



# Towards FAIR and scalable bioimage analysis workflows using OME-Zarr in Switzerland

Dr Virginie Uhlmann

|                                |                          |
|--------------------------------|--------------------------|
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# Towards FAIR and scalable bioimage analysis workflows using OME-Zarr in Switzerland Zürich

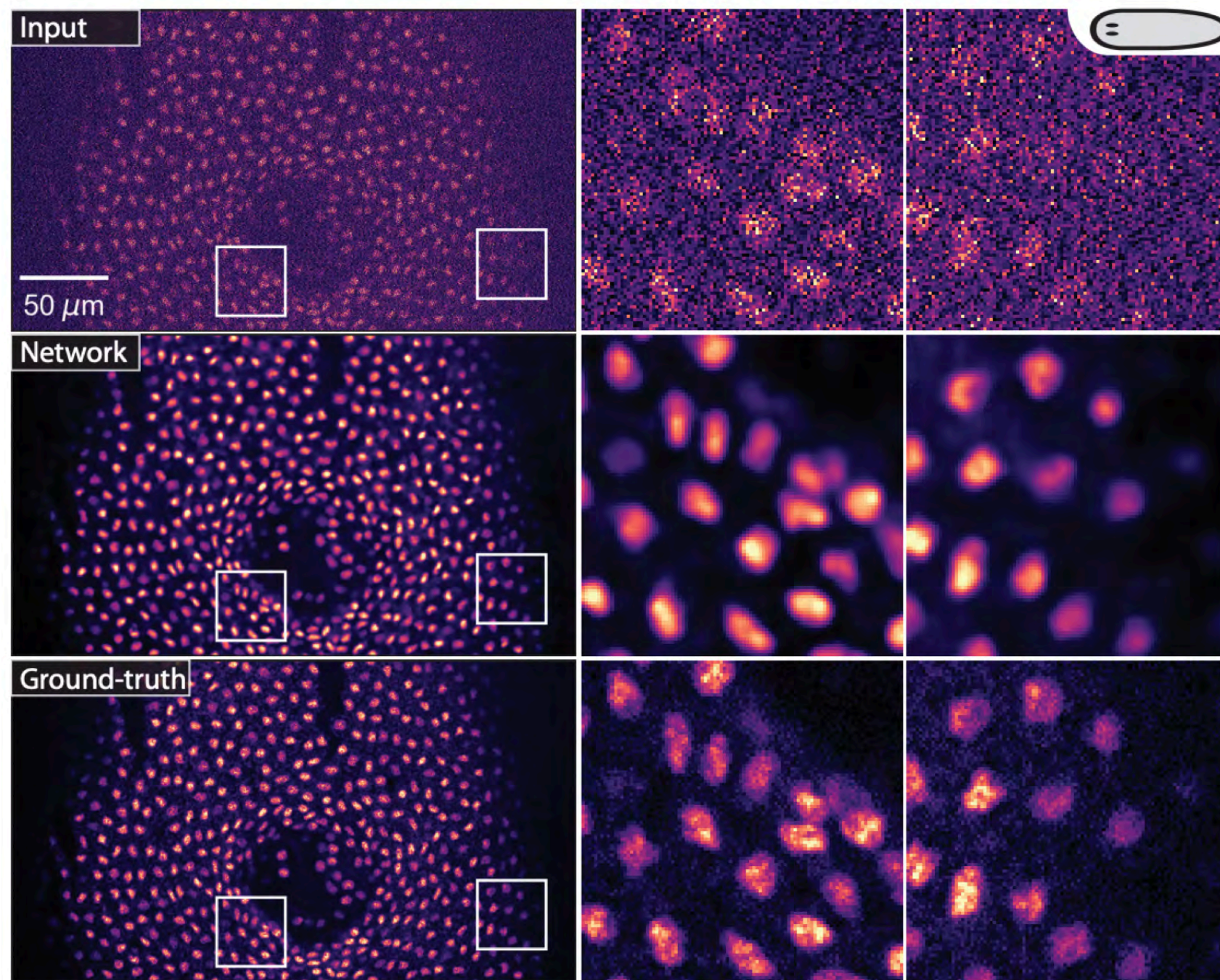
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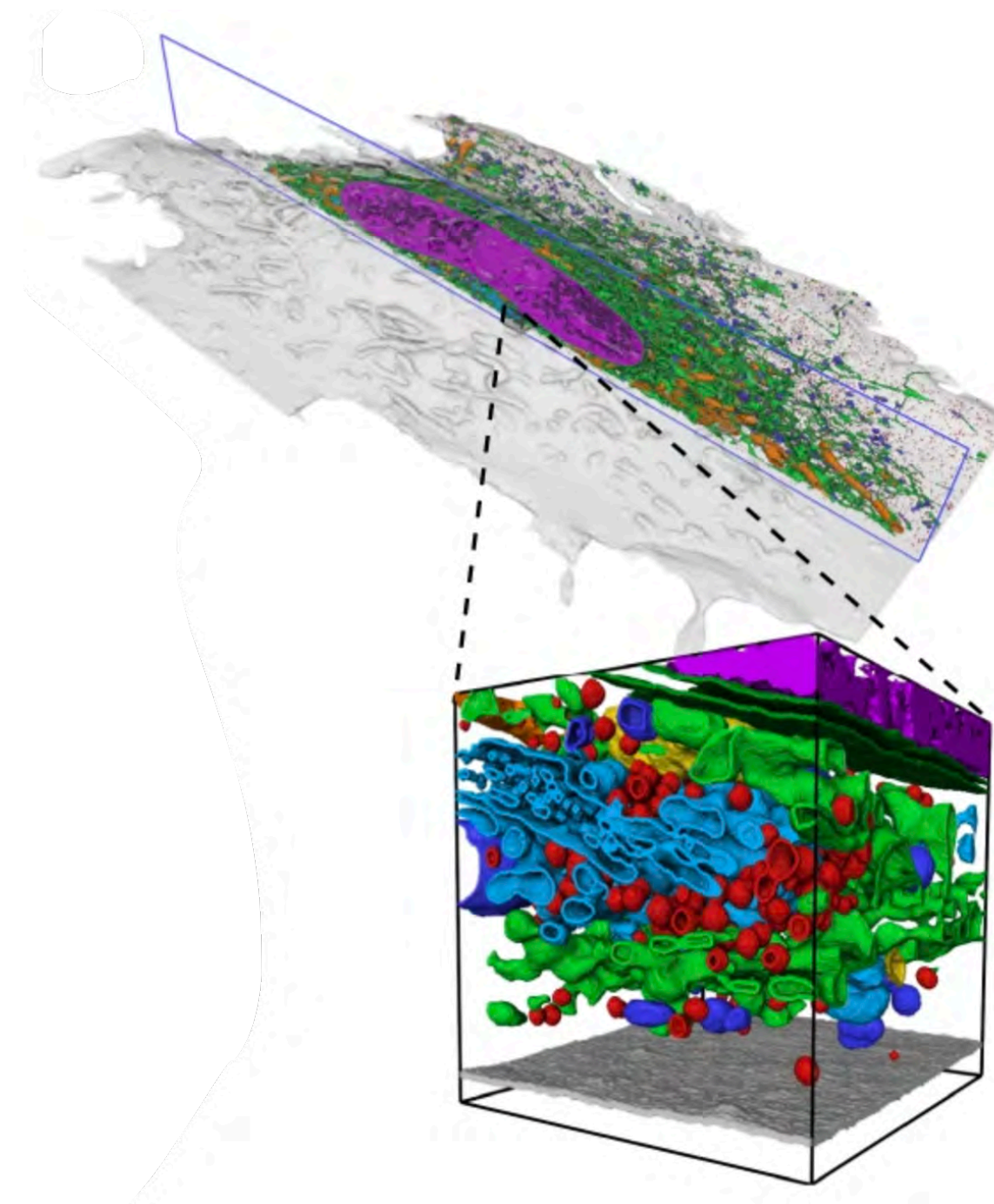
# Bioimage analysis in the machine learning era

