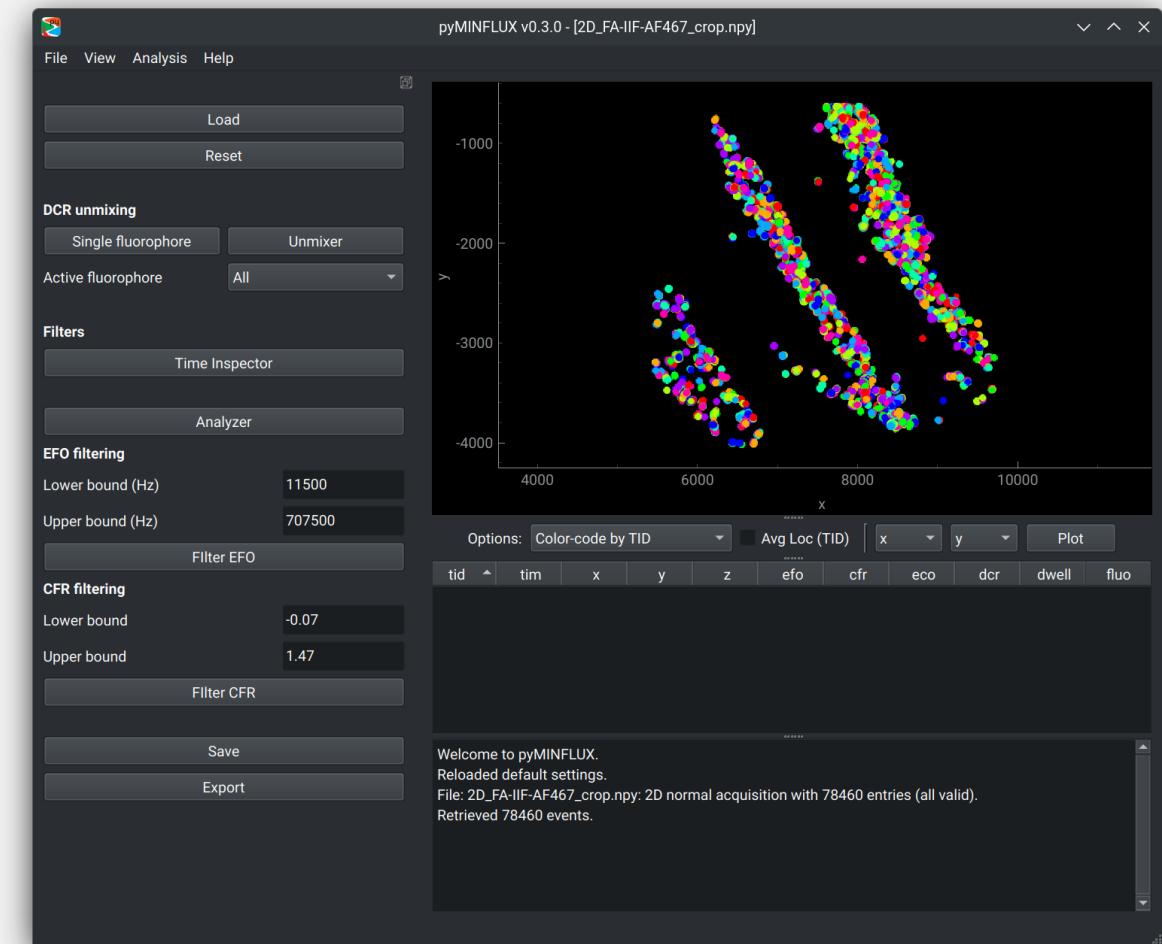


Collaborative expertise

Synergies between multi-disciplinary experts and
end users in software development

Aaron Ponti



About me

Education

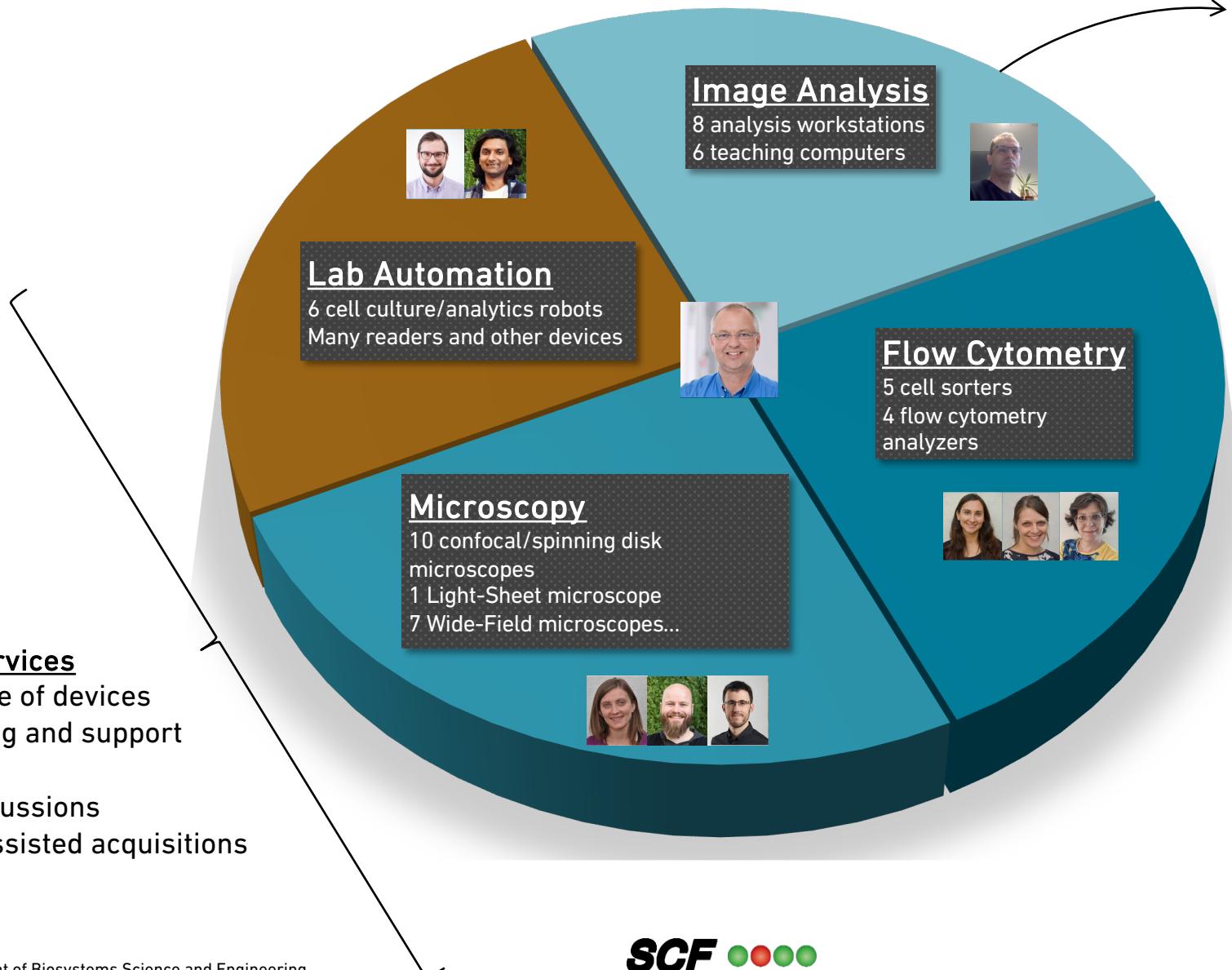
- M. Sc. Biotechnology
[D-BIOL ETH Zurich](#)
- PhD Image Analysis
[D-MAVT ETH Zurich](#)
- Post-doctoral fellow Image Analysis
[The Scripps Research Institute, San Diego, CA](#)

Briefly
D-INFK ETH Zurich

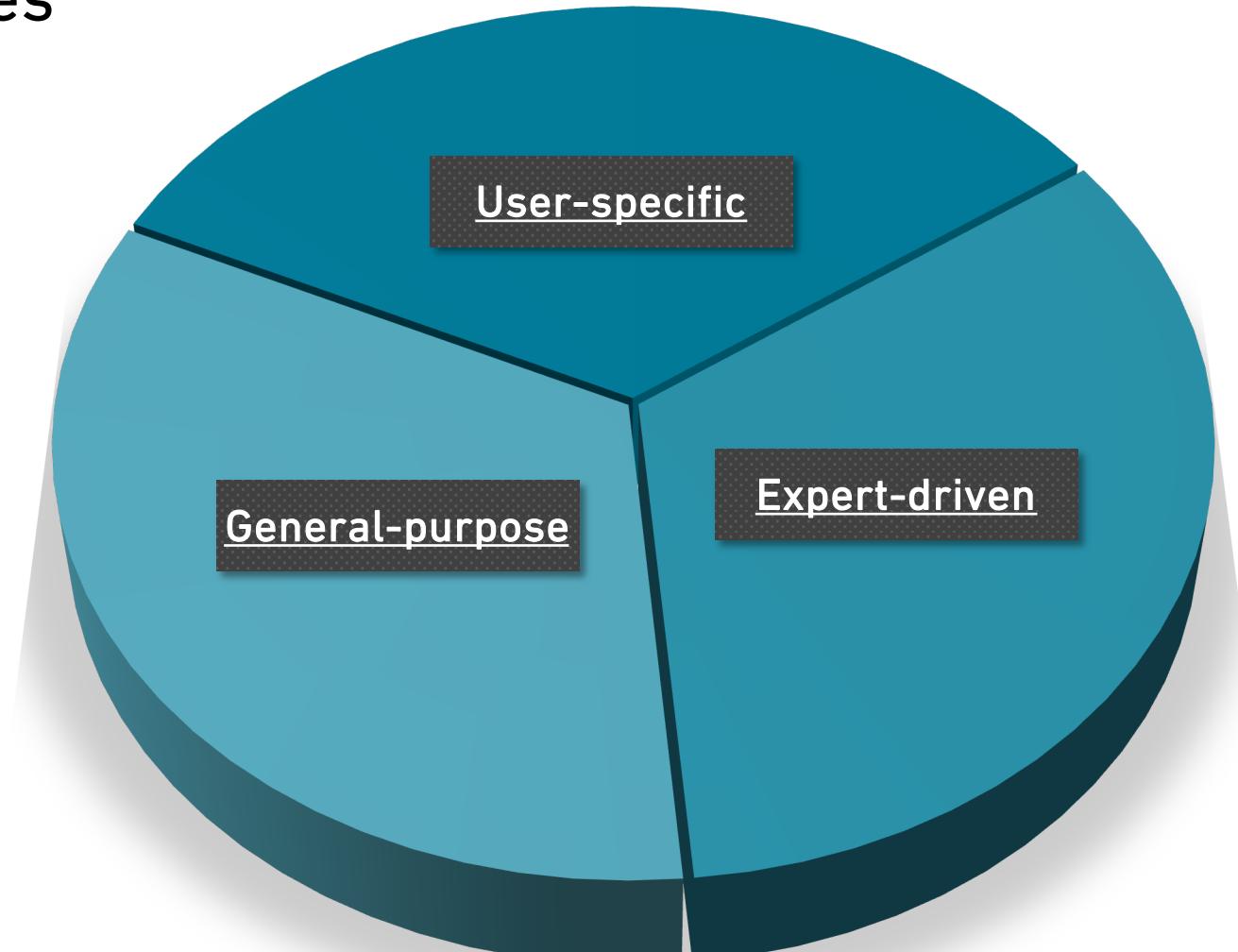
As a grown-up

- Image analysis specialist
[Friedrich Miescher Institute :: Facility for Advanced Imaging and Microscopy](#)
- Image Analysis Specialist & Software and Data Management Engineer
[D-BSSE ETH Zurich :: Single Cell Facility](#)

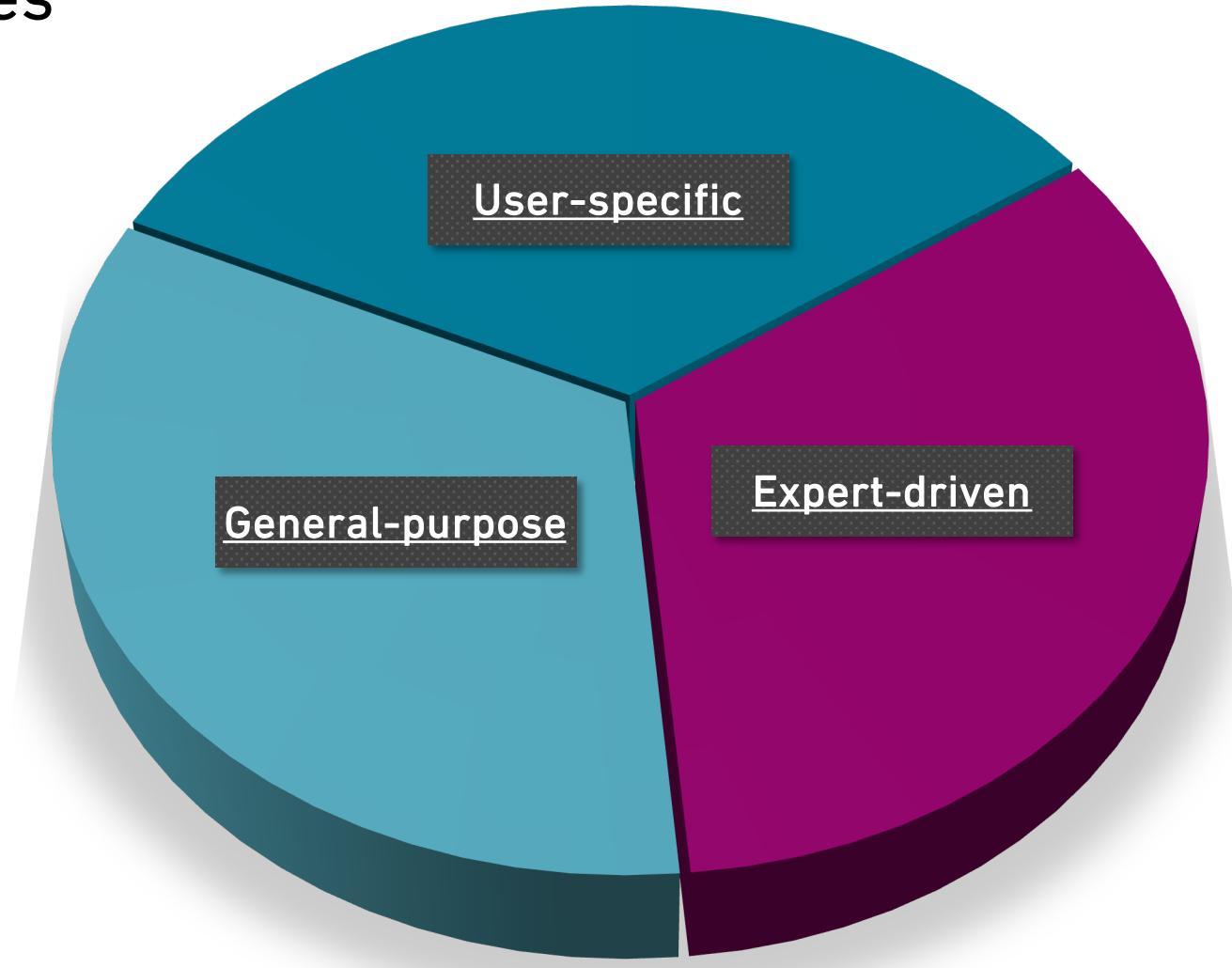
About us



IA project classes



IA project classes



Types of project

	User-specific projects	Expert-driven projects	General-purpose projects
Target audience	Single user	Several users	Many users
Specificity	Highly specialized	Specialized but scalable	Generalized
Team composition	Me (with user feedback)	Me and field experts (with user feedback)	Large and diverse team
Problem focus	Single, user-specific	Niche problems	Broad
Complexity	Varies	Complex	Moderate to complex
Scalability	Limited	Moderate	High
User input	Continuous	Initial and iterative (at release)	Initial and iterative (at release)
Project time	Short to moderate	Moderate to long	Long
Resource allocation	Moderate	High	Very high
Field knowledge	High (me)	Very high (experts)	Moderate
Code quality/testing	Minimal to moderate	High	Very high

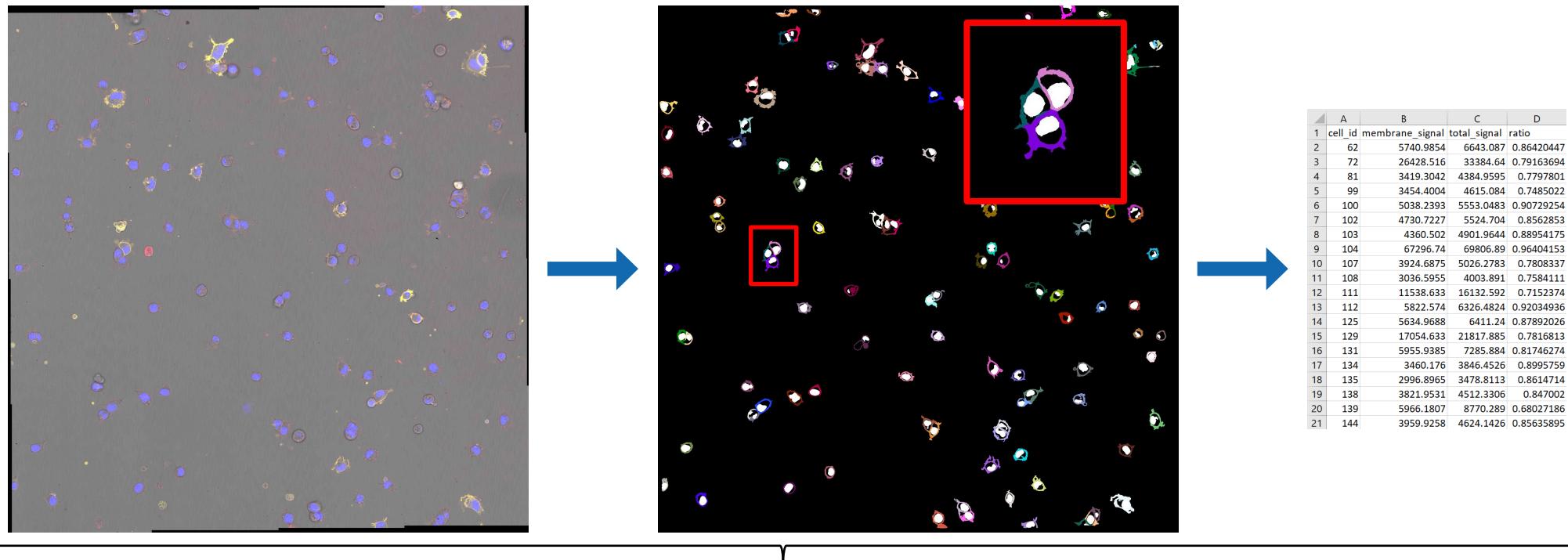
User-specific projects

User-specific projects	
Target audience	Single user
Specificity	Highly specialized
Team composition	Me (with user feedback)
Problem focus	Single, user-specific
Complexity	Varies
Scalability	Limited
User input	Continuous
Project time	Short to moderate
Resource allocation	Moderate
Field knowledge	High (me)
Code quality/testing	Minimal to moderate

User-specific projects :: Membrane localization study of a sensor



“ We designed a plasmid-based sensor consisting of two fusion-protein, that bind activated KRAS and can phosphorylate a synthetic transcription factor if it they dimerize. (...) As KRAS is a membrane protein and our sensor binds only to activated KRAS, membrane localization of our sensor-SYFP-fusion also tells us if KRAS is activated. (One of the) aim(s) of the study: investigate differences in membrane localization of the sensor between mutant and wild-type KRAS.

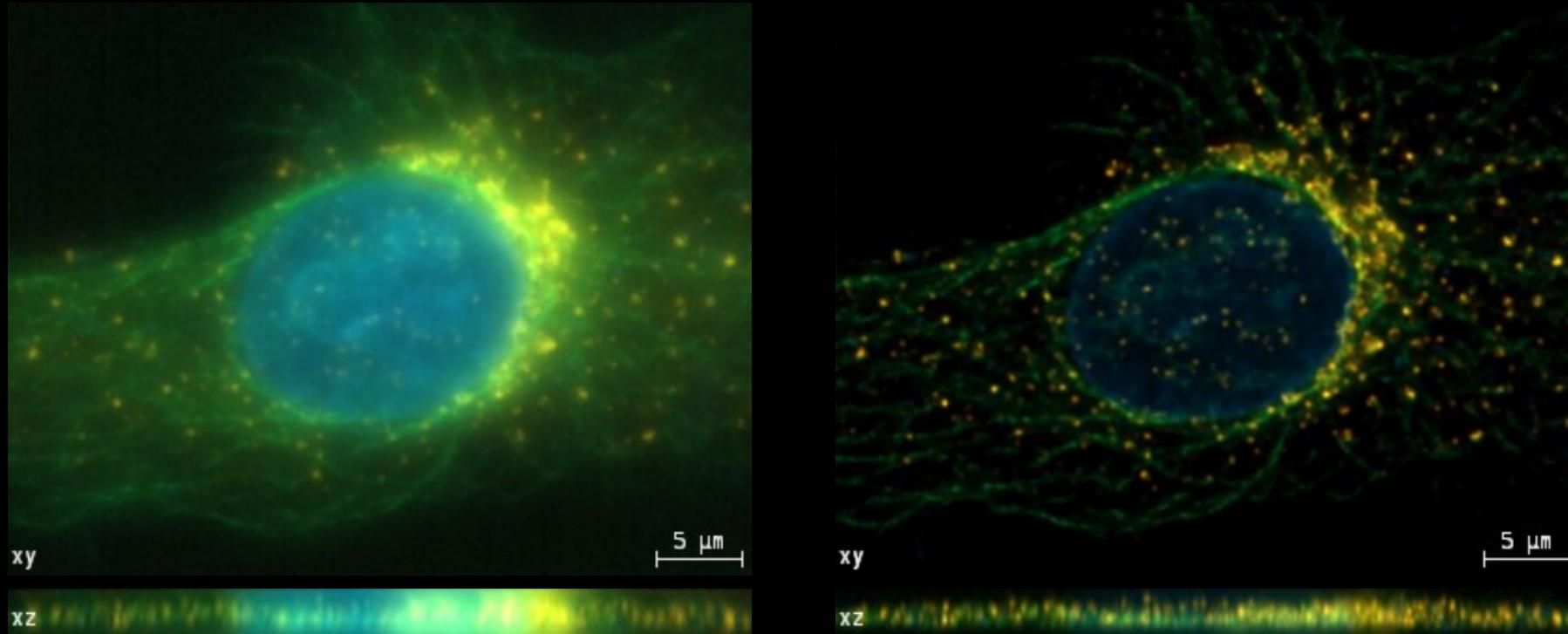


```
$ python analyze_membranes.py --folder E.GS3.56.1_reseeding --result result.csv --max-workers 8
```

General-purpose projects

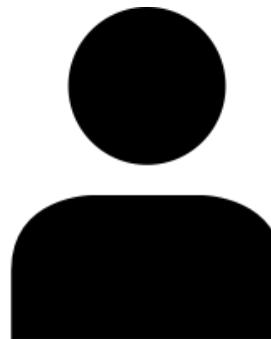
General-purpose projects	
Target audience	Many users
Specificity	Generalized
Team composition	Large and diverse team
Problem focus	Broad
Complexity	Moderate to complex
Scalability	High
User input	Initial and iterative (at release)
Project time	Long
Resource allocation	Very high
Field knowledge	Moderate
Code quality/testing	Very high

General-purpose projects :: Huygens Remote Manager (HRM)

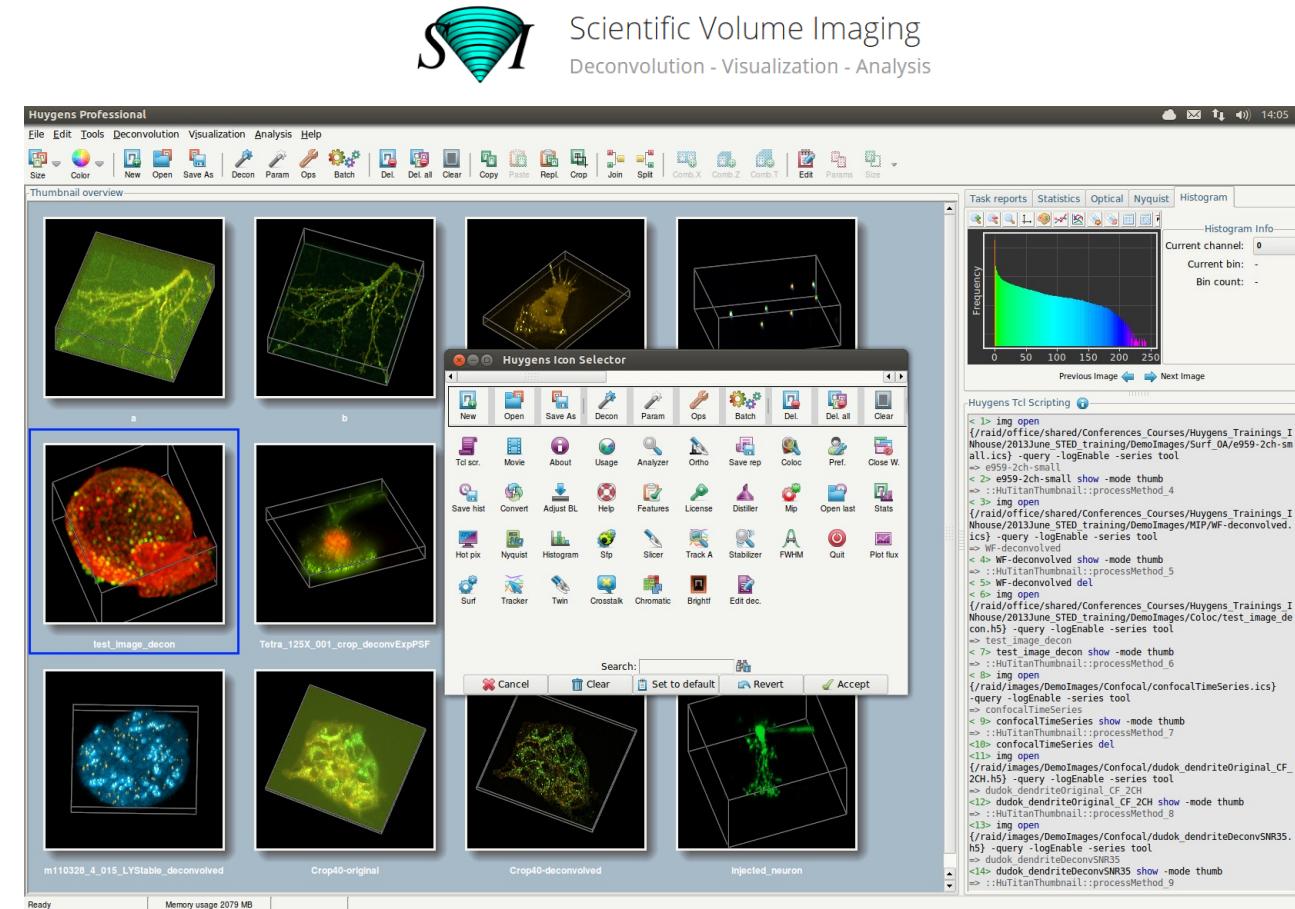


Deconvolution of an HeLa cell acquired on a widefield microscope.
Image courtesy Dr. Yury Belyaev. EMBL, Heidelberg, Germany.

