



BioImageIT: Integration of image data-management with analysis

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Why BioImage-IT?

Currently, there are very few software tools addressing both the data management and analysis.



Problem 1: Data management

- Hard drives: storage without metadata
 - Local Servers: storage with poor metadata integration
- ⇒ Data traceability (FAIR principles)

Problem 2: Processing & visualization tools

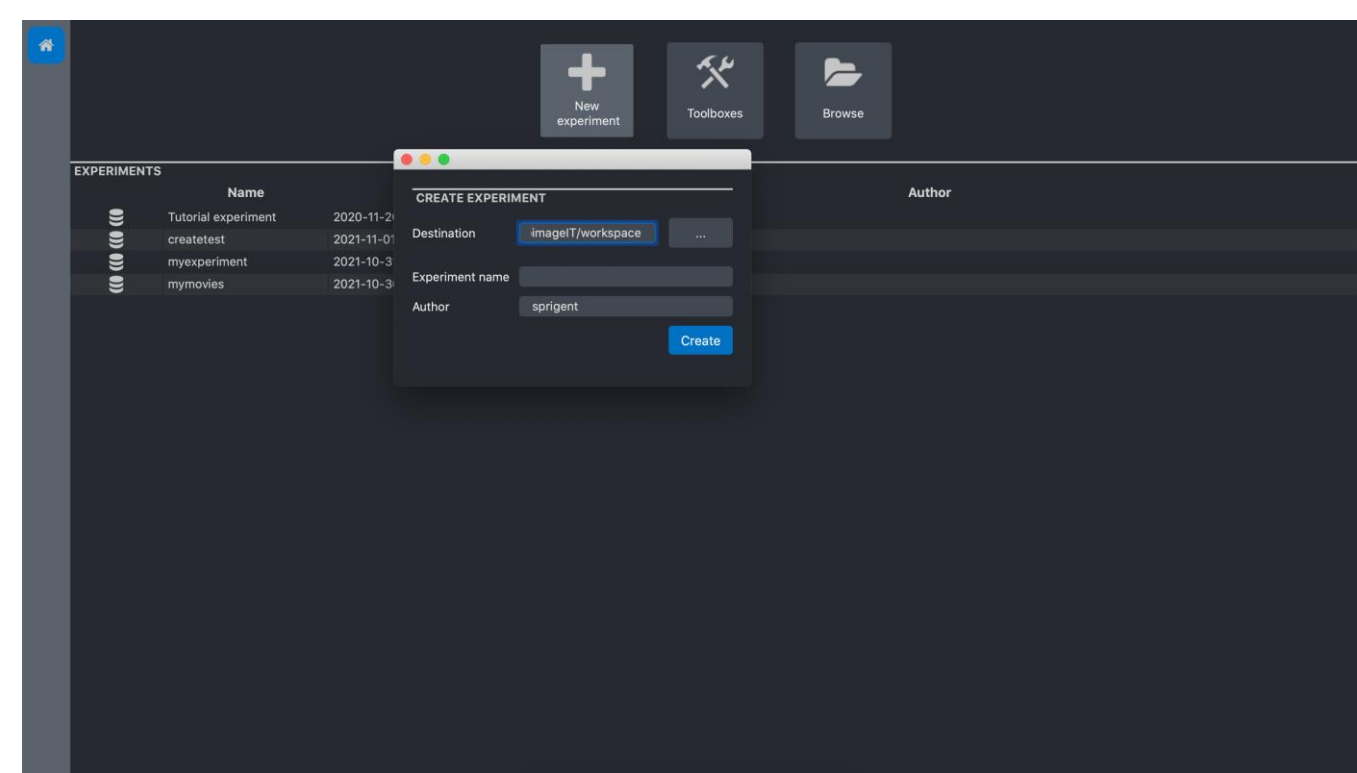
- Many languages
- For different systems (Linux, Apple, Microsoft)
- Needs for Documentations & reference test dataset

