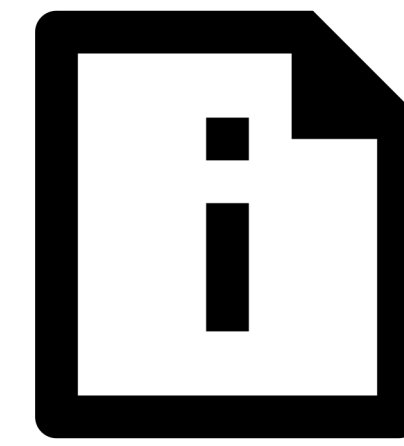




ABOUT MRI-CIA

MRI-CIA has been created in 2023, to answer the bioimage analysis needs of the users of the core imaging facility [Montpellier Ressources Imagerie](#) and the wider community. We offer comprehensive support for [bioimage analysis](#), from the start of a research project to publication. The [support](#) we provide is tailored to each individual case and can include one-on-one software [training](#) or the creation of [custom analysis tools](#). We handle various aspects of image analysis, such as for example:

- image data handling
- image restoration and registration
- quantitative image analysis and visualization
- instance segmentation and tracking
- morphological and intensity quantification
- colocalization analysis and spatial statistics

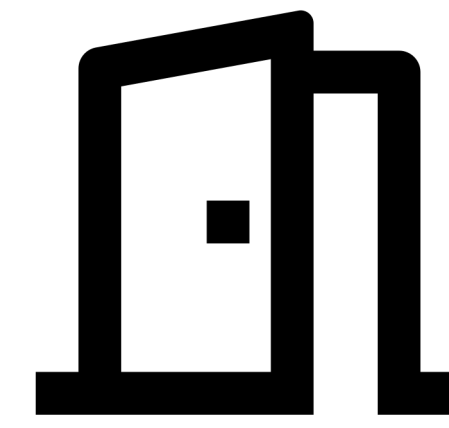


OPEN DESK SESSIONS

We do an open desk session every fortnight. Do you have questions about [image analysis](#)? Do you need help with a [script](#) or [macro](#)? Are you planning to start an image analysis [project](#) with us? Then come join us at the next open-desk session. The access is free and no inscription is needed, but we ask you to kindly give us some information, that will help us planning the session.