General-purpose projects :: Huygens Remote Manager (HRM)



Single-user desktop application



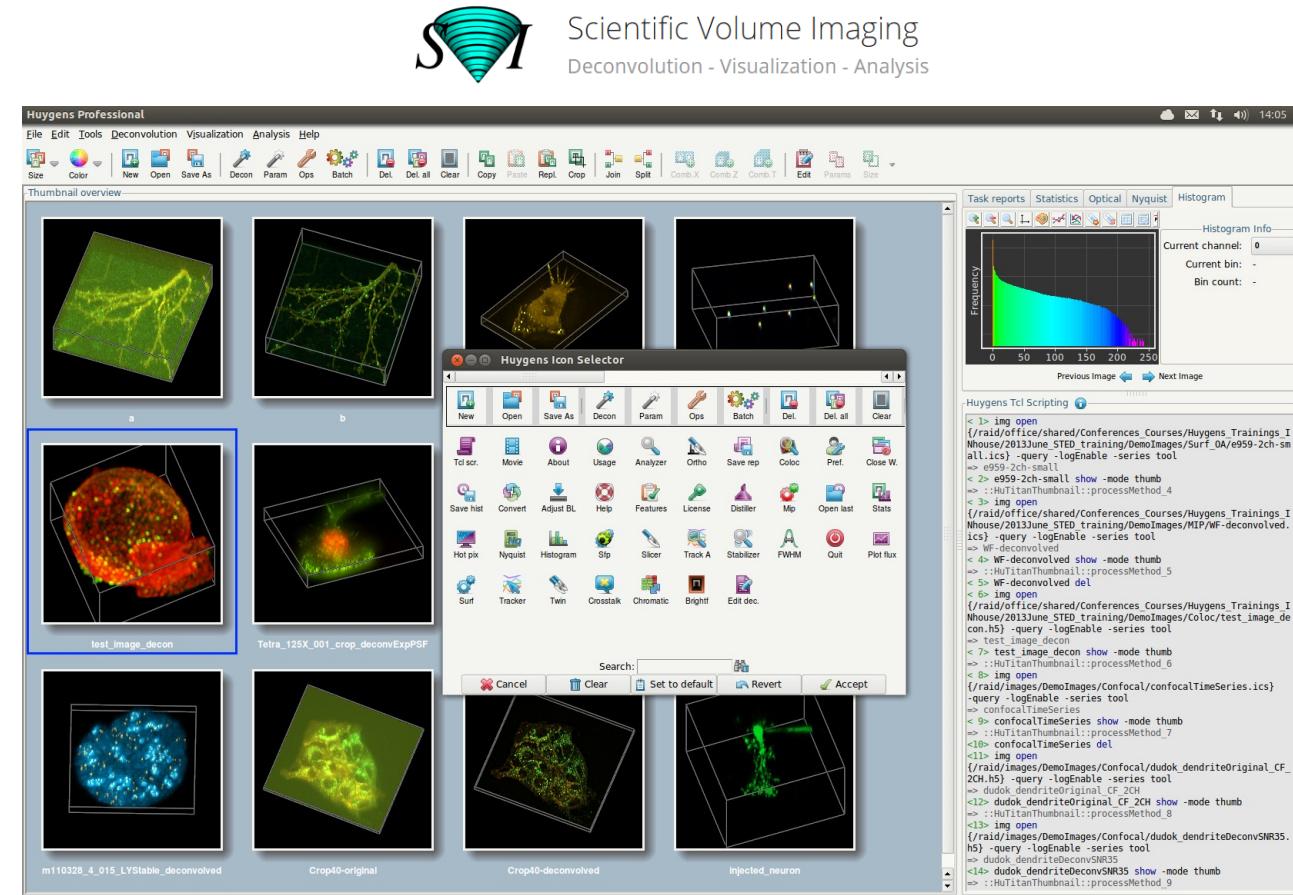
Huygens Professional

General-purpose projects :: Huygens Remote Manager (HRM)

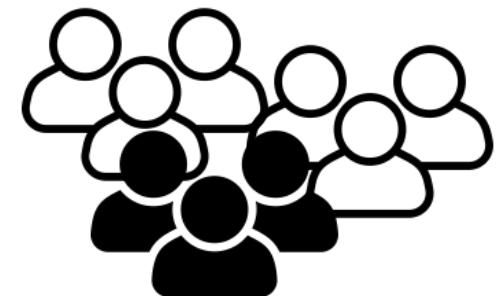
Our scope

Scientific facility with around
100 users

↑
1 workstation
↓



Huygens Professional

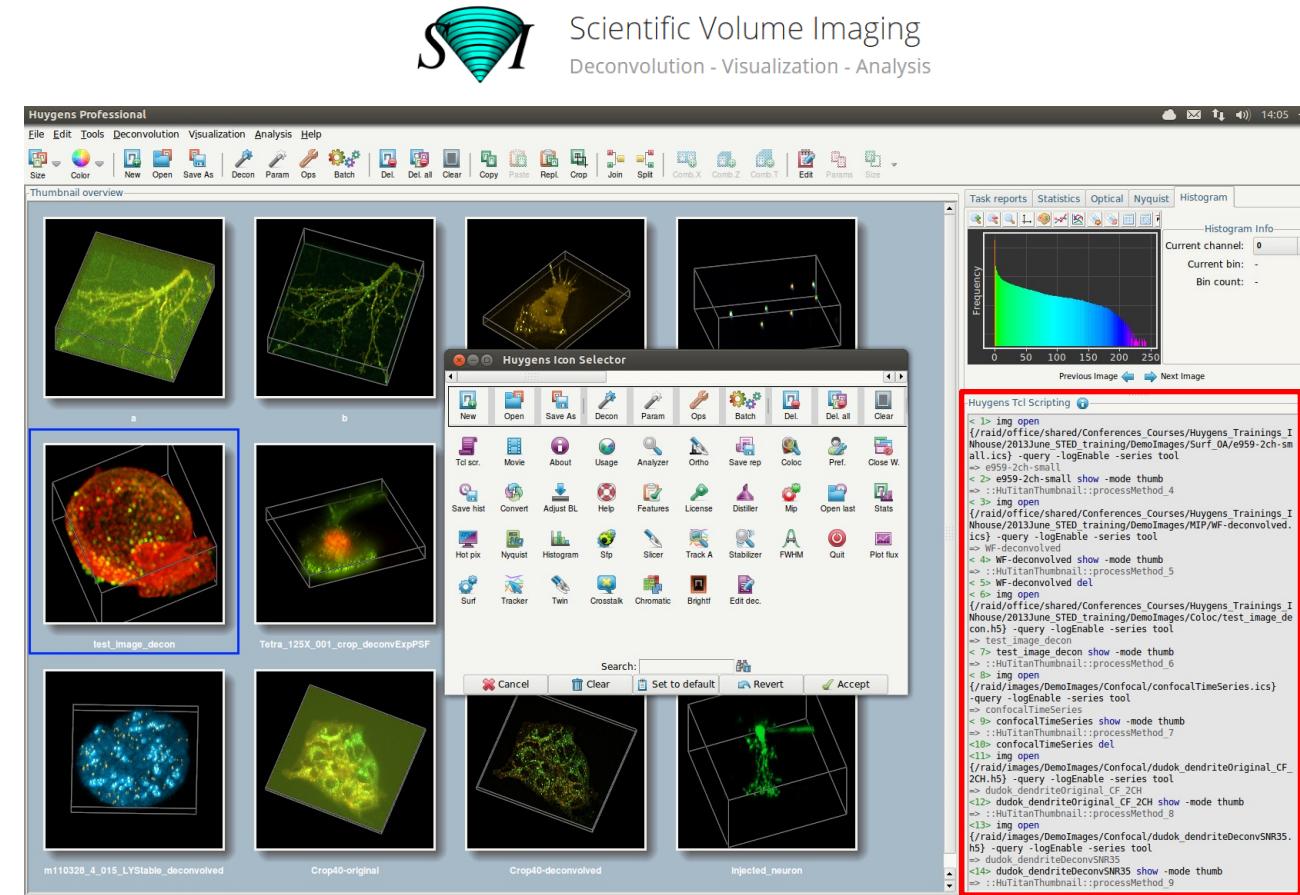
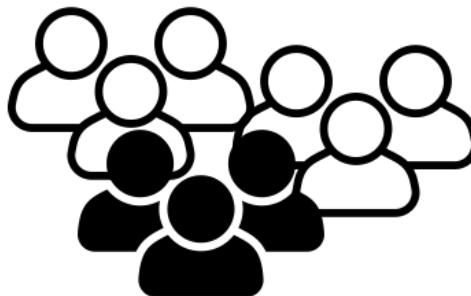


General-purpose projects :: Huygens Remote Manager (HRM)

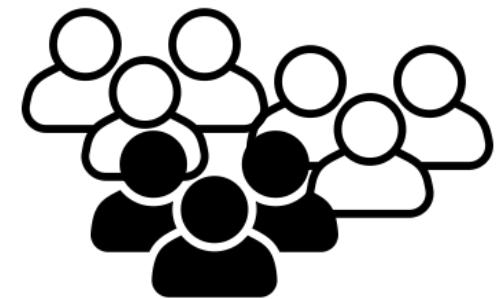
Our scope

Scientific facility with around
100 users

1 workstation



Huygens Professional



Fully scriptable

Huygens Core
Headless compute engine

General-purpose projects :: Huygens Remote Manager (HRM)

The Huygens Remote Manager is an easy to use interface to the Huygens Software by [Scientific Volume Imaging B.V.](#) that allows for multi-user, large-scale deconvolution and analysis.

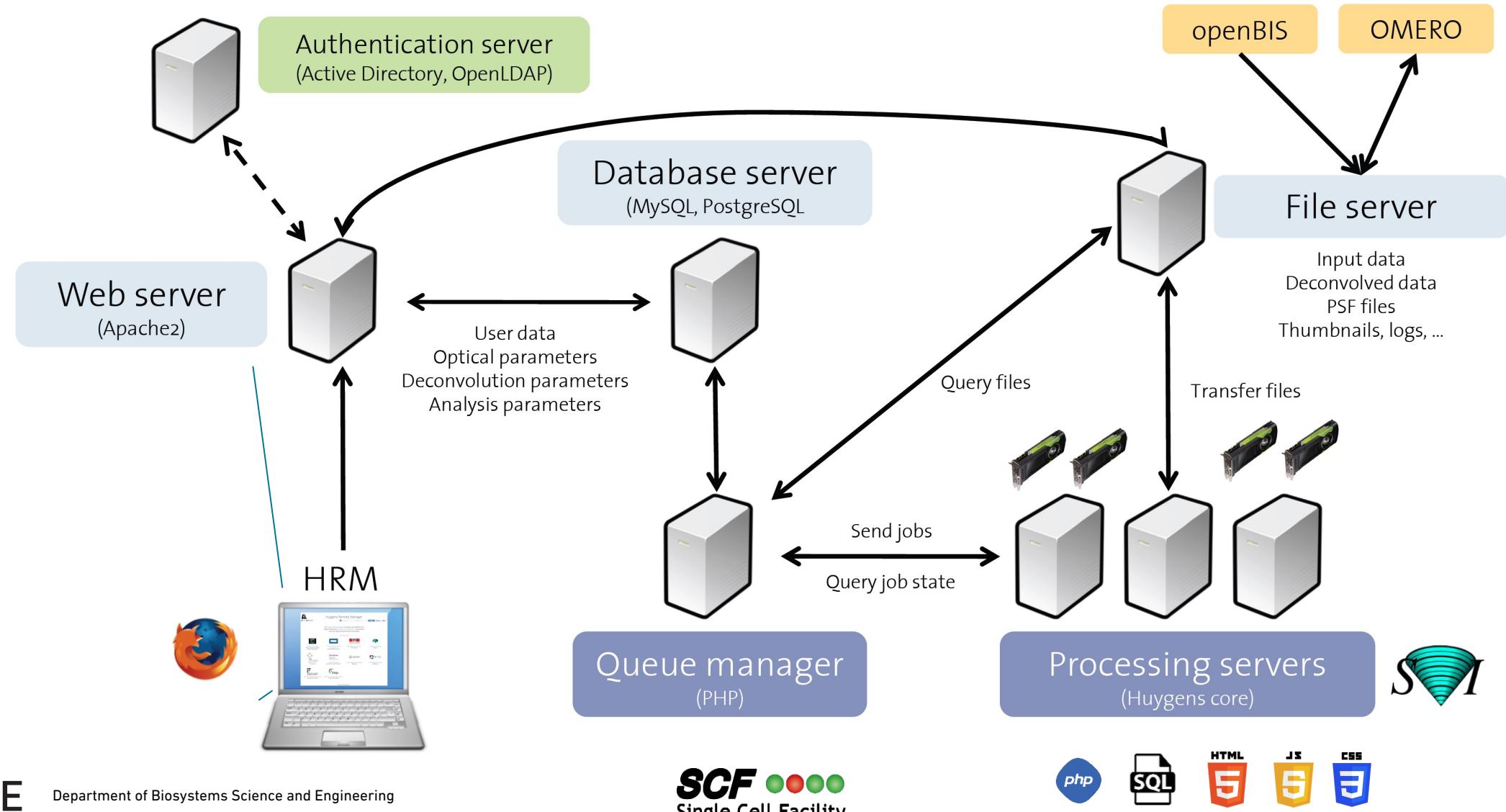
collaboration

 Montpellier RIO Imaging National Center for Scientific Research Montpellier	 Friedrich Miescher Institute for Biomedical Research	 Facility for Advanced Imaging and Microscopy Friedrich Miescher Institute	 Biolimaging and Optics platform EPF Lausanne	 Scientific Volume Imaging Hilversum
 Single-Cell Facility ETH Zurich	 University Basel The Center for Molecular Life Sciences	 Imaging Core Facility Biozentrum University of Basel	 Leibniz Institute for Neurobiology Magdeburg	 Combinatorial Neuroimaging Magdeburg
 Bioimage Light Microscopy Facility University of Fribourg	 Microscopy and Image Analysis Platform University of Freiburg	 Biolimaging Facility University of Manchester		

Huygens Remote Manager v3.9 Theme: [dark](#) [light](#)

<https://github.com/aarpon/hrm/>

General-purpose projects :: Huygens Remote Manager (HRM)



General-purpose projects :: openBIS Importer Toolset (oBIT)

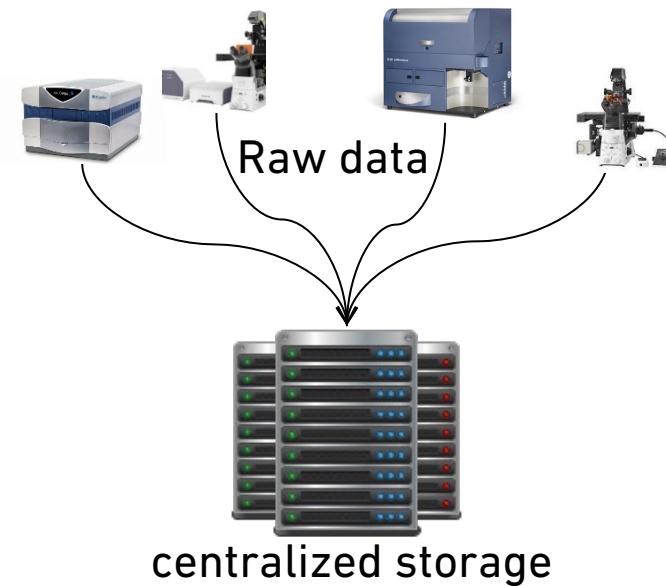
~ 40x at SCF/LAF



Raw data

General-purpose projects :: openBIS Importer Toolset (oBIT)

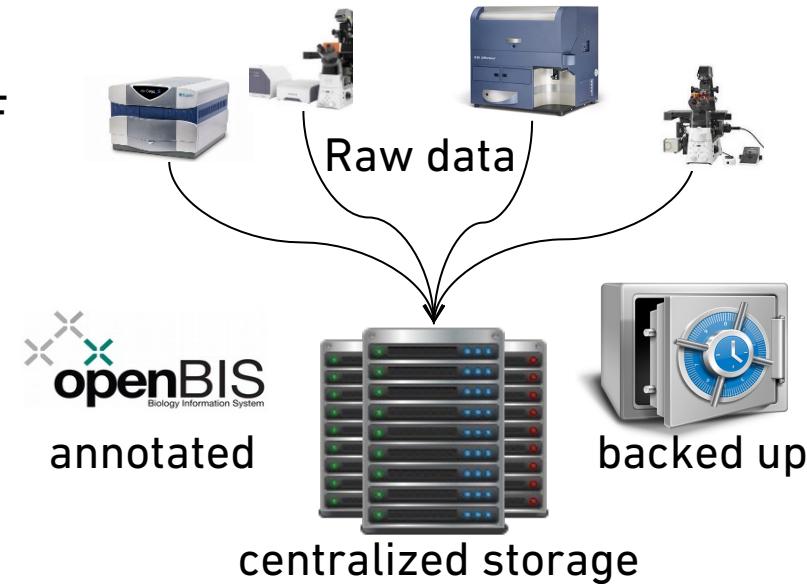
~ 40x at SCF/LAF



General-purpose projects :: openBIS Importer Toolset (oBIT)

~ 40x at SCF/LAF

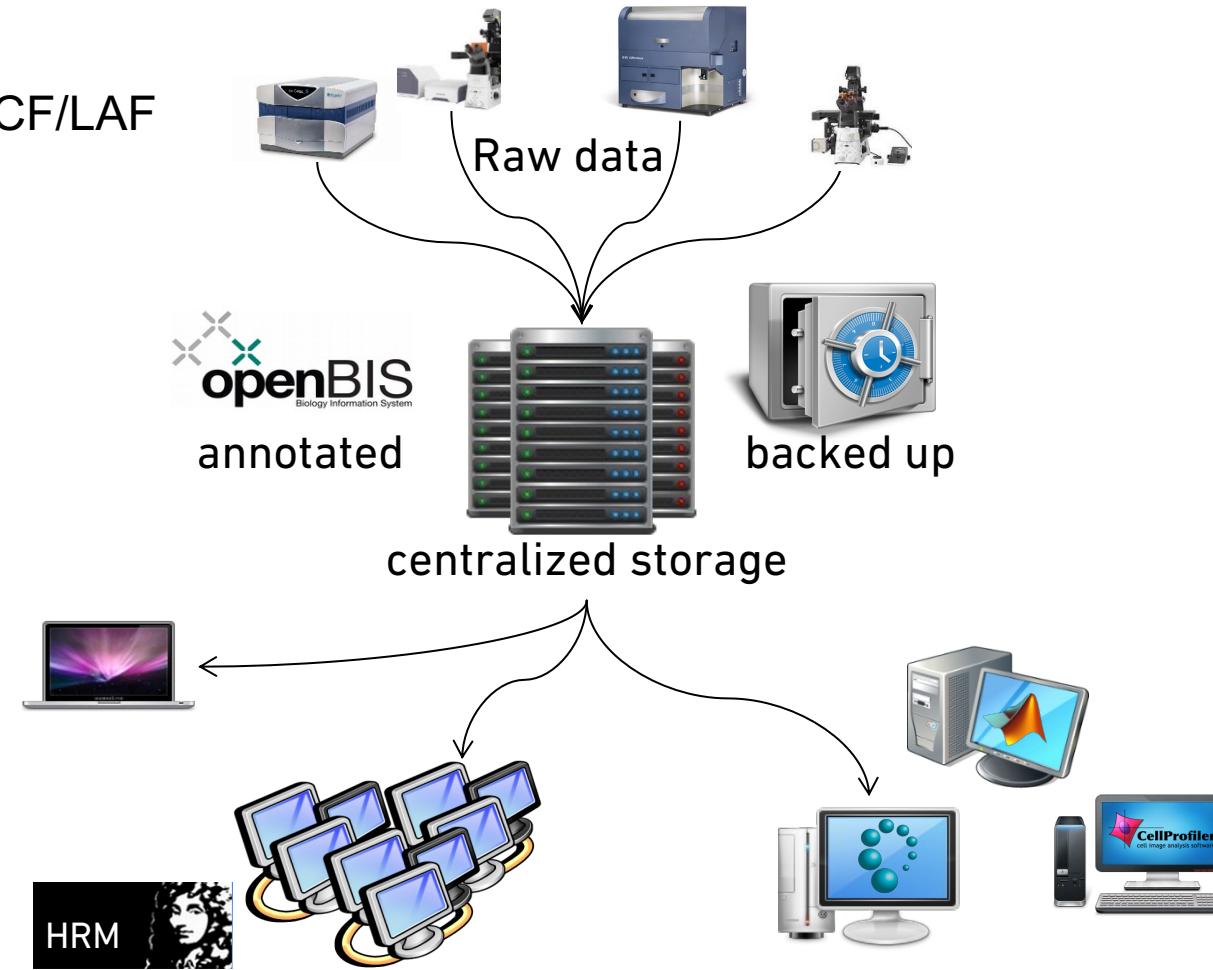
<https://sis.id.ethz.ch/>



General-purpose projects :: openBIS Importer Toolset (oBIT)

~ 40x at SCF/LAF

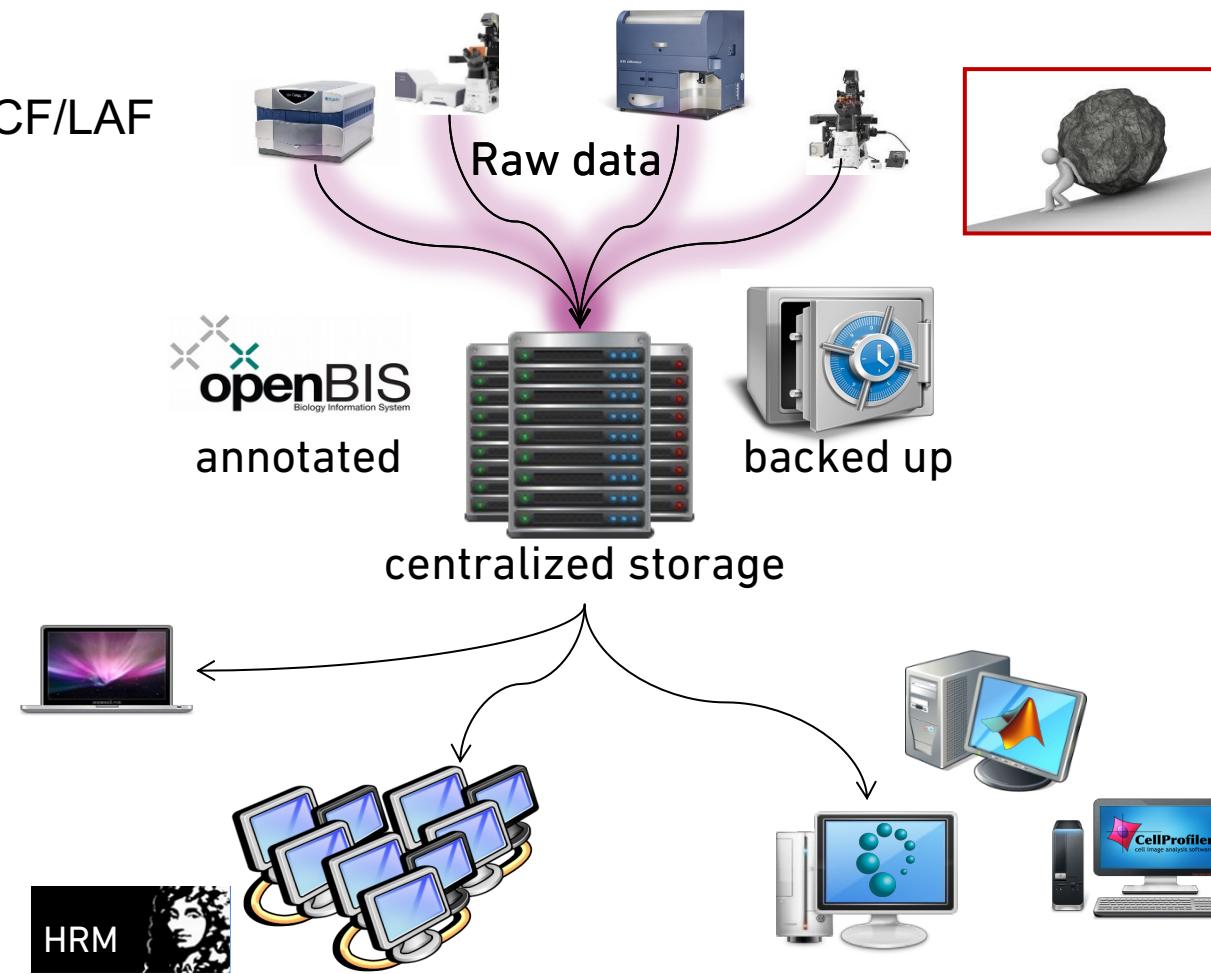
<https://sis.id.ethz.ch/>



General-purpose projects :: openBIS Importer Toolset (oBIT)

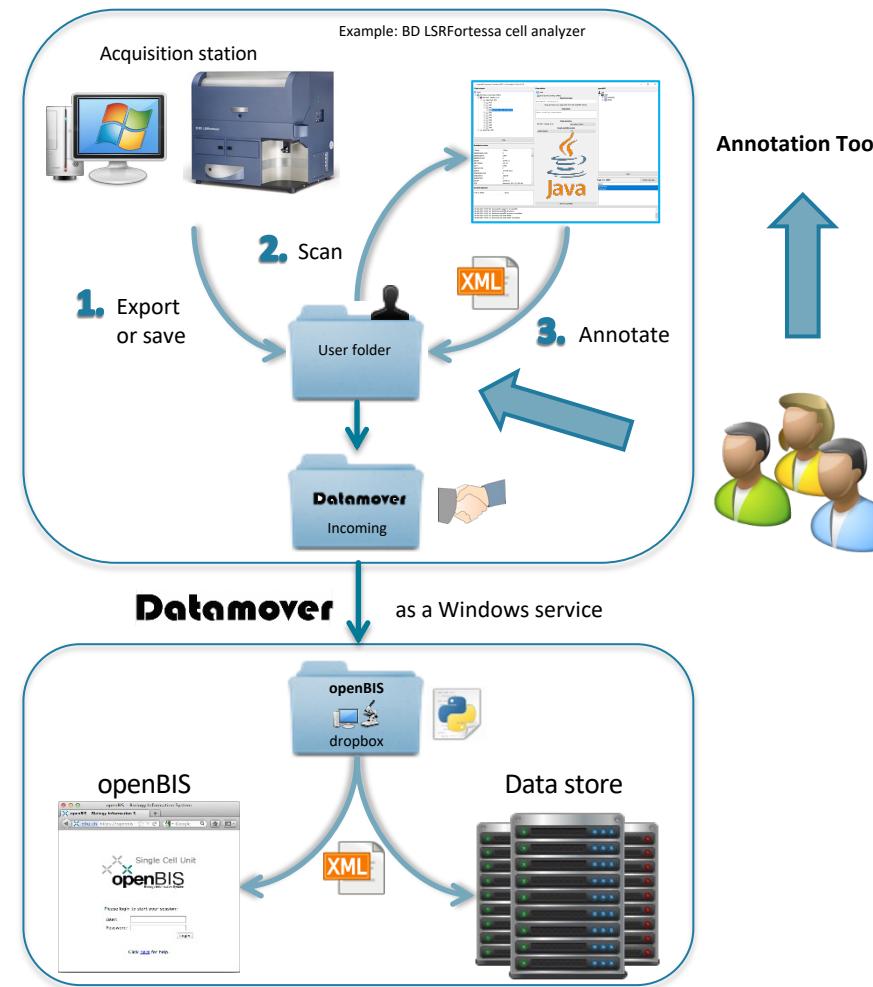
~ 40x at SCF/LAF

<https://sis.id.ethz.ch/>

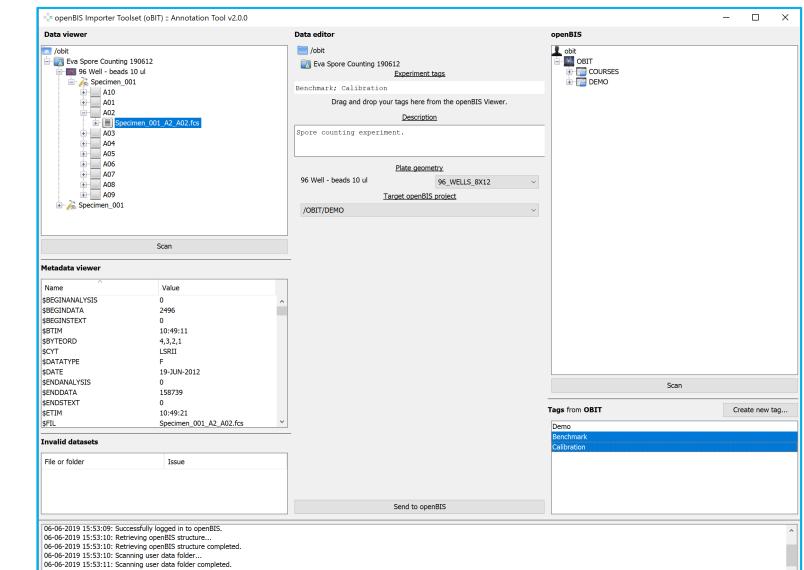


General-purpose projects :: openBIS Importer Toolset (oBIT)

New openBIS core technologies
Microscopy
Flow Cytometry



<https://github.com/aarpon/obit>



General-purpose projects :: openBIS Importer Toolset (oBIT)

New openBIS core technologies
Microscopy
Flow Cytometry

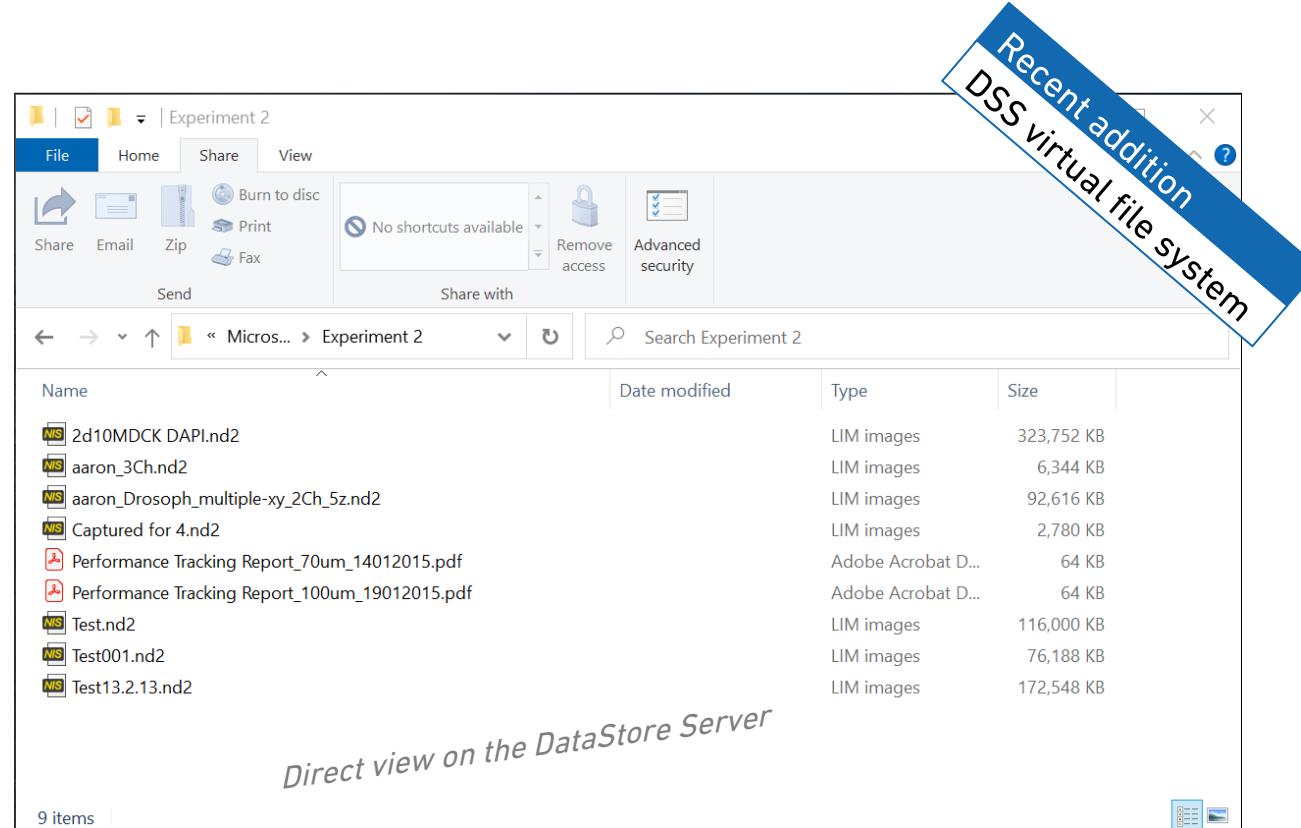
The figure displays four separate windows of the openBIS Importer Toolset (oBIT) interface:

- Microscopy Viewer:** Shows a microscopy image of MDCK cells stained with DAPI. It includes controls for Merge Channels, Filter (DAPI & TO), Resolution, and Depth (4 μm).
- File Uploader:** Shows a list of files ready for upload, including "2010MDCK.DAFlnd2" and "Experiment_2". It features a "Select files to upload" button and an "Auto upload on drop" checkbox.
- Lab Notebook:** A login screen for the Lab Notebook & Inventory Manager. It includes fields for Account and Password, and compatibility notes for Chrome and Firefox.
- Data Set:** Shows a flow cytometry plot of FSC-A vs FSC-H with data points. It includes sections for Identification Info, Data Set Type (FSC-A, FSC-H, Events in plot: 3551), and Metadata Fields.