## Image restoration



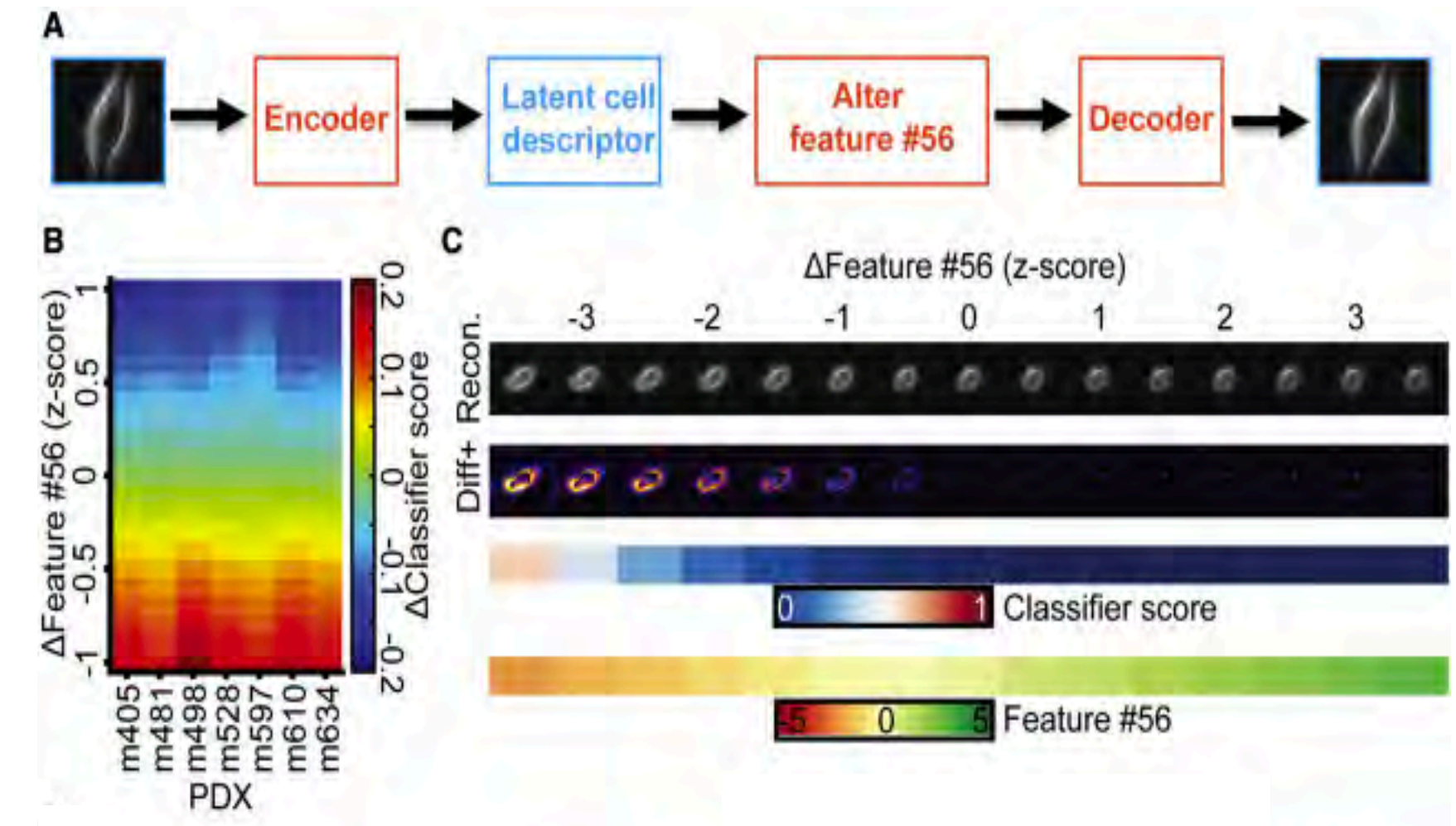
Weigert et al., Nat Methods, 2018

## Image partitioning



Heirich et al., Nature, 2021

## Image quantification



Zaritsky et al., Cell Syst, 2021



# Beyond analysis method development

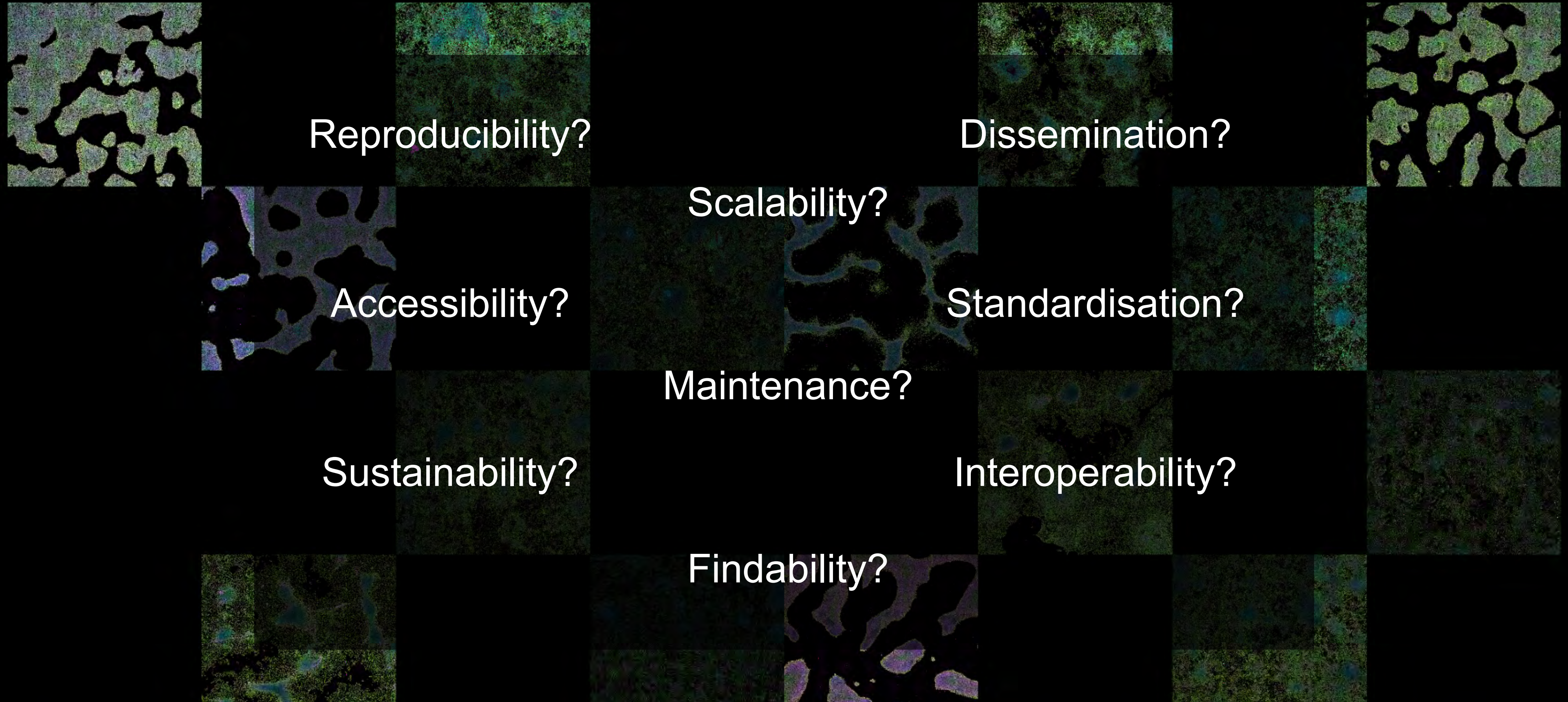


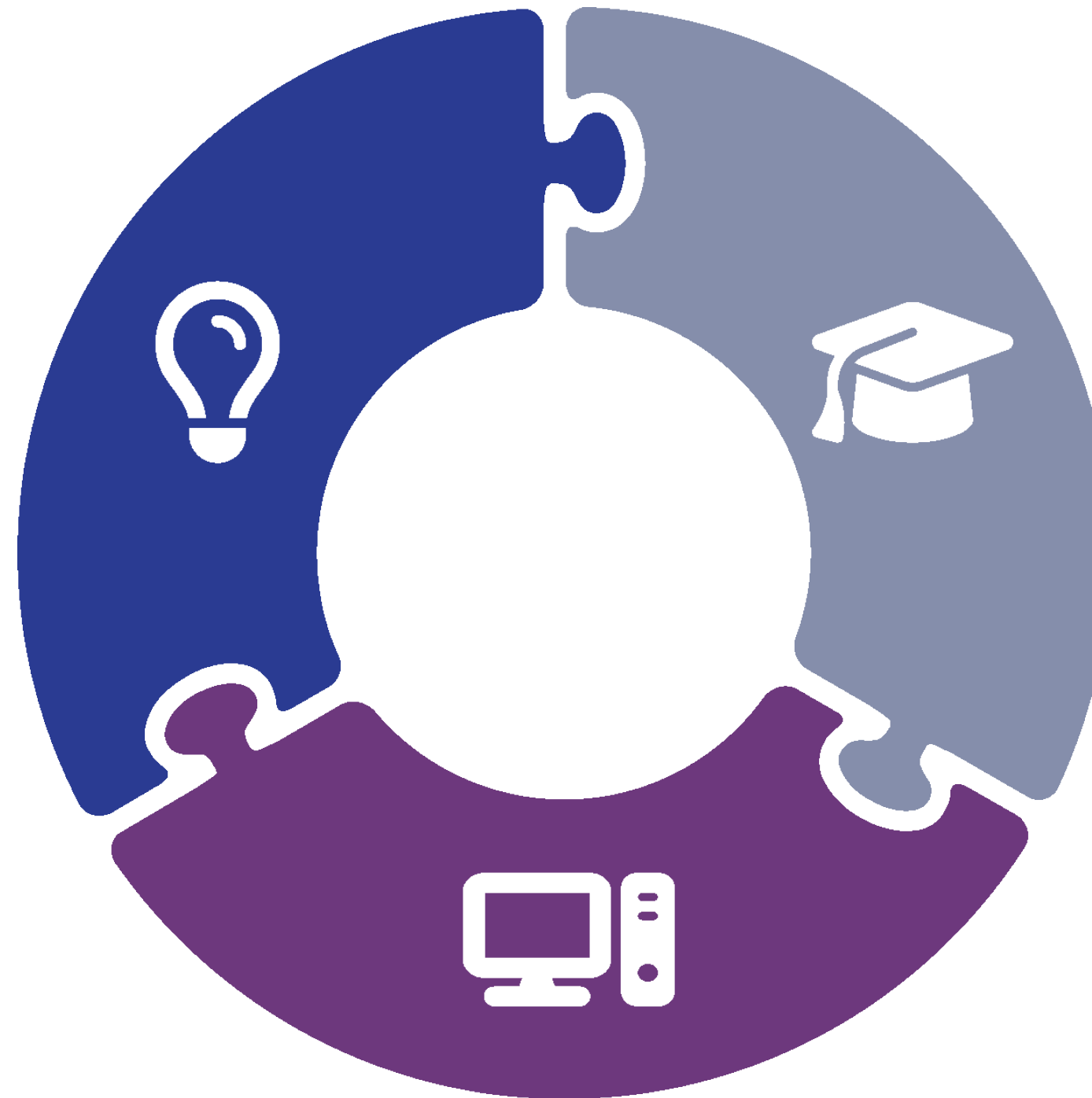
Image data courtesy of Joel Lüthi (UZH)



# The BioVisionCenter: Zürich's bioimage analysis hub

[www.biovisioncenter.uzh.ch](http://www.biovisioncenter.uzh.ch)

Make state-of-the-art  
bioimage analysis  
**at scale** accessible to all



Develop **FAIR standards**  
for bioimage analysis  
pipelines

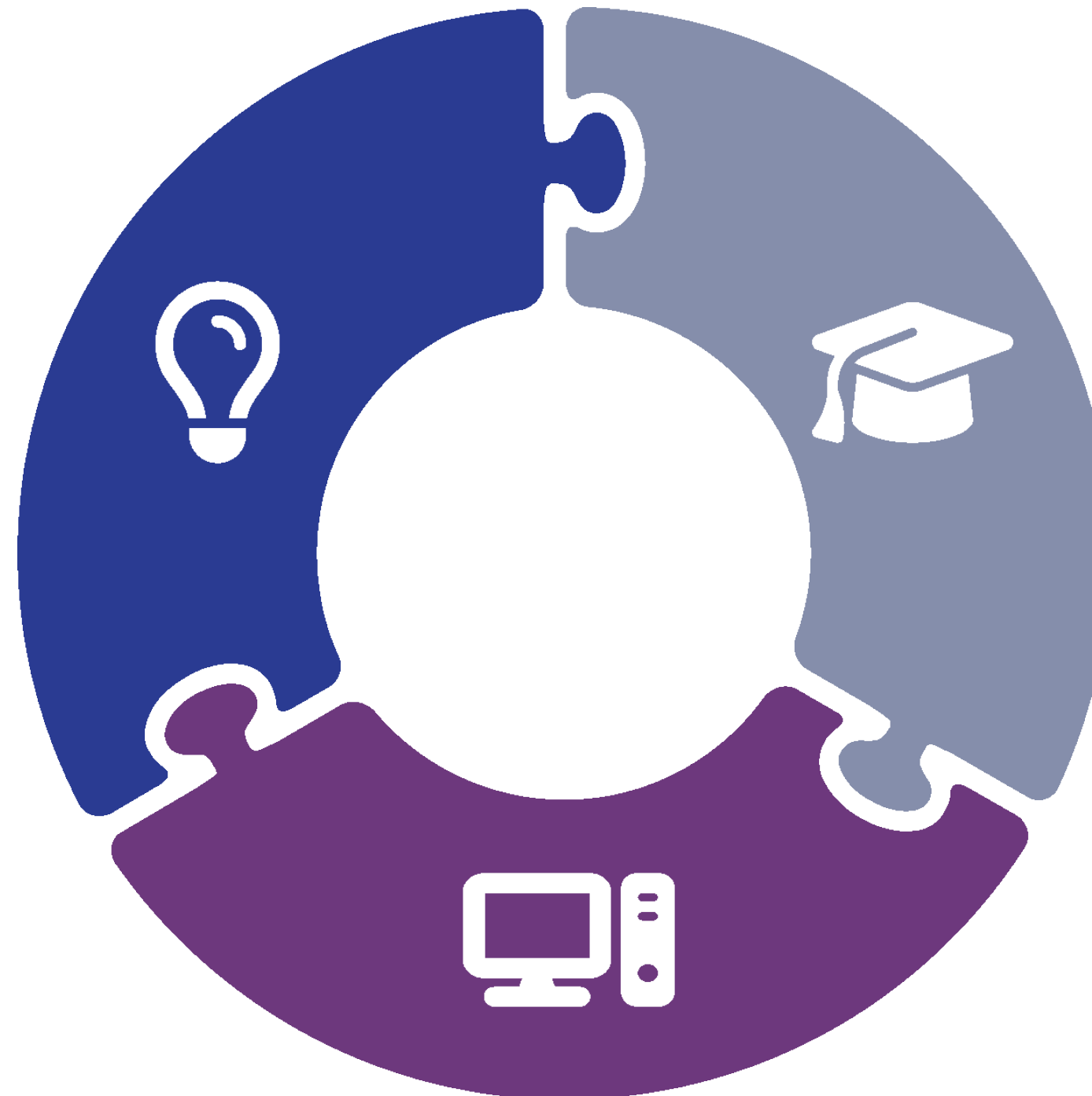
# The BioVisionCenter: Zürich's bioimage analysis hub

[www.biovisioncenter.uzh.ch](http://www.biovisioncenter.uzh.ch)

## BioVisionRIO

Research, Innovation, and Outreach

Open-source analysis platform  
incorporating state-of-the-art methods



## BioVisionEducation

Training

Bioimage analysis expertise for  
scientists at all career stages

## BioVisionServices

Service provision

Platform deployment and user support



# The BioVisionCenter: Zürich's bioimage analysis hub

## Open source

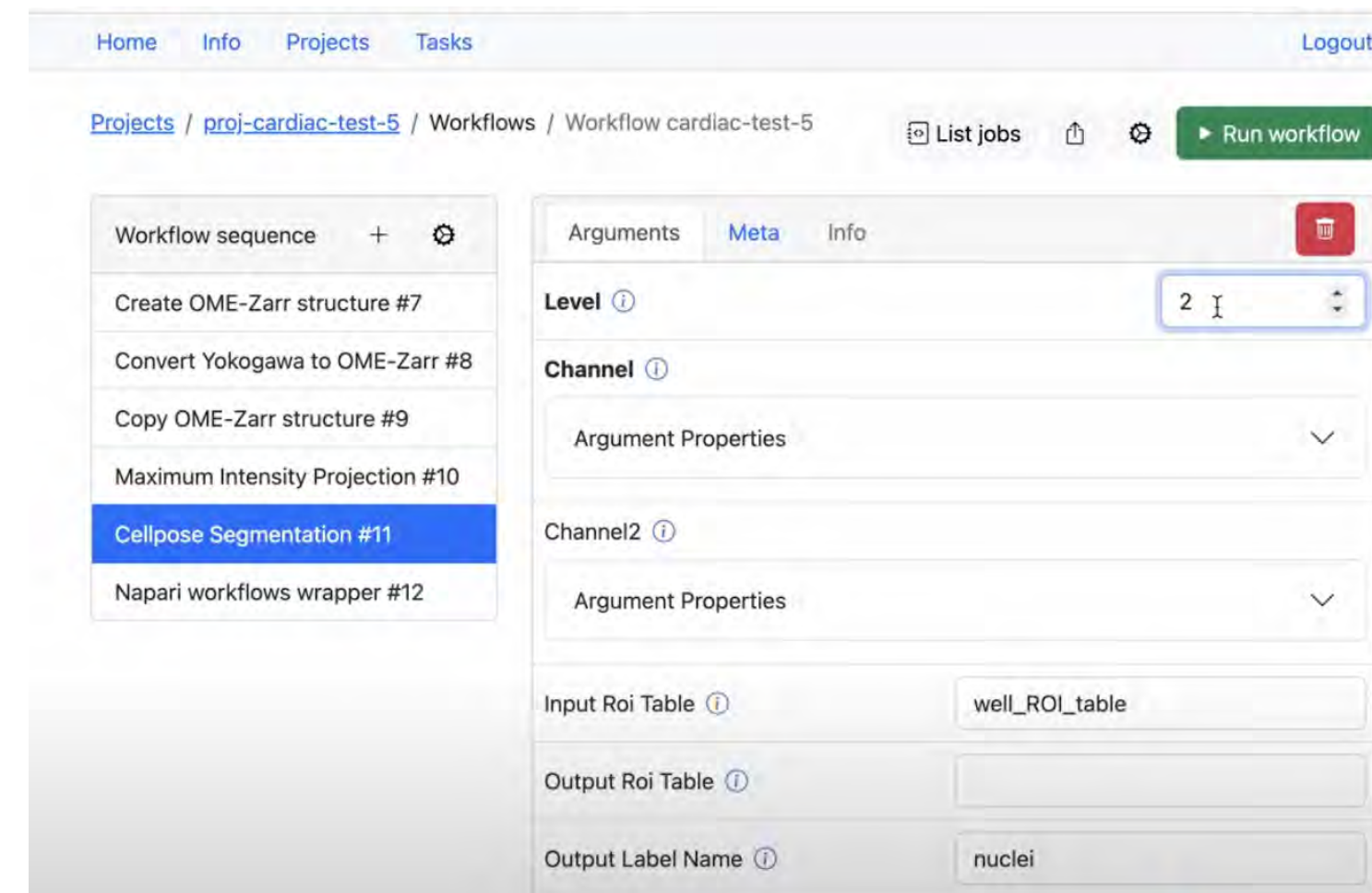
Our contributions are released under permissive free licenses