tinyurl.com/v9suznr6



PROJECTS

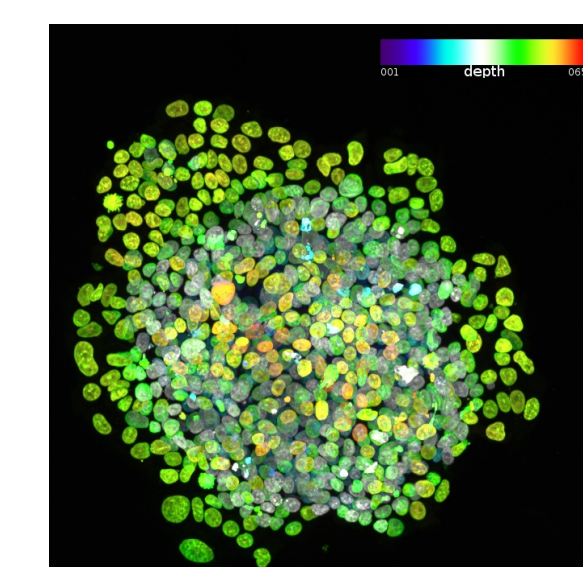
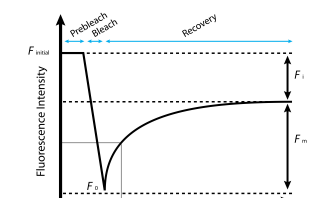
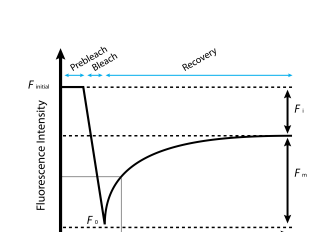
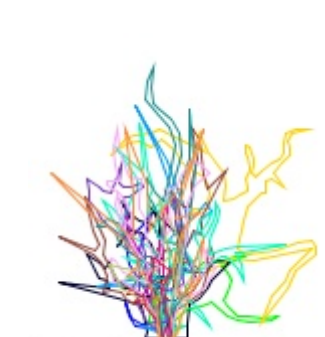
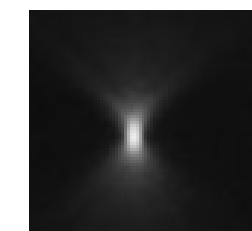
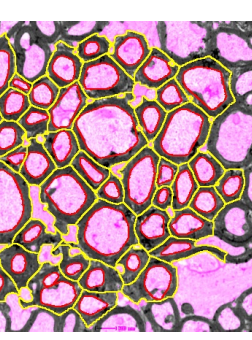
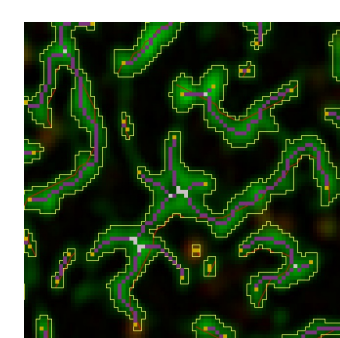
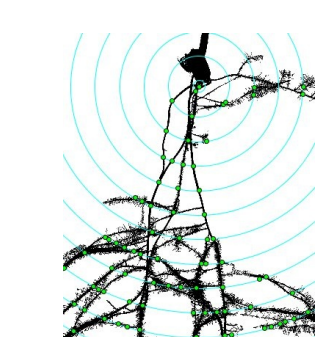
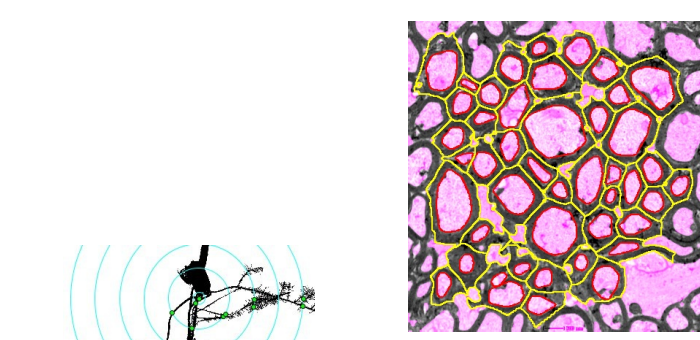
The service is [open](#) to the public and private sector without any institutional or geographic conditions. MRI-CIA accepts image analysis projects within the field of [life-science](#). The images to be analyzed, might be acquired on the MRI imaging core facility, but this is not a precondition for accessing the image analysis service.

The services provided by MRI-CIA include [training](#) and [consulting](#) in bio-image analysis and finding and [implementing solutions](#) for bio-image analysis problems. In the second case the preferred way is to [develop tools](#) and [train](#) the biologists to use them to perform their own analyses. In some cases, especially when new methods and technologies are involved, it can be preferable that MRI-CIA executes the analysis for the user.

The services of MRI-CIA, beyond the open desk sessions, are charged. We provide a free [quote](#) on request. Please find the current [tariffs](#) on our website.

Topics we often work on (non exhaustive) are:

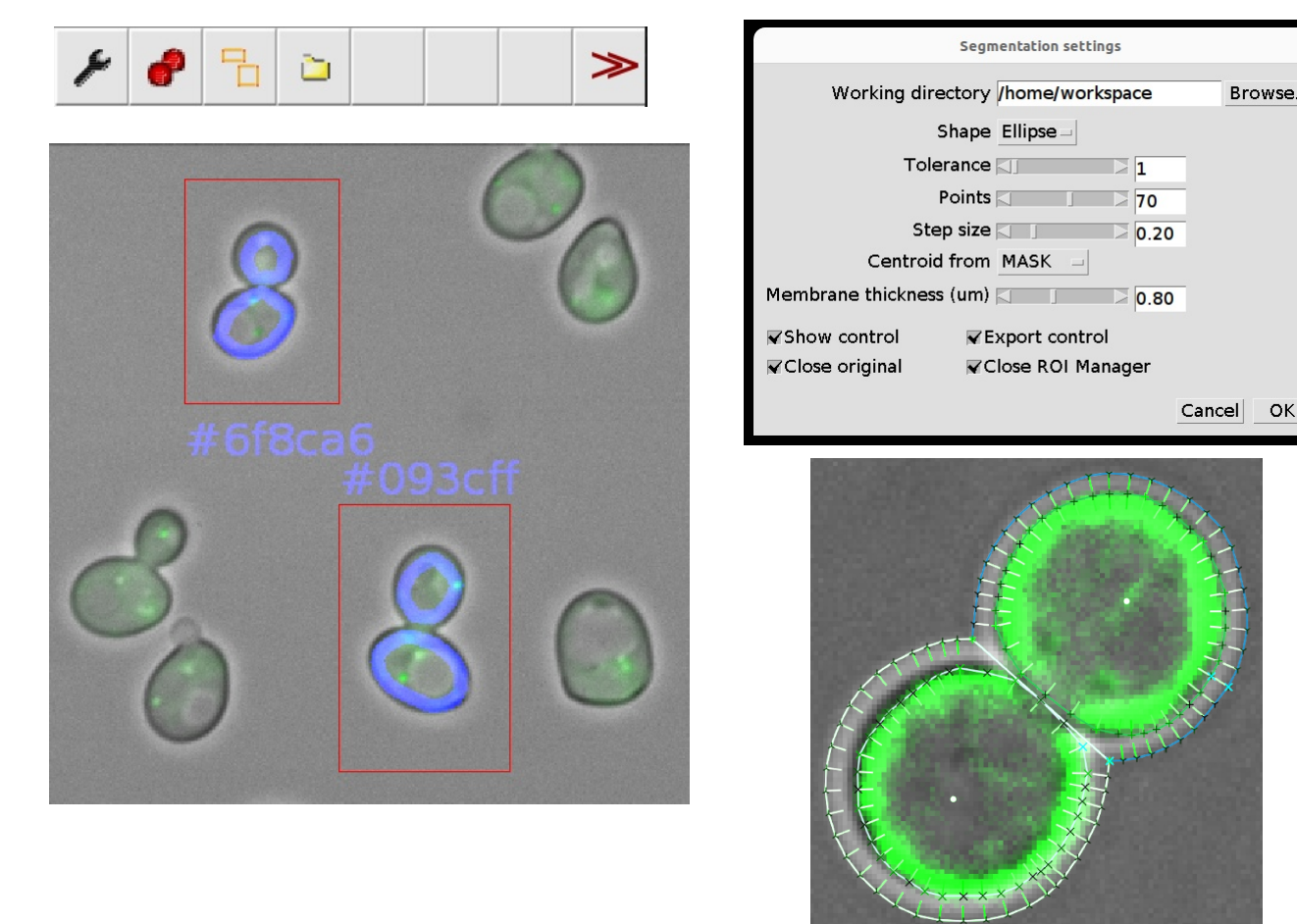
- Colocalization
- Intensity measurements
- Spot detection
- Cell morphology
- Filament Tracing
- Tracking
- Cell motility
- Cell lineage
- Object counting
- Clustering