Problem 3: link data to processing & visualization

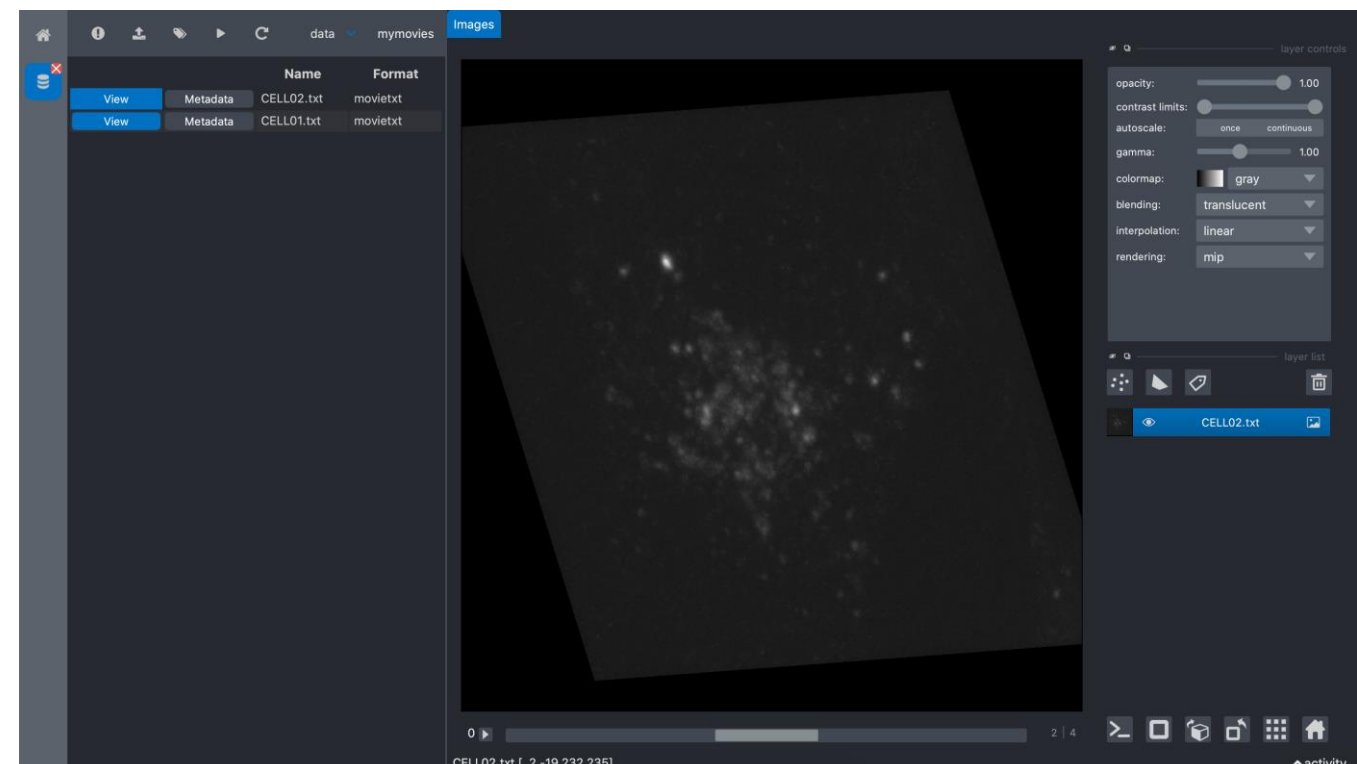
- Manual scripting
- Compatibility of data formats
- Main problem is to keep tracks of each processing steps with data rendering steps

1) Data Management

Referencing a new dataset (new experiment)

