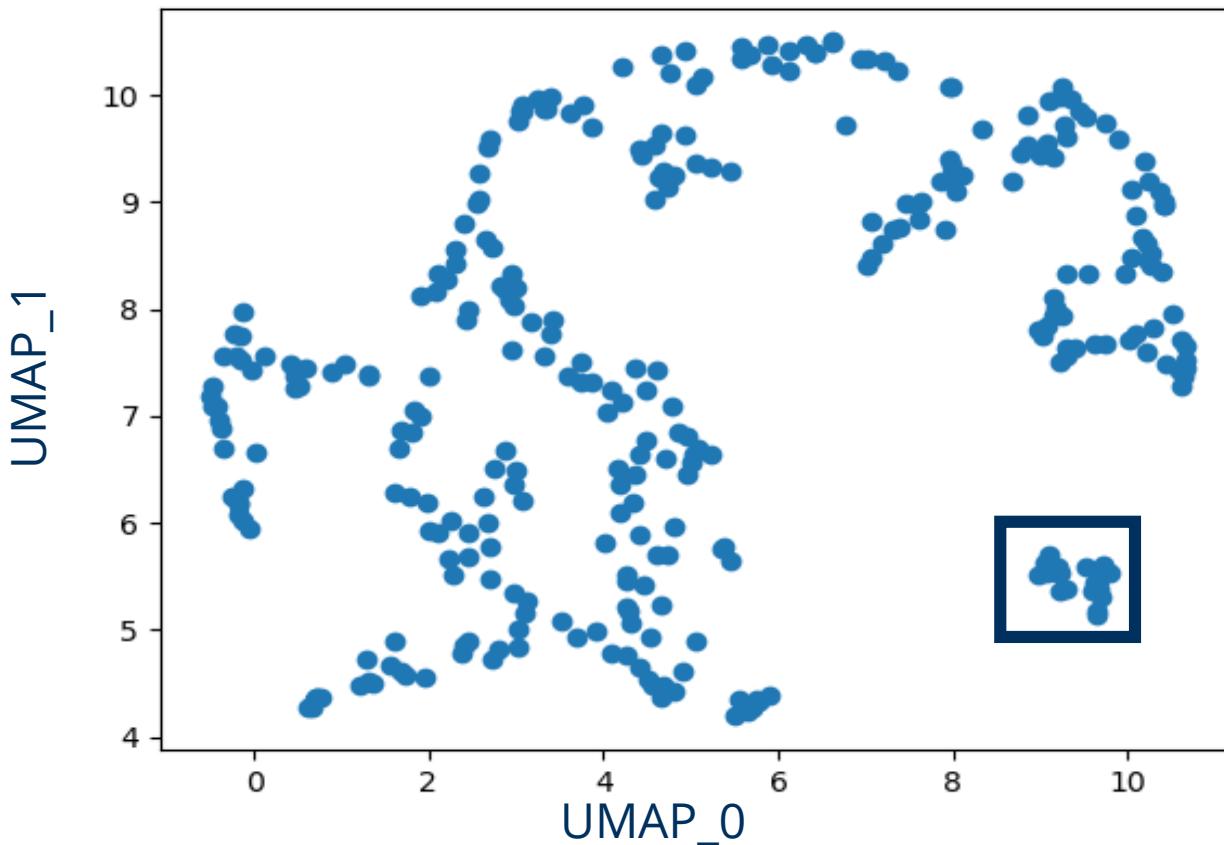


<https://umap-learn.readthedocs.io/en/latest/index.html>

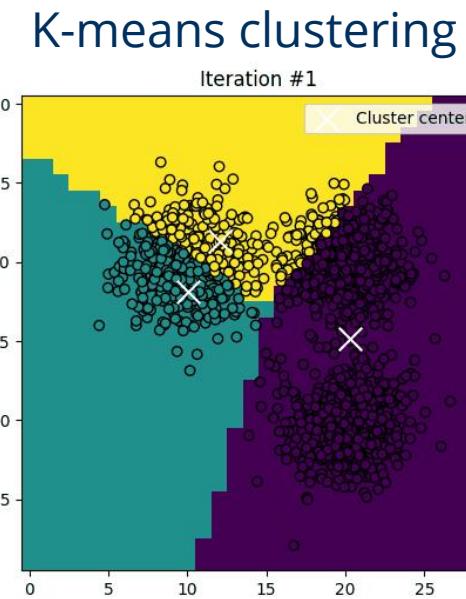
Clustering

Starting point: Feature space or dimensionality reduction reveals “groups” in our data

Can we automatically identify these groups?