tinyurl.com/ms824s4p

TOOLS DEVELOPED BY MRI-CIA

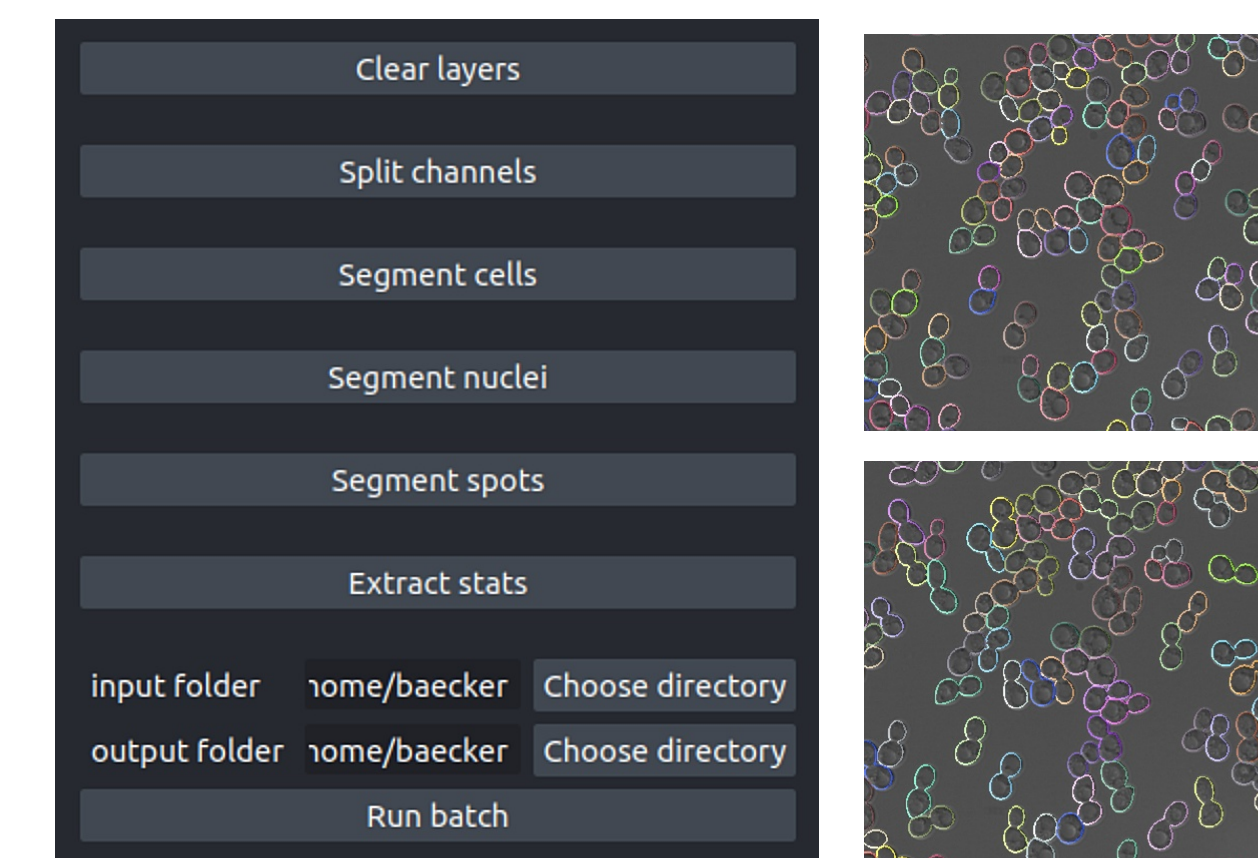
MD YEASTS



The tool measures the [intensity](#) of a fluorescent channel in the [membranes](#) of the mother and daughter cells of [budding yeast](#).