Integration into ELN



General-purpose projects :: openBIS Importer Toolset (oBIT)



ETH zürich

Scientific IT Services

Expert-driven projects

Expert-driven projects	
Target audience	Several users
Specificity	Specialized but scalable
Team composition	Me and field experts (with user feedback)
Problem focus	Niche problems
Complexity	Complex
Scalability	Moderate
User input	Initial and iterative (at release)
Project time	Moderate to long
Resource allocation	High
Field knowledge	Very high (experts)
Code quality/testing	High

Expert-driven projects

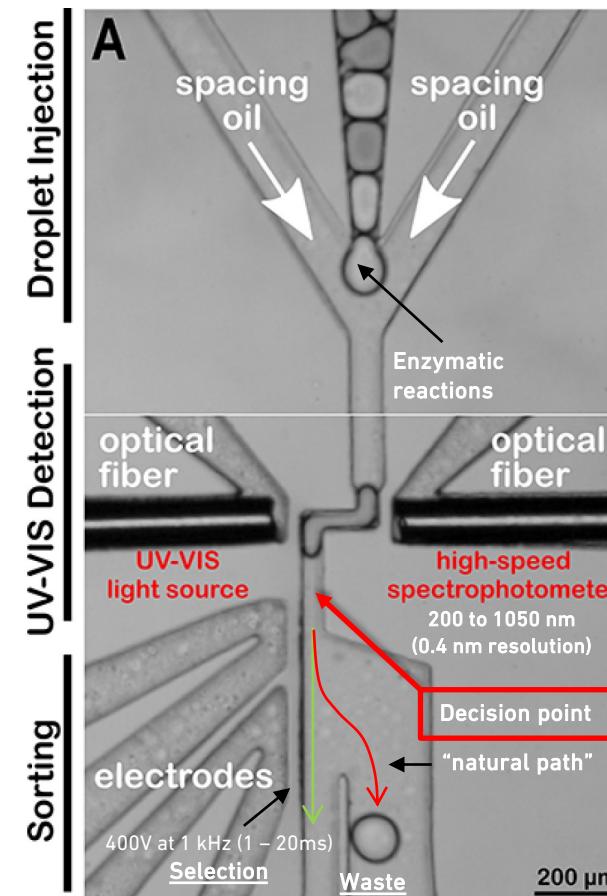
Expert-driven projects	
Target audience	Several users
Specificity	Complex problems
Technology	Python
Problem focus	Single-cell analysis
Complexity	Moderate
Scalability	Moderate
User input	Initial and iterative (at release)
Project time	Moderate to long
Resource allocation	High
Field knowledge	Very high (experts)
Code quality/testing	High

Expert-driven projects :: SpectraSorter

Duncombe T. A., Ponti A., Dittrich P. S. SoftwareX, Volume 19, 2022, 101160 DOI:10.1016/j.softx.2022.101160
Duncombe T. A., Ponti A., Seebeck F. P., Dittrich P. S. 2021. DOI: 10.1021/acs.analchem.1c02822

Goal

Design a **microfluidic platform** for the **high-throughput analysis** of (enzymatic) **reactions** inside small **droplets**.

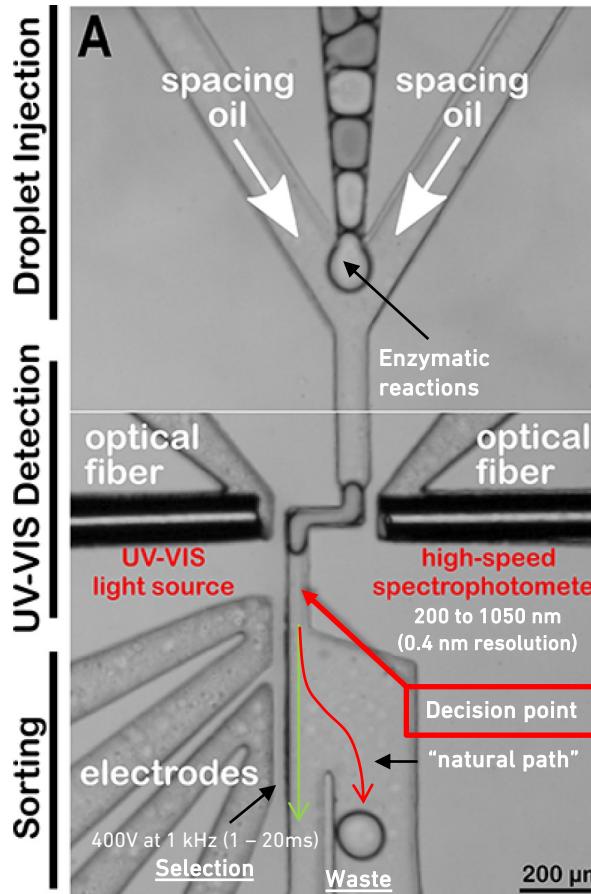


Expert: Todd Duncombe, Petra Dittrich Group, D-BSSE ETHZ

Expert-driven projects :: SpectraSorter

Duncombe T. A., Ponti A., Dittrich P. S. SoftwareX, Volume 19, 2022, 101160 DOI:10.1016/j.softx.2022.101160
 Duncombe T. A., Ponti A., Seebeck F. P., Dittrich P. S. 2021. DOI: 10.1021/acs.analchem.1c02822

UVADS: UV-vis spectra-activated droplet sorter



In **droplet microfluidic platforms**, droplets containing cells or reagents flow through capillaries. Inside each droplet, a reaction takes place, and the output is measured *by some means*. These platforms aim at achieving high-throughput and/or massively parallel analytics.

Previous approaches were very low throughput (1-10 droplets / second) and used fluorescence microscopy to measure single-wavelength absorbance in the visible spectrum.

Recent **label-free UV-vis spectroscopy** interrogates **molecular structures** directly by **chemical absorbance** of incident light over a large spectrum (200 to 1050 nm)

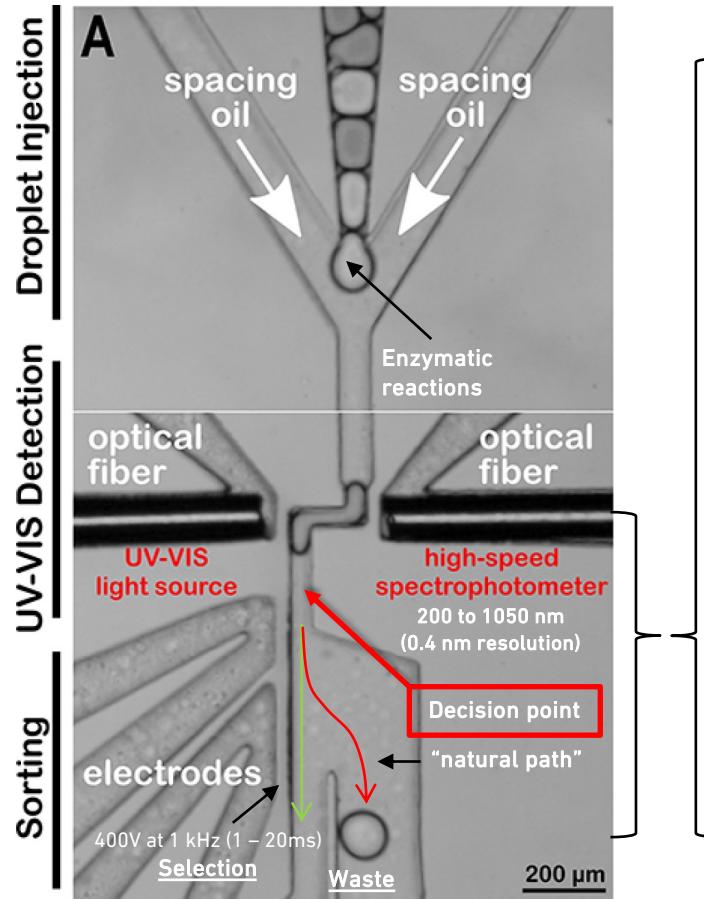
Our **microfluidic platform (UVADS)** can perform screening assays of enzymatic activity in **droplets** of bacterial micro-colonies by directly measuring the conversion to product by **UV-vis spectroscopy** and **sort** selected droplets using **electrodes**.

High-throughput label-free chemical identification in droplets and **on-demand** collection (via electrodes)

Expert-driven projects :: SpectraSorter

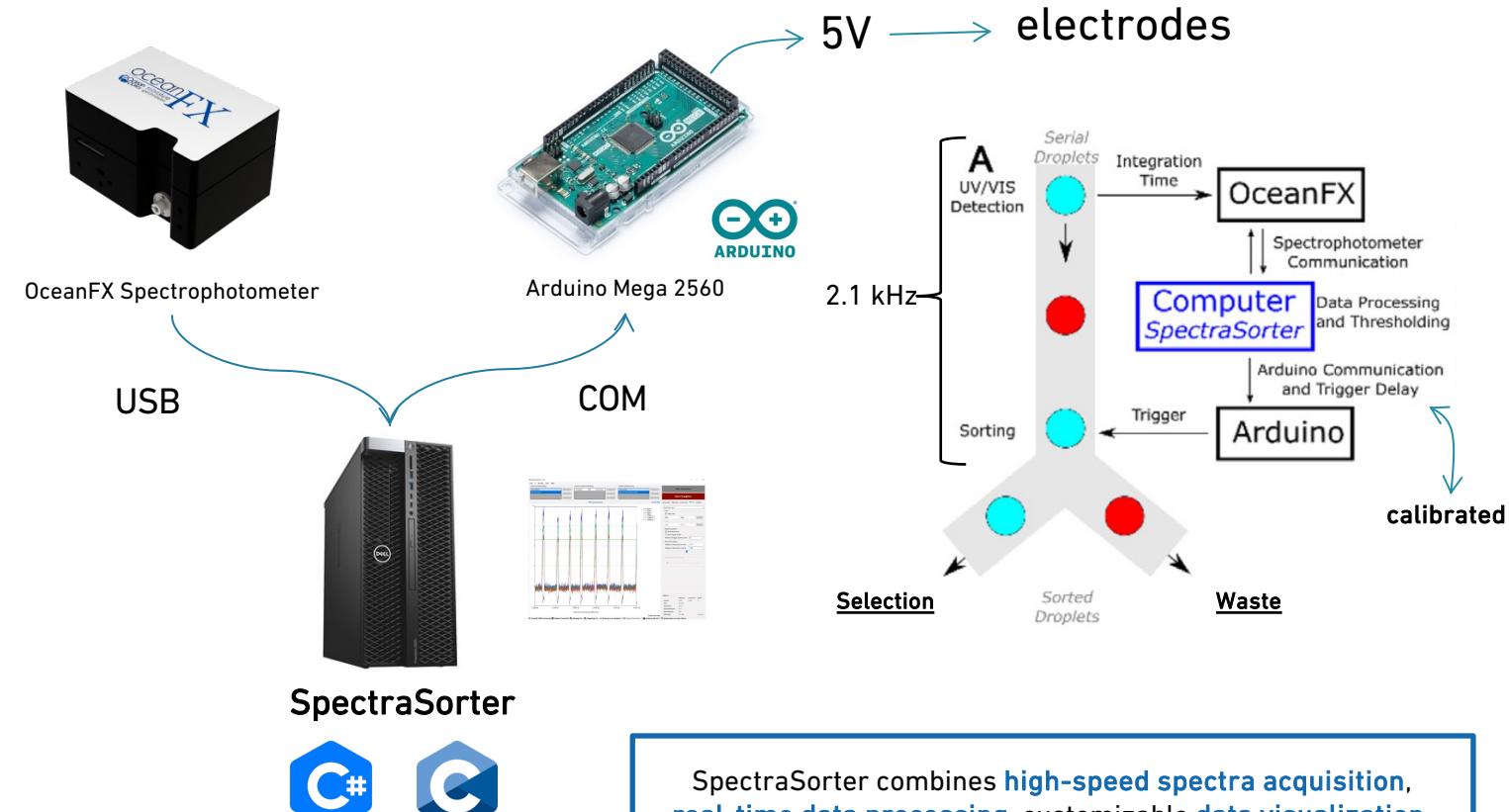
Duncombe T. A., Ponti A., Dittrich P. S. SoftwareX, Volume 19, 2022, 101160 DOI:10.1016/j.softx.2022.101160
 Duncombe T. A., Ponti A., Seebeck F. P., Dittrich P. S. 2021. DOI: 10.1021/acs.analchem.1c02822

UVADS: UV-vis spectra-activated droplet sorter



High-throughput label-free chemical identification in droplets and **on-demand** collection (via electrodes)

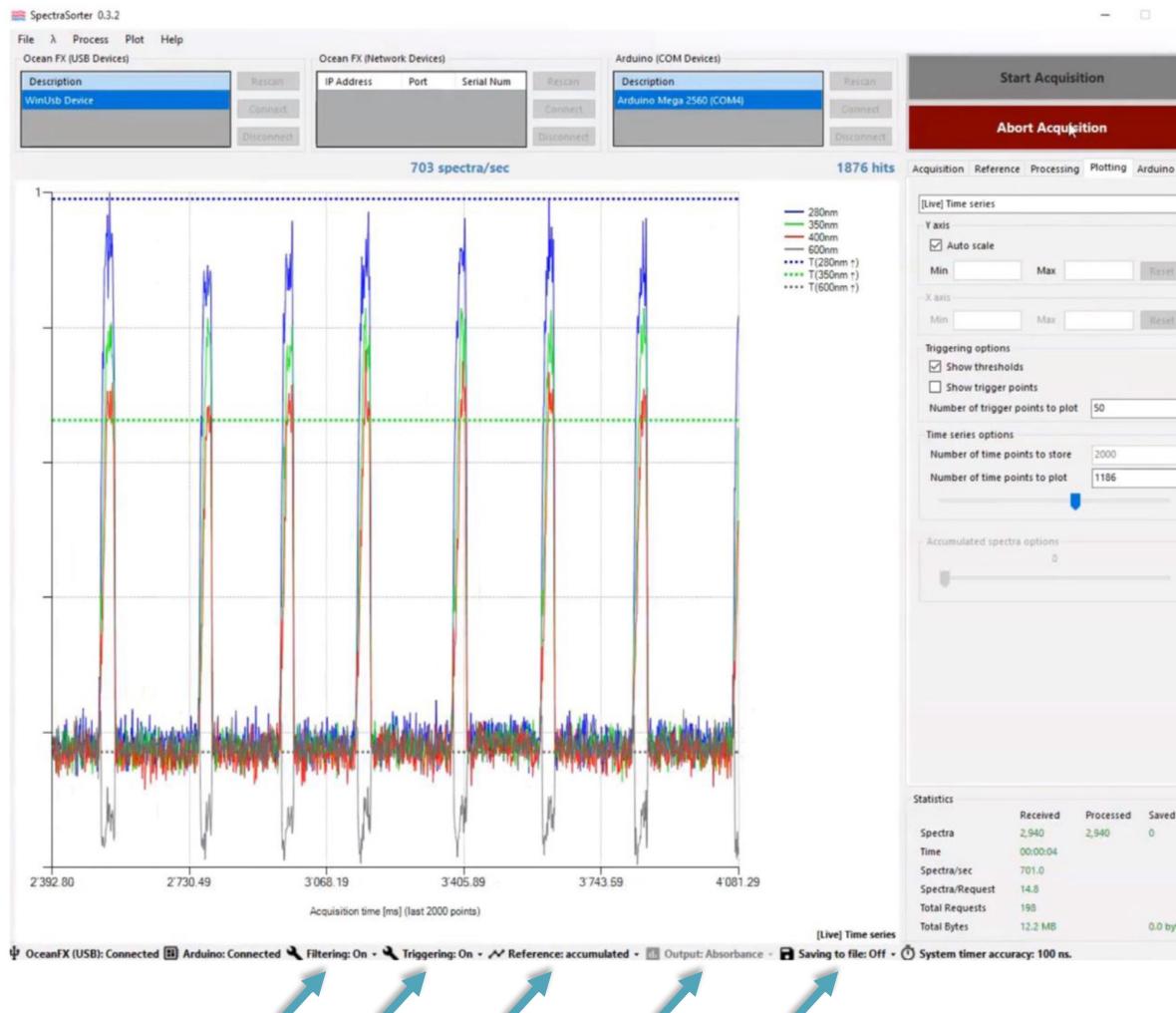
<https://github.com/SpectraSorter/SpectraSorter>



SpectraSorter combines **high-speed spectra acquisition**, **real-time data processing**, customizable **data visualization**, **precise control of external triggering** using any **multi-spectral feature**, **configuration management**, and more.

Expert-driven projects :: SpectraSorter

Duncombe T. A., Ponti A., Dittrich P. S. SoftwareX, Volume 19, 2022, 101160 DOI:10.1016/j.softx.2022.101160
 Duncombe T. A., Ponti A., Seebeck F. P., Dittrich P. S. 2021. DOI: 10.1021/acs.analchem.1c02822



SpectraSorter runs **four parallel queues**:

- **Acquisition** queue: collects up to 4500 spectra/s from the spectrometer
- **Compute** queue: performs all operations to decide if an event should trigger the Arduino microcontroller (low-pass filtering, transformation for absorbance or transmission, dark- and reference-correction, testing against all user-defined thresholds, triggering via Arduino)
- **Plotting** queue: plots the last spectrum at very low rate (10 Hz) for visual feedback
- **Saving** queue: writes to file the processed wavelengths (either a selection, a range, or the full spectrum)



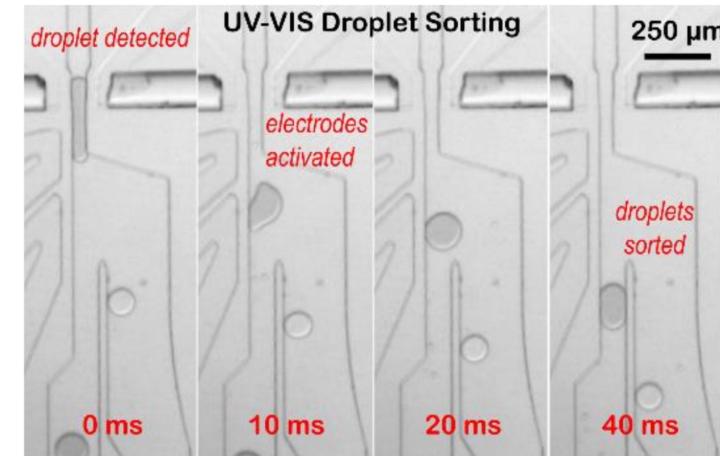
Expert-driven projects :: SpectraSorter

Duncombe T. A., Ponti A., Dittrich P. S. SoftwareX, Volume 19, 2022, 101160 DOI:10.1016/j.softx.2022.101160
 Duncombe T. A., Ponti A., Seebeck F. P., Dittrich P. S. 2021. DOI: 10.1021/acs.analchem.1c02822



The **Wavelength Hub** allows selection of any number of wavelengths that:

- act as a **threshold** for a **triggering event** (and in which way)
- will be displayed in the plotter as **time series** and/or as **full spectra**
- will be **saved** to disk



Expert-driven projects :: SpectraSorter

Expert contributions

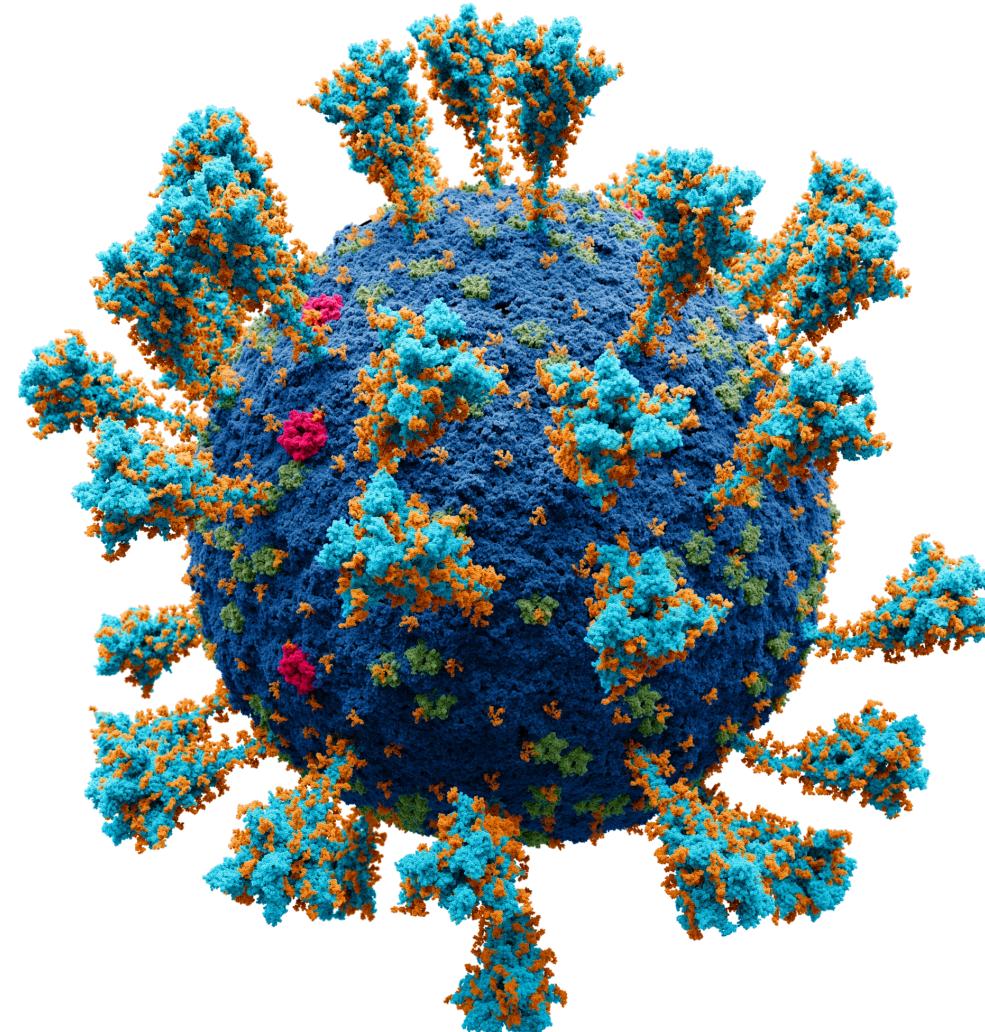
Todd Duncombe: development of the UVADS methodology and the microfluidics chip

Aaron Ponti: software development

Users

Petra Dittrich group

Expert-driven projects :: pyPOCQuant



<https://en.wikipedia.org/wiki/SARS-CoV-2>

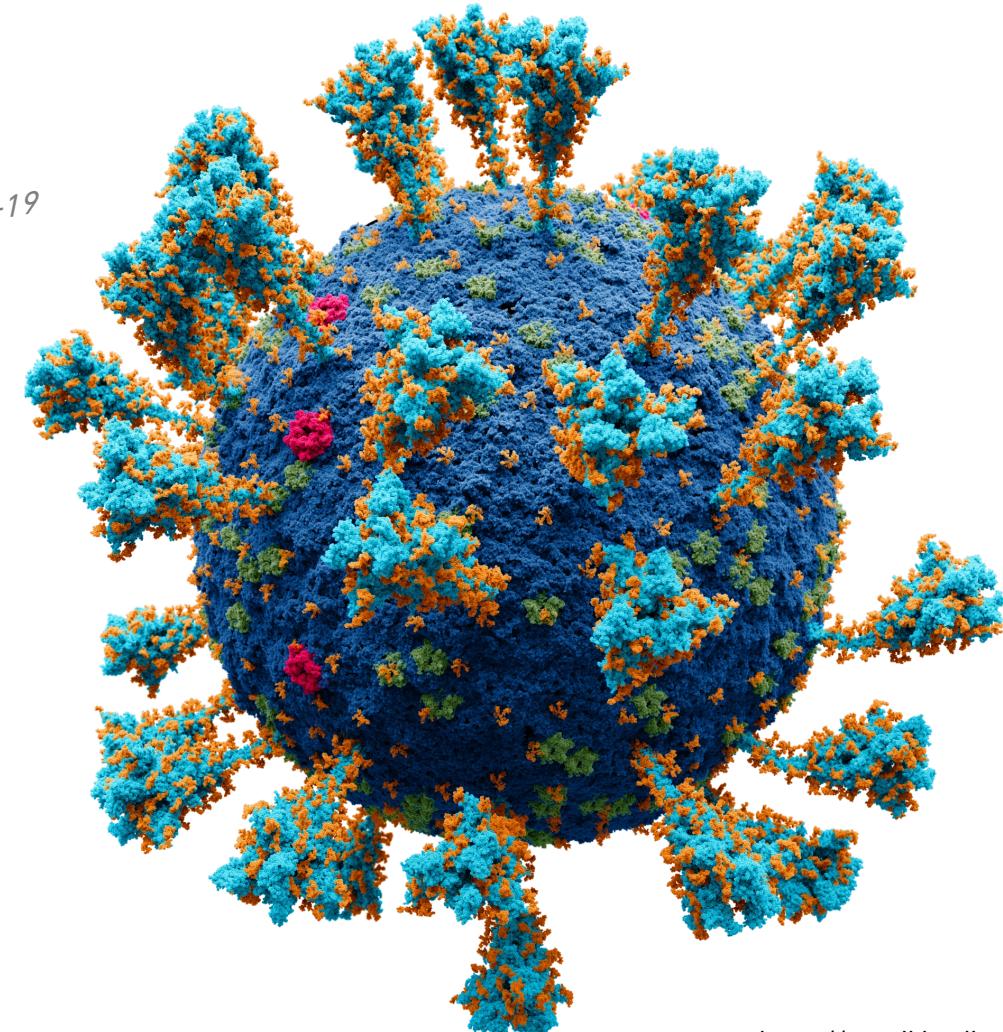
Expert-driven projects :: pyPOCQuant

On request by
Baselland Test Center (via Biolytix AG)



- Requirements**
1. **Quantify** the levels of **IgG** and **IgM** antibodies in patients' blood samples **over time** to study the body's immune response to SARS-CoV-2
 2. **Associate patient metadata** to each analysis and store the results in a database

*First wave of COVID-19
Spring 2020*



Experts:

Fabian Rudolf, Bundesamt für Gesundheit, CH

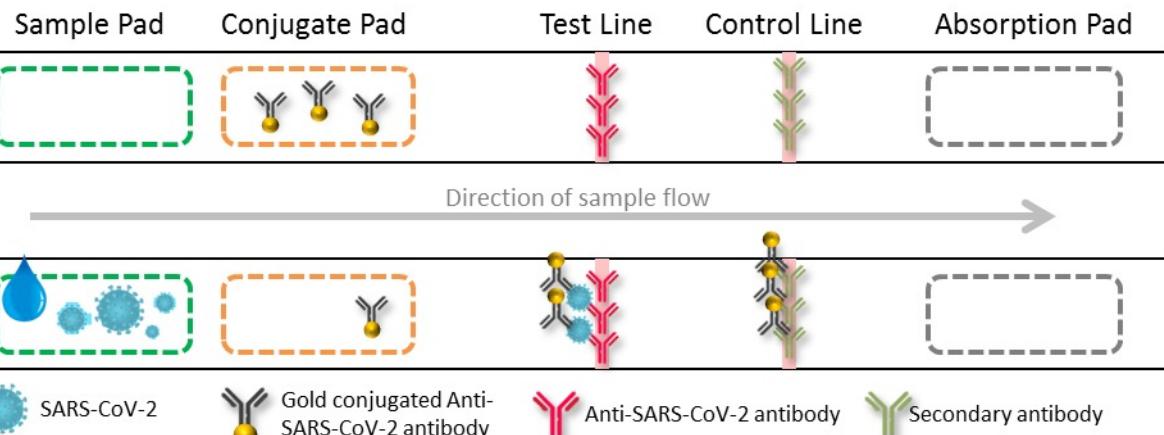
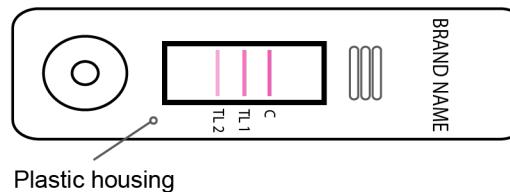
Andreas Cuny, Joerg Stelling group, D-BSSE ETHZ

<https://en.wikipedia.org/wiki/SARS-CoV-2>

Expert-driven projects :: pyPOCQuant

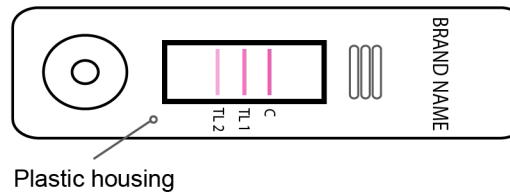
Image source: <https://www.acebiolab.com/EN/news/44>

Antigen (Ag) test

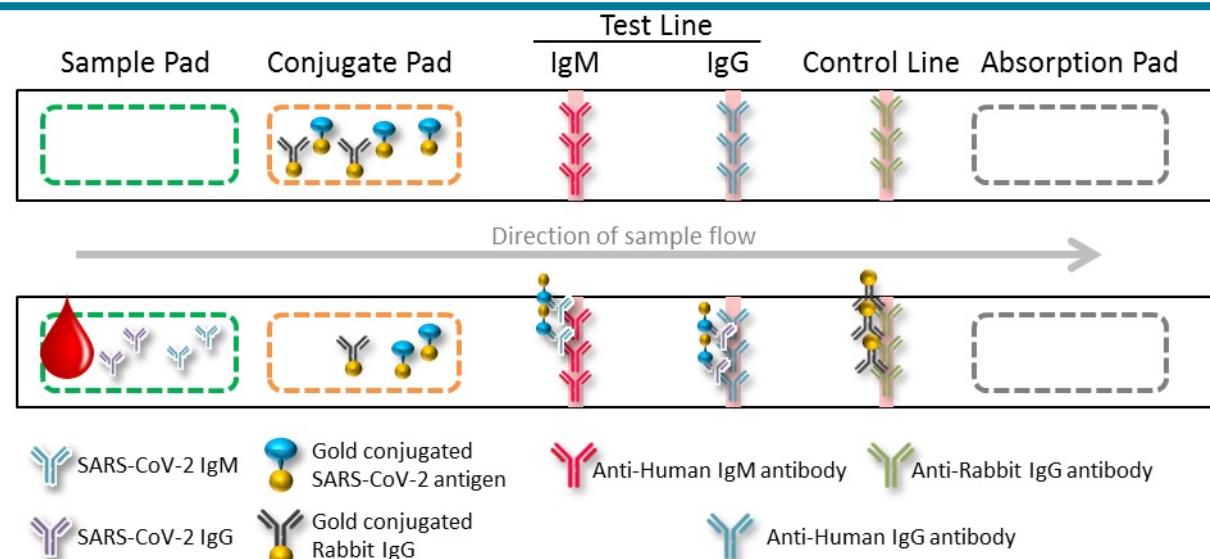


Lateral-flow point-of-care tests (POCTs)

Antibody (Ab) test



Lateral flow Point-Of-Care Tests (POCTs) are a valuable tool for rapidly detecting pathogens and the associated immune response in humans and animals.