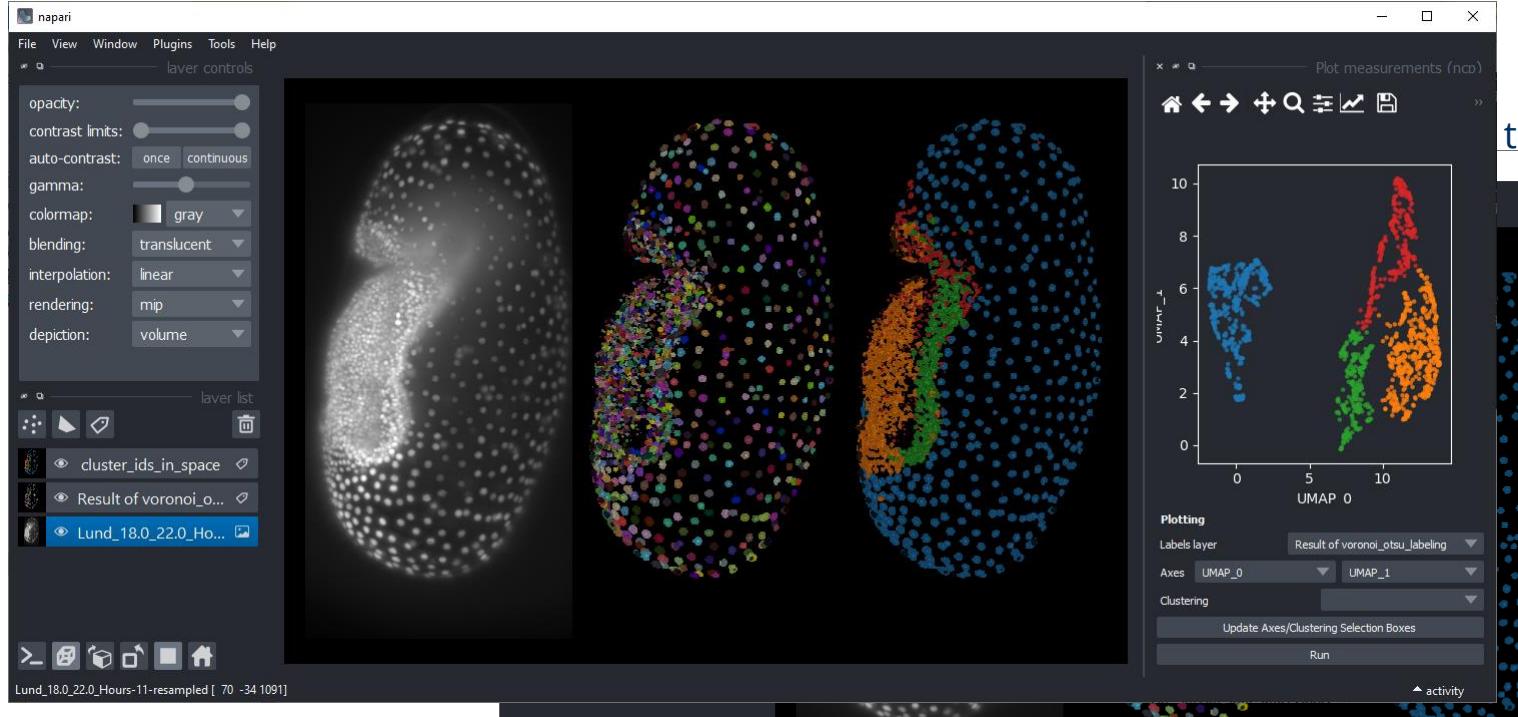


→ **Clustering** allows to stratify data into groups *without previous annotations*



Dimensionality reduction

Uniform manifold approximation and projection (UMAP)