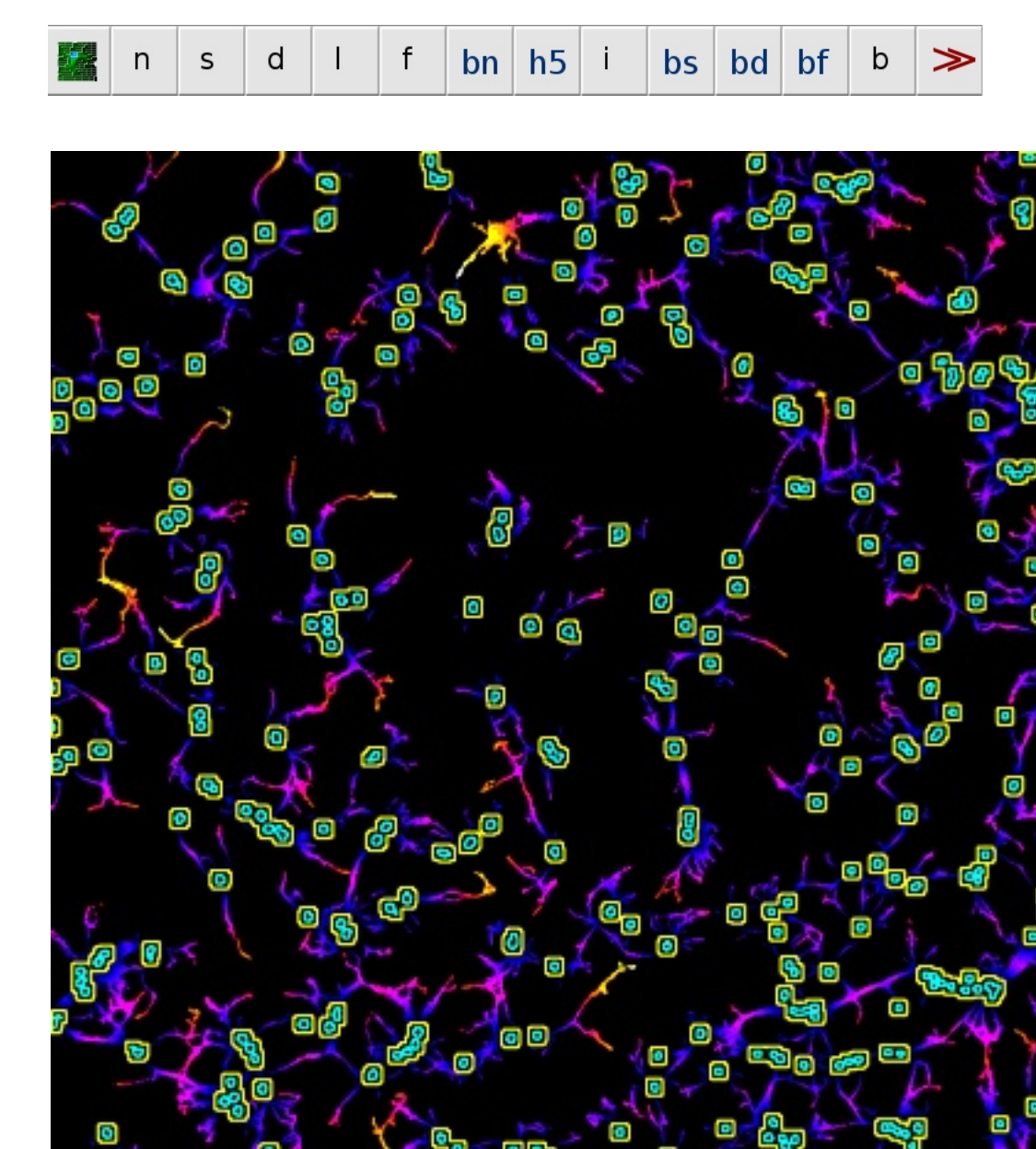
[Moving n-gons](#) are used to find the membrane and to split the cells. An ngon starts as an ellipse or box around the budding yeast. It moves towards the center and stops according to some criteria. The [curvature](#) is used to find the splitting points.

SPOTS IN YEASTS



The napari-plugin analyzes [lipid droplets](#) in budding yeast cells. The cells are segmented with [cellpose](#) in the brightfield channel. In the result the mother-daughter pairs are separated. They are reconnected using the [Hopcraft-Karp algorithm](#). The cells are considered as a bipartite graph, in which the cells with nucleus form one partition and those without the other. The tool reports the [number](#) of droplets per cell, their [areas](#) and [intensities](#) and their [positions](#) within the cell