Expert-driven projects :: pyPOCQuant

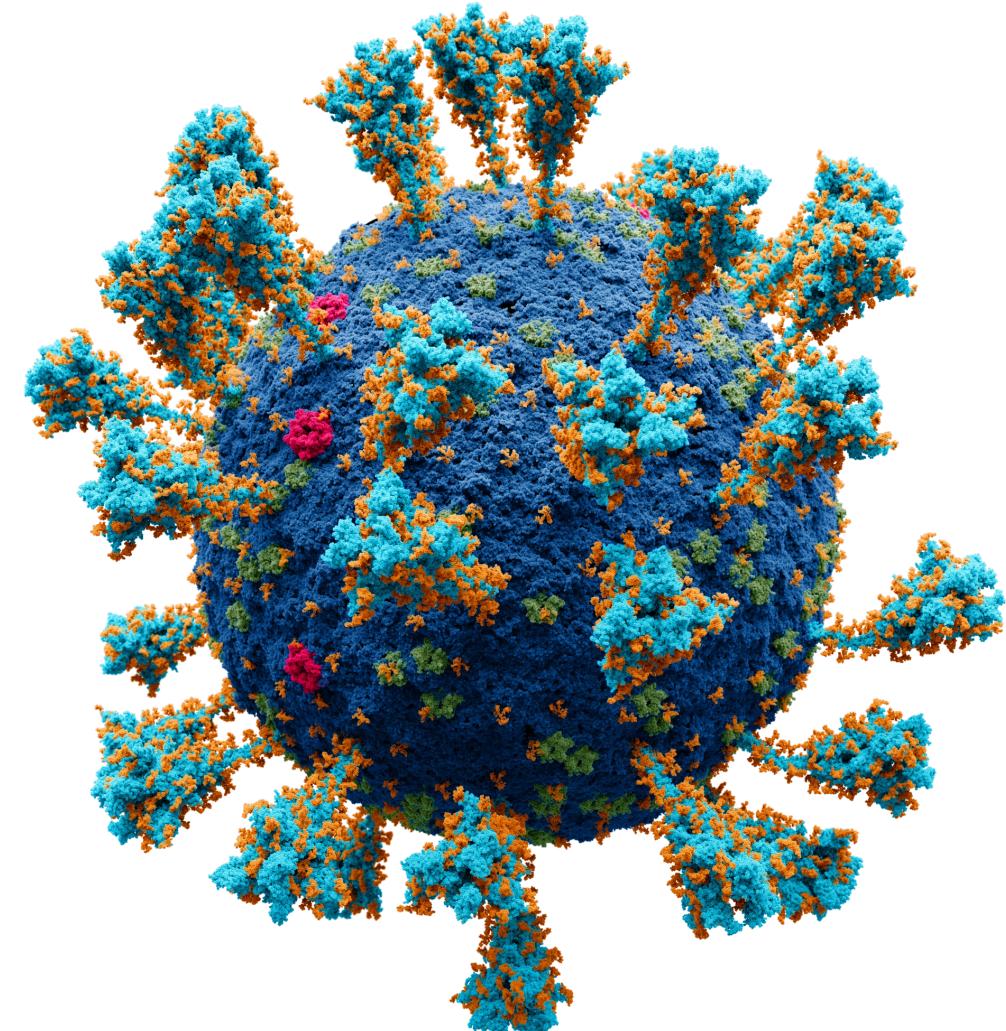
We don't want to waste any test!

Sudden, high demand for **robust** and **quantitative** analysis of POCTs from **different vendors** and from **large numbers** of images

Which ones are quantitative?

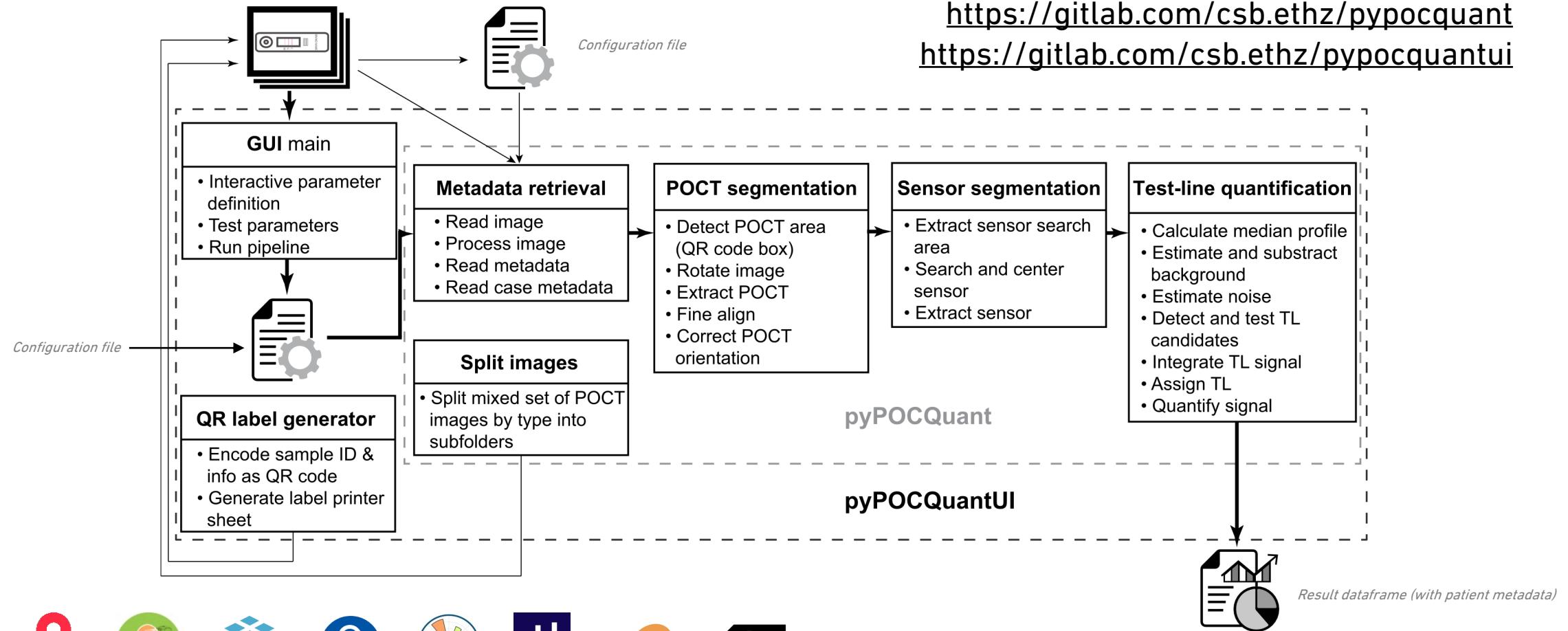
No freely available pipelines for robust, large-scale **batch processing**

There were commercial readers, but they were slow, expensive, proprietary, and only compatible with certain types of tests.



<https://en.wikipedia.org/wiki/SARS-CoV-2>

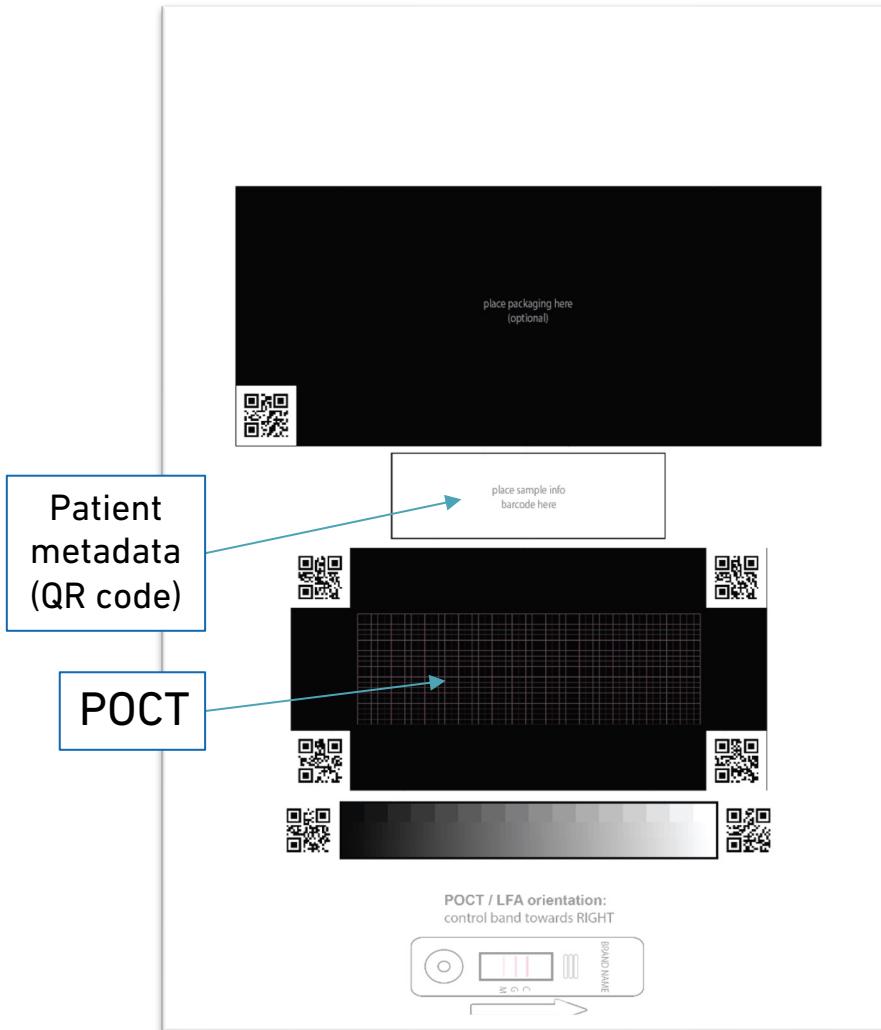
Expert-driven projects :: pyPOCQuant



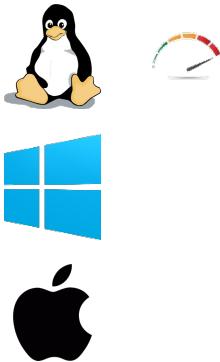
Expert-driven projects :: pyPOCQuant

- We needed to be able to analyse batches of **hundreds to thousands of tests** with very low failure rate
- However, several parameters strongly affect the robustness of our quantitative analysis:
 - **illumination variability** (given by acquisitions performed at different times of the day, weather conditions, shadows, reflections)
 - **scaling and orientation of the images** (due to freehand shots with cameras or smartphones)
 - **intensity corrections** by the camera (intensity stretching, white balancing, and compression) **and its file formats** (*e.g.*, RAW vs. JPG)
 - **different sizes, colors, and shapes** of POCTs from different vendors
 - **random positioning** and **orientation** of the POCT in the field of view
 - often **difficult localization** of the detector window

Expert-driven projects :: pyPOCQuant



Expert-driven projects :: pyPOCQuant



Interactively create
and save a
configuration for
batch processing

The screenshot shows the pyPOCQuant software interface. On the left, the configuration parameters are listed:

- File**: Input folder (1) C:\Users\Localadmin\Desktop\ui_images\sample_image, Output folder (2) C:\Users\Localadmin\Desktop\ui_images\sample_image\pipeline, File list (3) IMG_8489.JPG, Img0619.jpg.
- Parameter** section:
 - Runtime parameters**: Number of cores (max=96) (10) set to 2, QC checked, Verbose checked.
 - Basic parameters**: Number of sensor bands (5) set to 3, Control band index (-1), Sensor band names: 0 igm, 1 igg, 2 ctl.
 - Band expected relative location**: 0 set to 0.25.
- Test parameters**: Run (11) set to 9.
- Log**: Extracting POCT from image finished successfully. (5)

On the right, the software displays a sample image of a COVID-19 IgG/IgM test strip. Annotations include:

- User defines window and test line positions (and number) (7) pointing to the red dashed box around the M, G, and C lines.
- Automatic extraction of POCT (8) pointing to the image of the physical test strip.

Expert-driven projects :: pyPOCQuant

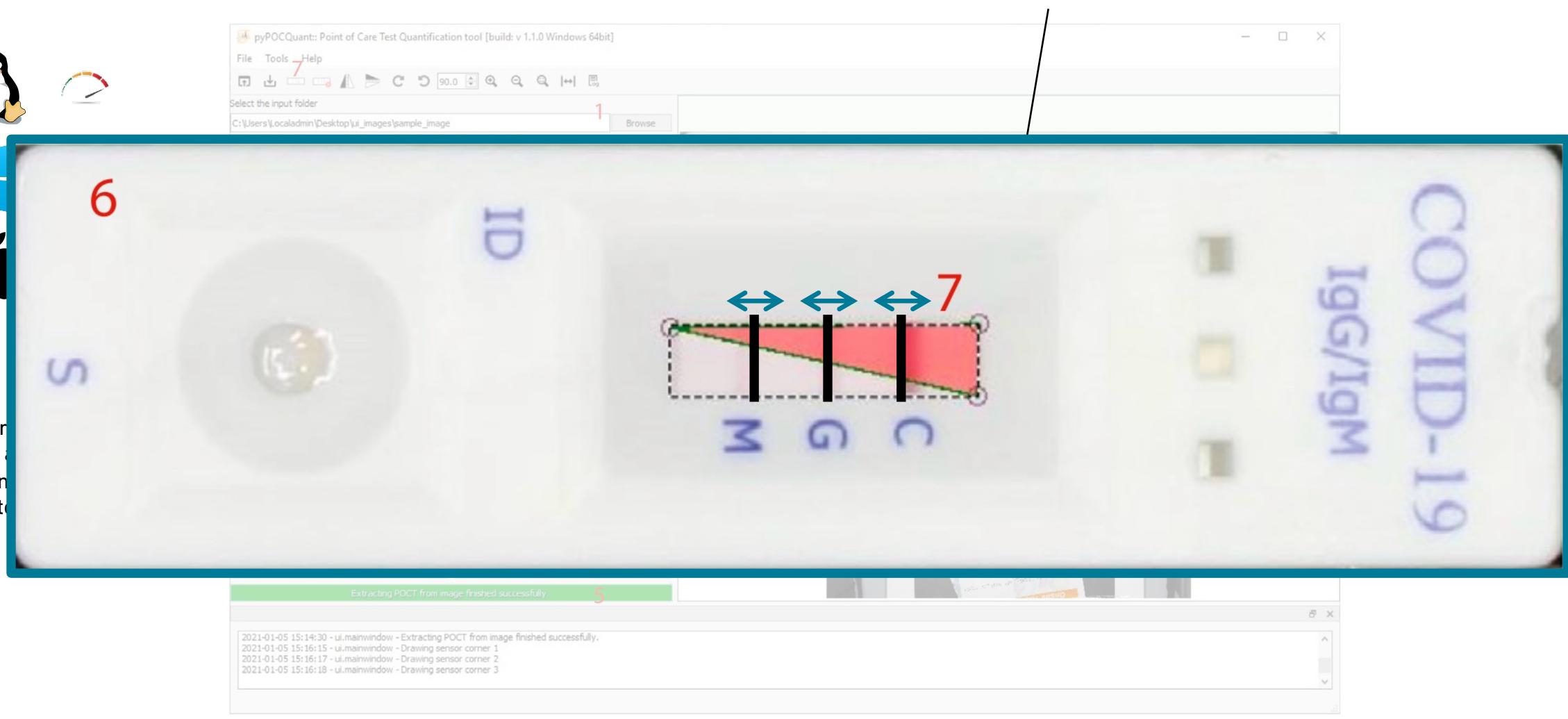


Inter

con

bat

User defines window and test line positions (and number)



Expert-driven projects :: pyPOCQuant

Run from console

```
python pyPOCQuant.py -f examples/images -o examples/images/results -s examples/config.conf -w 4
```



Run from scripts or notebooks

```
from pypocquant.lib.pipeline import run_pipeline
from pypocquant.lib.settings import default_settings

# Get the default settings
settings = default_settings()

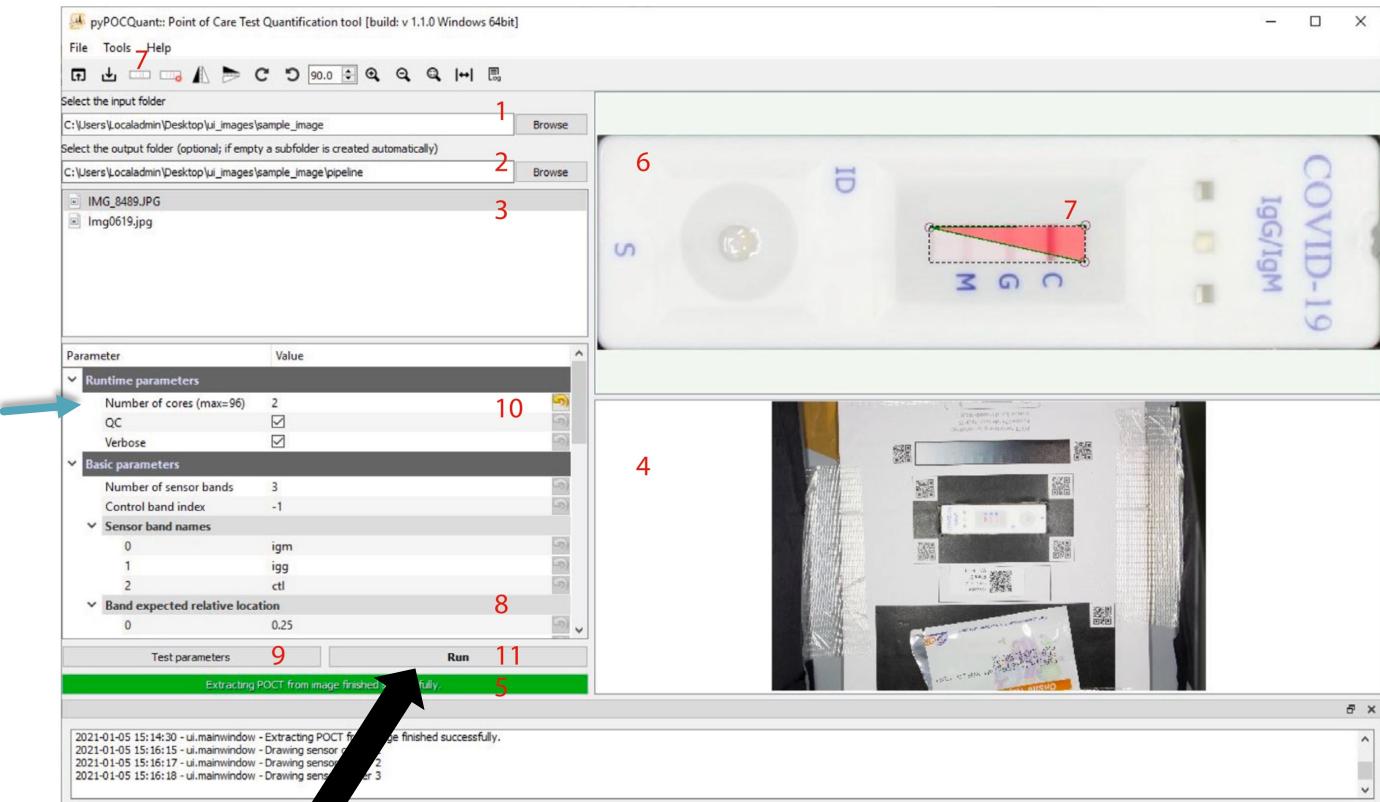
# Change settings manually as needed
settings["sensor_band_names"] = ('igm', 'igg', 'ctl')

# Alternatively, load existing settings file
# from pypocquant.lib.settings import Load_settings
# settings = Load_settings('full/path/to/settings/file.conf')

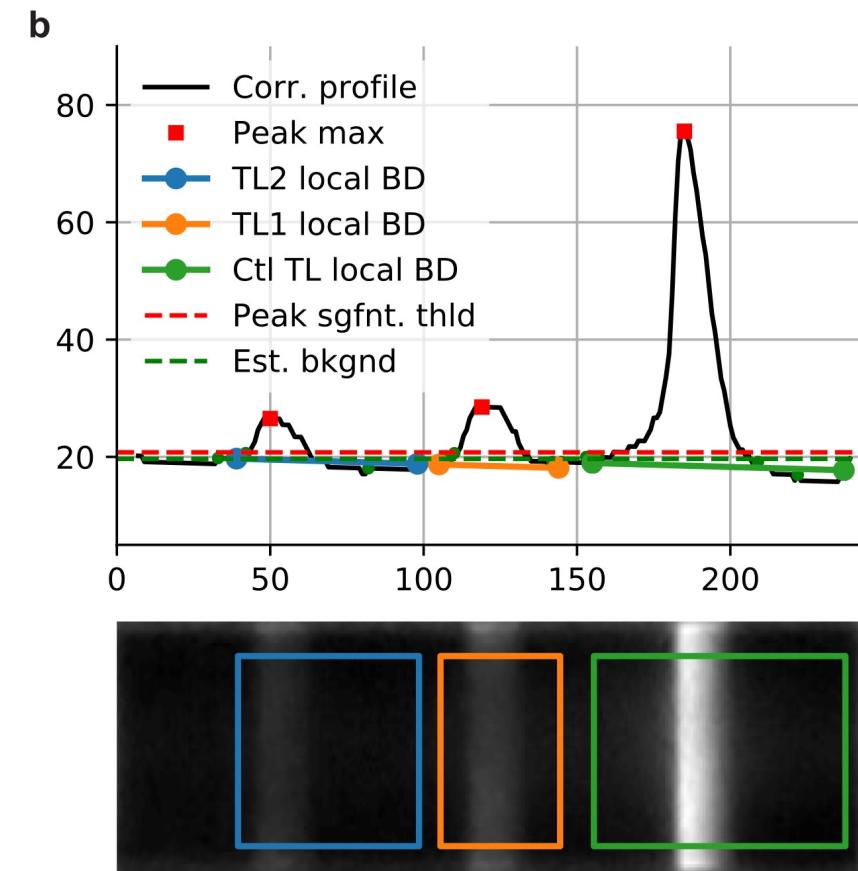
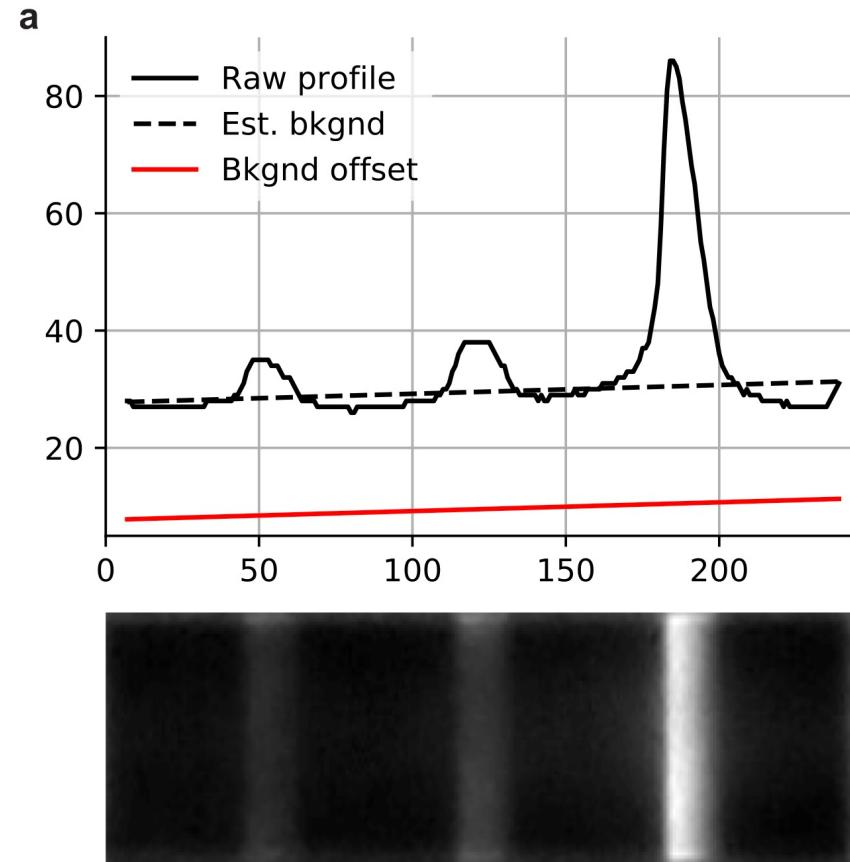
# Set final argument
input_folder_path = 'full/path/to/input/folder'
results_folder_path = 'full/path/to/results/folder'
max_workers = 8

# Run the pipeline
run_pipeline(
    input_folder_path,
    results_folder_path,
    **settings,
    max_workers=max_workers
)
```

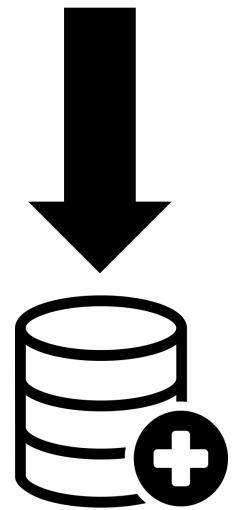

Run from user interface



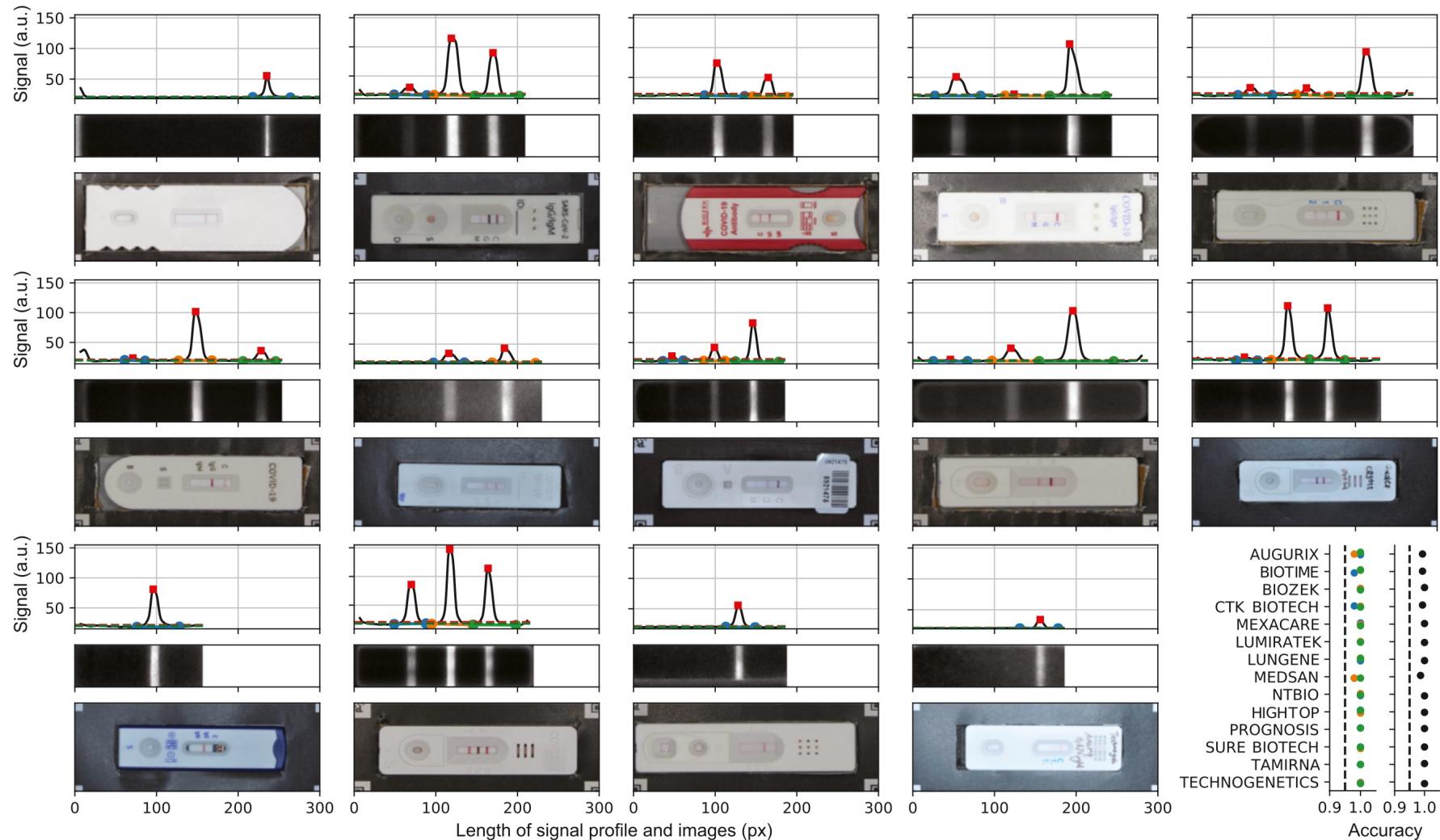
Expert-driven projects :: pyPOCQuant



Analysis results
Patient metadata
Experiment metadata



Expert-driven projects :: pyPOCQuant



Expert-driven projects :: pyPOCQuant

Cuny A. P., Rudolf F., Ponti A. SoftwareX 15:2021, 100710. DOI: 10.1016/j.softx.2021.100710

Work by [Andreas Cuny](#)

Expert contributions

Fabian Rudolf: development of the testing methodology, field work, and project management

Andreas Cuny: development of hardware components of pyPOCQuant, application development

Aaron Ponti: computer vision algorithm development, application development



Users

- Baselland Test Center (via Biolytix AG)
- Swiss Tropical and Health Institute (TPH), Basel
- Fachhochschule Nordwestschweiz (FHNW), Muttenz
- Swiss Armed Forces ← Large-scale testing before Rekrutenschule Summer 2020
- Canton Grisons and Swiss Federal Office of Public Health (Kantonaler Führungsstab Graubünden)
- Purdue University, Indiana, USA
- Test centers in Argentina and Greece

New hardware prototype (with touch screen and Raspberry Pi 4 Model B) for the Swiss Armed Forces