Laura Žigutytė
@zigutyte

Ryan Savill
@RyanSavill4

Marcelo L. Zoccoler
Robert Haase,
Thorsten Wagner,
Johannes Soltwedel

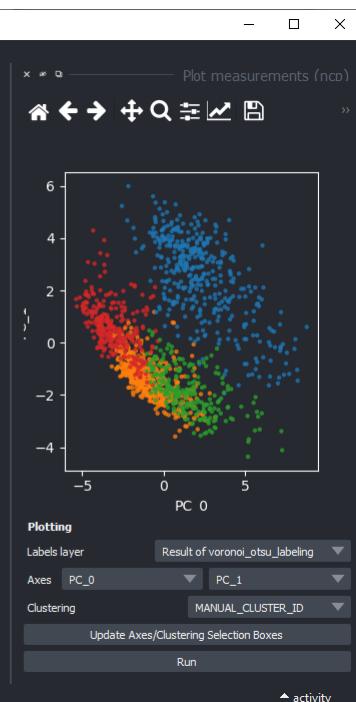
<https://github.com/BiAPoL/napari-clusters-plotter>

Image Data Source: Daniela Vorkel, Myers lab, MPI-CBG/CSBD Dresden

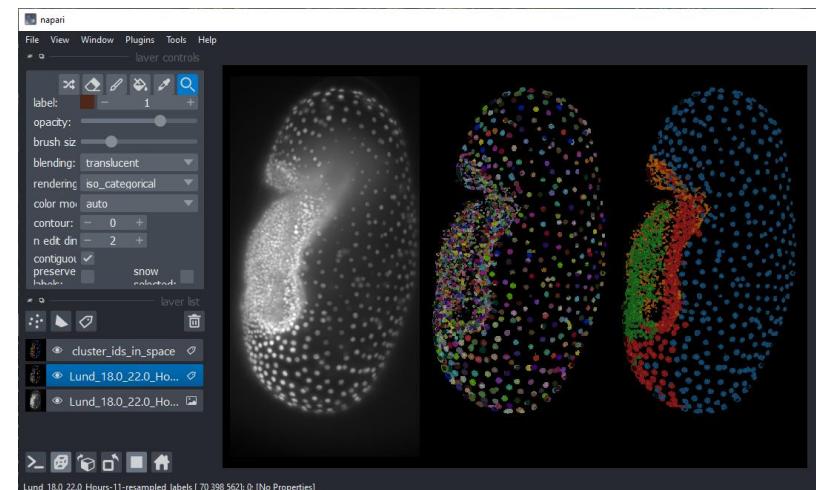
t-distributed stochastic neighbor embedding (t-SNE)



Principal component analysis (PCA)



Clustering



Laura Žigutytė
@zigutyte

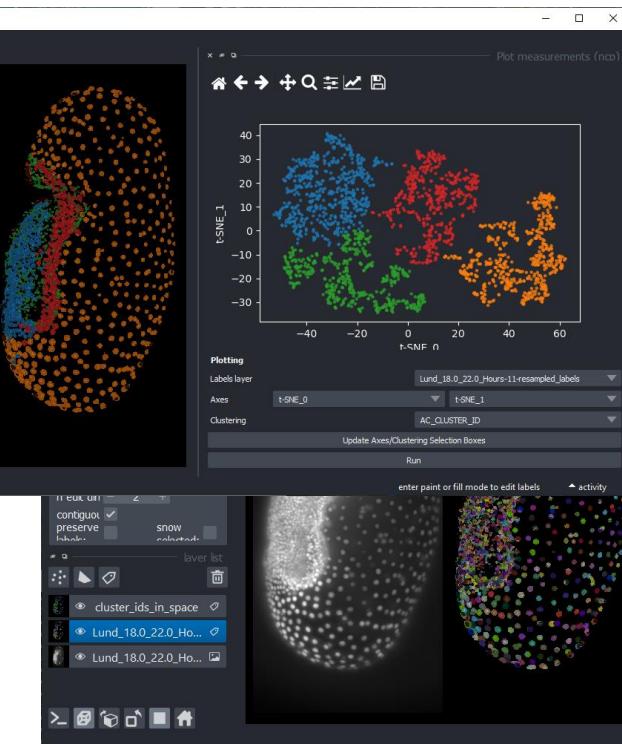
Ryan Savill
@RyanSavill4

Marcelo L. Zoccoler
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Thorsten Wagner,
Johannes Soltwedel