**open source**  
initiative®

## FAIRness

Our platform is designed to be accessible to all



## Community

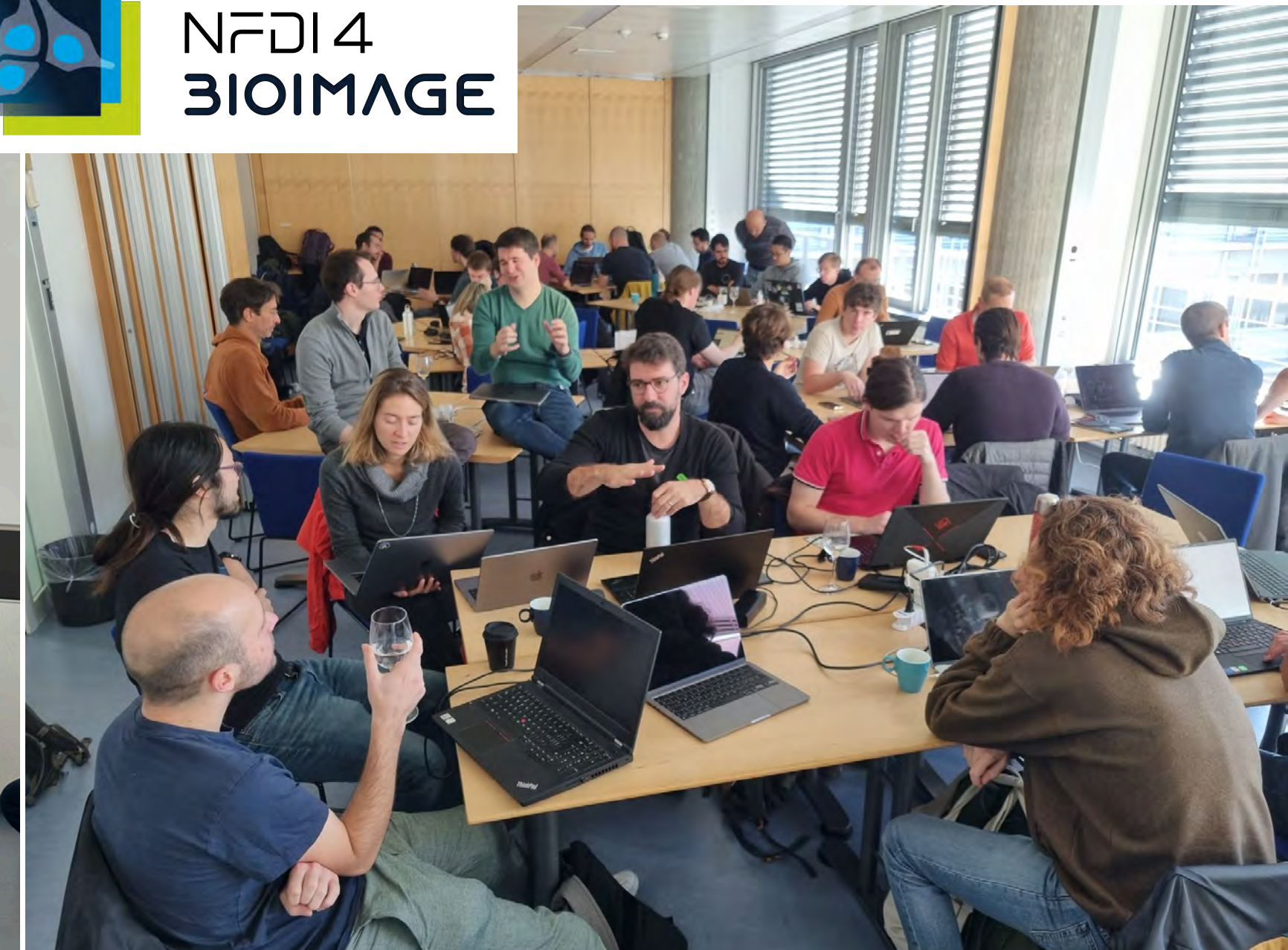
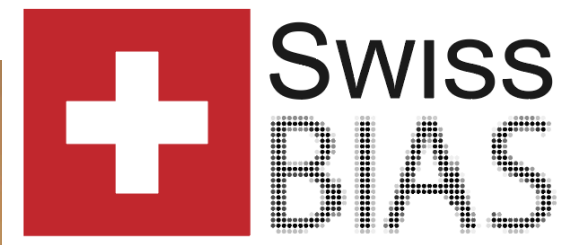
We promote work from the community and actively contribute to it





# BioVisionCenter community events

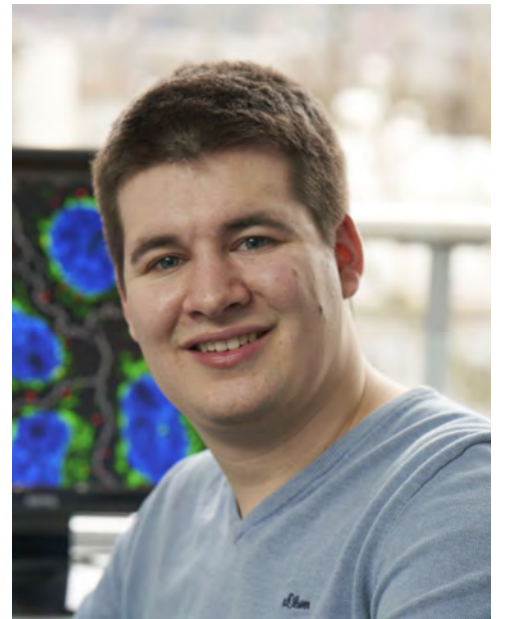
Recent next generation bioimage analysis workflows and OME-NGFF hackathon at the BioVisionCenter (Nov 6-8, 2023)



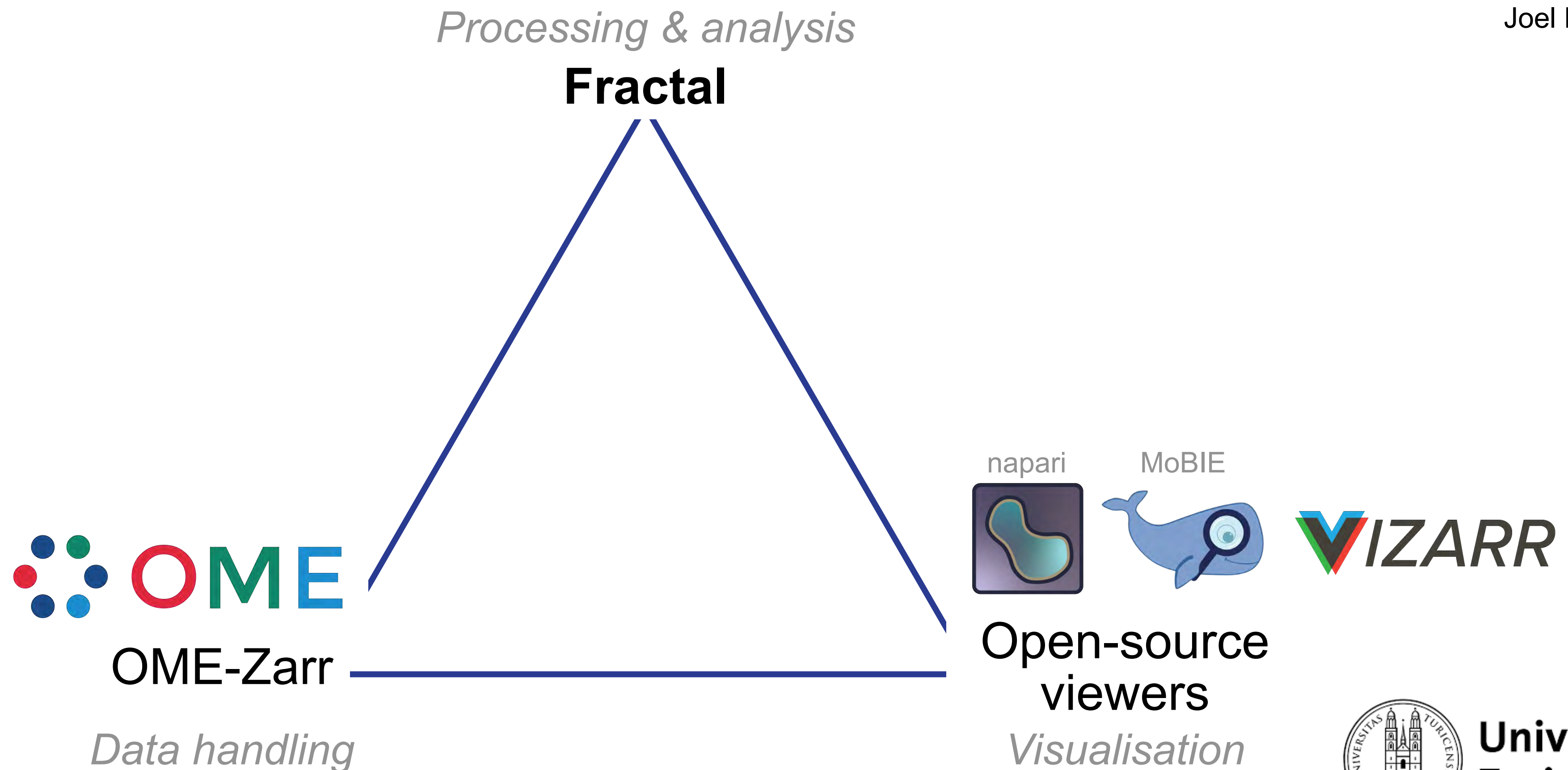


# The Fractal analytics platform

Fractal is a framework built on open-source standards for storage & visualization to streamline bioimage analysis workflows

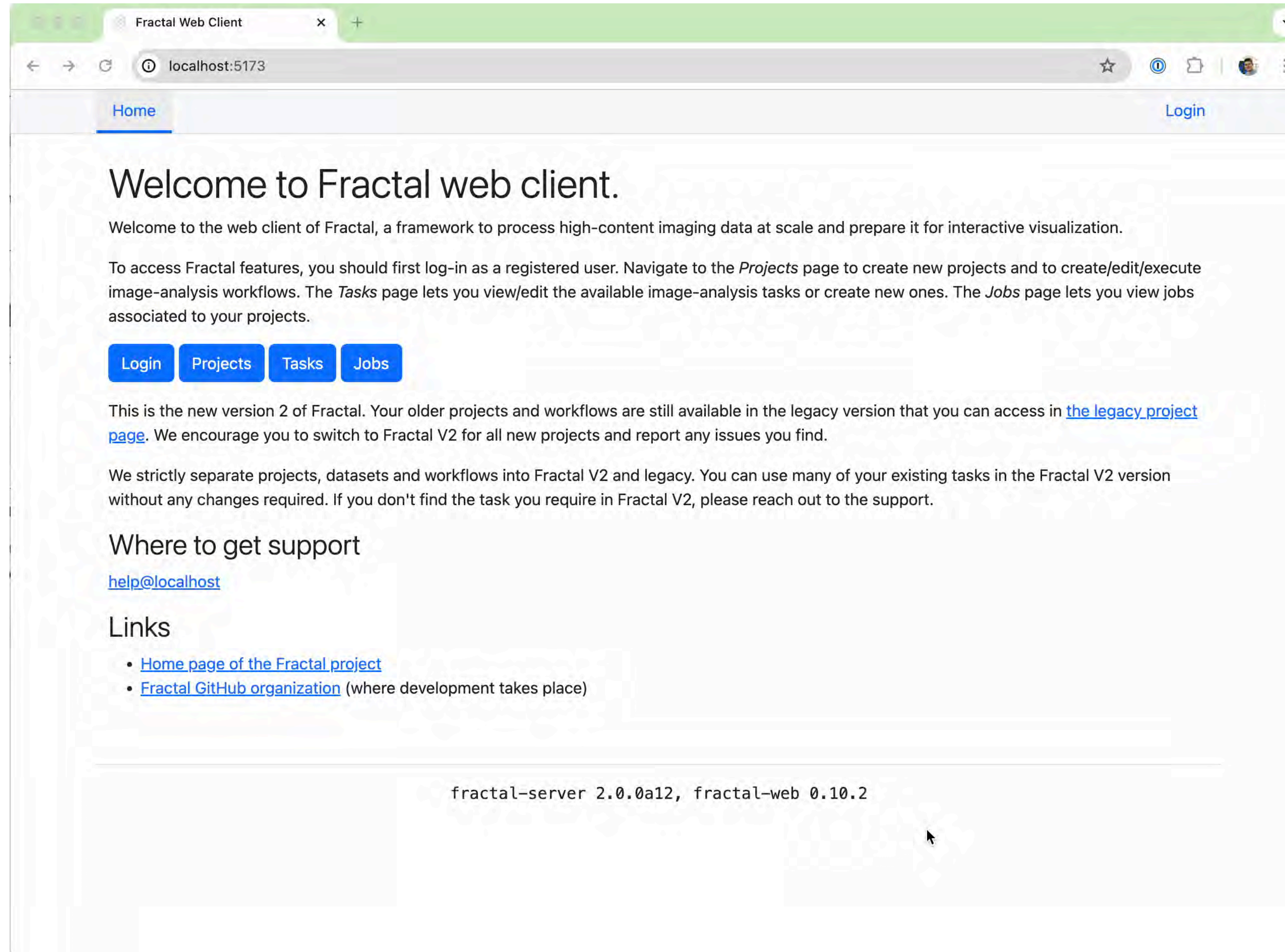


Joel Lüthi





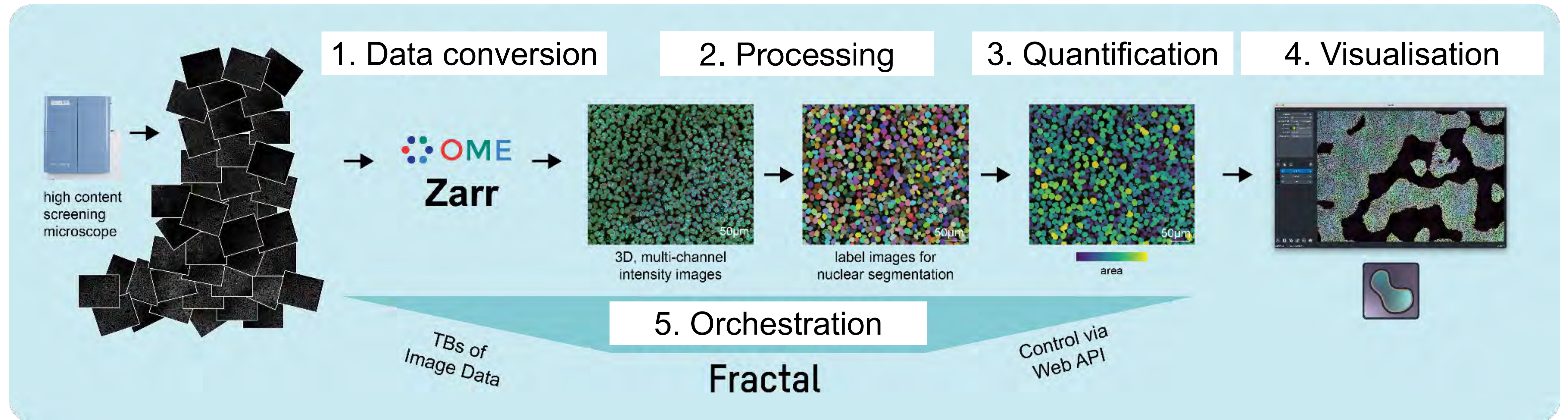
# The Fractal analytics platform



The screenshot shows a web browser window titled "Fractal Web Client" at the URL "localhost:5173". The page has a light blue header with "Home" on the left and "Login" on the right. The main content area features a large heading "Welcome to Fractal web client." followed by a paragraph: "Welcome to the web client of Fractal, a framework to process high-content imaging data at scale and prepare it for interactive visualization." Below this is another paragraph: "To access Fractal features, you should first log-in as a registered user. Navigate to the *Projects* page to create new projects and to create/edit/execute image-analysis workflows. The *Tasks* page lets you view/edit the available image-analysis tasks or create new ones. The *Jobs* page lets you view jobs associated to your projects." A row of four blue buttons labeled "Login", "Projects", "Tasks", and "Jobs" is positioned below the text. Further down, a paragraph states: "This is the new version 2 of Fractal. Your older projects and workflows are still available in the legacy version that you can access in [the legacy project page](#). We encourage you to switch to Fractal V2 for all new projects and report any issues you find." Another paragraph follows: "We strictly separate projects, datasets and workflows into Fractal V2 and legacy. You can use many of your existing tasks in the Fractal V2 version without any changes required. If you don't find the task you require in Fractal V2, please reach out to the support." The section "Where to get support" includes the email link [help@localhost](mailto:help@localhost). The "Links" section contains two bullet points: [Home page of the Fractal project](#) and [Fractal GitHub organization](#) (where development takes place). At the bottom of the page, the footer text reads "fractal-server 2.0.0a12, fractal-web 0.10.2".