NEURITE ANALYZER

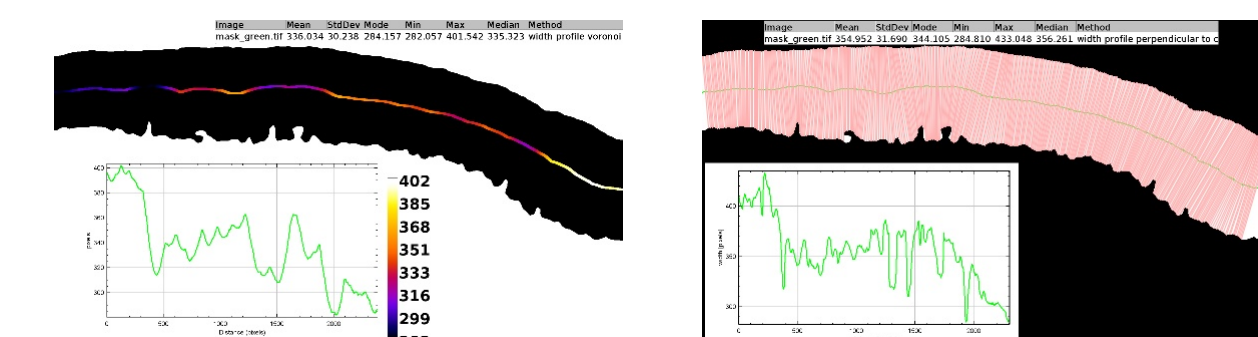


The workflow allows to analyze [RNA-FISH](#) spots on neurites. It counts the spots per cell and measures their distance to the soma along the neurite.

The images are acquired with the Phenix Opera and consist of 10x10 fields of 1000x1000 pixels each. They are exported and reconstructed with the help of the [MRI-Opera-Export-Tools](#).

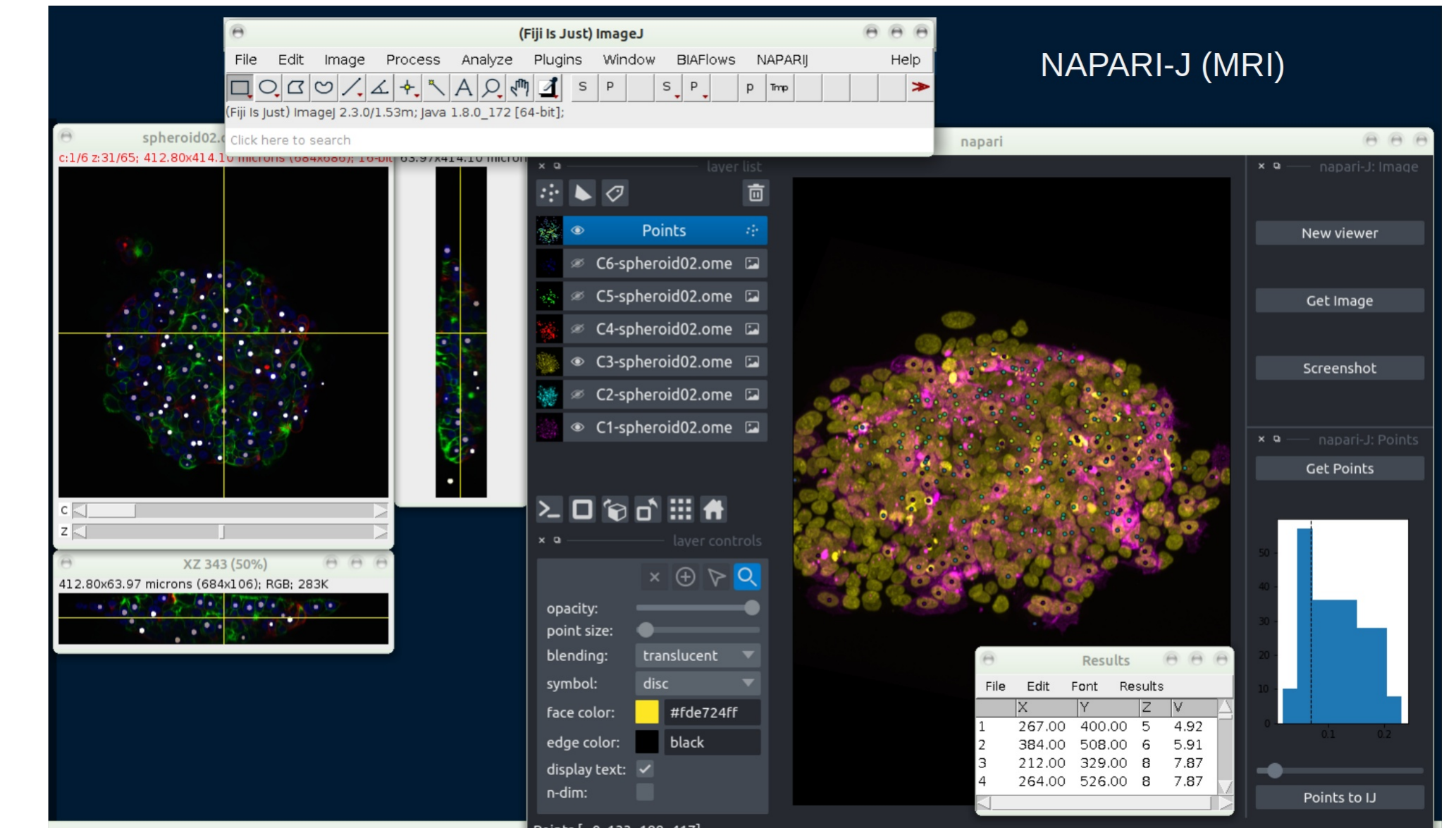
The neurites are segmented with a pre-trained [Ilastik](#) classifier. The distances are calculated using the [Geodesic Distance Map](#) from the FIJI-plugin [MorphoLibJ](#). Each point on a neurite is labelled with the identity of the closest connected soma