Adapted user interface (and template) for the new hardware

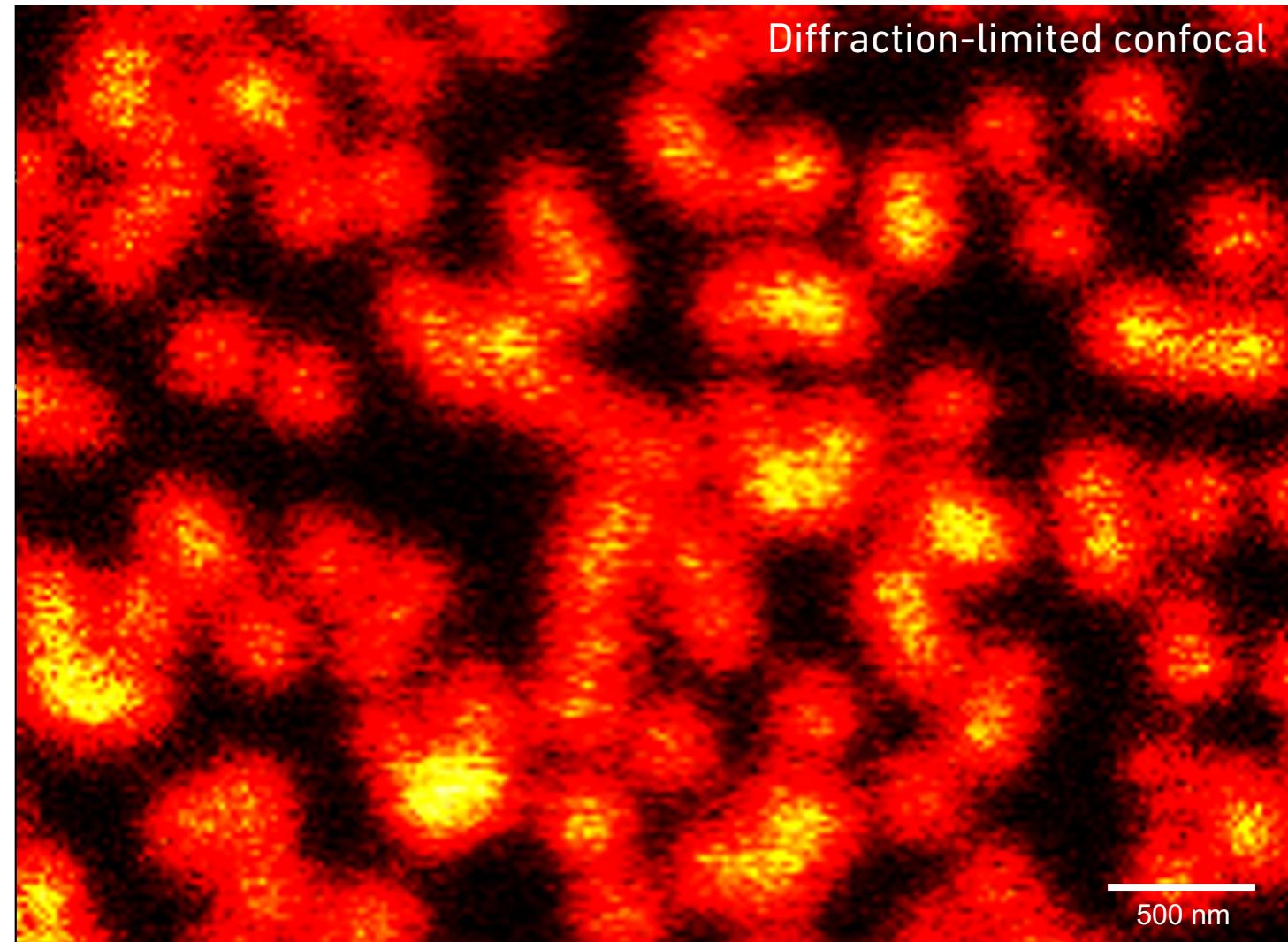
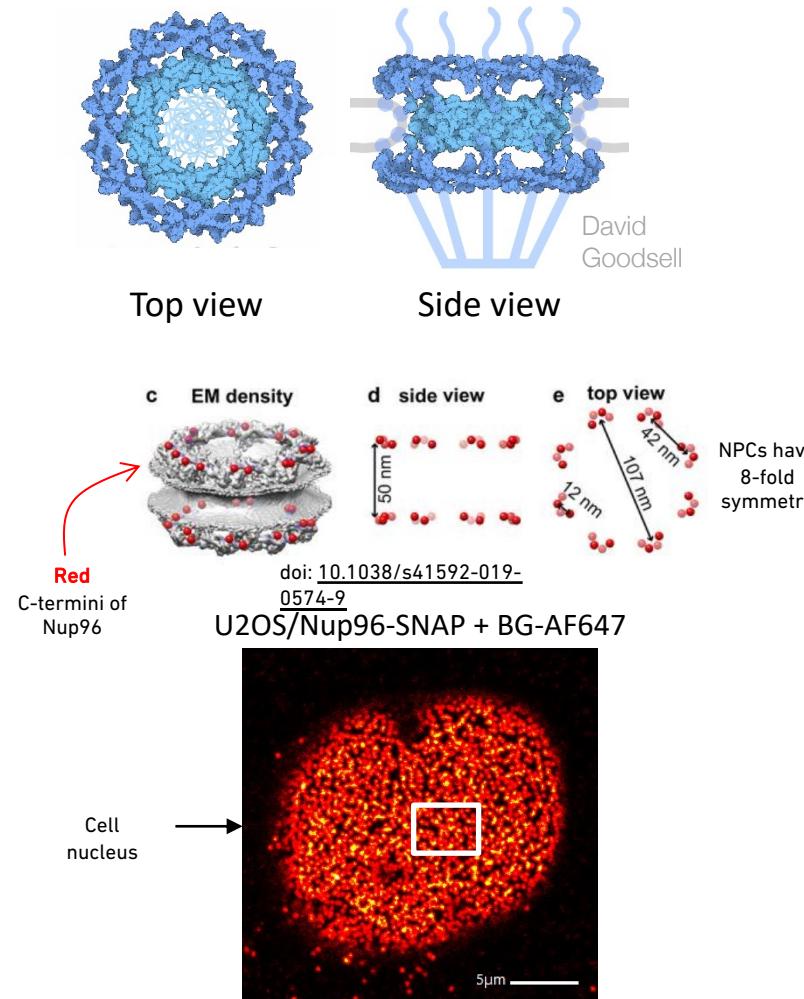
Expert-driven projects :: pyMINFLUX



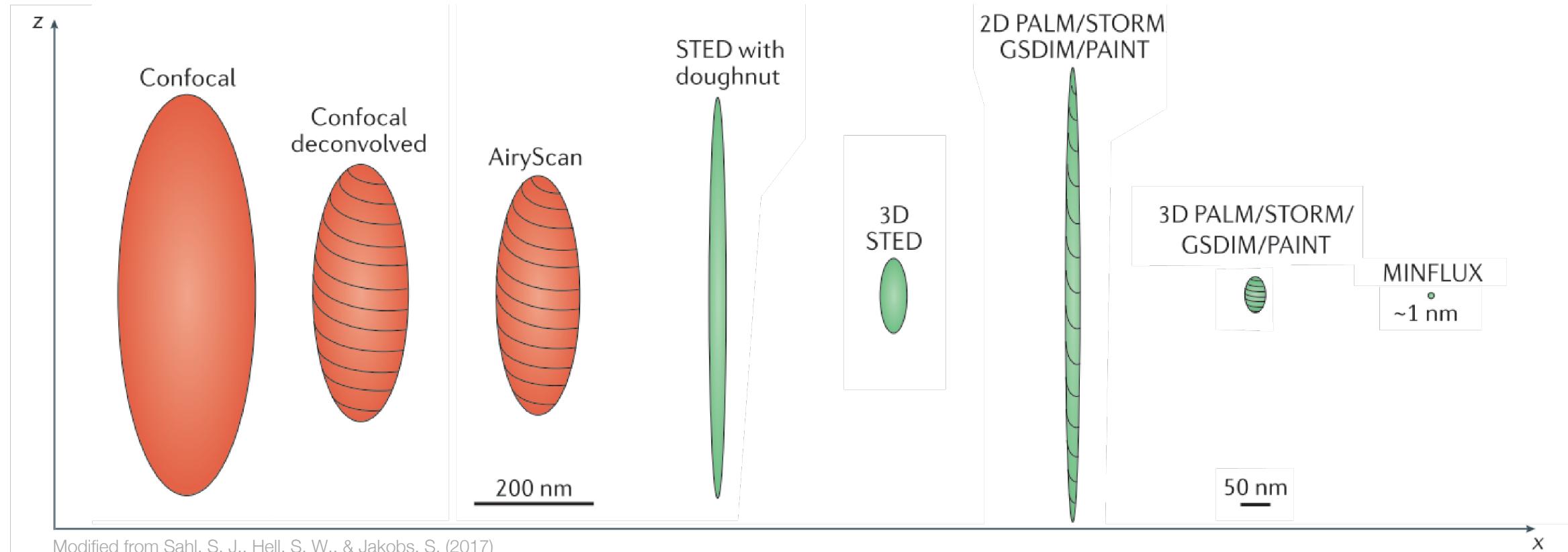
Expert: [Javier Casares Arias](#), Single Cell Facility, D-BSSE ETHZ

Expert-driven projects :: pyMINFLUX

QC sample: Nuclear pore complex imaging



Expert-driven projects :: pyMINFLUX



XY	200 nm	150 nm	120 nm	30 nm	50 nm	20 nm	20 nm	1 nm
Z	600 nm	400 nm	350 nm	600 nm	150 nm	600 nm	100 nm	1 nm

Expert-driven projects :: pyMINFLUX

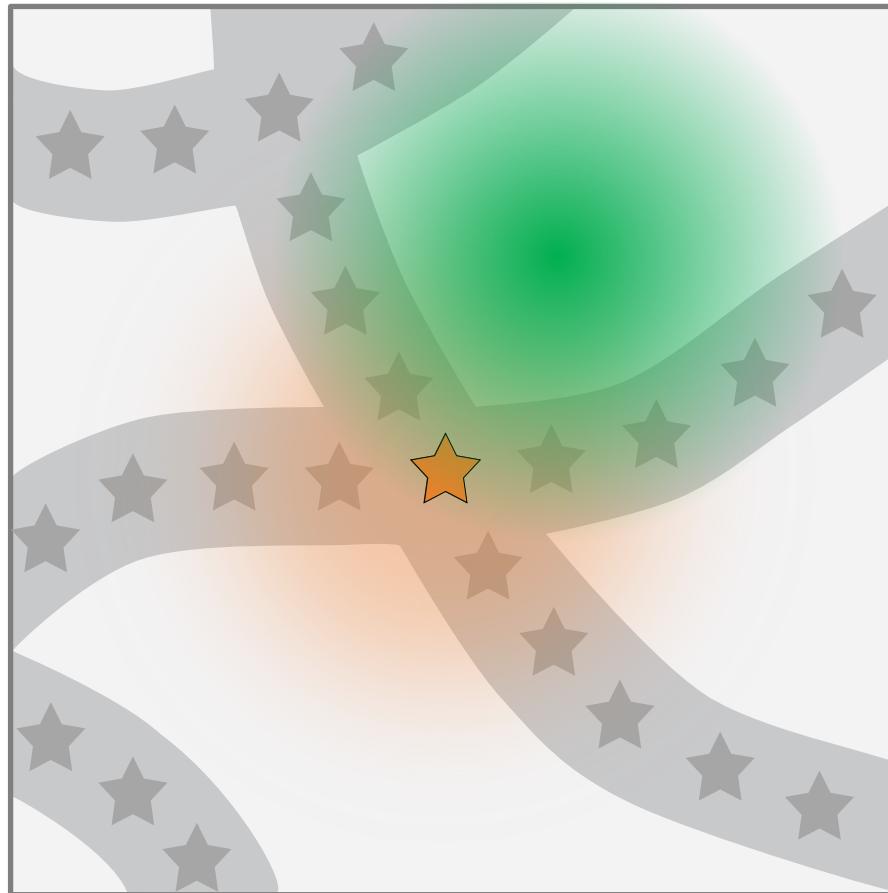
When the minimum at the center of the **excitation donut** and the fluorophore overlap there is no excitation, and thus no emission

Beam position = Fluorophore position



Expert-driven projects :: pyMINFLUX

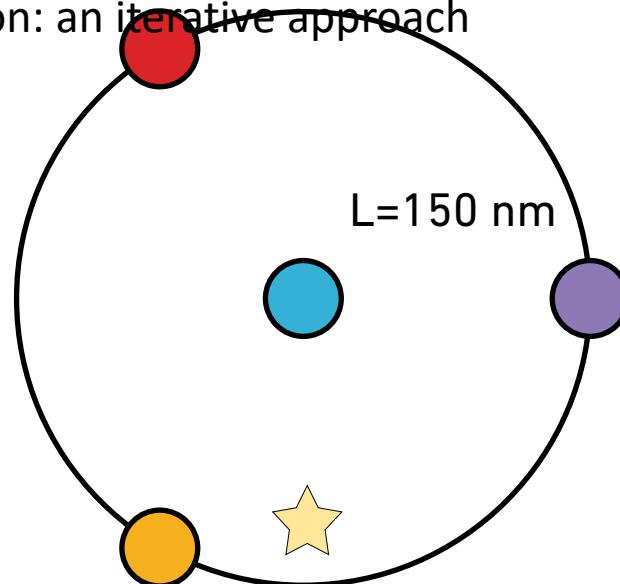
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

Expert-driven projects :: pyMINFLUX

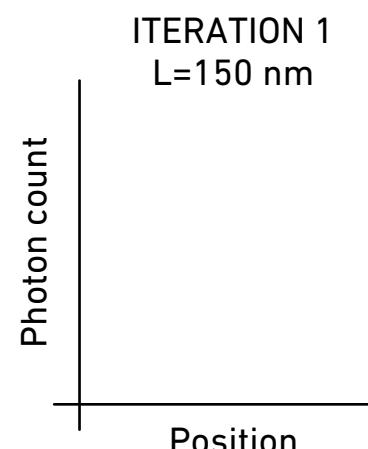
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

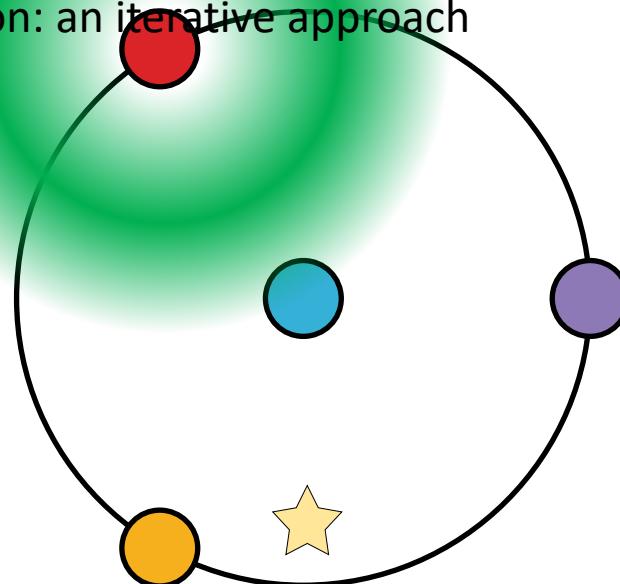
MINFLUX iteration:

1. Define scanning region according to previous estimation



Expert-driven projects :: pyMINFLUX

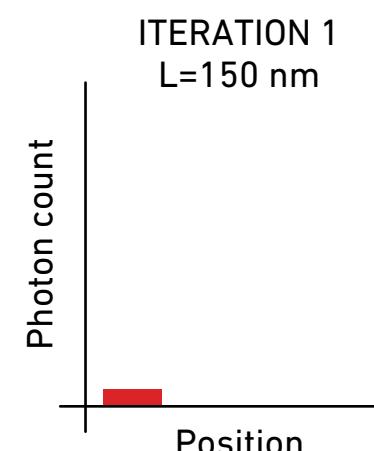
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

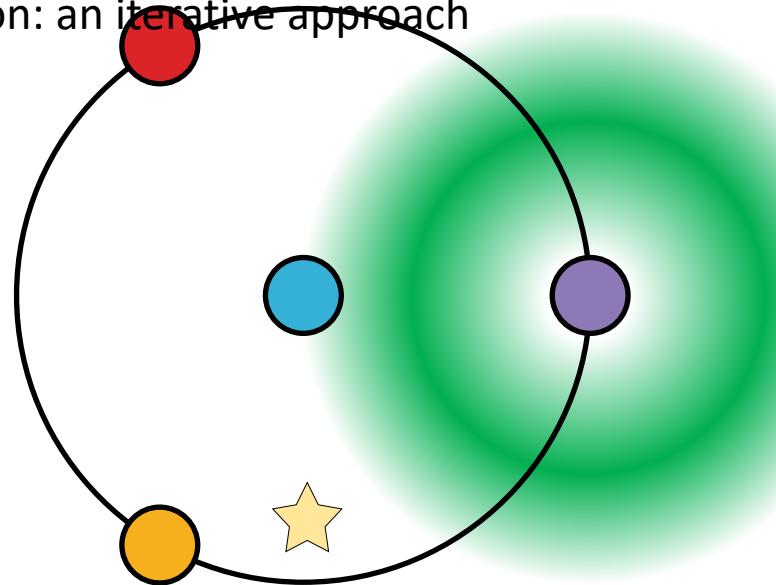
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern



Expert-driven projects :: pyMINFLUX

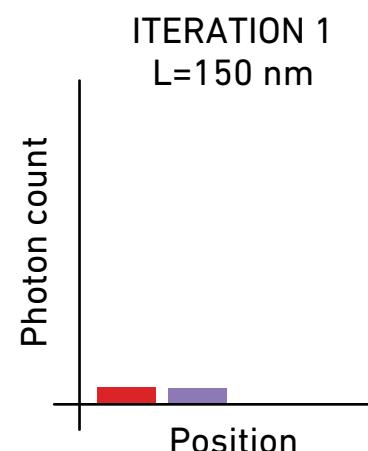
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

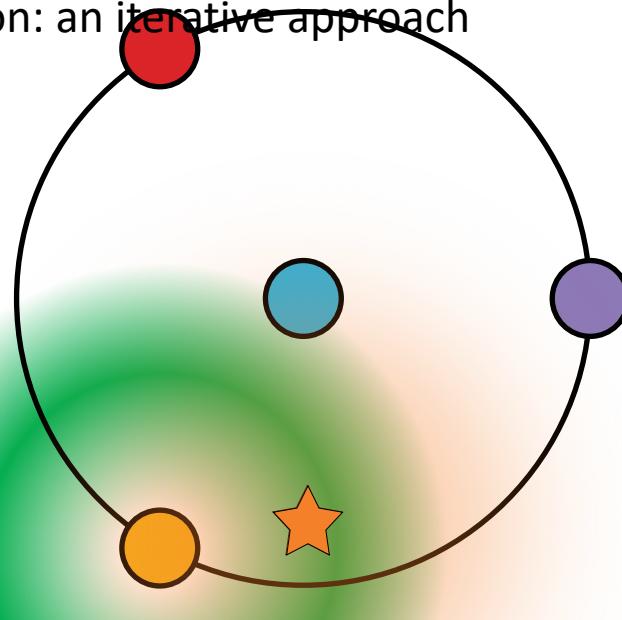
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern



Expert-driven projects :: pyMINFLUX

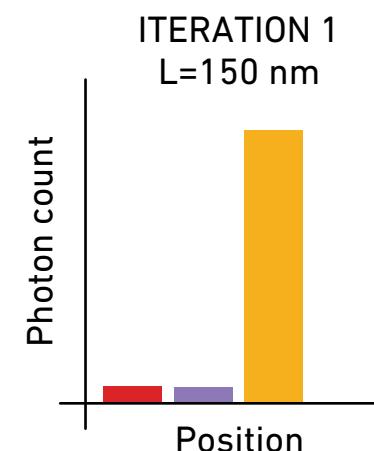
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

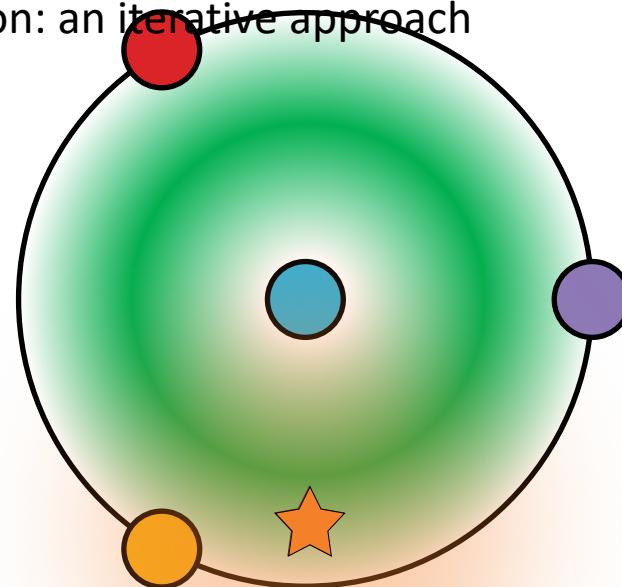
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern



Expert-driven projects :: pyMINFLUX

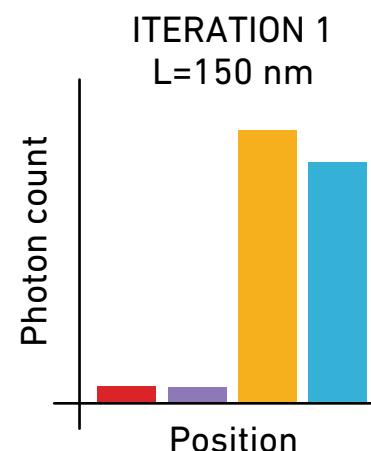
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

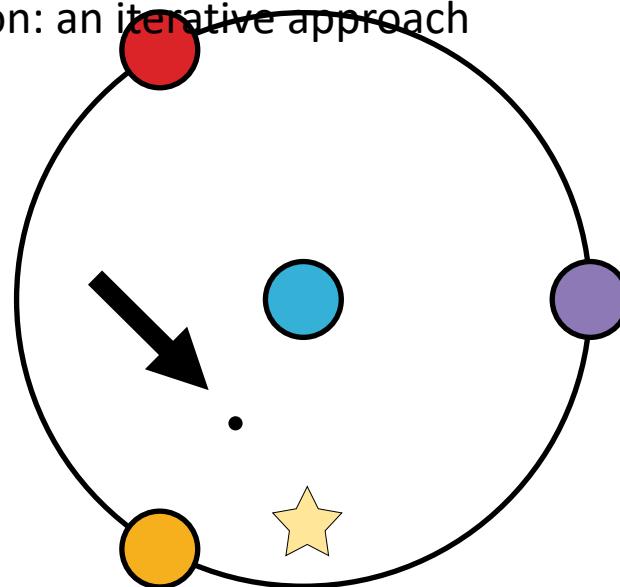
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern



Expert-driven projects :: pyMINFLUX

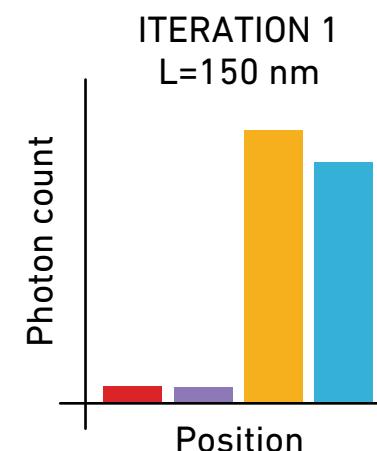
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

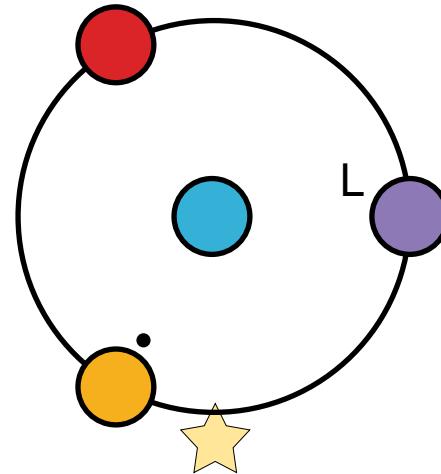
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation



Expert-driven projects :: pyMINFLUX

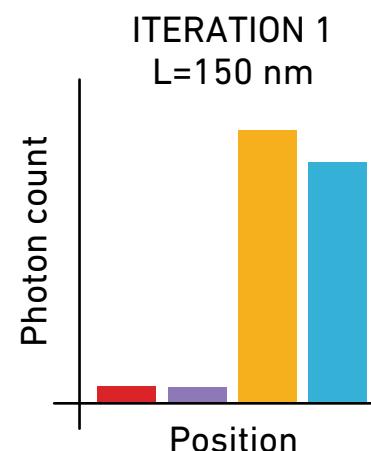
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

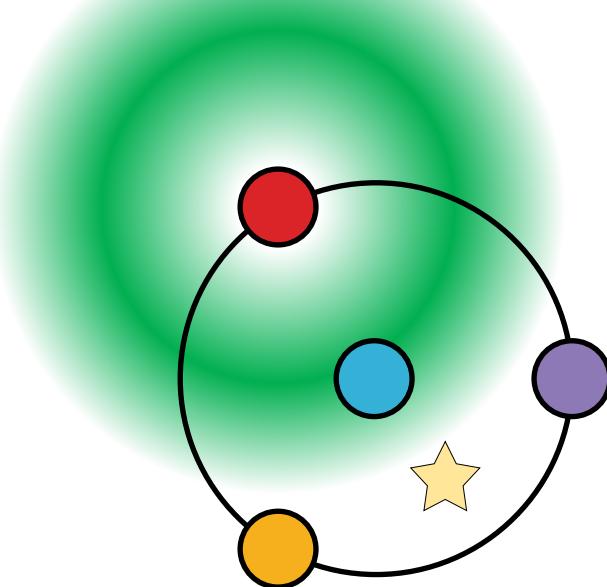
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

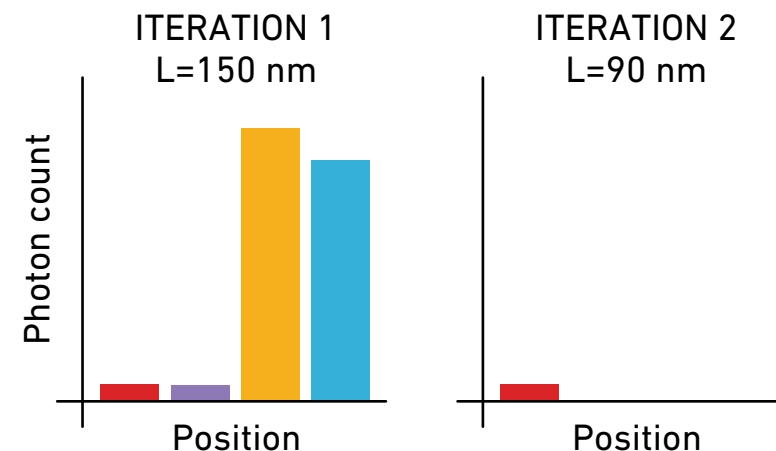
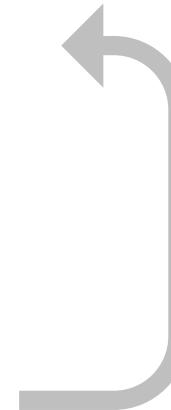
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

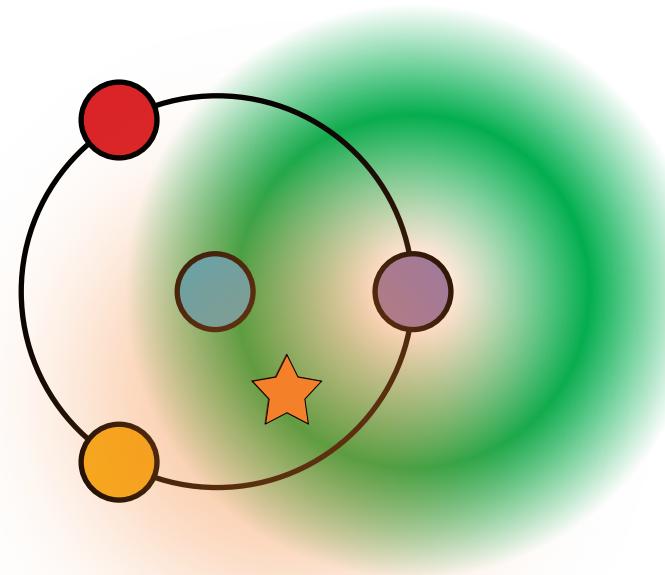
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

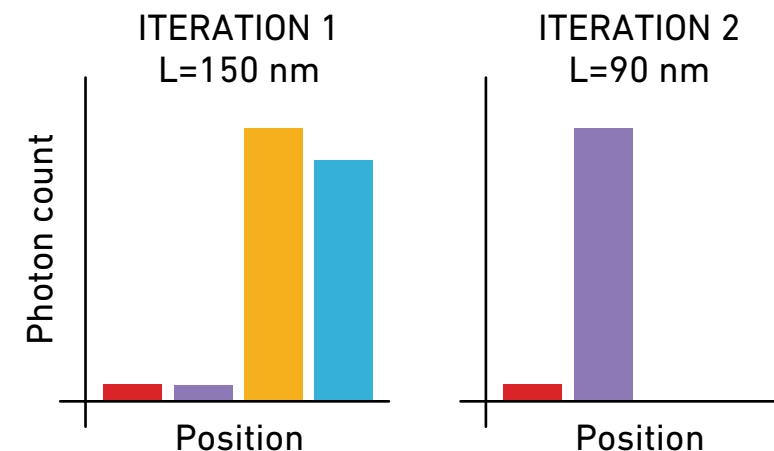
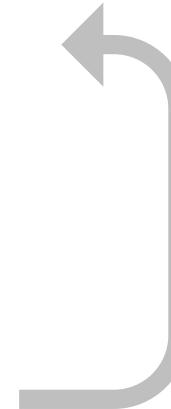
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



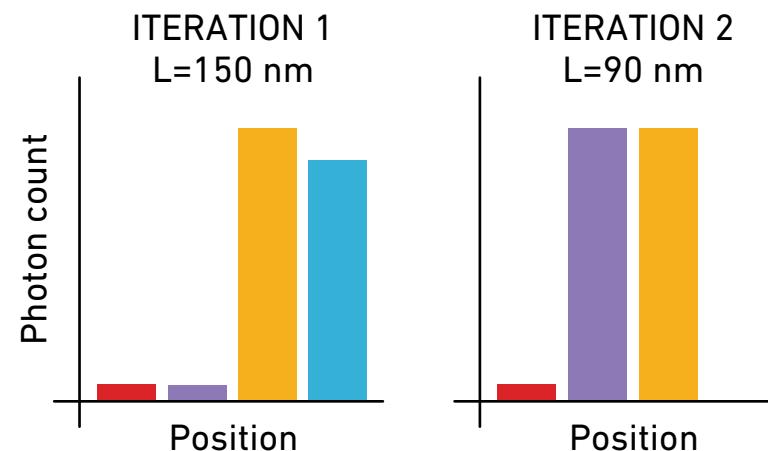
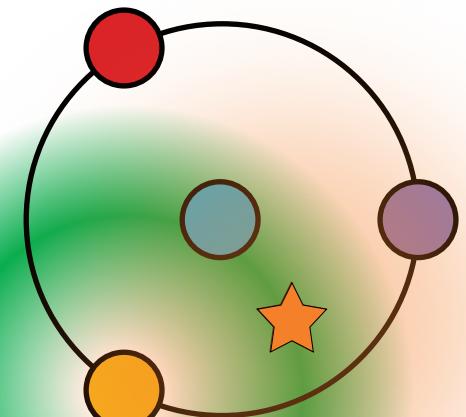
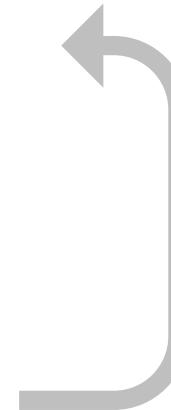
Expert-driven projects :: pyMINFLUX