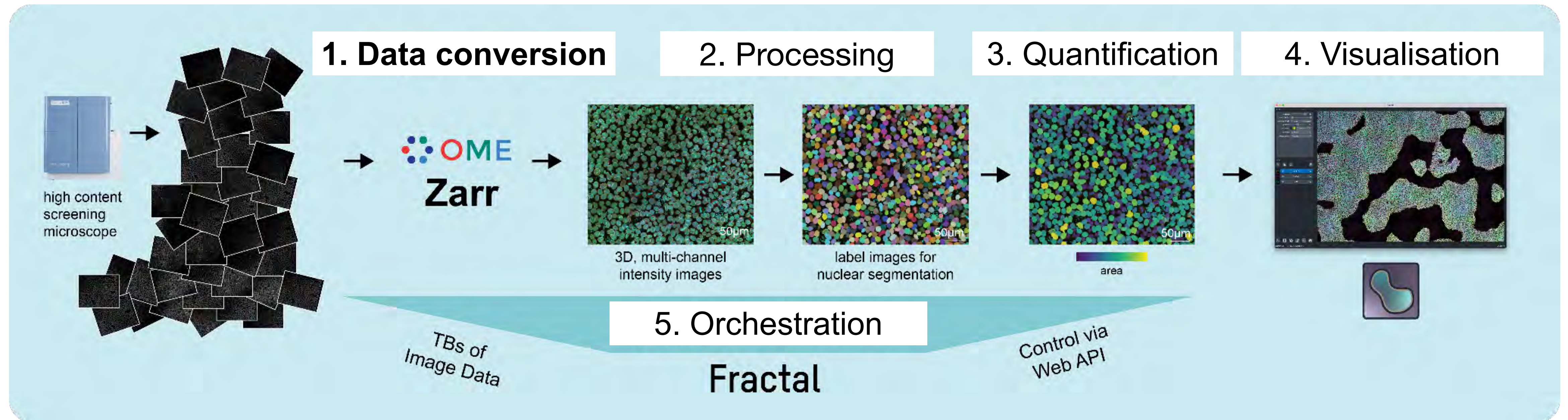
# The Fractal analytics platform



[fractal-analytics-platform.github.io](https://fractal-analytics-platform.github.io)



# The Fractal analytics platform



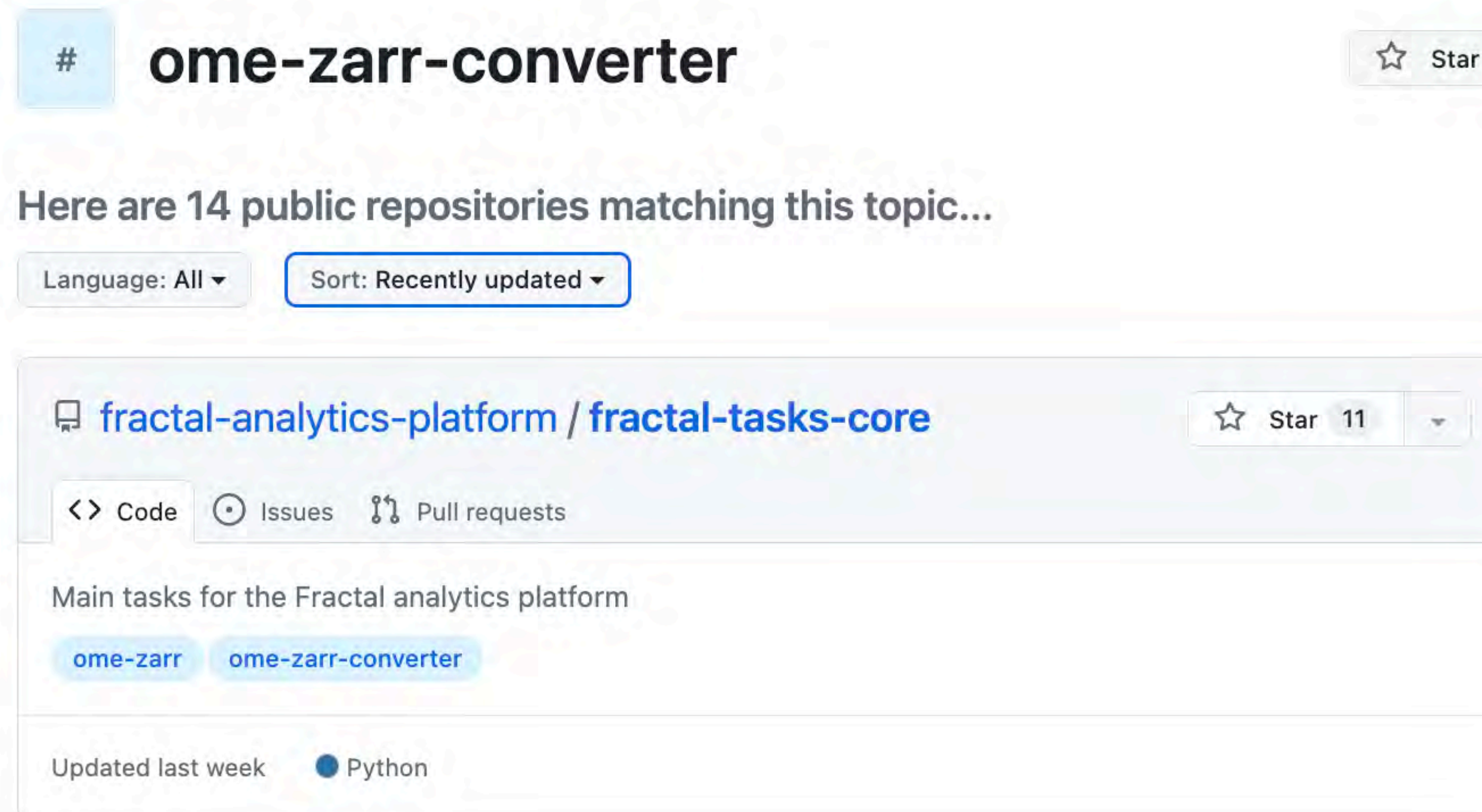
[fractal-analytics-platform.github.io](https://fractal-analytics-platform.github.io)



# Data conversion to OME-Zarr

We are currently implementing our own converters, using existing libraries whenever we can...

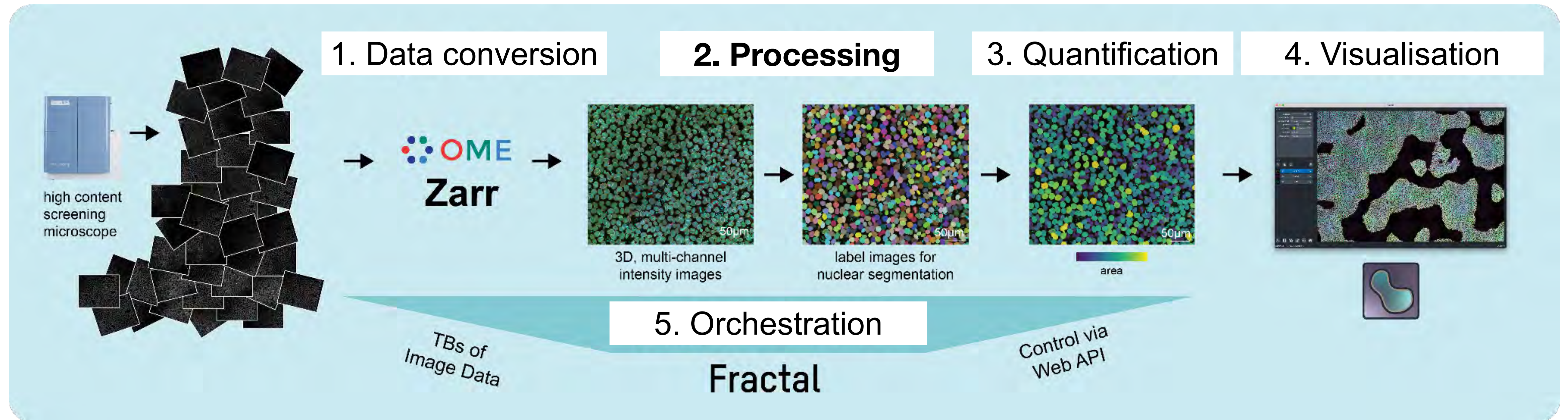
...and are keen to find ways to work together as a community on that topic!



The screenshot shows a GitHub search result for the topic `# ome-zarr-converter`. The search results are filtered by language (All) and sorted by 'Recently updated'. The top result is the repository `fractal-analytics-platform / fractal-tasks-core`, which has 11 stars. The repository description includes 'Main tasks for the Fractal analytics platform' and lists `ome-zarr` and `ome-zarr-converter` as sub-projects. The repository is updated last week and is written in Python.



# The Fractal analytics platform



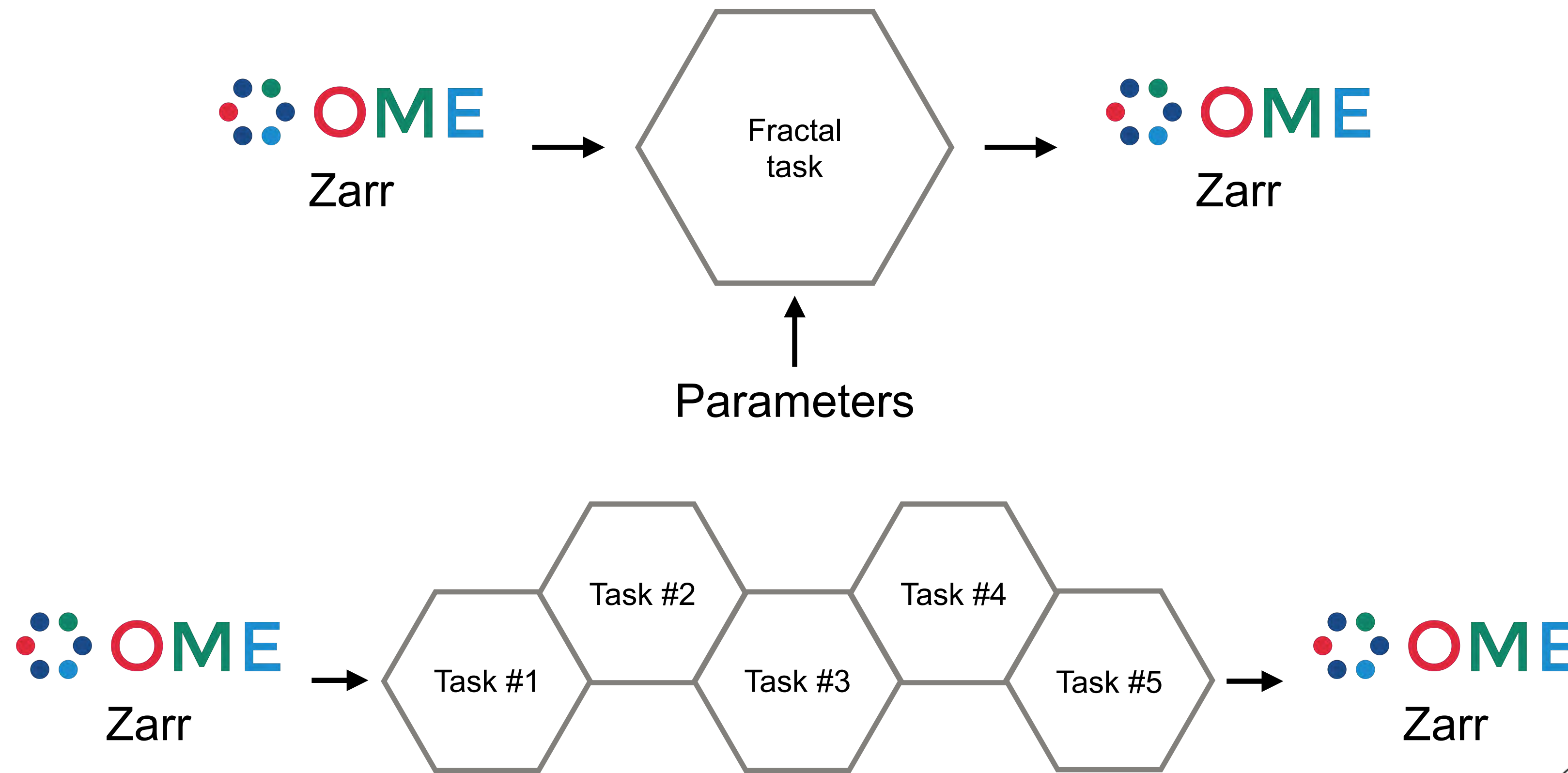
[fractal-analytics-platform.github.io](https://fractal-analytics-platform.github.io)