<https://github.com/BiAPoL/napari-clusters-plotter>

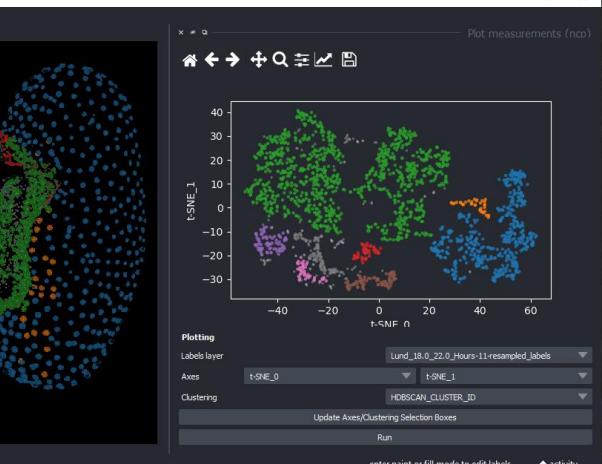
Image Data Source: Daniela Vorkel, Myers lab, MPI-CBG/CSBD Dresden

K-means clustering



Agglomerative clustering

Hierarchical Density-Based
Spatial Clustering of
Applications with Noise
(HDBSCAN)



Data Exploration

... using interactive clustering

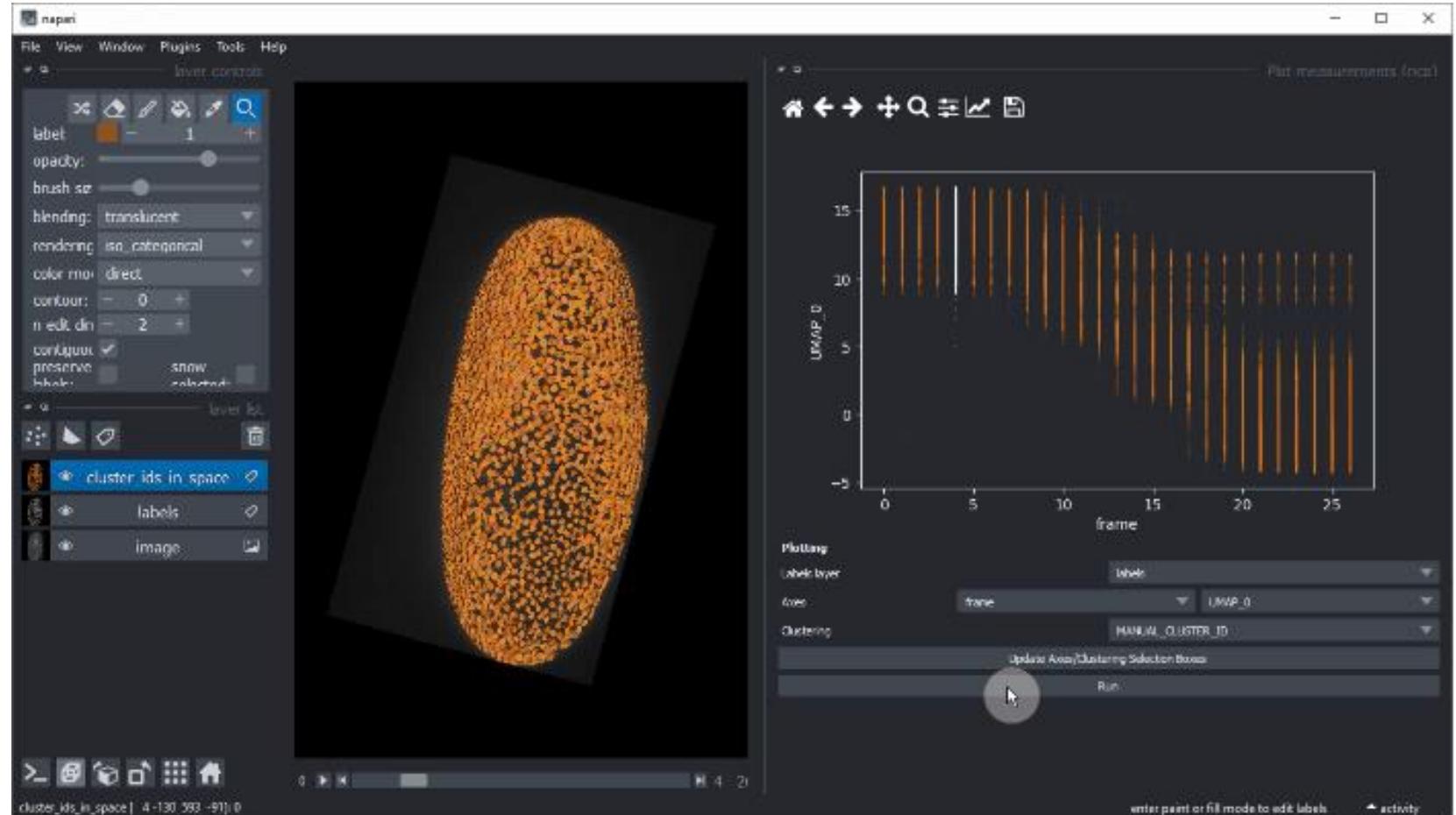
Multi-layer
analysis
coming soon
in 0.9.0!