WIDTH PROFILE TOOLS



The tools estimate the width-profile of an object given as a binary mask. Four methods are provided: as [local thickness](#), as [voronoi distance](#) between two parts of the contour-line, perpendicular to the axis of inertia and at regular distances using rays perpendicular to a [centerline](#) segment.

NAPARI-J

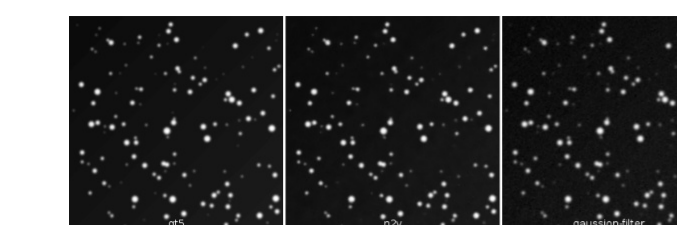


A plugin to exchange data with FIJI and to use FIJI image analysis from napari. Current features are:

- get the active image from FIJI
- send a screenshot to FIJI
- get a set of points from the FIJI results table
- filter the points in napari
- send the filtered points back to FIJI

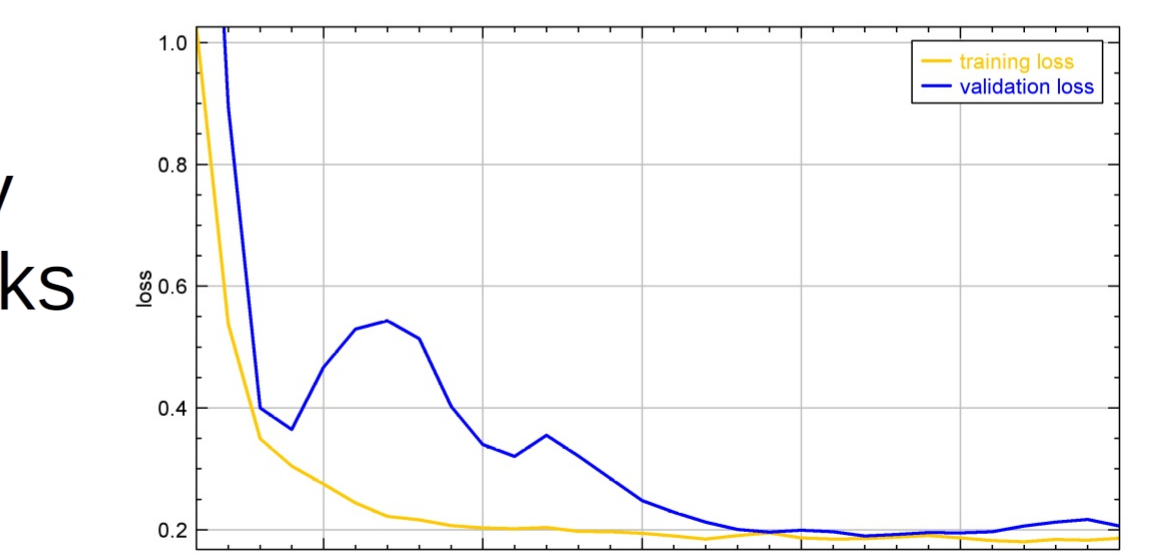


DL4MIC



DL4Mic (MRI)

- Easily train, validate and use DL-models from within FIJI