# Image processing with Fractal tasks



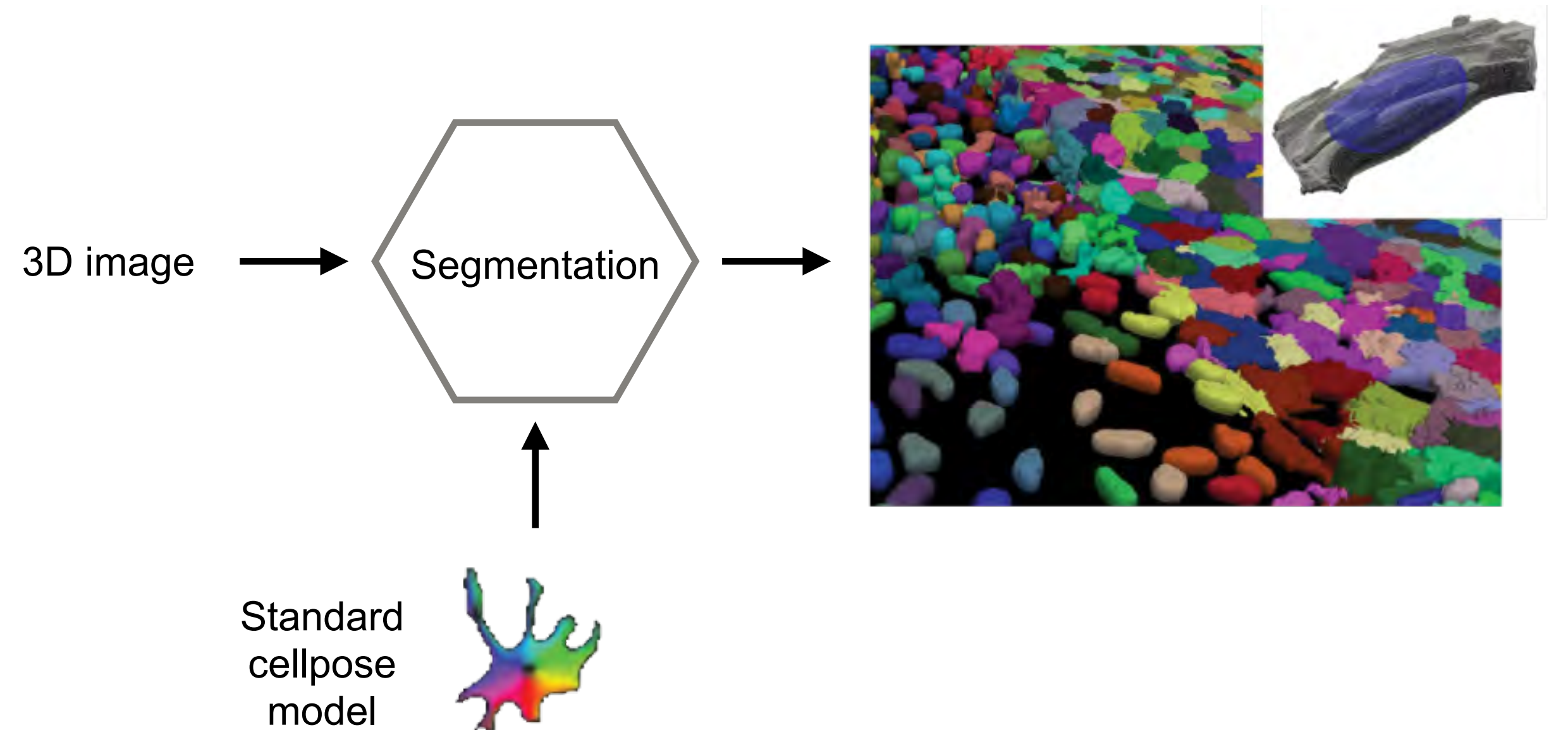
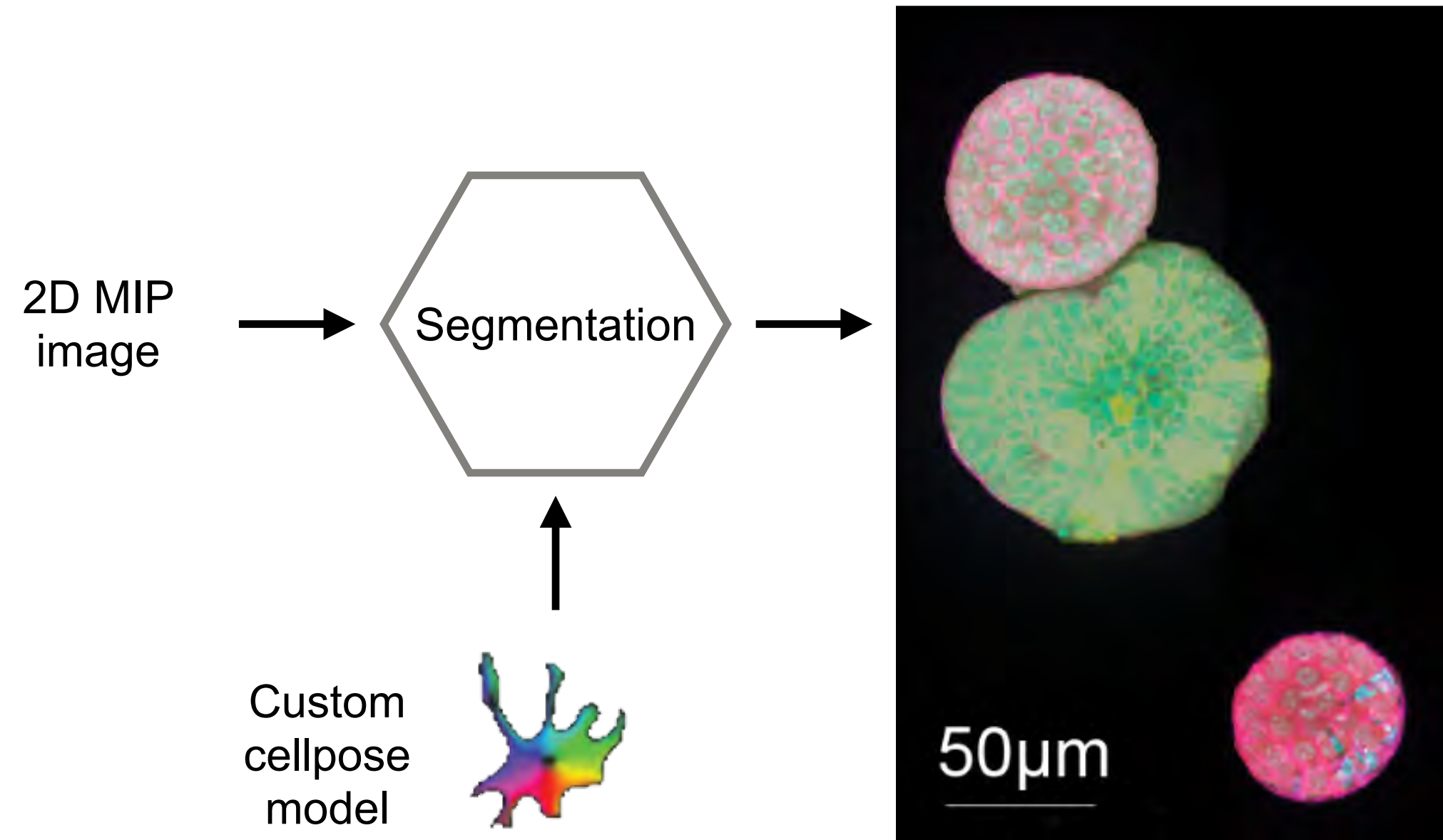
Fractal tasks are building blocks that process OME-Zarr





# Image processing with Fractal tasks

Fractal tasks can flexibly handle different combinations of inputs and parameters  
(e.g., segment a whole well or loop over ROIs, 2D or 3D, full res or downscaled, ...)





# Towards easier task building

We are working hard to make it easy to develop custom Fractal tasks, and for this we need good tools to manipulate OME-Zarrs

```
# Process the image with an image processing approach of your choice
label_img = custom_process_img(
    array_zyx.compute(),
    custom_argument=custom_argument,
)

def custom_process_img(
    int_img: np.array, custom_argument: int
) -> np.array:
    """
    Image processing function, to be replaced with your custom logic

    Numpy image & parameters in, label image out

    Args:
        int_img: Intensity image as a numpy array
        custom_argument: integer parameter

    Returns:
        label_img: np.array
    """

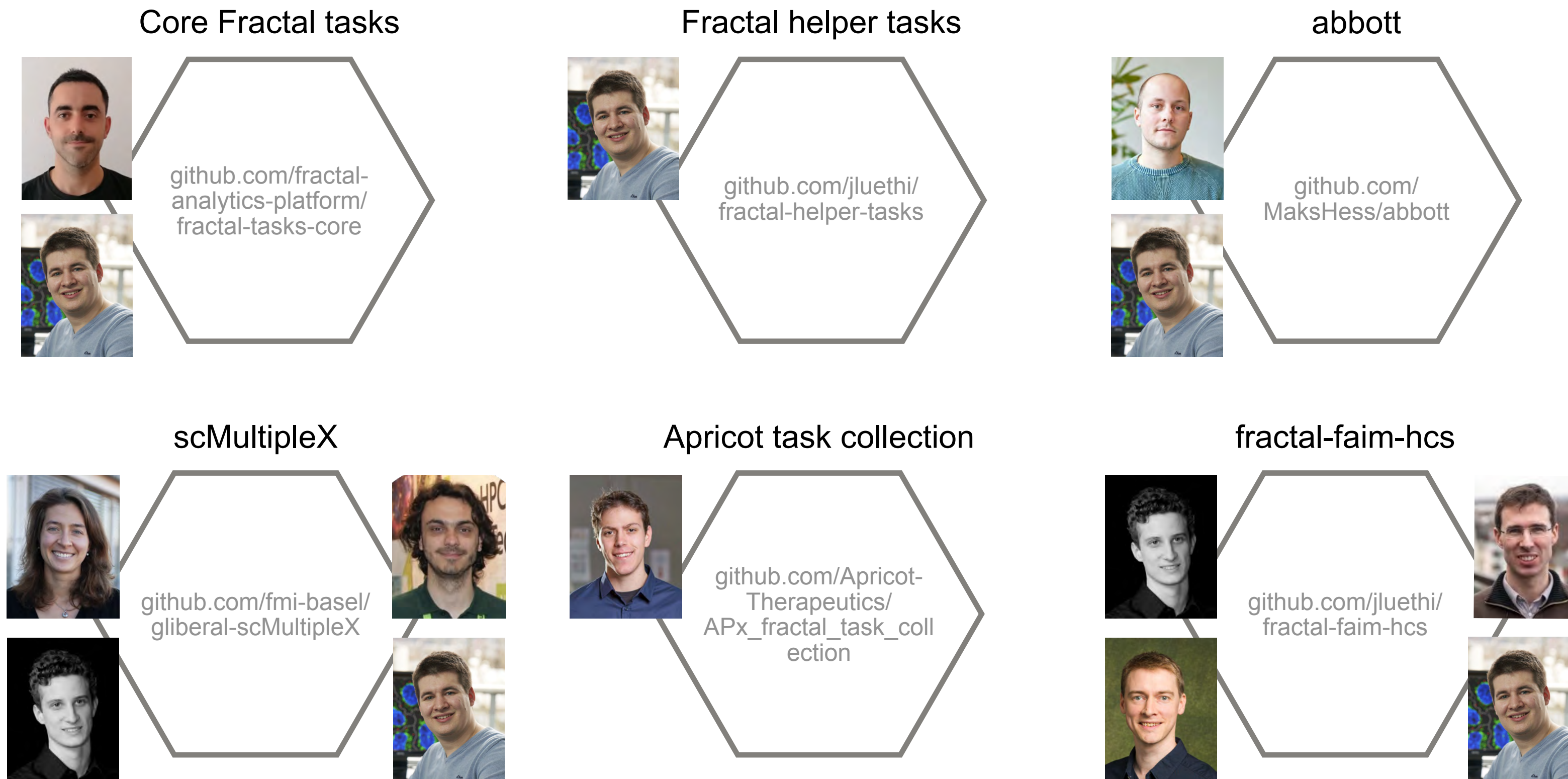
    # Add your own operations here
```

[github.com/fractal-analytics-platform/fractal-tasks-template](https://github.com/fractal-analytics-platform/fractal-tasks-template)



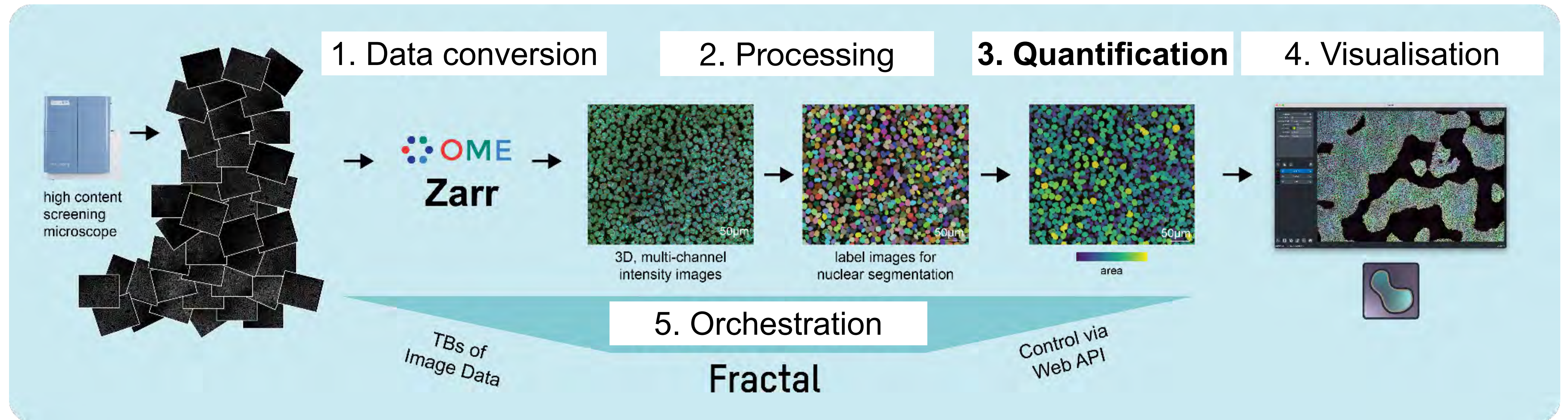
# Currently available task packages

Task packages are actively being developed by us - and the community





# The Fractal analytics platform



[fractal-analytics-platform.github.io](https://fractal-analytics-platform.github.io)



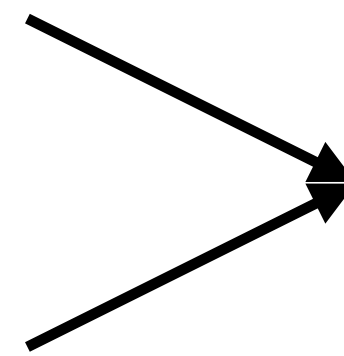
# Storing quantification results along with labels and data

Fractal extracts measurements to OME-Zarrs and stores them in AnnData tables

[github.com/ome/ngff/pull/64](https://github.com/ome/ngff/pull/64)