Localization: an iterative approach

Estimate fluorophore position with spot-shaped beam

MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



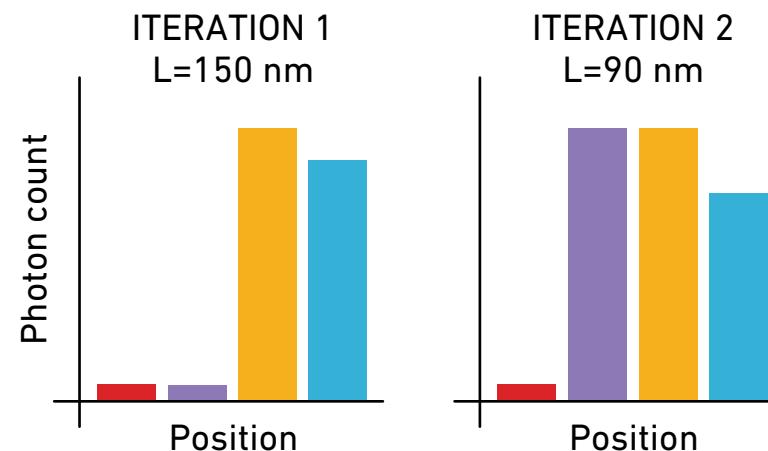
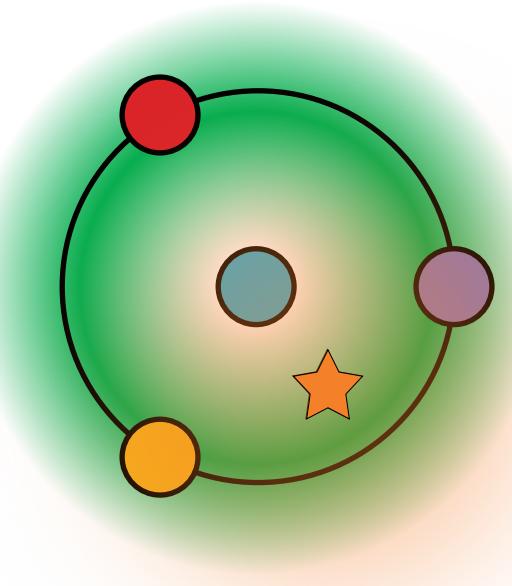
Expert-driven projects :: pyMINFLUX

Localization: an iterative approach

Estimate fluorophore position with spot-shaped beam

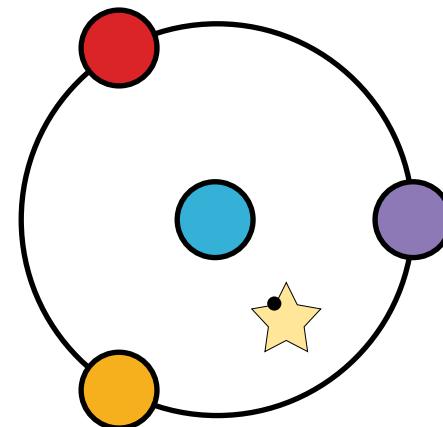
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

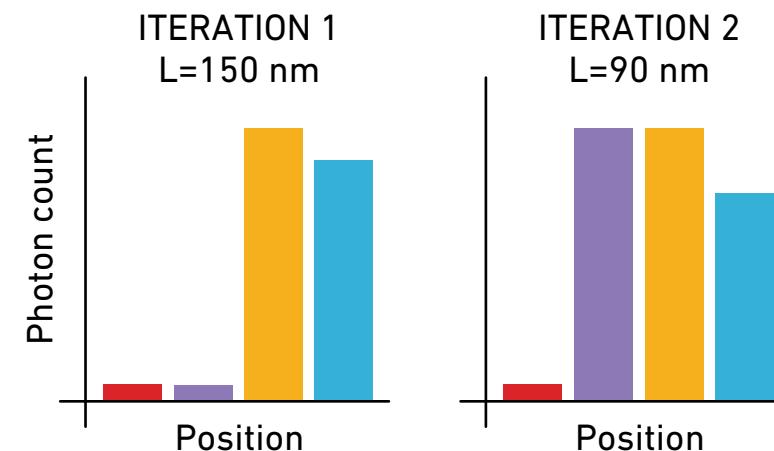
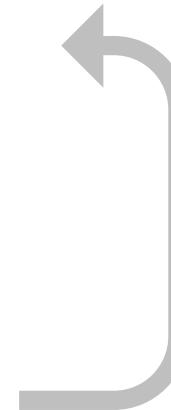
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



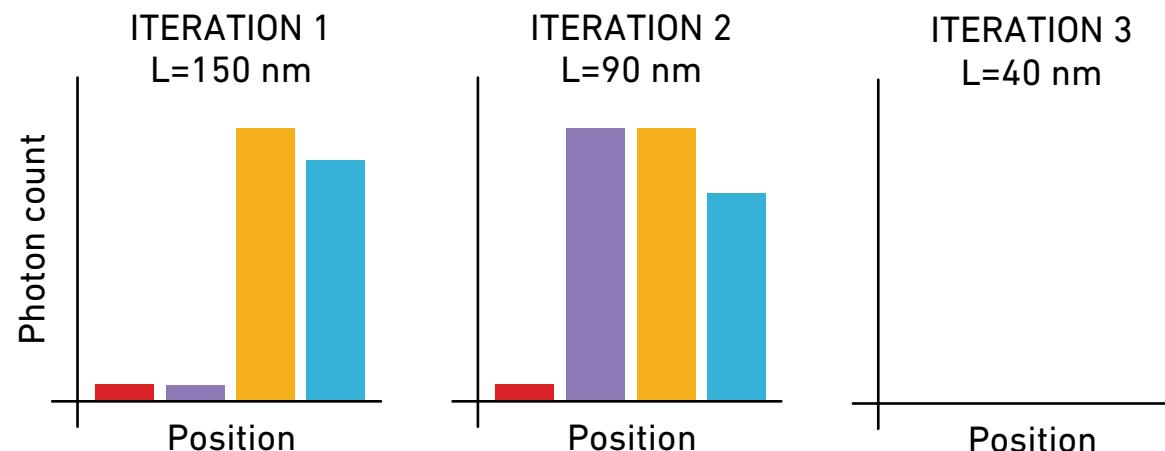
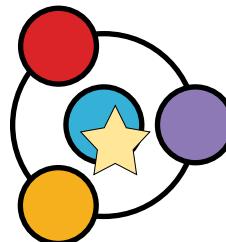
Expert-driven projects :: pyMINFLUX

Localization: an iterative approach

Estimate fluorophore position with spot-shaped beam

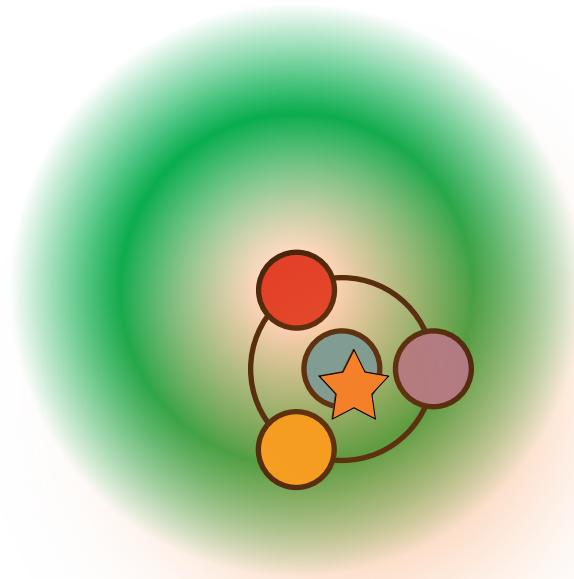
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

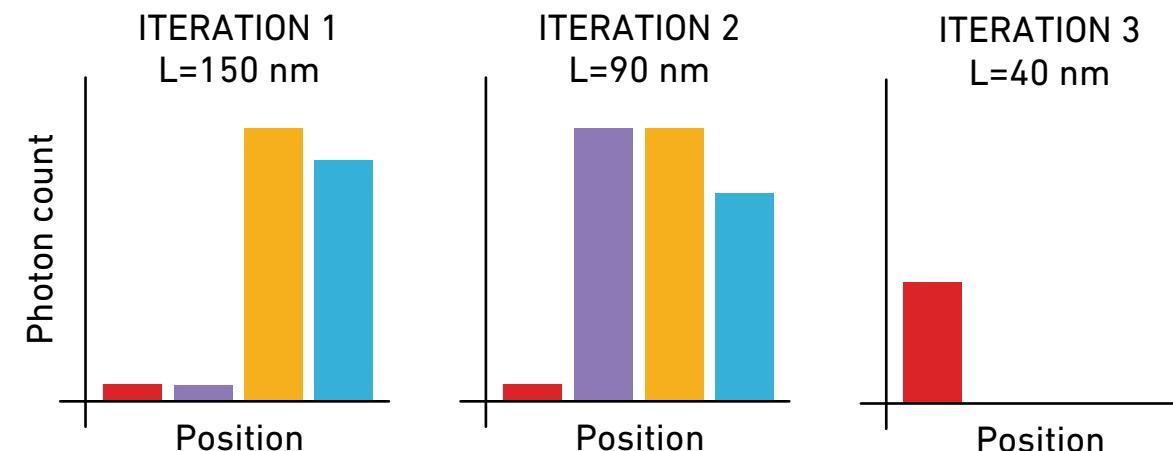
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

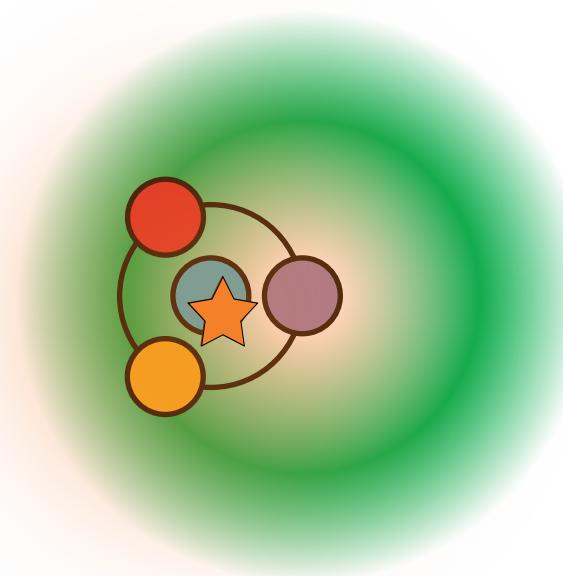
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

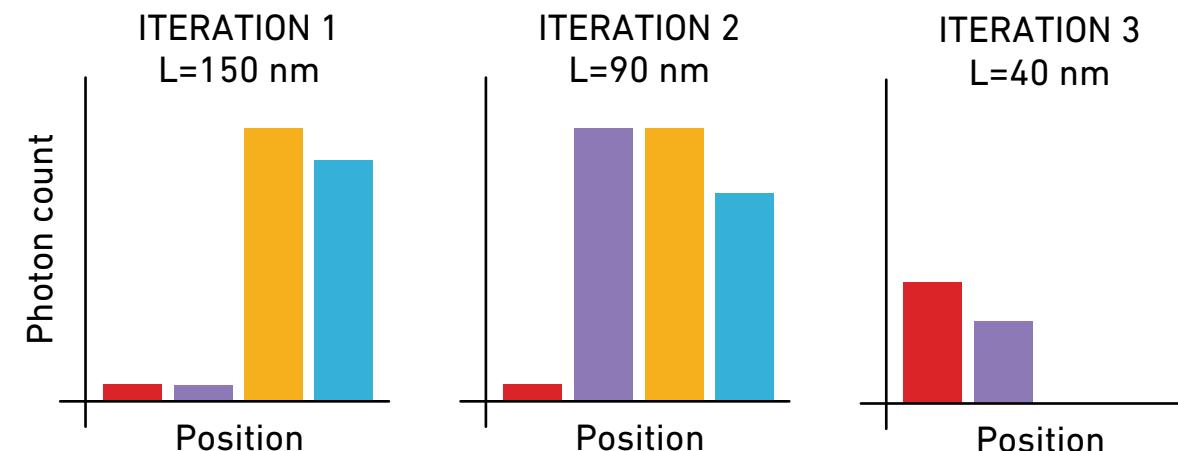
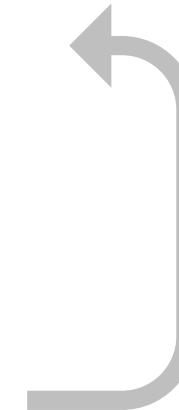
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

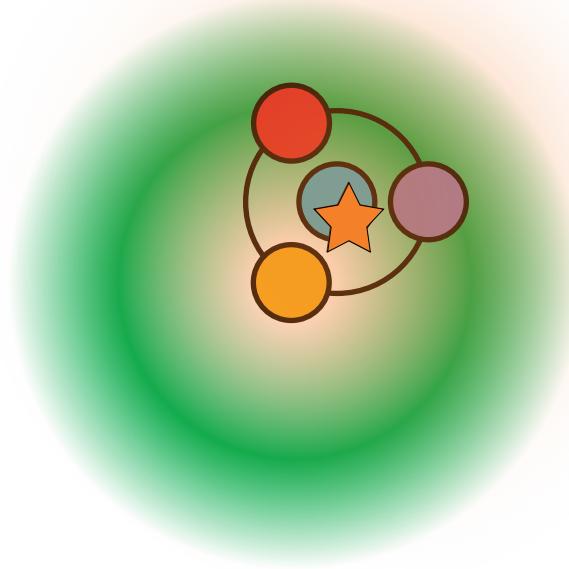
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

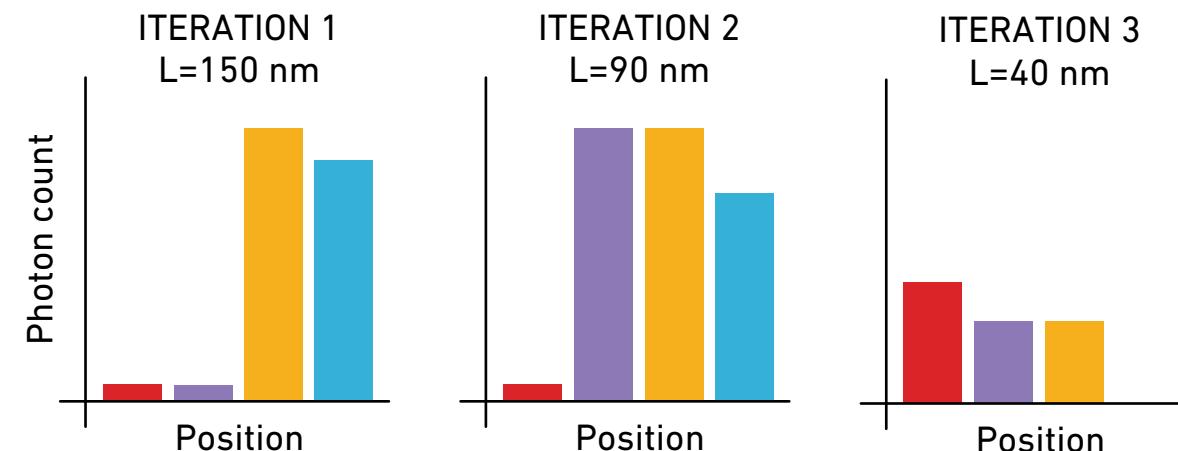
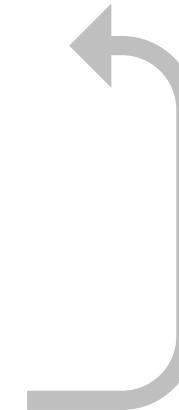
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

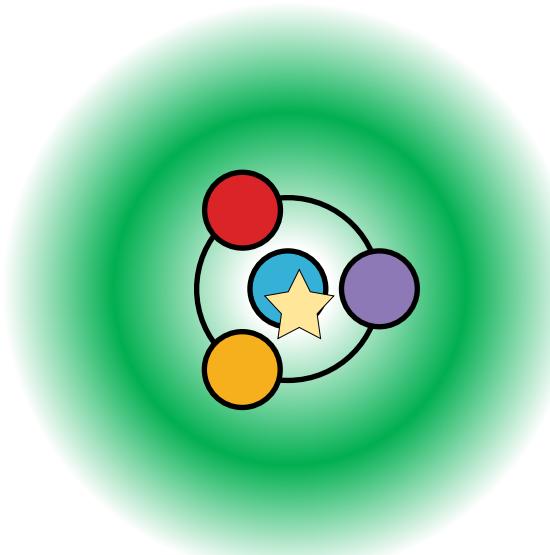
MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

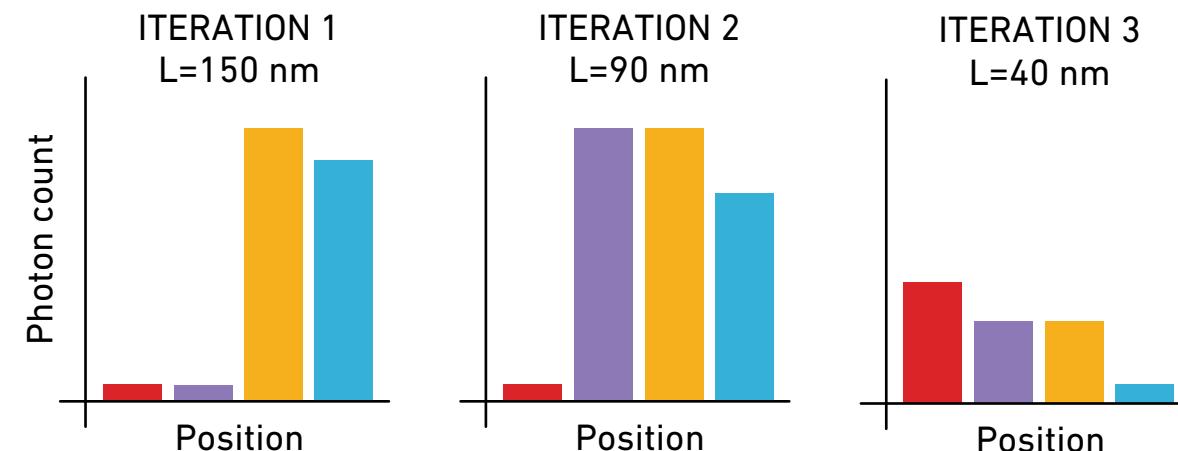
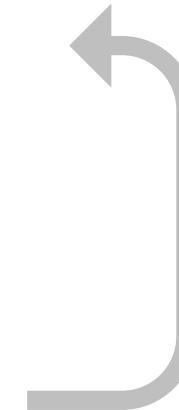
Localization: an iterative approach



Estimate fluorophore position with spot-shaped beam

MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

Localization: an iterative approach

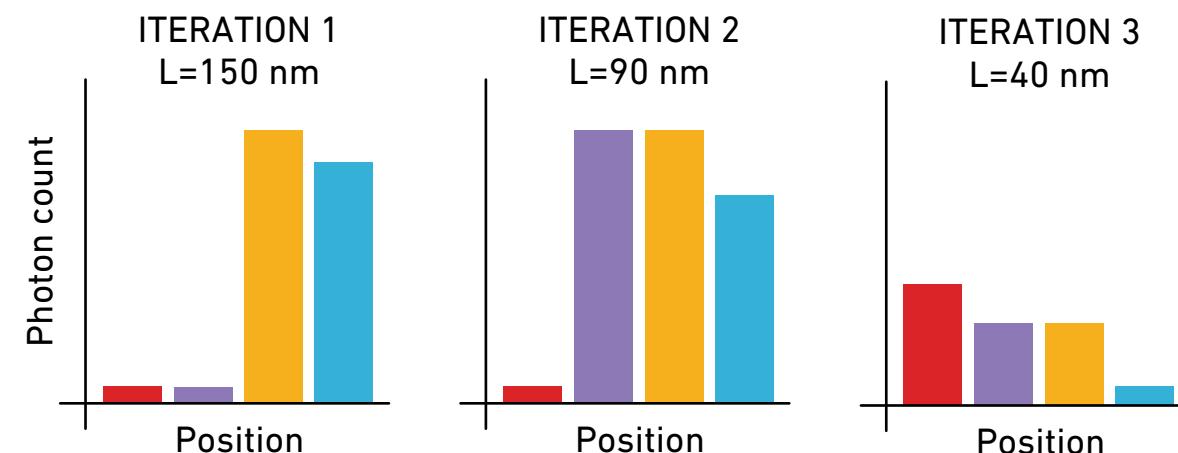


FLUOROPHORE LOCALIZATION

Estimate fluorophore position with spot-shaped beam

MINFLUX iteration:

1. Define scanning region according to previous estimation
2. Register emitted photons from every position in the pattern
3. Analyse photon counts and refine fluorophore position estimation
4. Decrease “L”



Expert-driven projects :: pyMINFLUX

Operation modalities

Localization



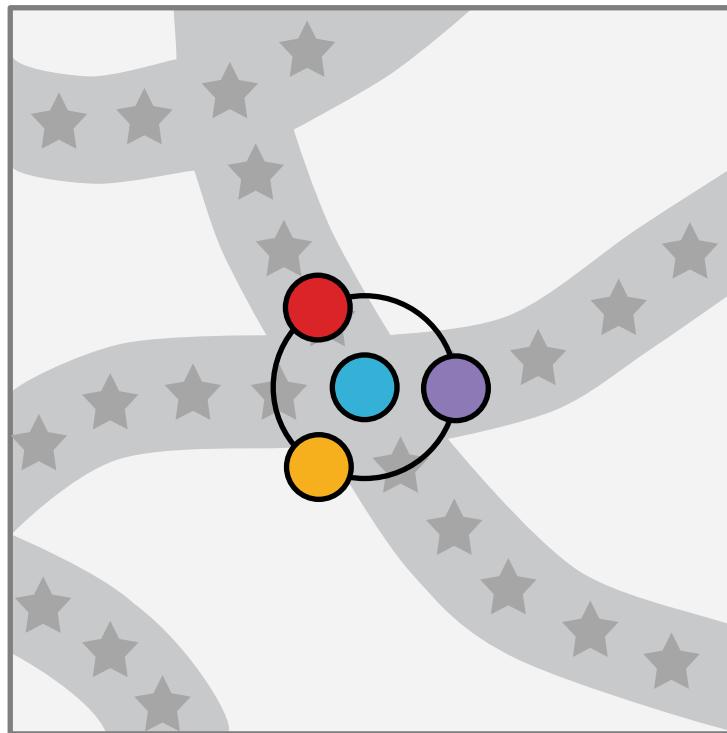
Important: only very few fluorophores must be emitting at any given time!