Laura Žigutytė
@zigutyte

Ryan Savill
@RyanSavill4

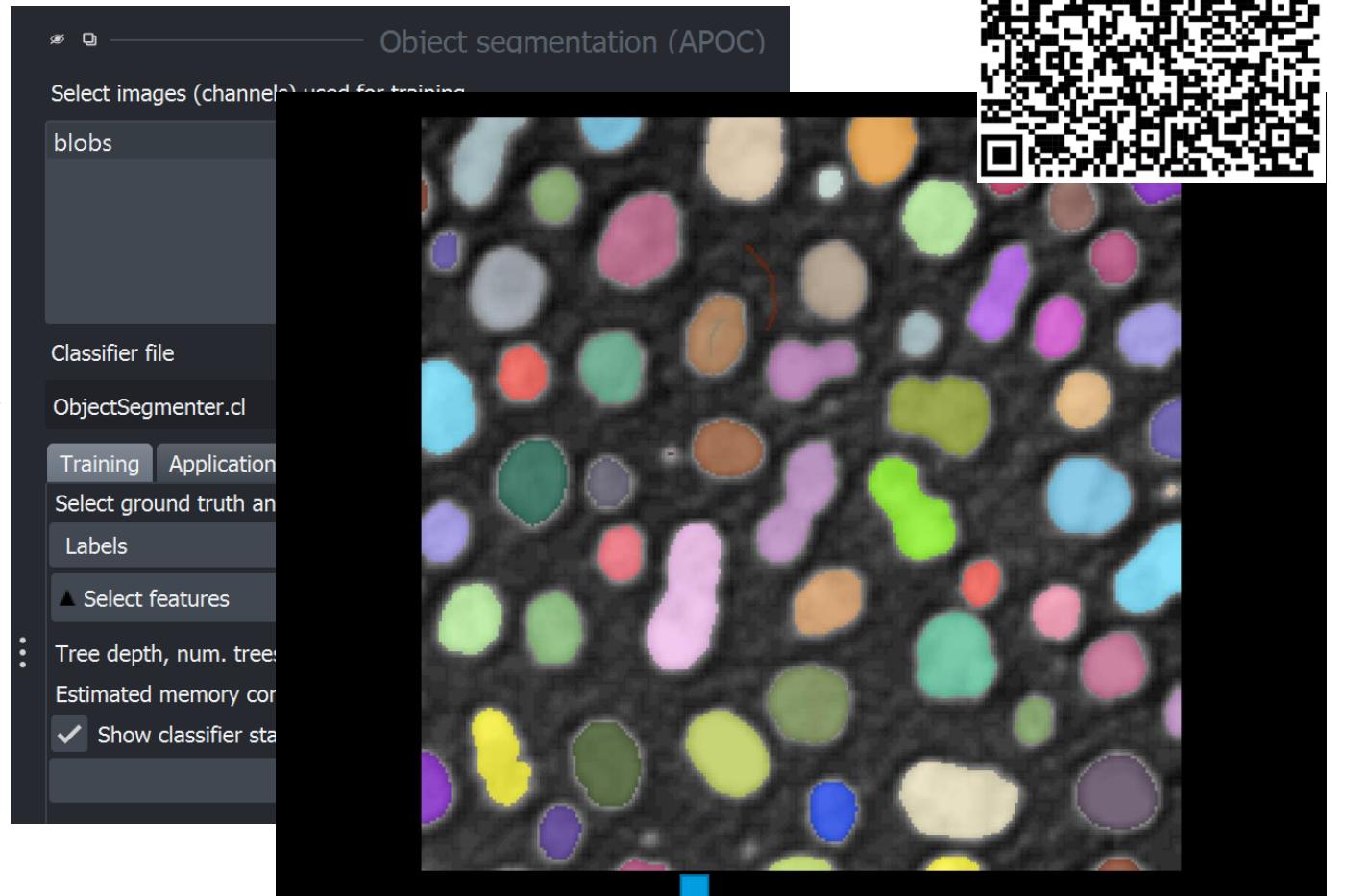