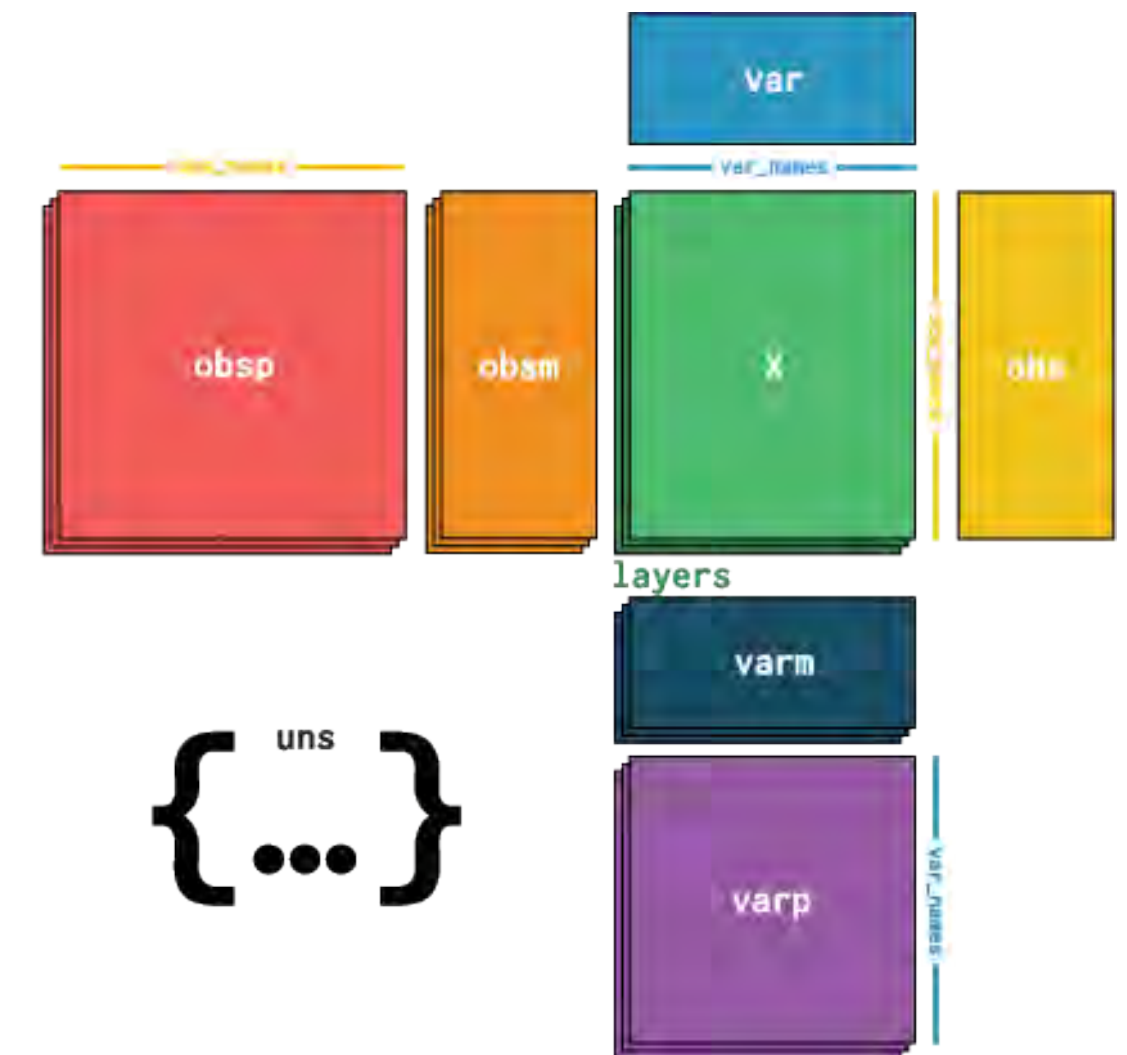
DAPI intensity image

Nuclei labels  
(instance segmentation)



scikit-image regionprops

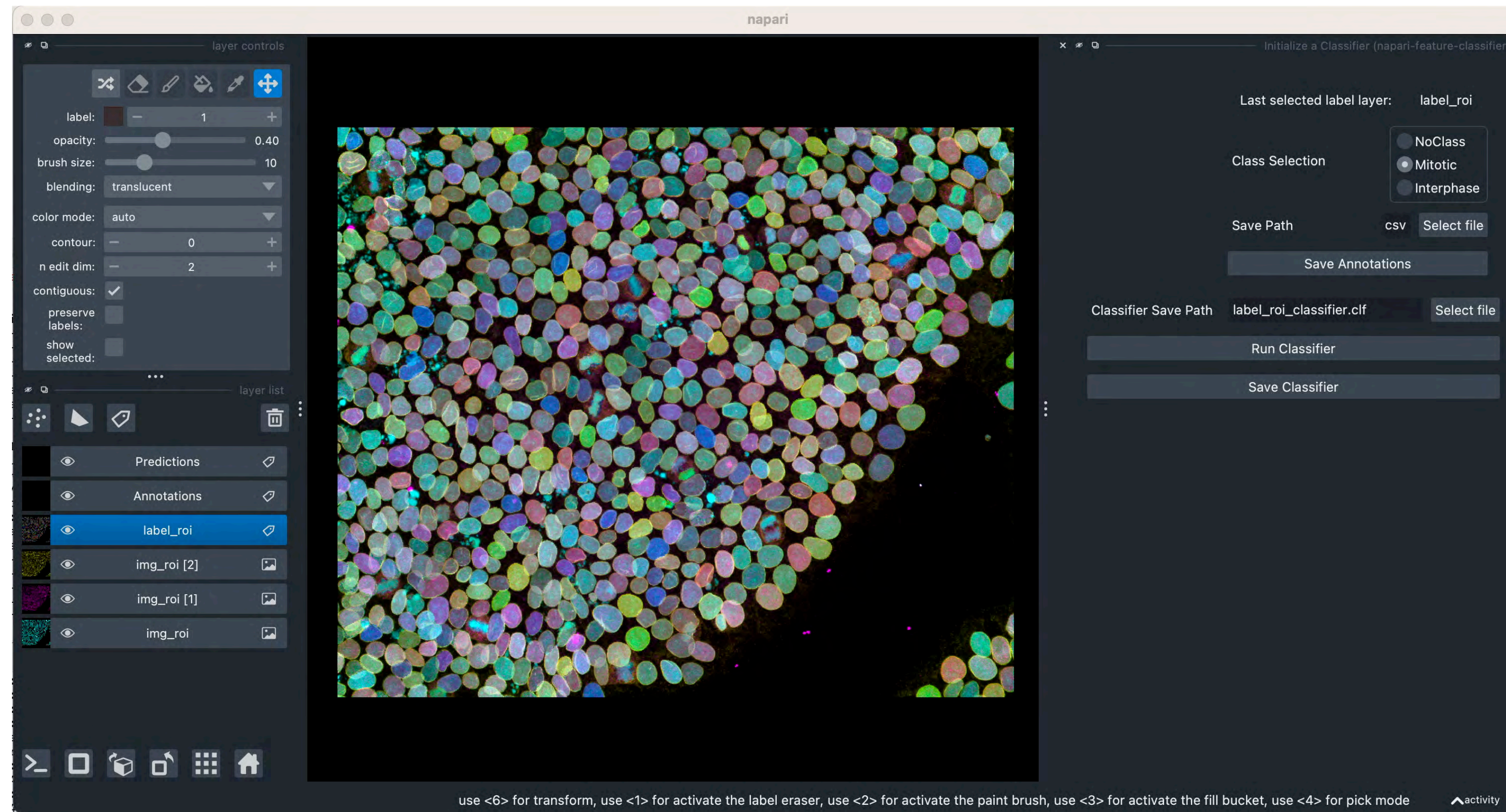
|       | area   | mean_intensity | standard_deviation_intensity |
|-------|--------|----------------|------------------------------|
| label |        |                |                              |
| 1     | 2400.0 | 264.030426     | 71.719330                    |
| 2     | 528.0  | 251.848480     | 121.864410                   |
| 3     | 1536.0 | 200.345047     | 62.951511                    |
| 4     | 5856.0 | 305.467712     | 95.109253                    |
| 5     | 2768.0 | 241.529617     | 68.545265                    |
| ...   | ...    | ...            | ...                          |





# OME-Zarr containers allow for integrated analysis

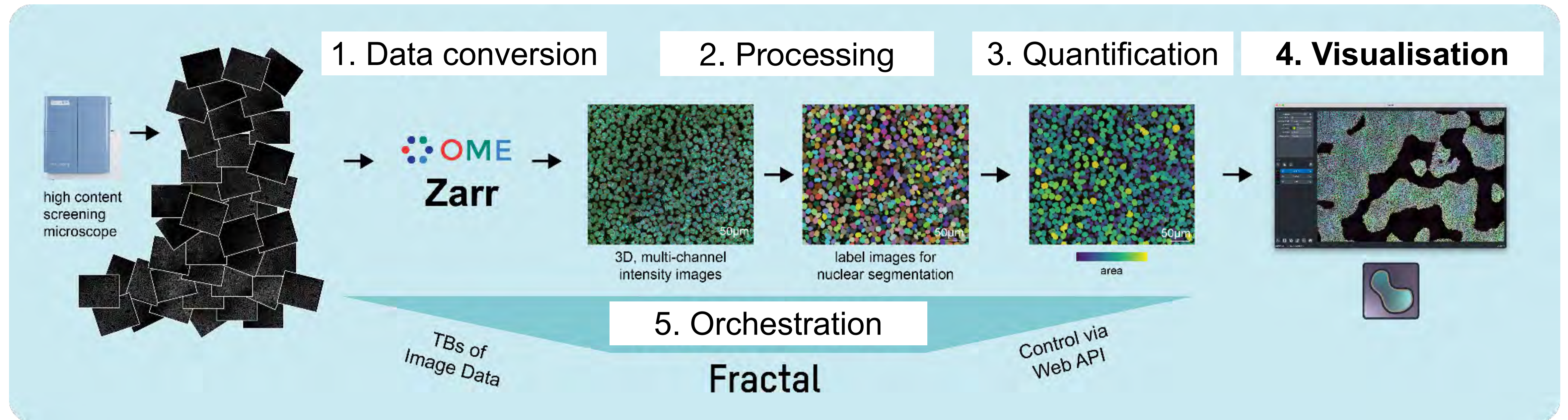
Keeping images, labels, and measurements together enables interactive data exploration



napari-OME-Zarr-roi-loader and napari-feature-classifier plugins (Maks Hess & Joel Lüthi)



# The Fractal analytics platform

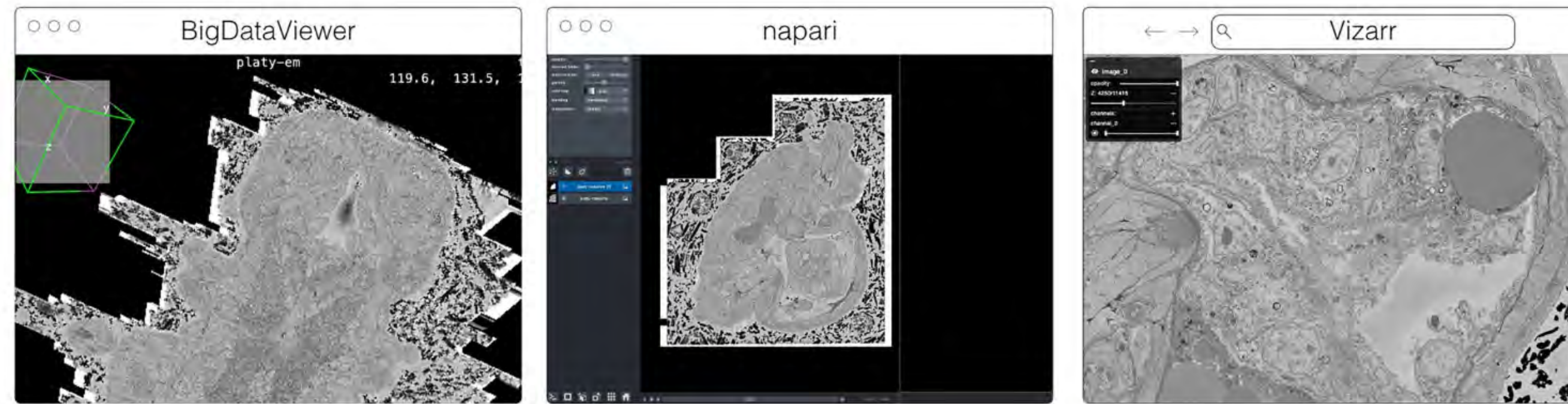


[fractal-analytics-platform.github.io](https://fractal-analytics-platform.github.io)



# Many good viewer options are available for OME-Zarrs

We are relying on open-source OME-Zarr viewers and are actively exploring web-based solutions

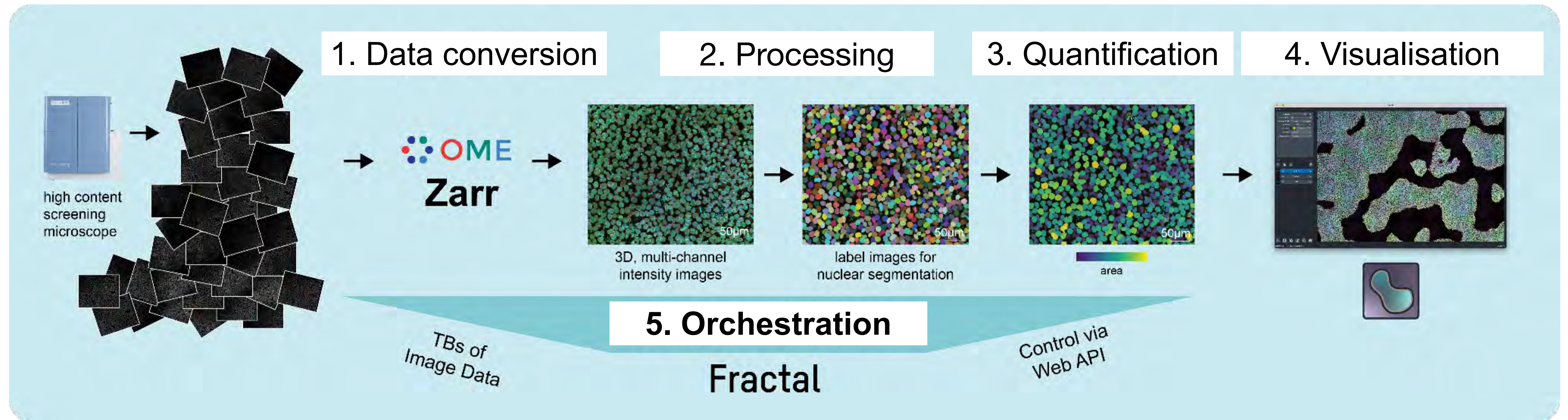


| Visualization tool     | Use                   | Language/framework       |
|------------------------|-----------------------|--------------------------|
| AGAVE                  | Linux, MacOS, Windows | C++, OpenGL              |
| ITKWidgets             | Web (Jupyter)         | Python, WASM             |
| MoBIE/BigDataViewer    | Linux, MacOS, Windows | Java                     |
| napari                 | Desktop               | Python                   |
| Neuroglancer           | Web                   | WebGL                    |
| Validator              | Web                   | Svelte                   |
| Viv                    | Web                   | React, deck.gl           |
| webKnossos             | Web                   | React, WebGL             |
| website-3d-cell-viewer | Web                   | React, TypeScript, WebGL |

An up-to-date version of the table is maintained at <https://ngff.openmicroscopy.org/tools> and contributions are welcome