1. Fluorophores are localized 1 by 1

Expert-driven projects :: pyMINFLUX

Operation modalities

Localization

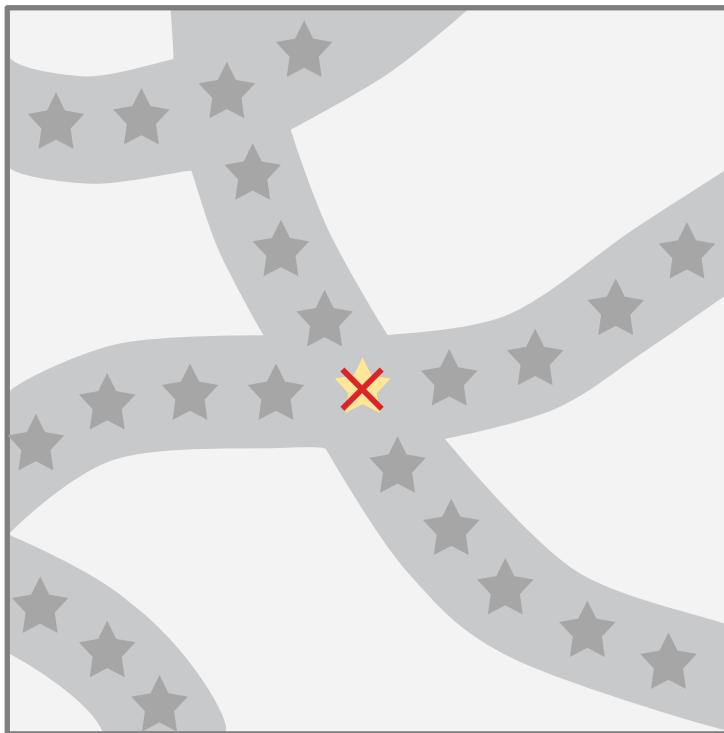


1. Fluorophores are localized 1 by 1

Expert-driven projects :: pyMINFLUX

Operation modalities

Localization

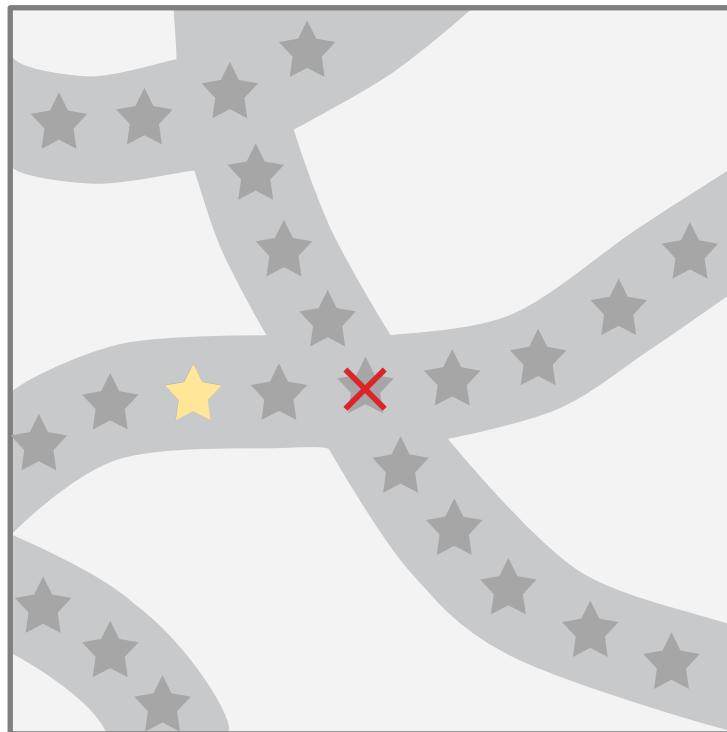


1. Fluorophores are localized 1 by 1

Expert-driven projects :: pyMINFLUX

Operation modalities

Localization

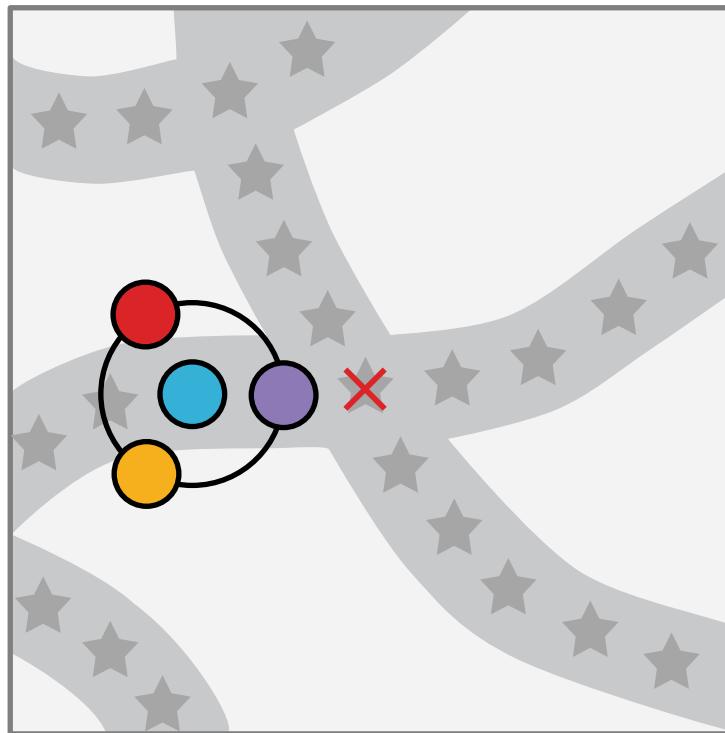


1. Fluorophores are localized 1 by 1

Expert-driven projects :: pyMINFLUX

Operation modalities

Localization

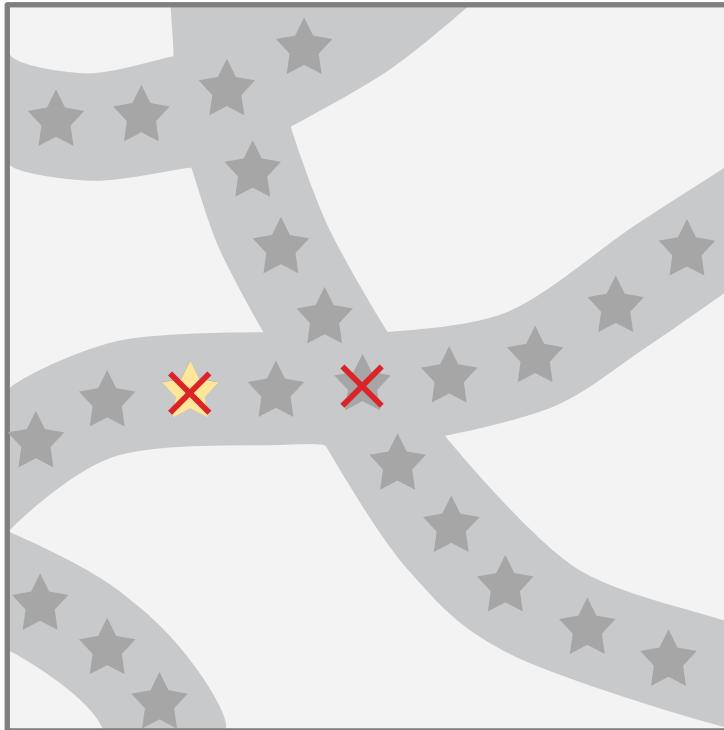


1. Fluorophores are localized 1 by 1

Expert-driven projects :: pyMINFLUX

Operation modalities

Localization

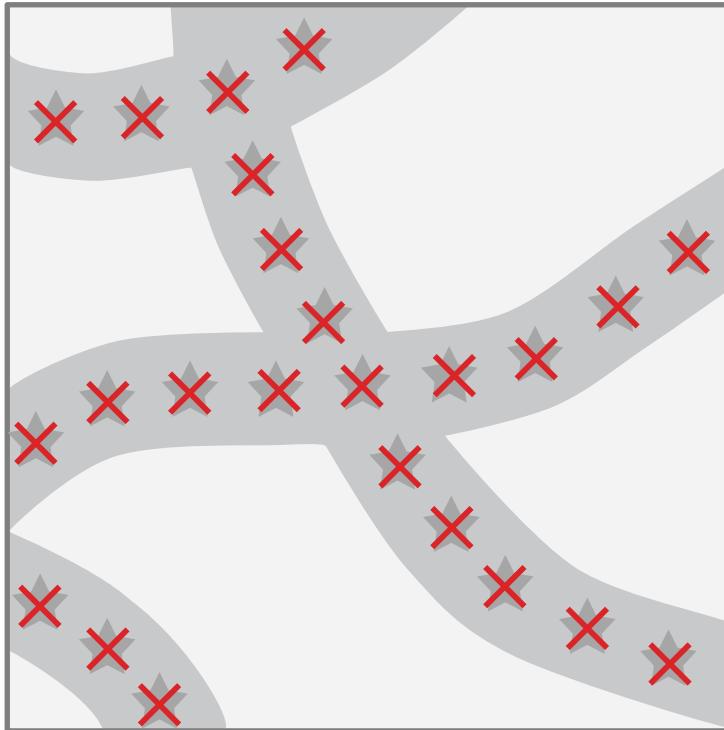


1. Fluorophores are localized 1 by 1

Expert-driven projects :: pyMINFLUX

Operation modalities

Localization

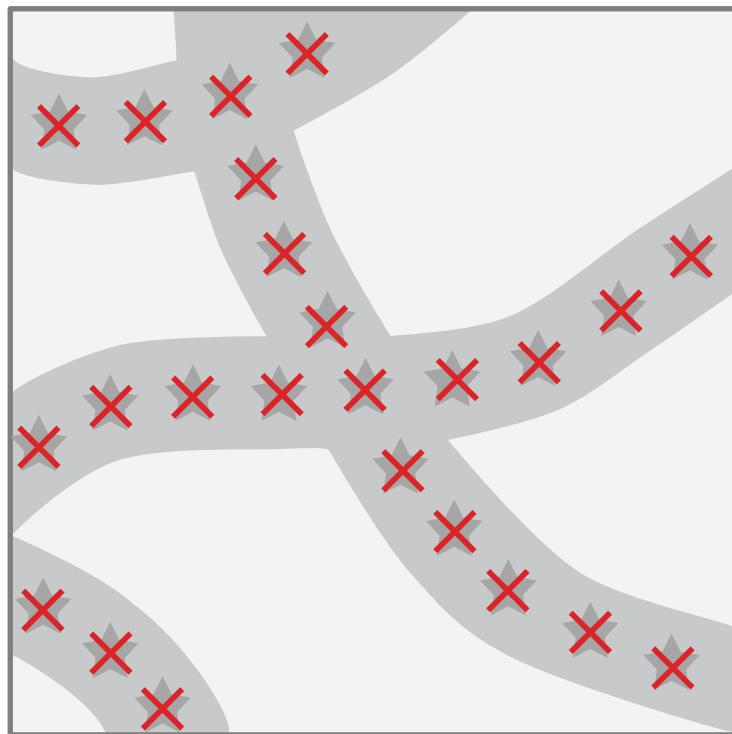


1. Fluorophores are localized 1 by 1

Expert-driven projects :: pyMINFLUX

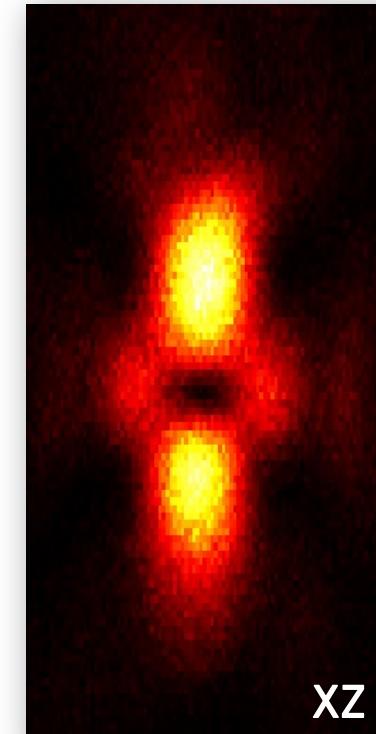
Operation modalities

Localization



3 nm - 2D

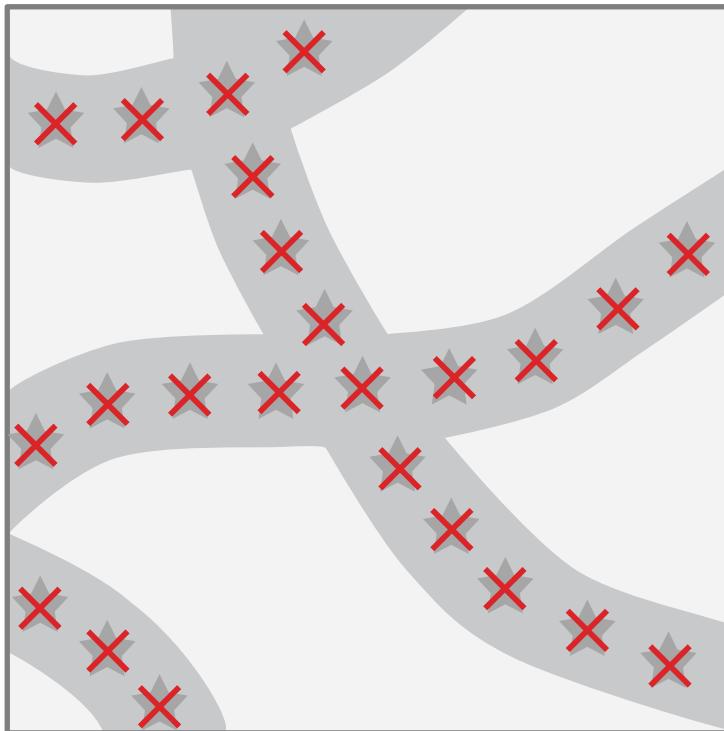
5 nm - 3D



Expert-driven projects :: pyMINFLUX

Operation modalities

Localization



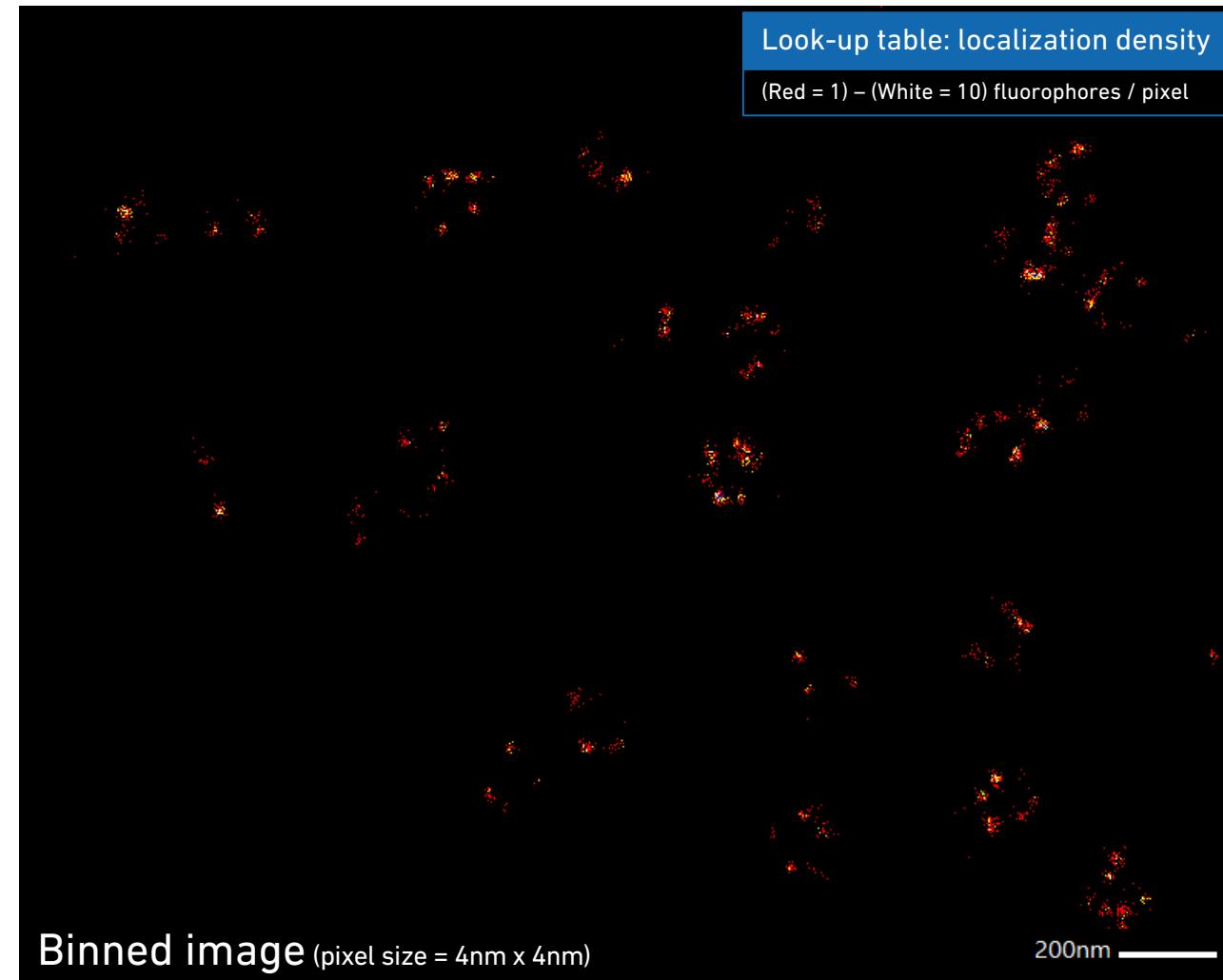
1. Fluorophores are localized 1 by 1
2. Coordinates turned into an image

Expert-driven projects :: pyMINFLUX

At this stage, we hadn't bought the microscope yet...

- What we had:
- No localization data
 - Low-res raster images

Testing phase



Expert-driven projects :: pyMINFLUX

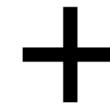
Now, we bought the microscope



iMSPECTOR

Acquisition
Data export
Developed for STED
Pixel-based
MINFLUX data visualization requires “binning”
Licensed
Viewer version available
Windows-only

Production



Paraview

3D rendering software
Built-in Inspector bridge
Tools + Plugins
Open-source
Cross-platform

Missing features

Click-and-inspect
Localization precision
Fluorophore unmixing
Filtering options
Metrics comparison

Not facility-friendly

Fully open raw data format
NumPy, MATLAB or JSON

Documentation from Abberior



Expert-driven projects :: pyMINFLUX

<https://github.com/bsse-scf/pyMINFLUX>



pyMINFLUX



Tailored for MINFLUX data

Open-access and cross-platform
GUI-Independent API

Visualization, filtering and analysis tools

Selection tool

Data viewer

Customizable scatter plot

2-Color MINFLUX unmixing

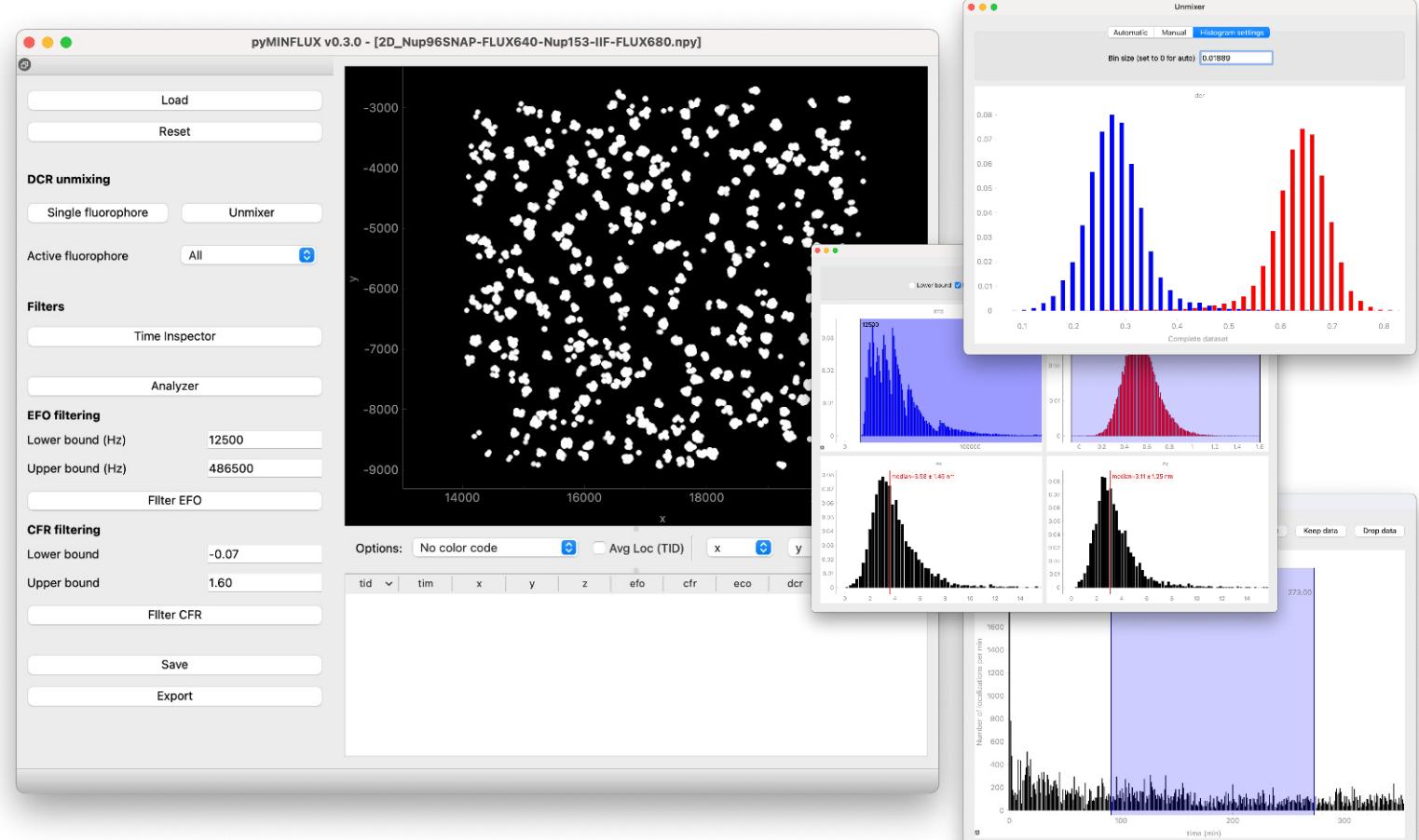
Localization precision calculation

Manual and automatic filtering

Fourier-ring correlation analysis

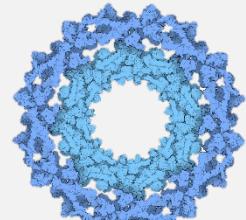
Integration with Paraview

Custom .pmx format (metadata, processing parameters, ...)

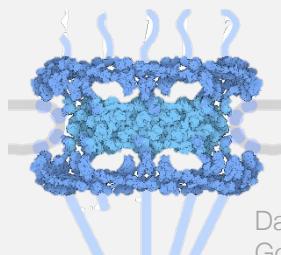


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



David
Goodsell

Side view

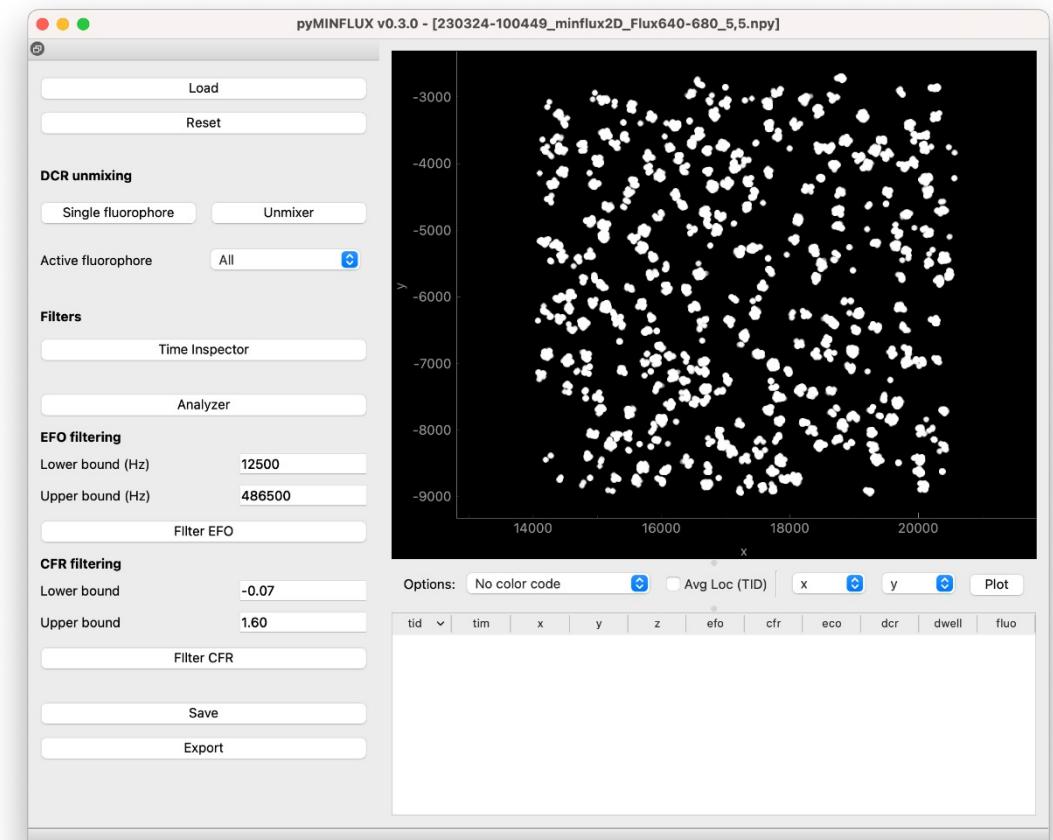
U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