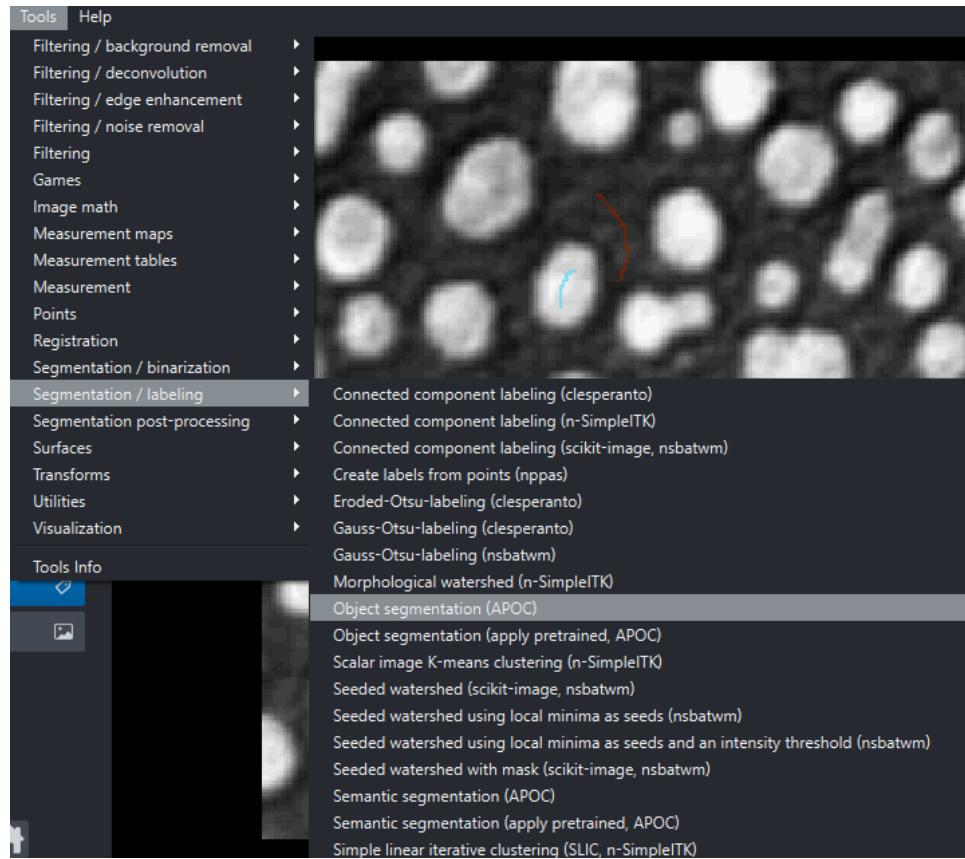
Marcelo L. Zoccoler
Robert Haase,
Thorsten Wagner,
Johannes Soltwedel