# The Fractal analytics platform

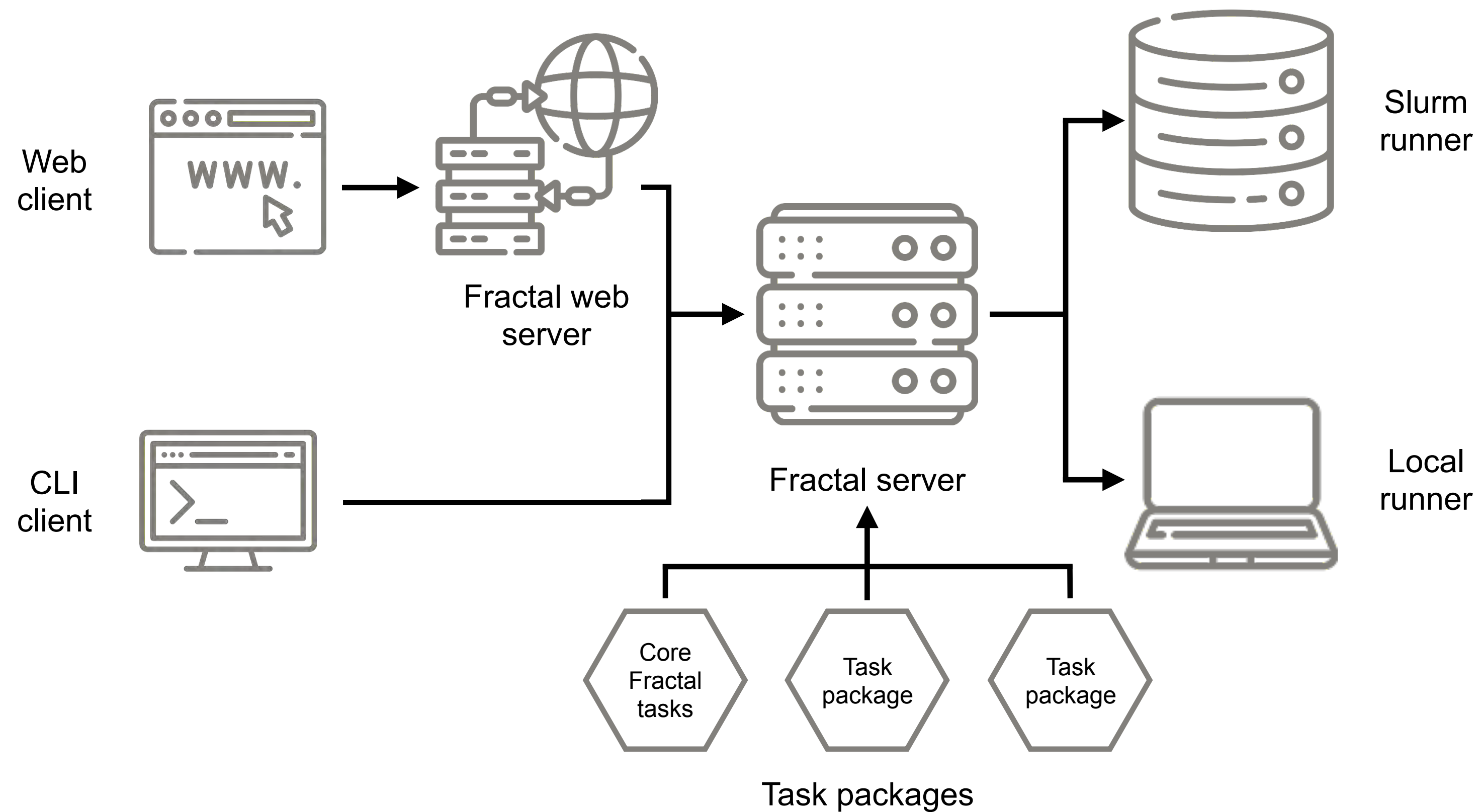


[fractal-analytics-platform.github.io](https://fractal-analytics-platform.github.io)



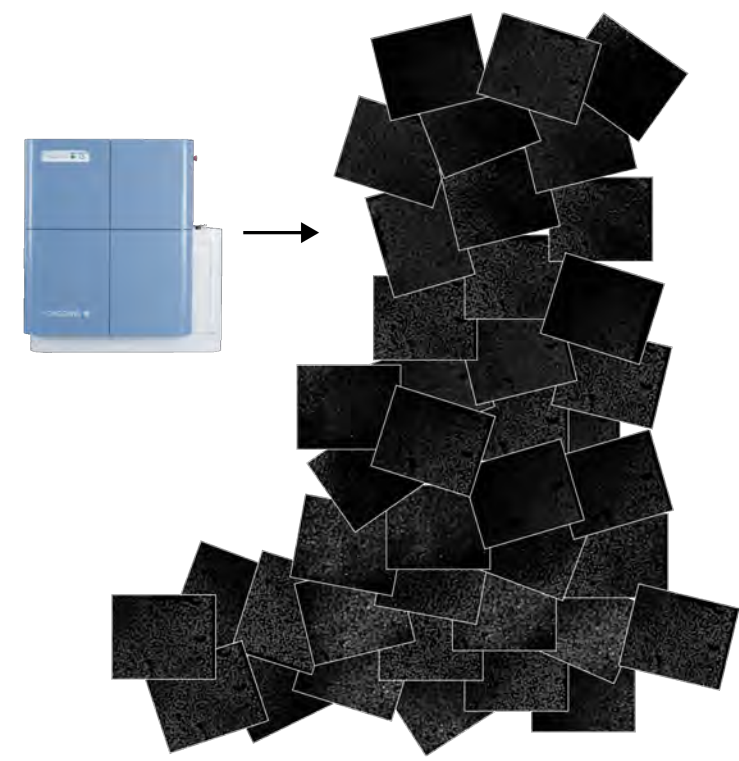
# Fractal uses a modular orchestration system

Our Fractal server runs where the compute is  
(personal laptop or HPC)

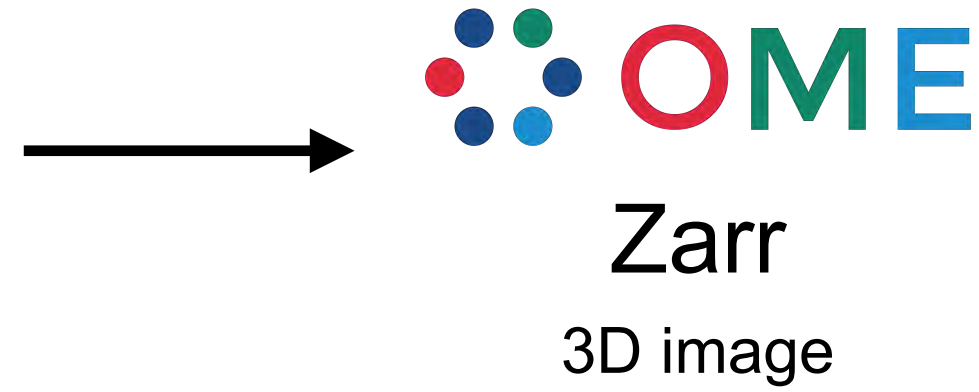




# Example workflow



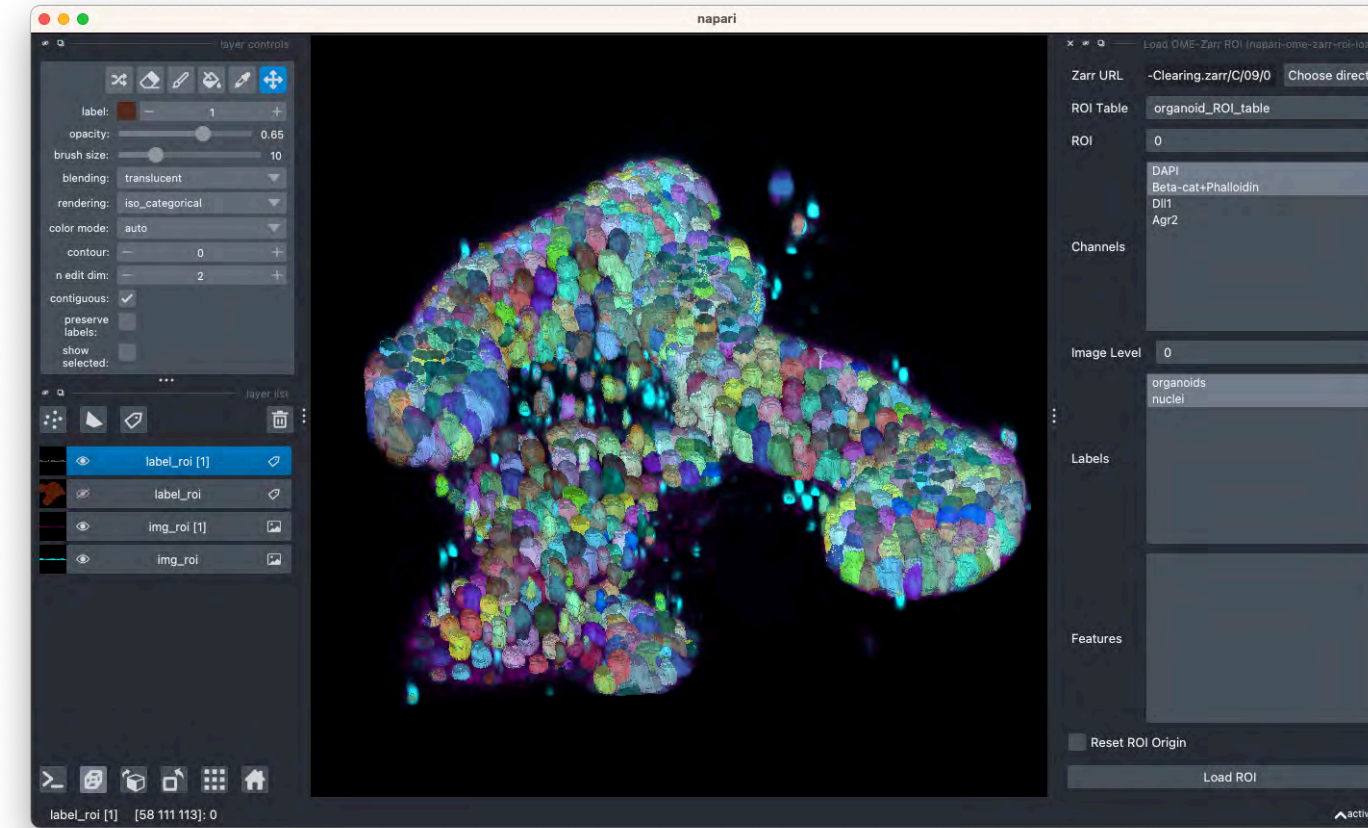
3D HCI images  
(Yokogawa or Molecular  
Devices system)