pyMINFLUX workflow

Raw data import

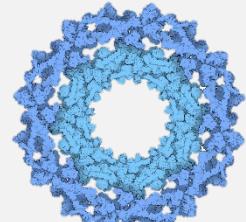


Manual inspection

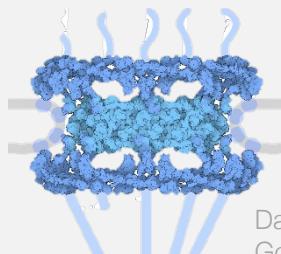


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



David
Goodsell

Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

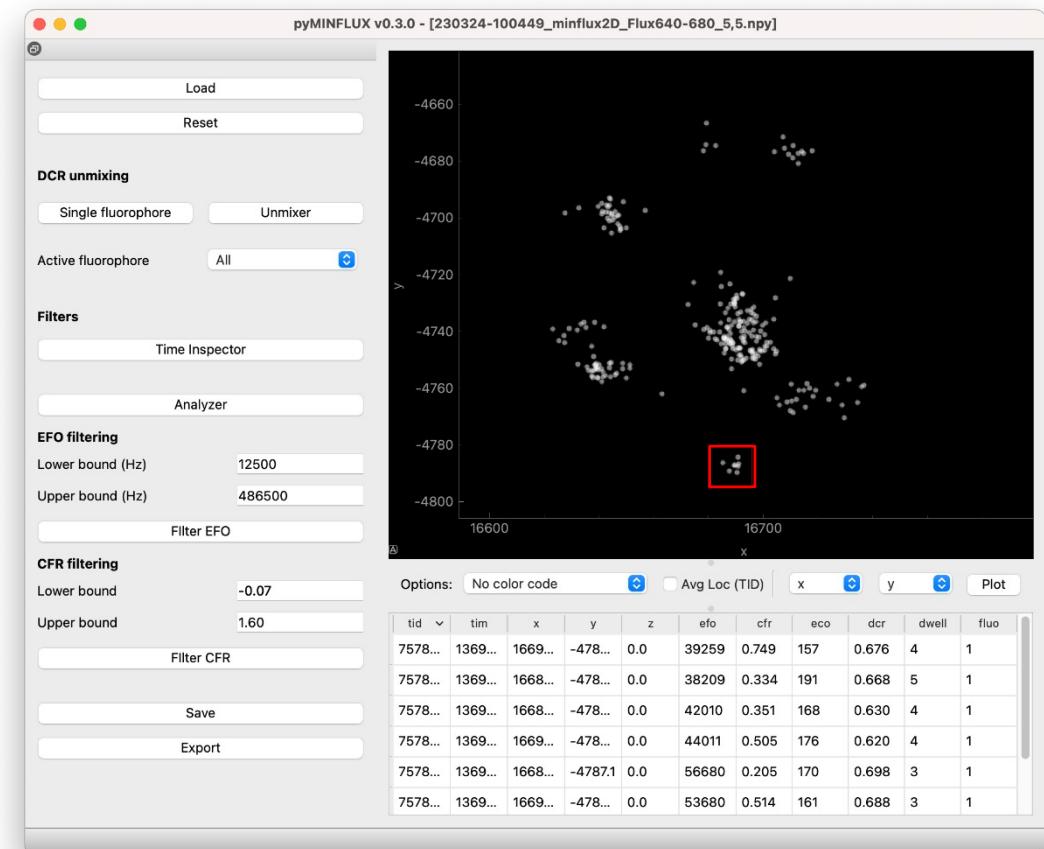
pyMINFLUX workflow

Raw data import



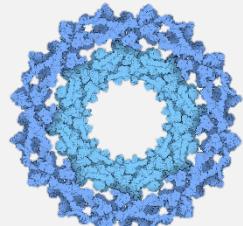
Manual inspection

Dataset navigation

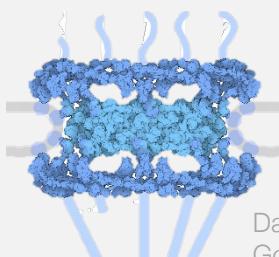


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



David
Goodsell

Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

pyMINFLUX workflow

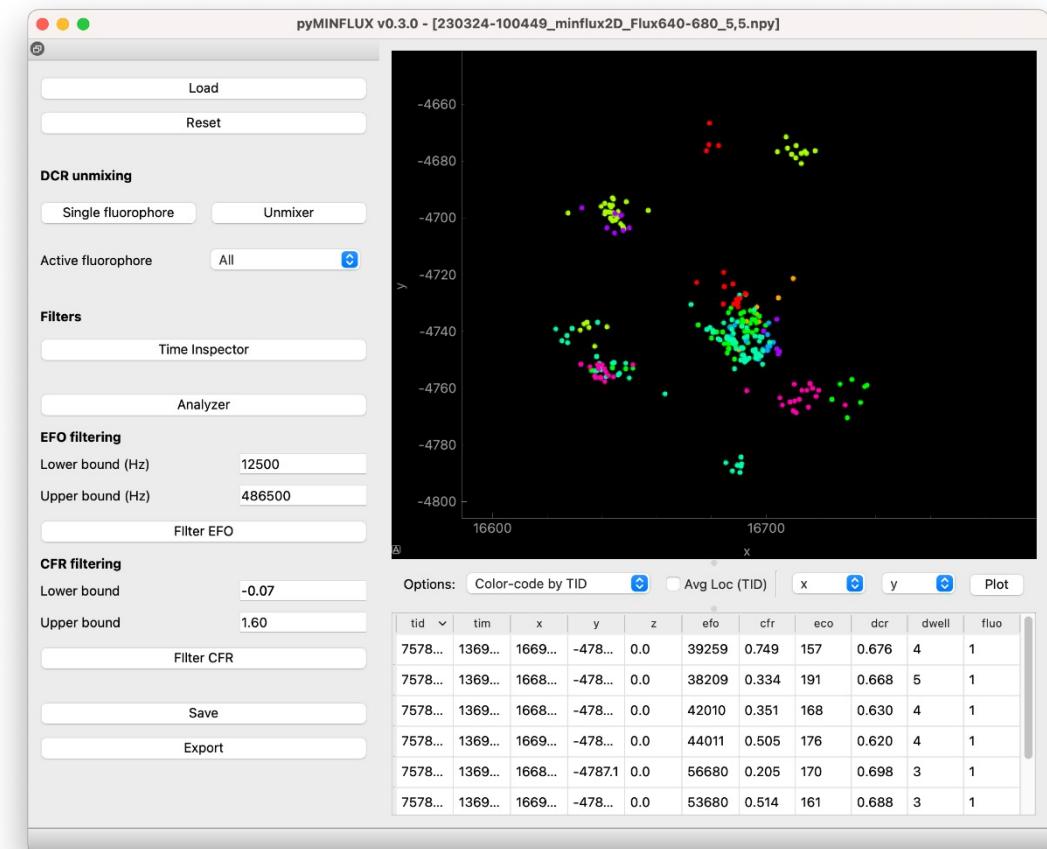
Raw data import



Manual inspection

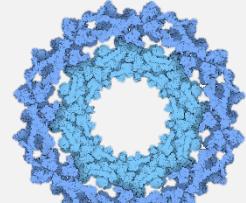
Dataset navigation

Trace coloring

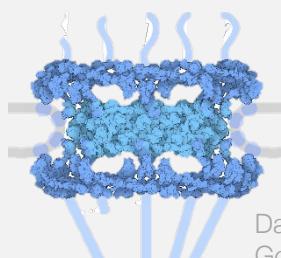


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



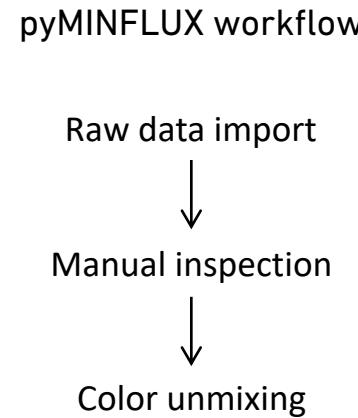
Top view



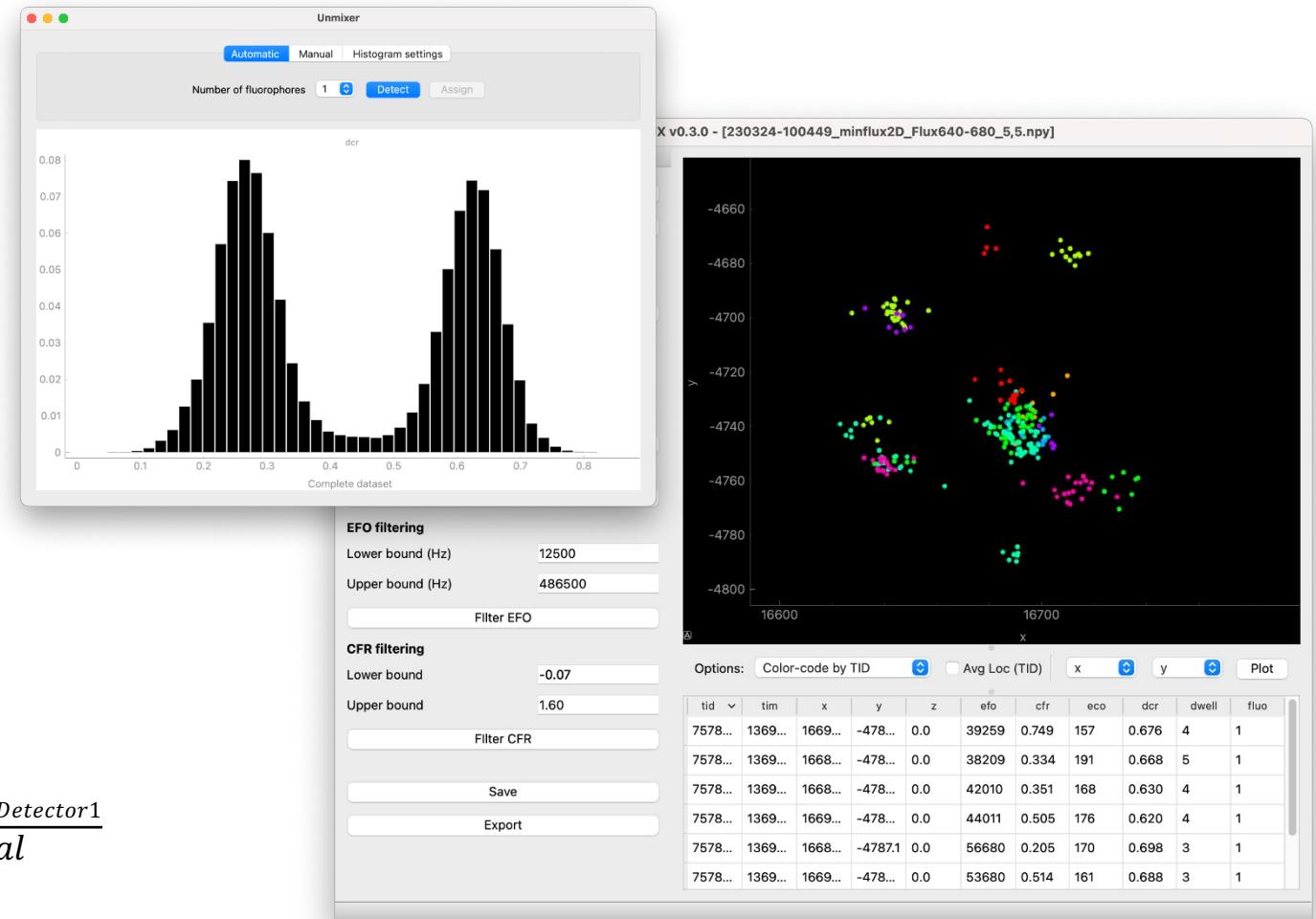
David
Goodsell

Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

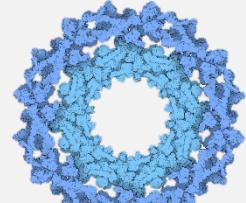


$$dcr = \frac{\text{Photons}_{\text{Detector}1}}{\text{Total}}$$

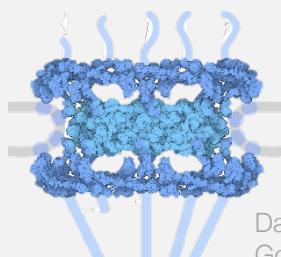


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

pyMINFLUX workflow

Raw data import



Manual inspection

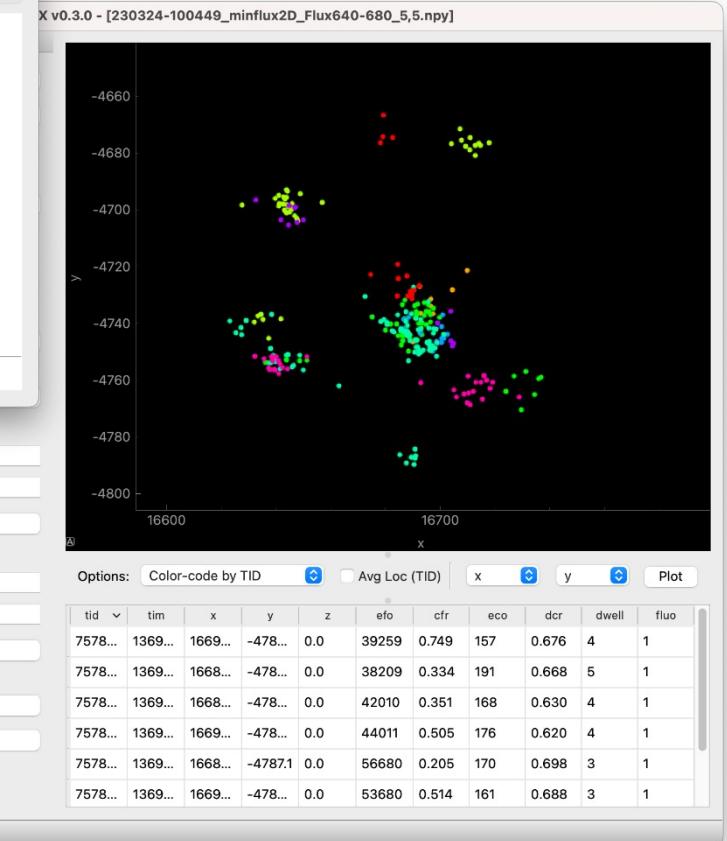


Color unmixing

Automatic filtering

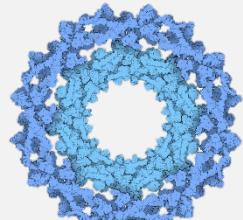
Gaussian mixture model

$$dcr = \frac{\text{Photons}_{\text{Detector}1}}{\text{Total}}$$

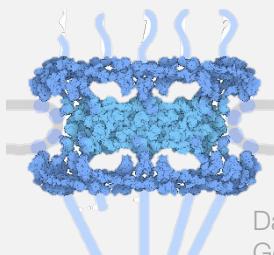


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



David
Goodsell

Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

pyMINFLUX workflow

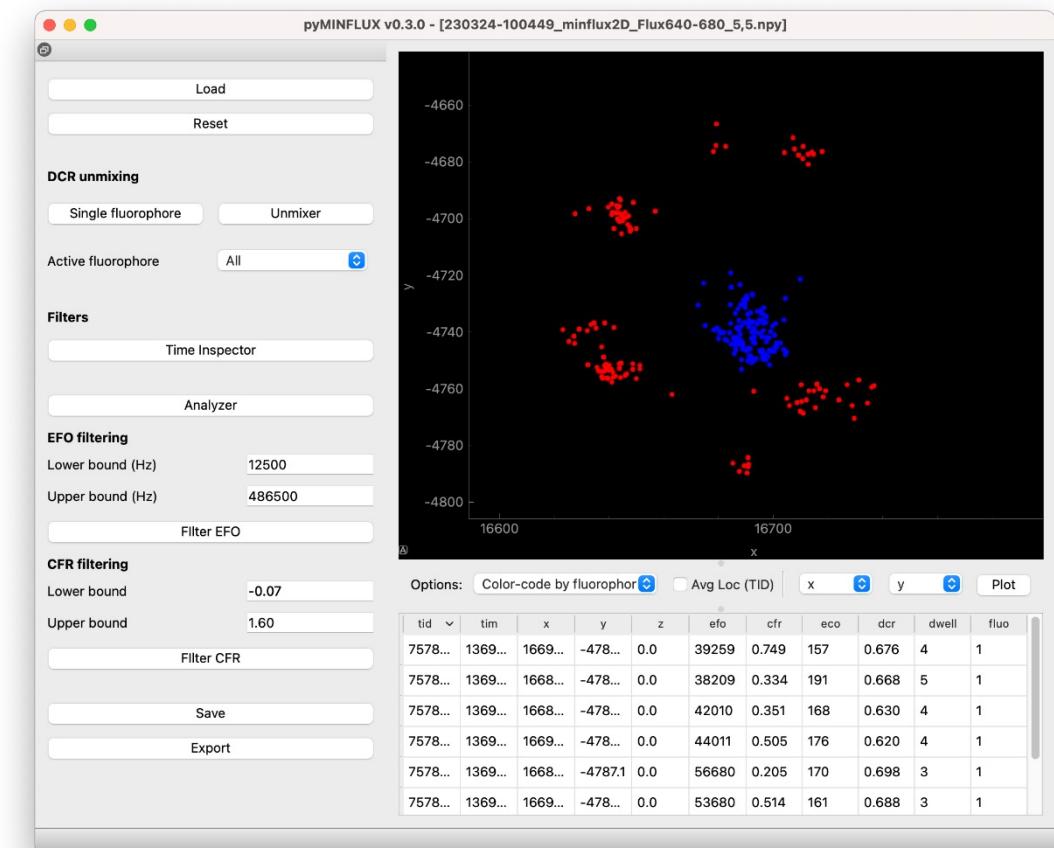
Raw data import



Manual inspection

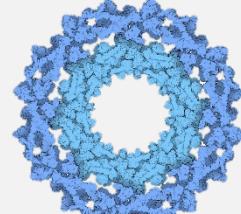


Color unmixing

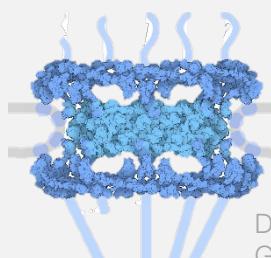


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



David
Goodsell

Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

pyMINFLUX workflow

Raw data import



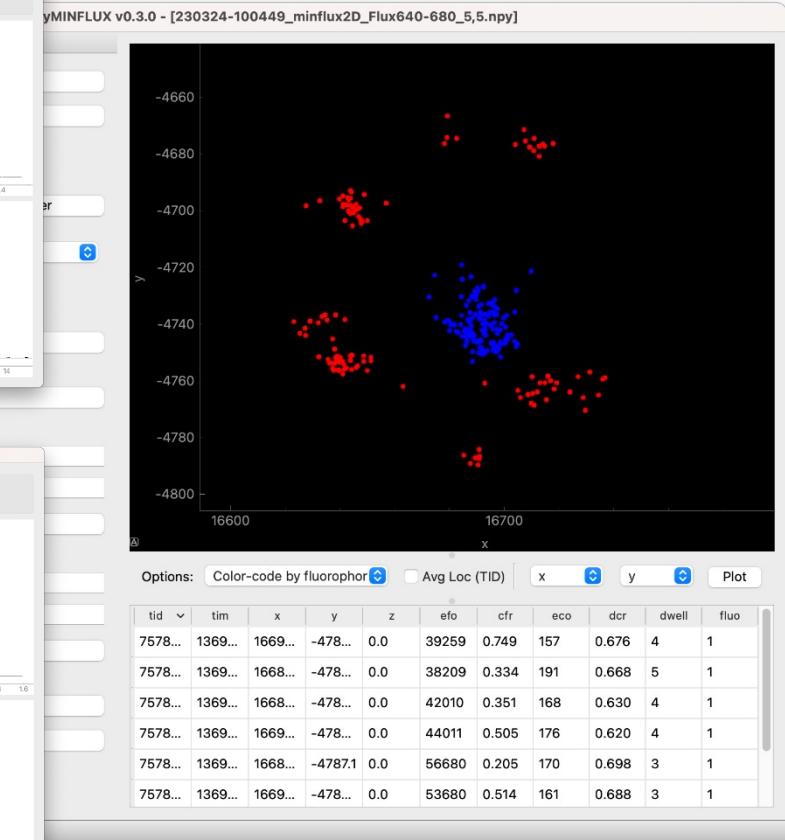
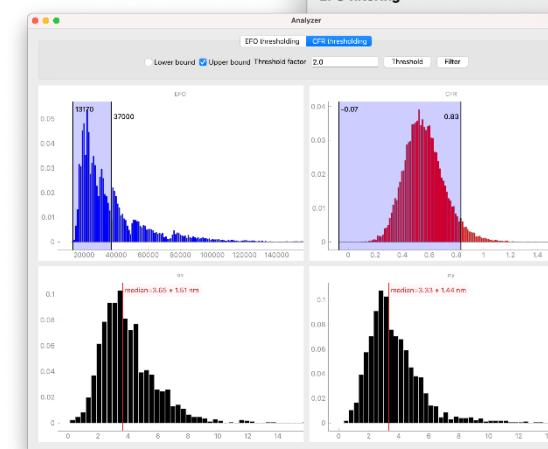
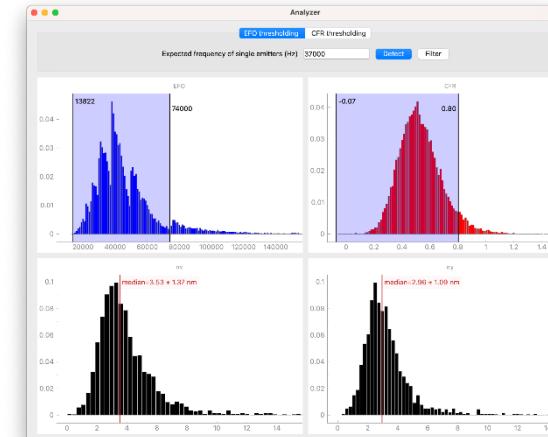
Manual inspection



Color unmixing

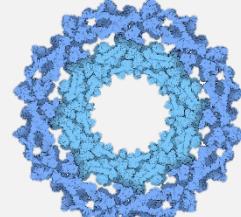


Per-fluorophore filtering

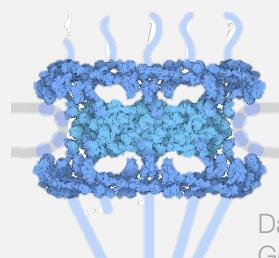


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



David
Goodsell

Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

pyMINFLUX workflow

Raw data import



Manual inspection



Color unmixing

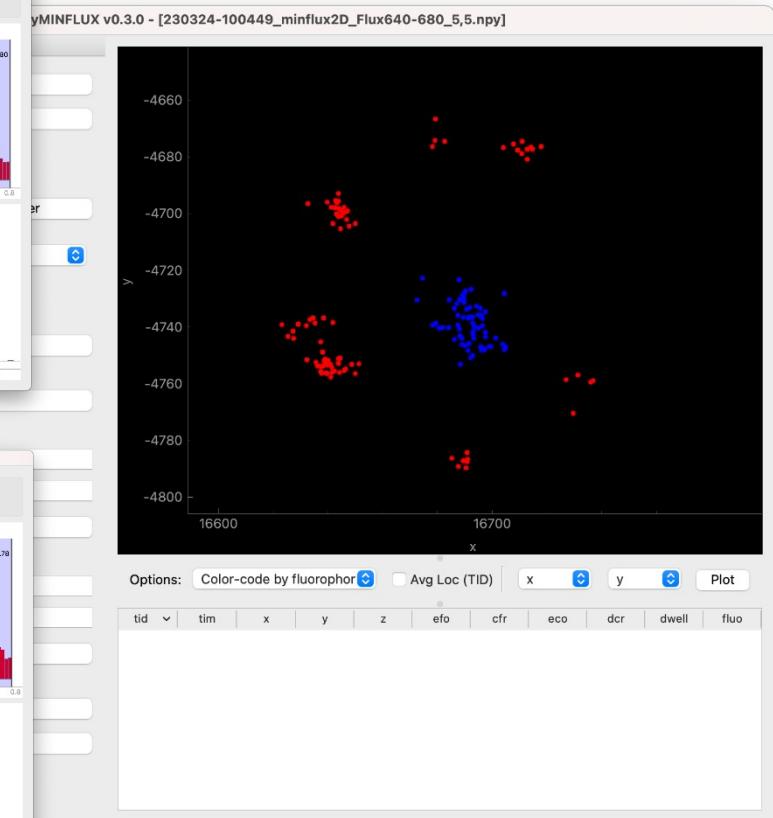
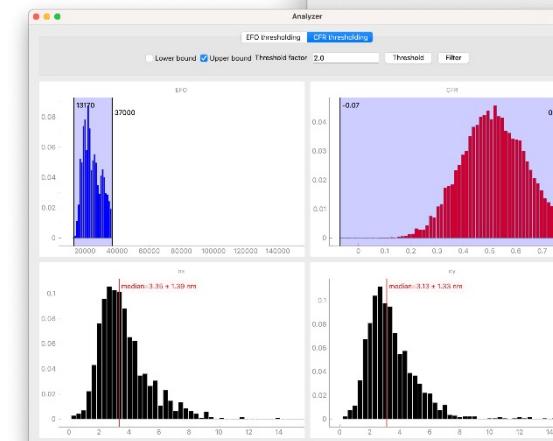
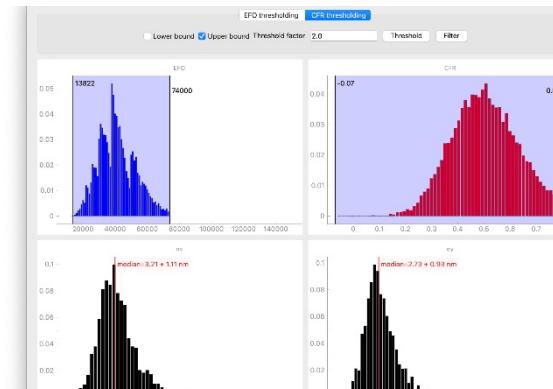


Per-fluorophore filtering

Emission frequency

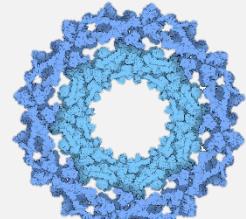
Recentering
estimator

Localization
precision

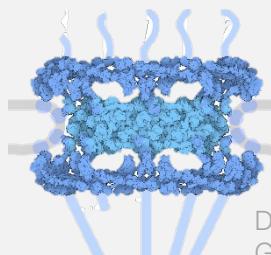


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex

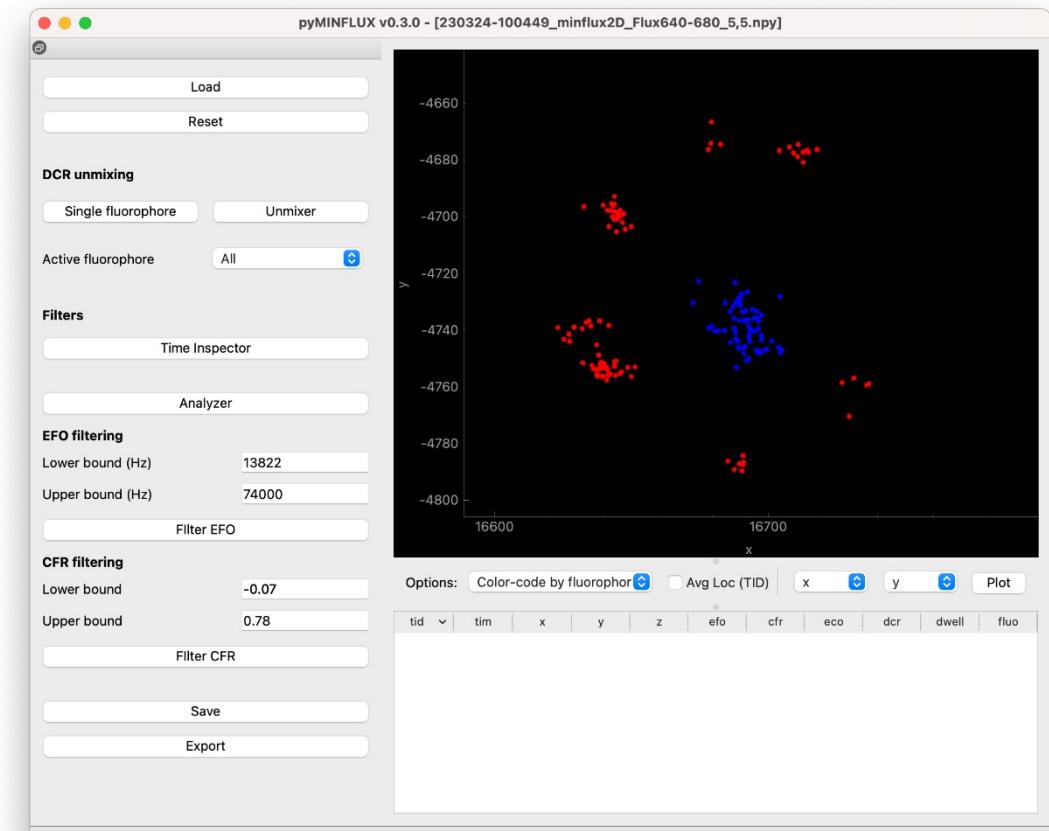
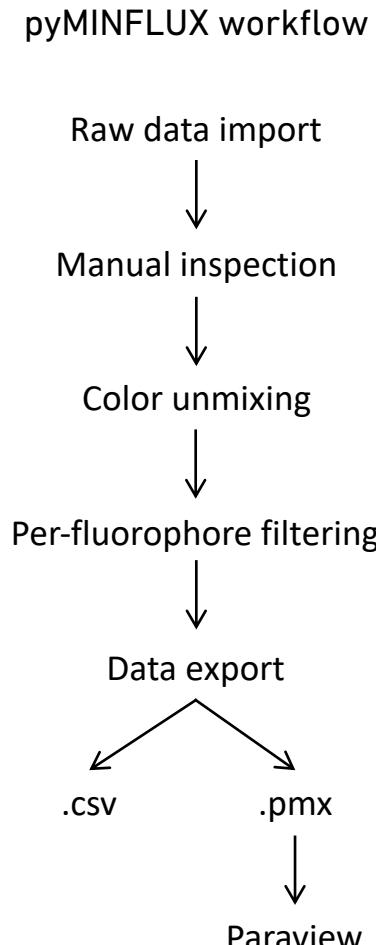


Top view



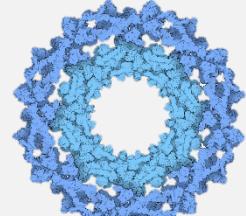
David
Goodsell

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

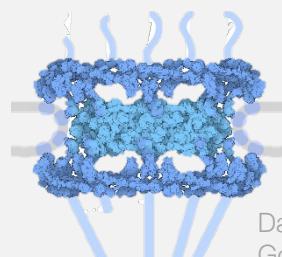


Expert-driven projects :: pyMINFLUX

QC sample
Nuclear pore complex



Top view



Side view

U2OS Nup96-SNAP cells
BG-Abberior Flux 640
Ms-Nup153 + 2^{ary} Flux 680
GLOX-MEA (10-15 mM)

pyMINFLUX workflow

Raw data import



Manual inspection



Color unmixing



Per-fluorophore filtering



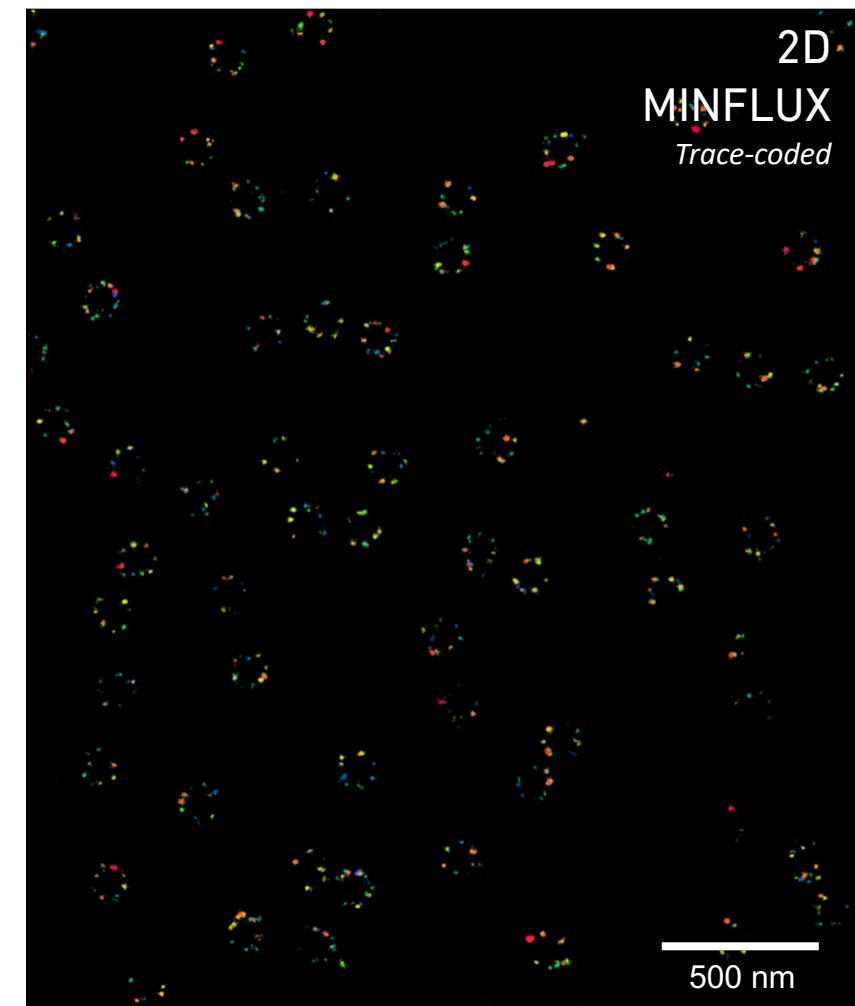
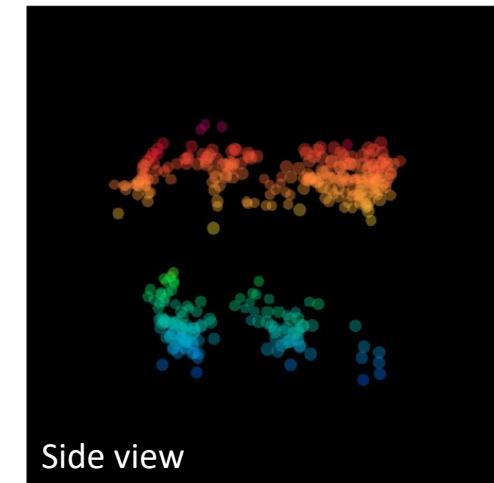
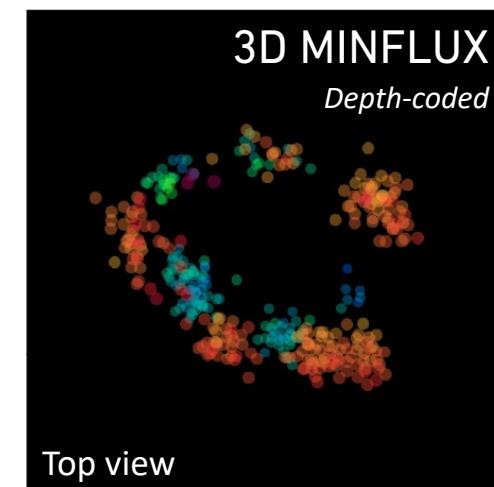
Data export

.csv

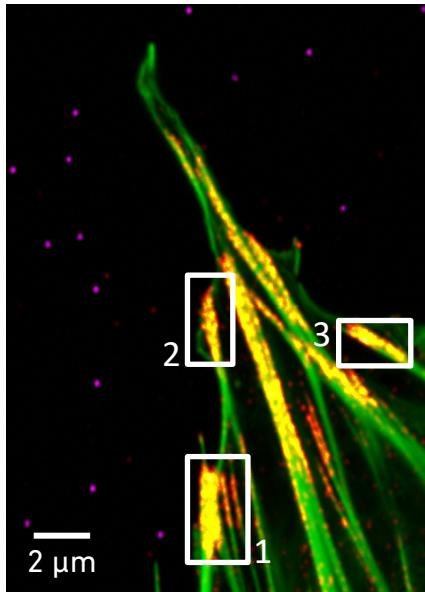
.pmx



Paraview



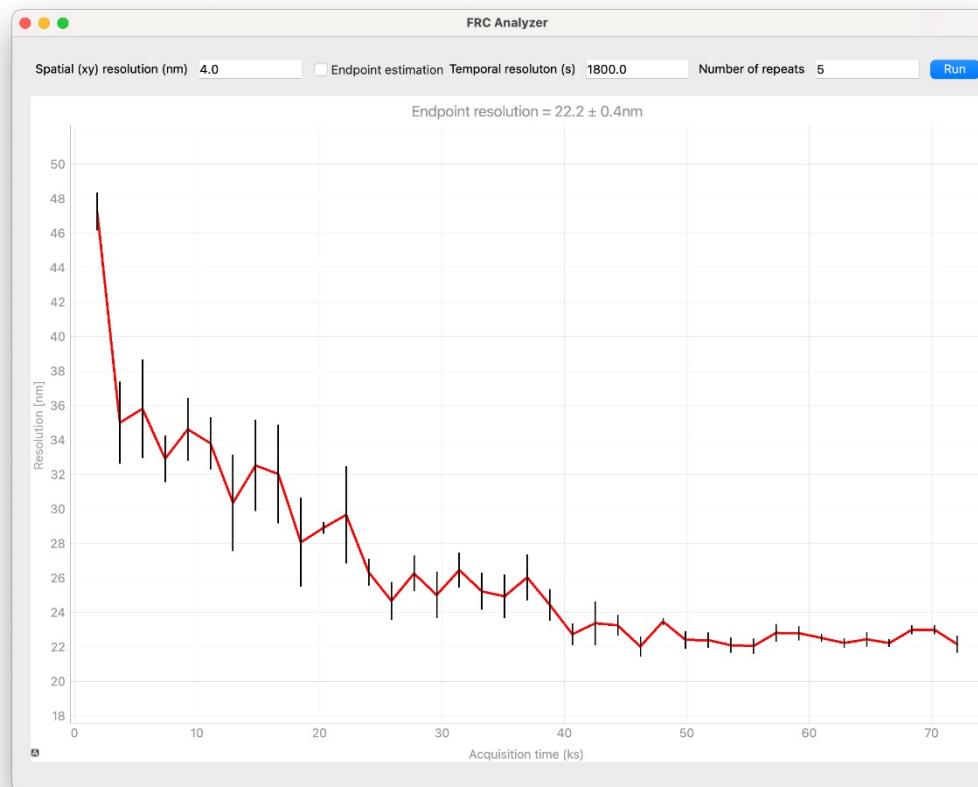
Expert-driven projects :: pyMINFLUX



MEFs
Phalloidin-AF488
Rat-Integrin + 2^{ary} AF568
Gold nanoparticles

Rb anti Paxillin
sdAb DNA-PAINT Atto 655

Fourier-ring correlation analysis ("endpoint indicator")



Nico Strohmeyer, D-BSSE

Expert-driven projects :: pyMINFLUX

Expert contributions

Javier Casares Arias: MINFLUX specialist, designed a lot of controlled experiments to test filtering and analysis strategies

Aaron Ponti: development of pyMINFLUX

Users

- D-BSSE, Daniel Mueller Group (Michele Nava, Nico Strohmeyer, Matilde Lucioli, Krishna Kasuba)
- D-BSSE, Timm Schroeder Group (Germán Camargo)
- University of Basel, Thomas Ward Group (Michaela Slánská)
- University of Heidelberg (Charlotte Kaplan)

Summary

There are different classes of (image analysis) projects with different types of requirements and target audiences:

- **User-specific projects** usually have a small scope and are solved in a tight feedback loop with the end user.
- **General-purpose projects** target large audiences with less specific sets of functionality and often require larger development teams and better software engineering practices.
- **Expert-driven projects** require tight collaboration between experts with different sets of field knowledge with the goal of creating tools that appeal to reasonably large but niche audiences.

Acknowledgments



Thomas Horn (head of SCF and LAF)

Microscopy

Erica Montani

Javier Casares Arias

Tom Lummen

Lab Automation

Sant Kumar

Daniel Gerngross

Flow Cytometry

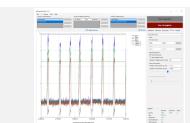
Mariangela Di Tacchio

Aleksandra Gumienny

Chiara Cavallini

SpectraSorter

Todd Duncombe, D-BSSE



pyPOCQuant

Fabian Rudolf, D-BSSE and BAG

Andreas Cuny, D-BSSE



pyMINFLUX

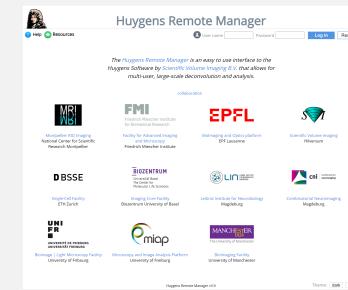
Javier Casares Arias, D-BSSE



User-specific project

Gabriel Senn, D-BSSE

HRM



Volker Bäcker, Montpellier Rio Imaging

Daniel Sevilla, Scientific Volume Imaging

Niko Ehrenfeuchter, Biozentrum

Torsten Stöter, Leibniz Institute for Neurobiology

Felix Meyenhofer, University of Fribourg

Olivier Burri, EPFL

Egor Zindy University of Manchester.

Asheesh Gulati EPFL

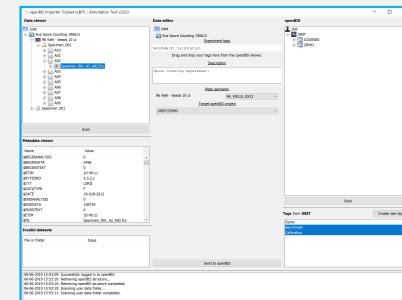
Alessandra Griffa, EPFL

José Viña, Scientific Volume Imaging

Kevin Namink, Scientific Volume Imaging

Frederik Grüll Biozentrum

oBIT



Bernd Rinn, SIS

Chandrasekhar Ramakrishnan, SIS

Juan Fuentes Serna, SIS

Franz-Josef Elmer, SIS

Caterina Barillari, SIS

Piotr Kupczyk, SIS

Antti Luomi, SIS

Jakub Straszewski, SIS

Manuel Kohler, SIS

Vernon Bailey, ITSC

John Ryan, ITSC

Vincenzo Spanò, ITSC

Martin Fox, ITSC

DBSSE

All the users!