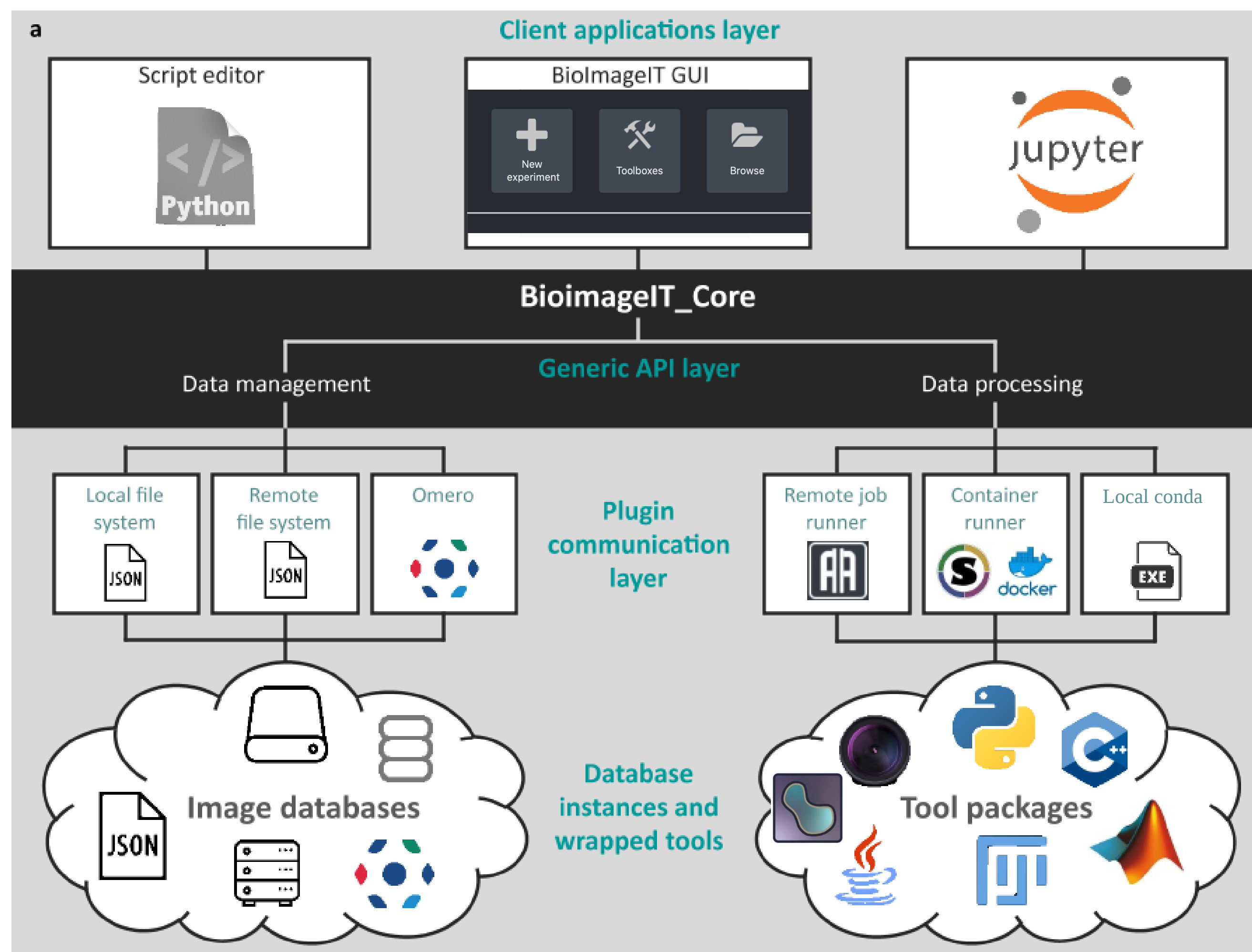


Instant control of dataset integration (use Napari)