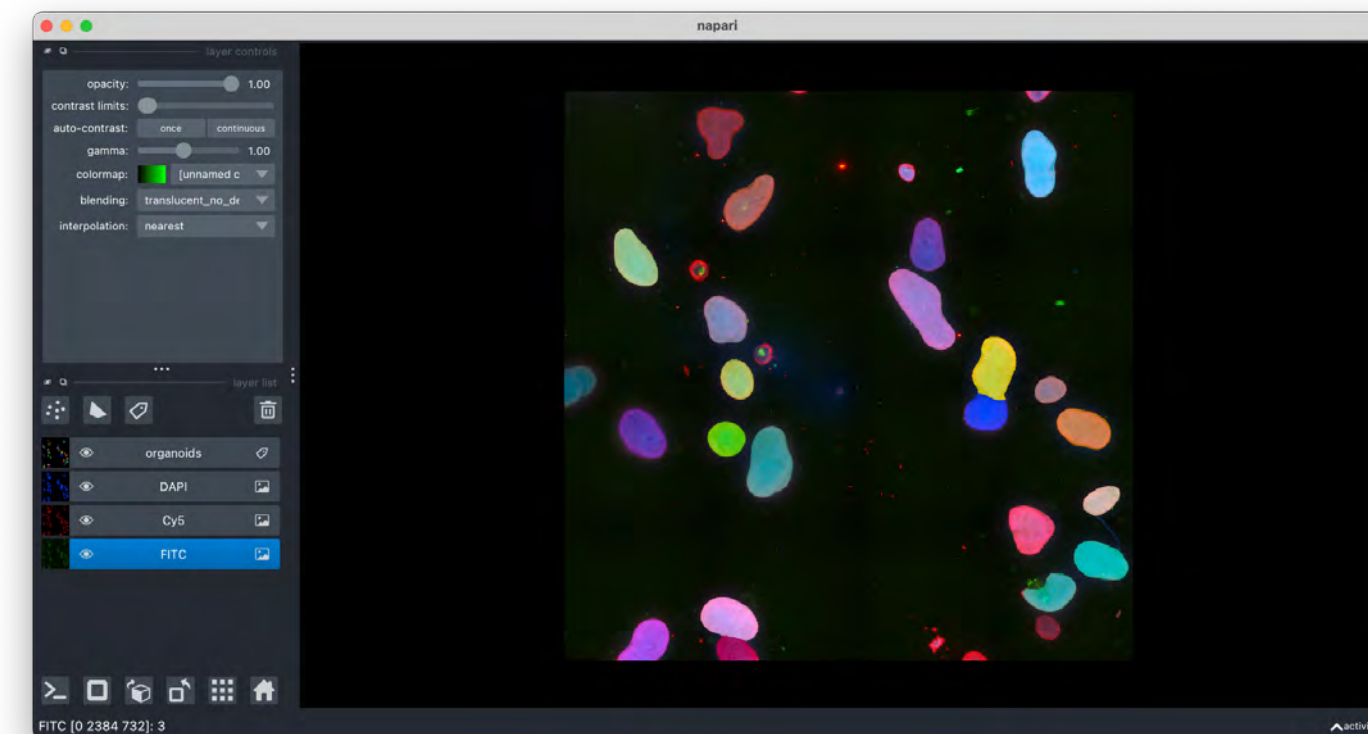
Maximum  
intensity  
projection



3D nuclei segmentation



3D  
measurements



2D  
measurements

2D organoid segmentation



# Initial roadmap: focusing on high-data-volume modalities

High-Content Imaging

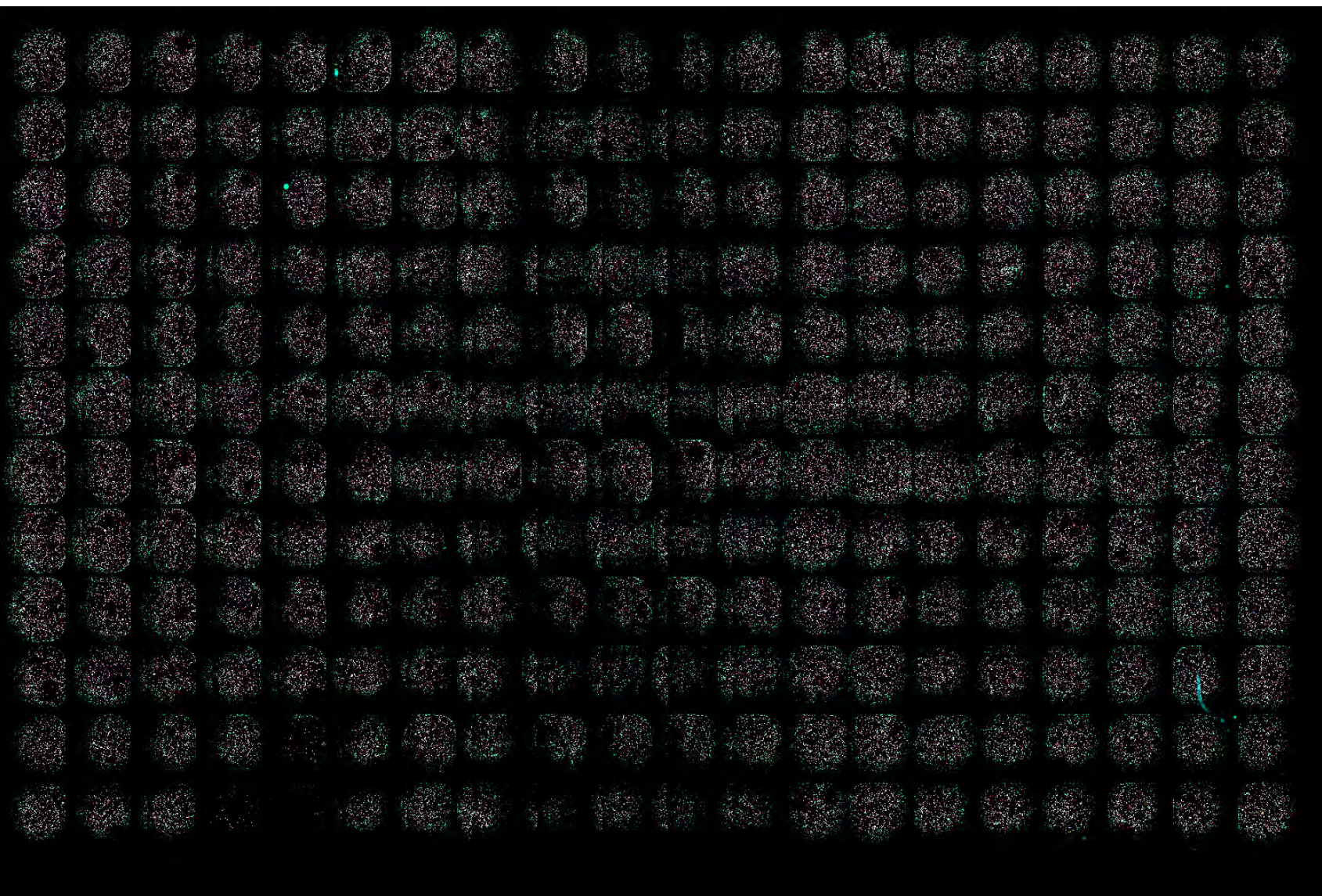


Image courtesy of Kelvin Groot (Pelkmans lab, UZH)

Lightsheet

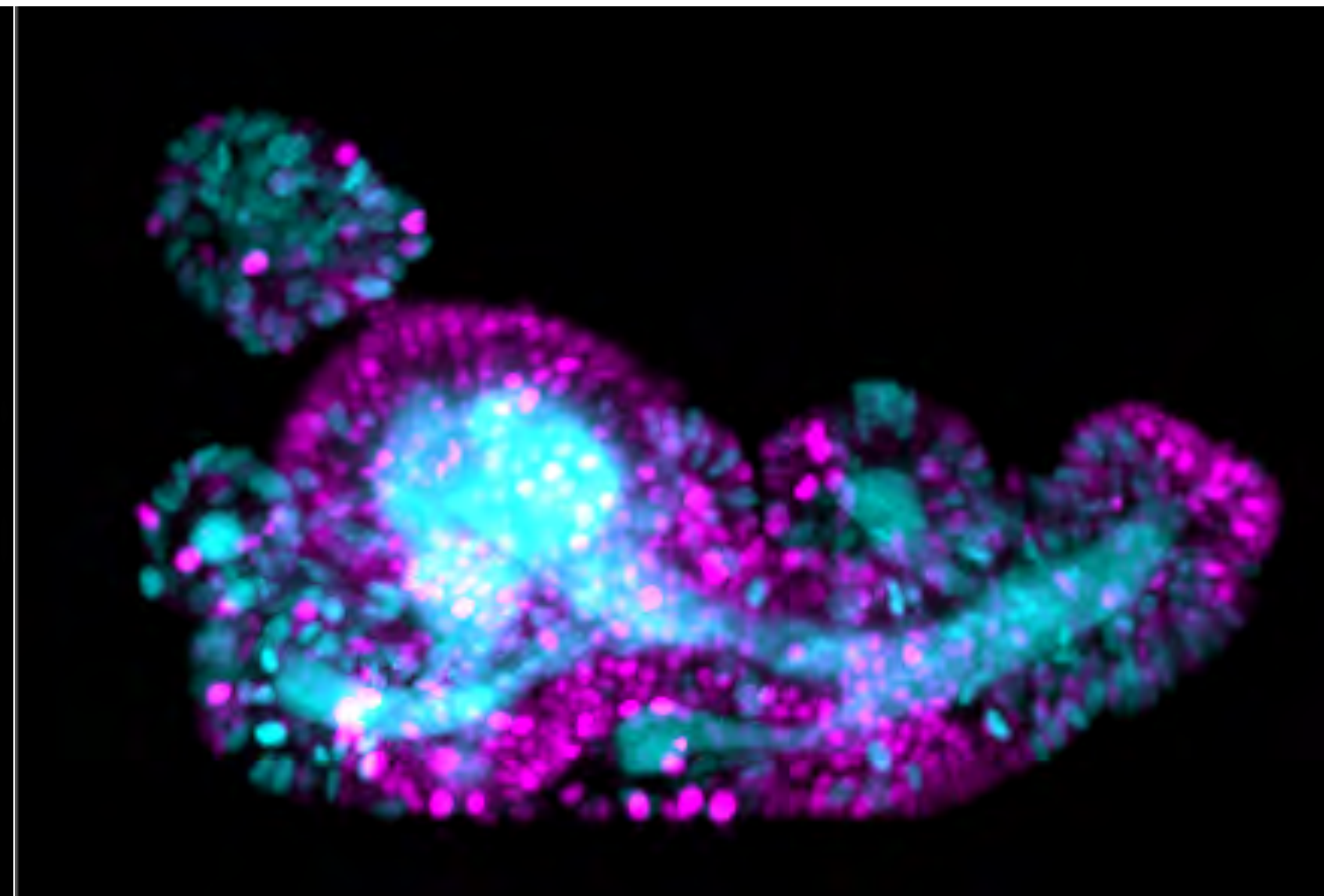
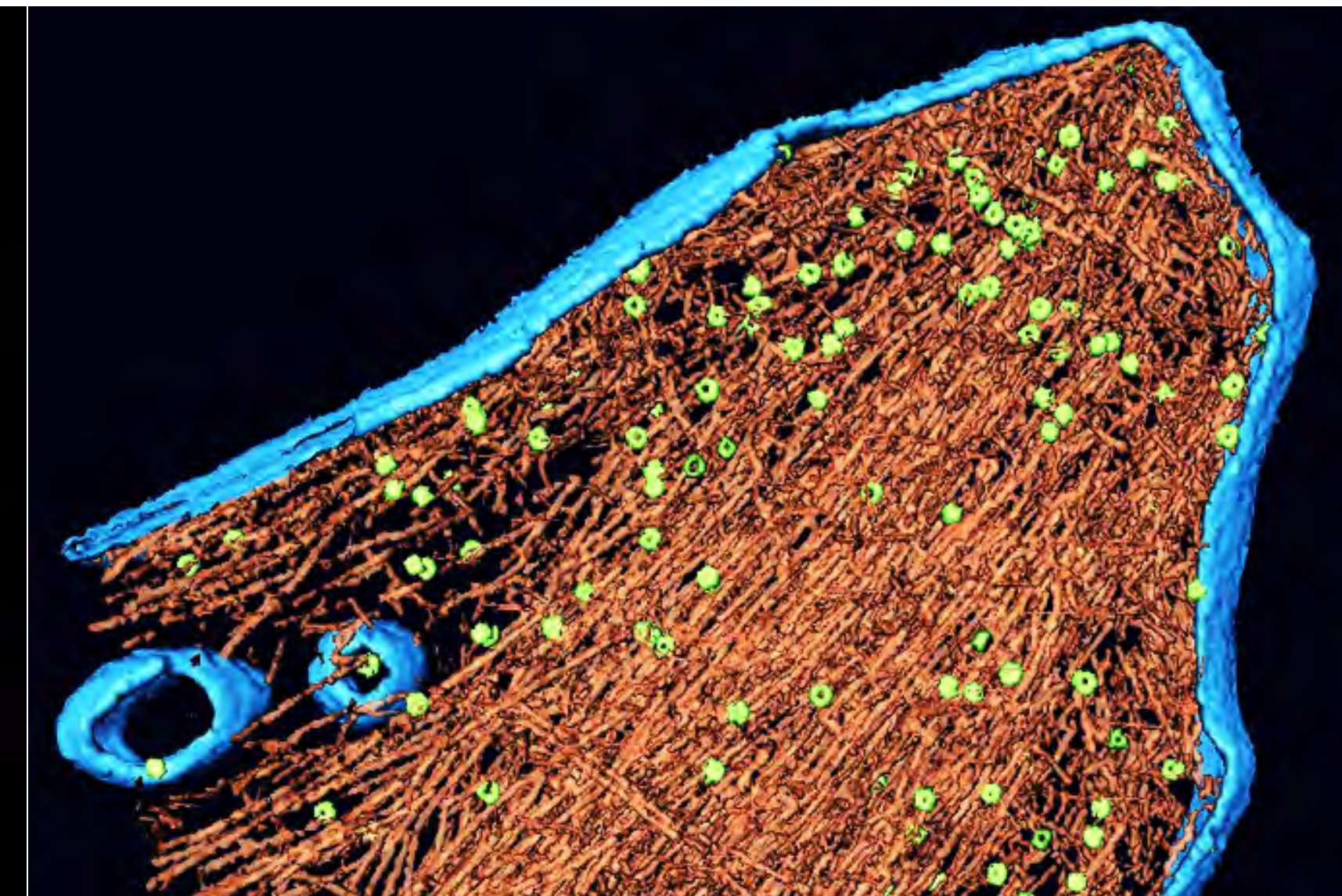


Image courtesy of Liberali lab (FMI)

Electron microscopy+tomography



Patla et al., 2010 (Medalia lab, UZH)



# Fractal is under active development

We are developing Fractal in the open under a permissive open-source license (BSD3)

[fractal-analytics-platform.github.io](https://fractal-analytics-platform.github.io)

| Component         | GitHub Repository                  | Documentation                           | Package                                    |
|-------------------|------------------------------------|---|--|
| <b>server</b>     | <a href="#">fractal-server</a>     | <a href="#">fractal-server docs</a>     | <a href="#">fractal-server on PyPI</a>     |
| <b>client</b>     | <a href="#">fractal-client</a>     | <a href="#">fractal-client docs</a>     | <a href="#">fractal-client on PyPI</a>     |
| <b>web client</b> | <a href="#">fractal-web</a>        | <a href="#">fractal-web docs</a>        | -  |
| <b>core tasks</b> | <a href="#">fractal-tasks-core</a> | <a href="#">fractal-tasks-core docs</a> | <a href="#">fractal-tasks-core on PyPI</a> |

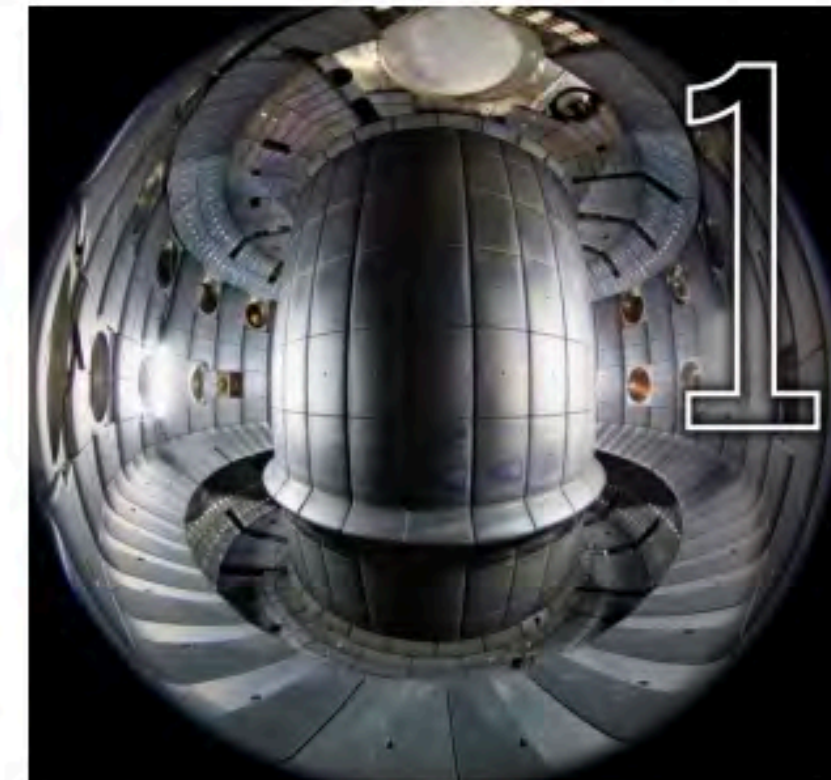


# Some things are happening in Switzerland

The Swiss Academy of Science is preparing an update to its Thematic Roadmaps, with a SwissBiImaging chapter!



Thematic Roadmaps  
2021



Swiss Roadmap for Research Infrastructures in view of the  
2025-2028 ERI Dispatch  
(Roadmap for Research Infrastructures 2023)

Part I: National Research Infrastructures

Schweizerische Eidgenossenschaft  
Confédération suisse  
Confederazione Svizzera  
Confederaziun svizra  
Swiss Confederation

Federal Department of Economic Affairs,  
Education and Research SER  
State Secretariat for Education,  
Research and Innovation SERI

Swiss Roadmap  
2023



# Gratitude

Thank you for your attention!



**UZH**  
**BioVision**  
**Center**



Incoming RSE  
(20% FTE committed to OME-  
NGFF implementation)