- A framework to easily integrate new networks
- Runs in python



(N ^o)	Reference image	(N ^o)	Test image	SNR (dB)	PSNR (dB)	RMSE	MAE
(1)	gt5	(1)	noise	19.20405144	26.72729932	8.52853583	6.72216094
(1)	gt5	(1)	n2v	38.72119838	46.28991626	0.90160670	0.58652819
(1)	gt5	(1)	gaussian-filter	34.12542003	41.69413791	1.53040385	1.08228281

Deep Learning for Microscopy

WORKSHOPS

ImageJ Macro Programming

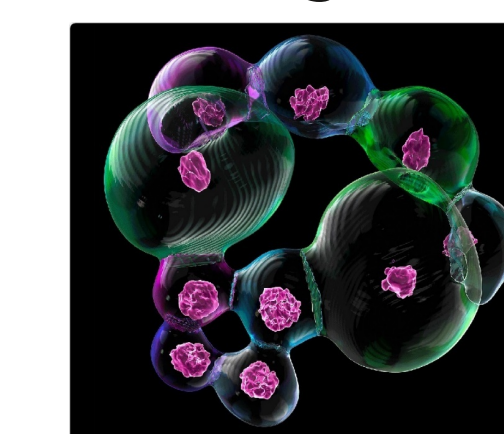
```

setBatchMode(true);
while(next()) {
  run("Analyze Image");
}
setBatchMode("exit and display");

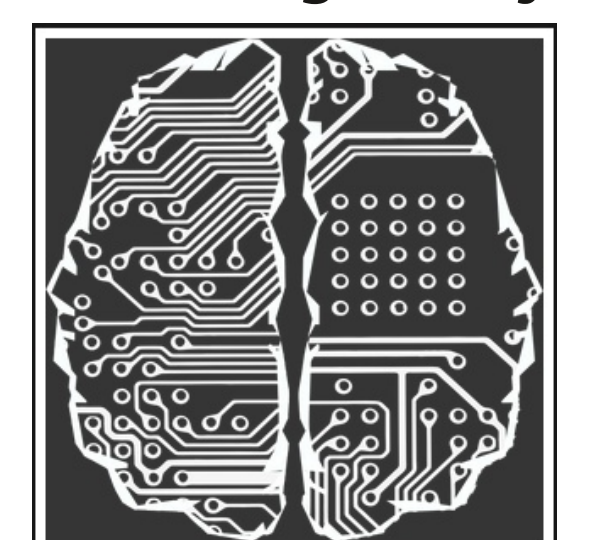
```

<https://tinyurl.com/2p8tsnbc>

3D Bio-Image Analysis



Machine Learning (ML/DL) for bio-image analysis



<https://tinyurl.com/daxb3mnn>

Check out the upcoming Biocampus workshops: www.biocampus.cnrs.fr/index.php/en/workshops-registration