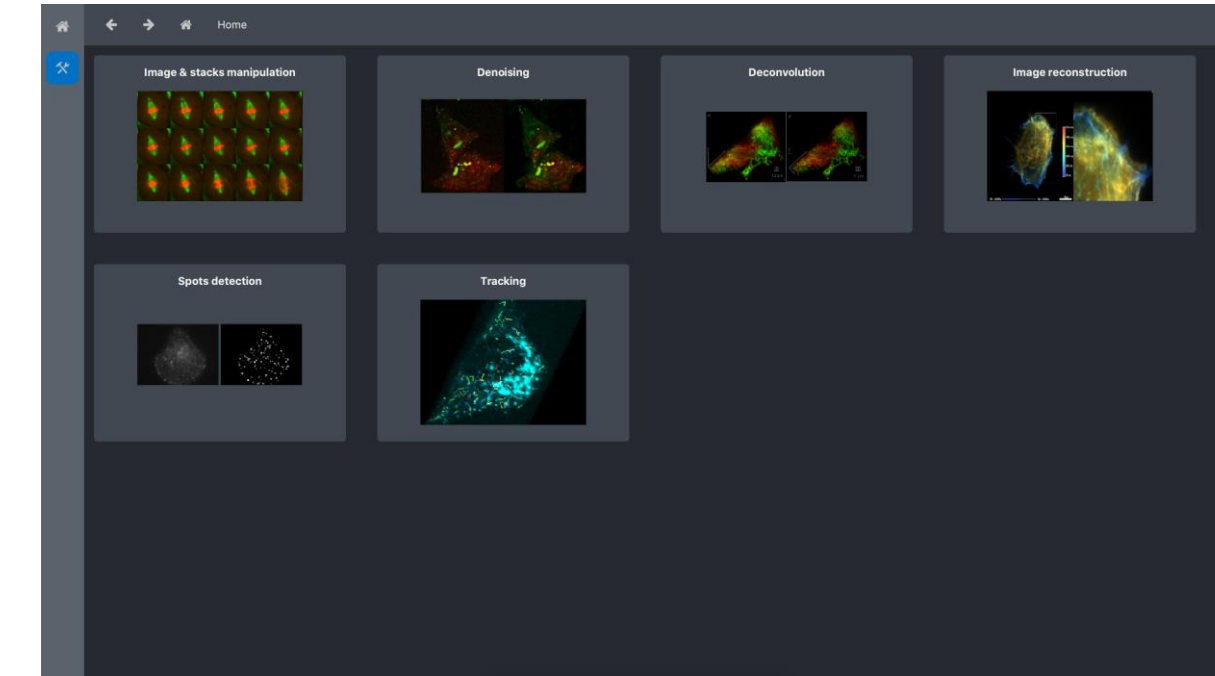
..... (SEE 2 or 3)