<https://github.com/BiAPoL/napari-clusters-plotter>

Image Data Source: Daniela Vorkel, Myers lab, MPI-CBG/CSBD Dresden

Exercise: Object segmentation



1. Activate the environment and open napari

```
mamba activate amhct  
napari
```

2. Open the blobs image

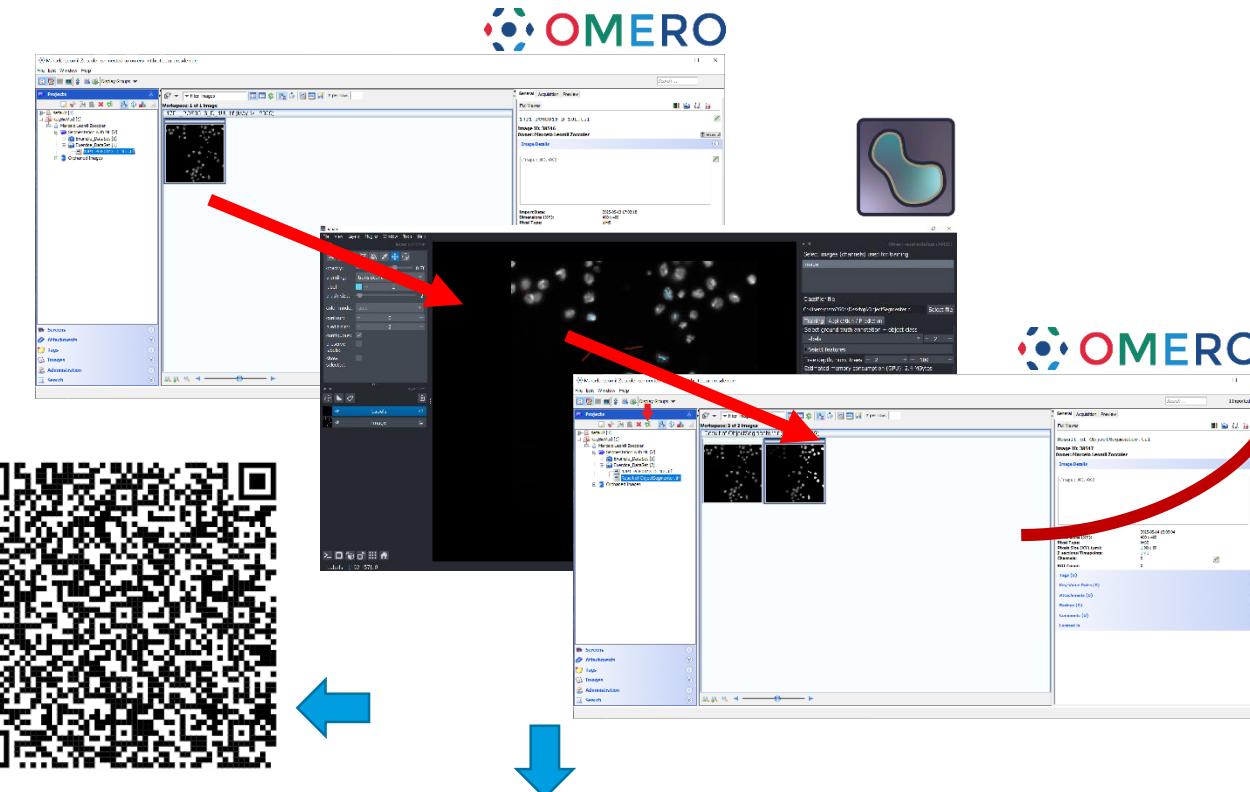
3. Perform object segmentation on blobs sample dataset

<https://imagej.nih.gov/ij/images/>

https://biapol.github.io/AMHCT_Bio_Image_Analysis_2025/interactive_pixel_classification/readme.html

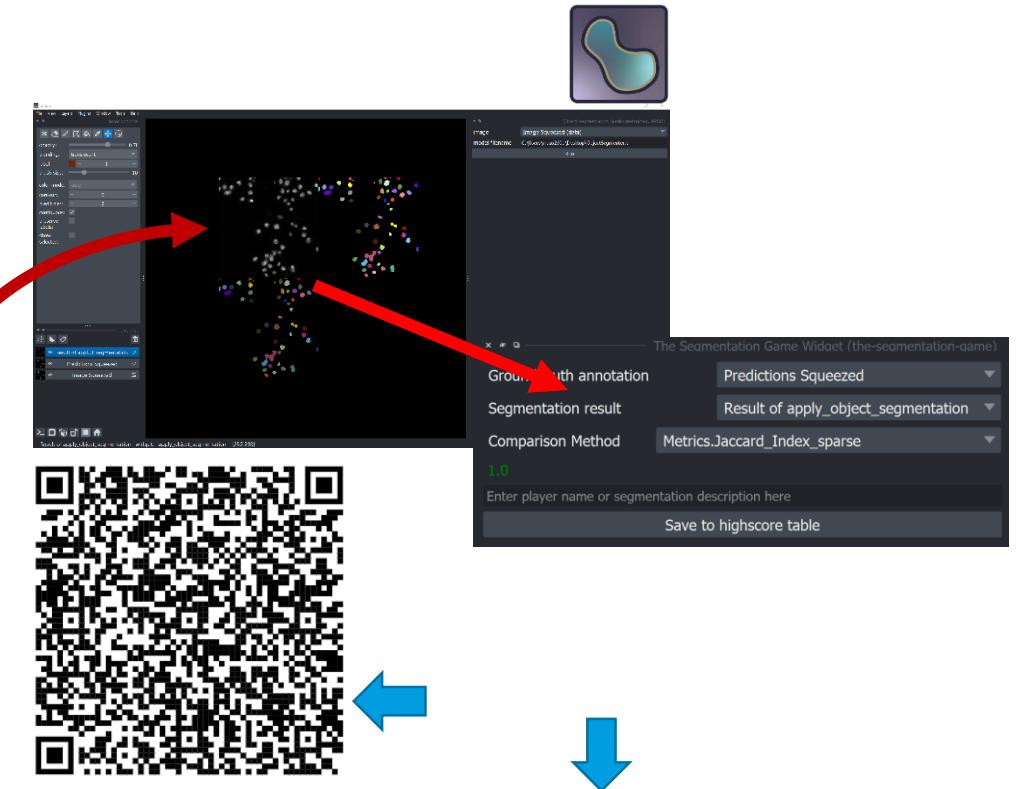
Exercise: Recording and Reproducing a Bio-Image Analysis Workflow

Creating a workflow:



https://biapol.github.io/AMHCT_Bio_Image_Analysis_2025/napari_apoc_omero_workflow/workflow_creation.html

Reproducing your colleague's workflow:



https://biapol.github.io/AMHCT_Bio_Image_Analysis_2025/napari_apoc_omero_workflow/workflow_reproduction.html

Discussion

- How many succeeded in **creating** the workflow?
- How many succeeded in **reproducing** the workflow?
- Which were key items to ensure reproducibility?
- Which part was the hardest?
- What could hamper reproducibility?

Further resources:

Napari-hub:

www.napari-hub.org

BiaPoL image analysis course materials:

<https://github.com/BiAPoL/Bio-image Analysis with Python>

Bio-image analysis materials:

<https://bioimagebook.github.io/README.html>

<https://haesleinhuepf.github.io/BioImageAnalysisNotebooks/intro.html>

Bio-Image Workflow Tools:

<https://galaxyproject.org/>

<https://github.com/nextflow-io/nextflow>

Image Science Community Forum:

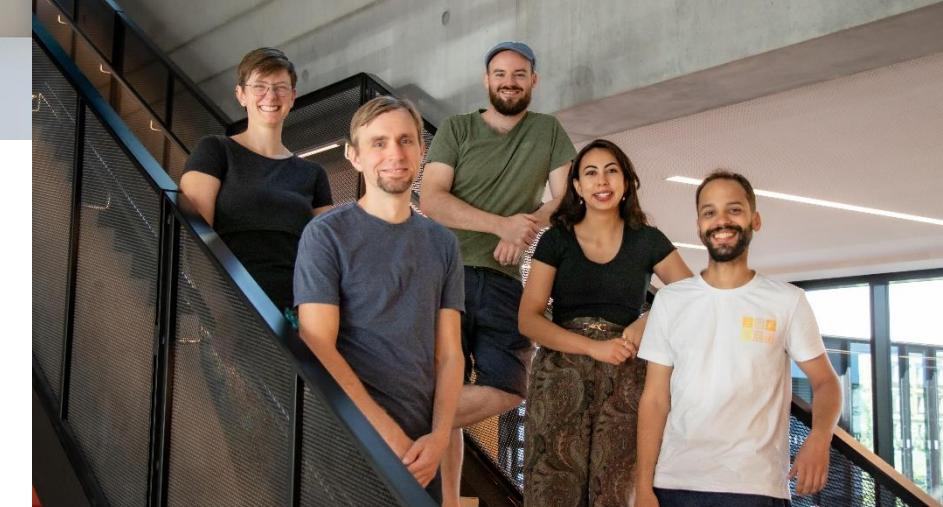
<https://forum.image.sc/>

Acknowledgements



BiAPoL team

- Marcelo Zoccoler
 - Johannes Soltwedel
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- Robert Haase
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 - Svetlana Iarovenko
 - Ryan George Savill
 - Laura Zigutyte
 - Somashekhar Kulkarni
 - Maleeha Hassan
 - Tina Smejka



Networks



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