BioImage-IT offers a turnkey solution

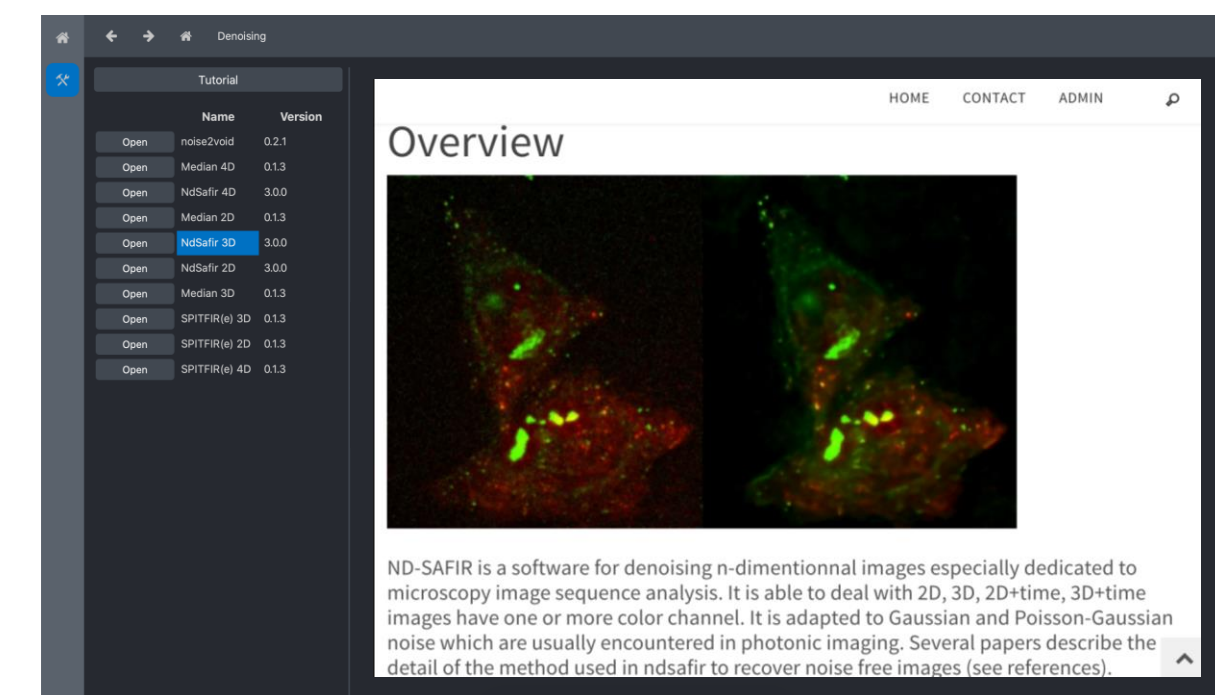


2) User Interface Toolbox

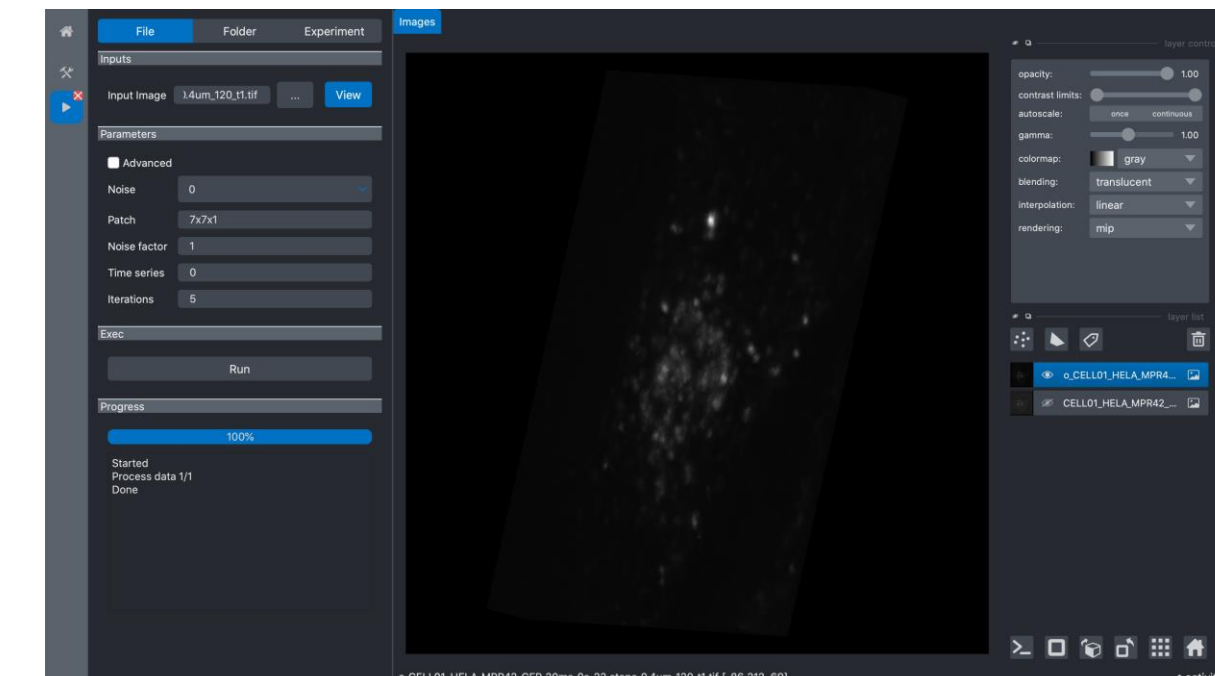
Toolboxes finder



Documentation



Tool runner



3) Developers tools /expert mode

Pipeline

```
from bioimagepy.experiment import Experiment
# create an experiment
my_experiment = Experiment()
my_experiment.create(name="myexperiment",
                    author="Sylvain Prigent",
                    uri="...")
print("experiment created")

# import the data
my_experiment.import_dir(dir_uri="./synthetic_data/data/",
                        filter=".tif$",
                        author="Sylvain Prigent",
                        format='tif',
                        date='2019-03-17',
                        copy_data=True)

# show the experiment directory
list_files('./myexperiment')
```

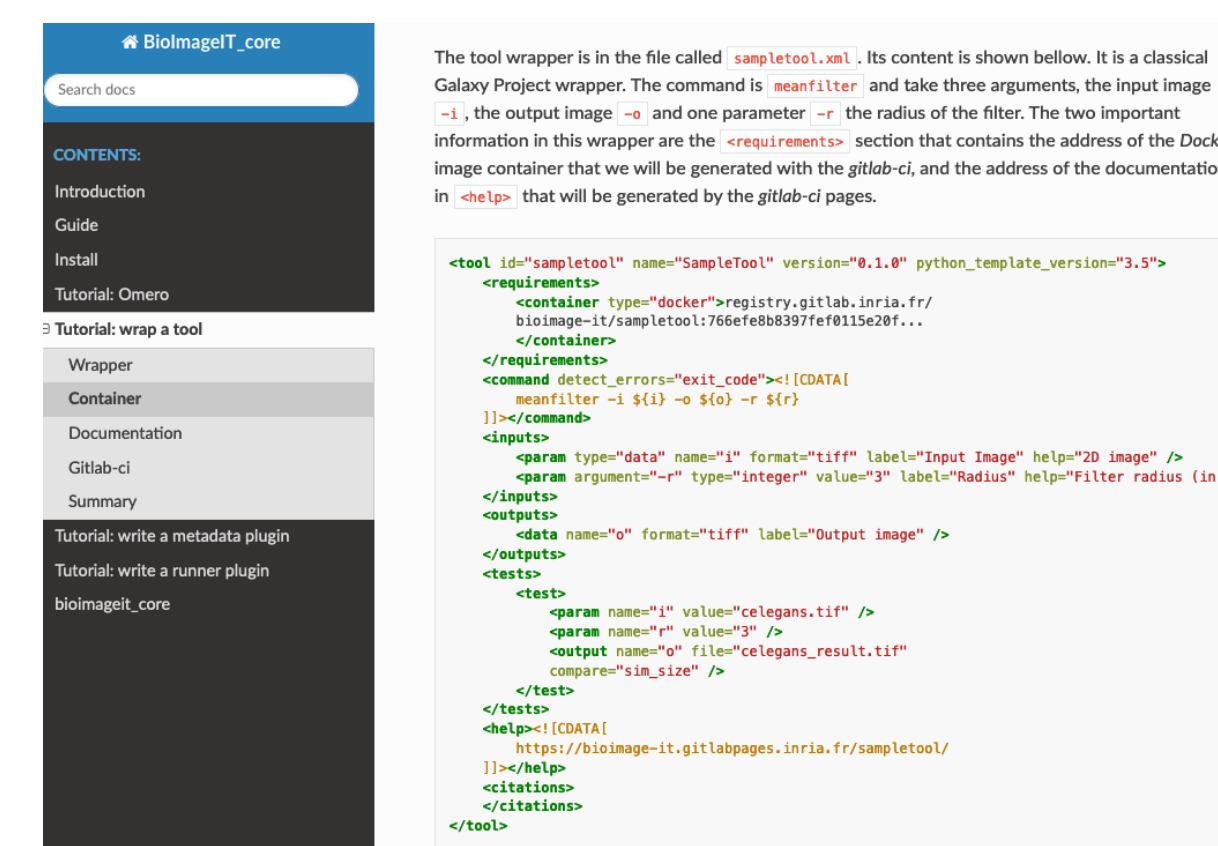
```
from bioimagepy.experiment import Experiment
from bioimagepy.pipeline import Pipeline
ConfigAccess('./bioimagepy/config_sample.json')
my_experiment = Experiment('./userdata/myexperiment')
pipeline = Pipeline(my_experiment)

process1 = pipeline.add_process(ProcessAccess().get('svecon2d_v0.1.0'))
process1.set_parameters('sigma', 2, 'regularization', 2, 'weighting', 0.1, 'method', 'SV')
process1.set_dataset_name('deconv')
process1.add_input('data')
process1.run()

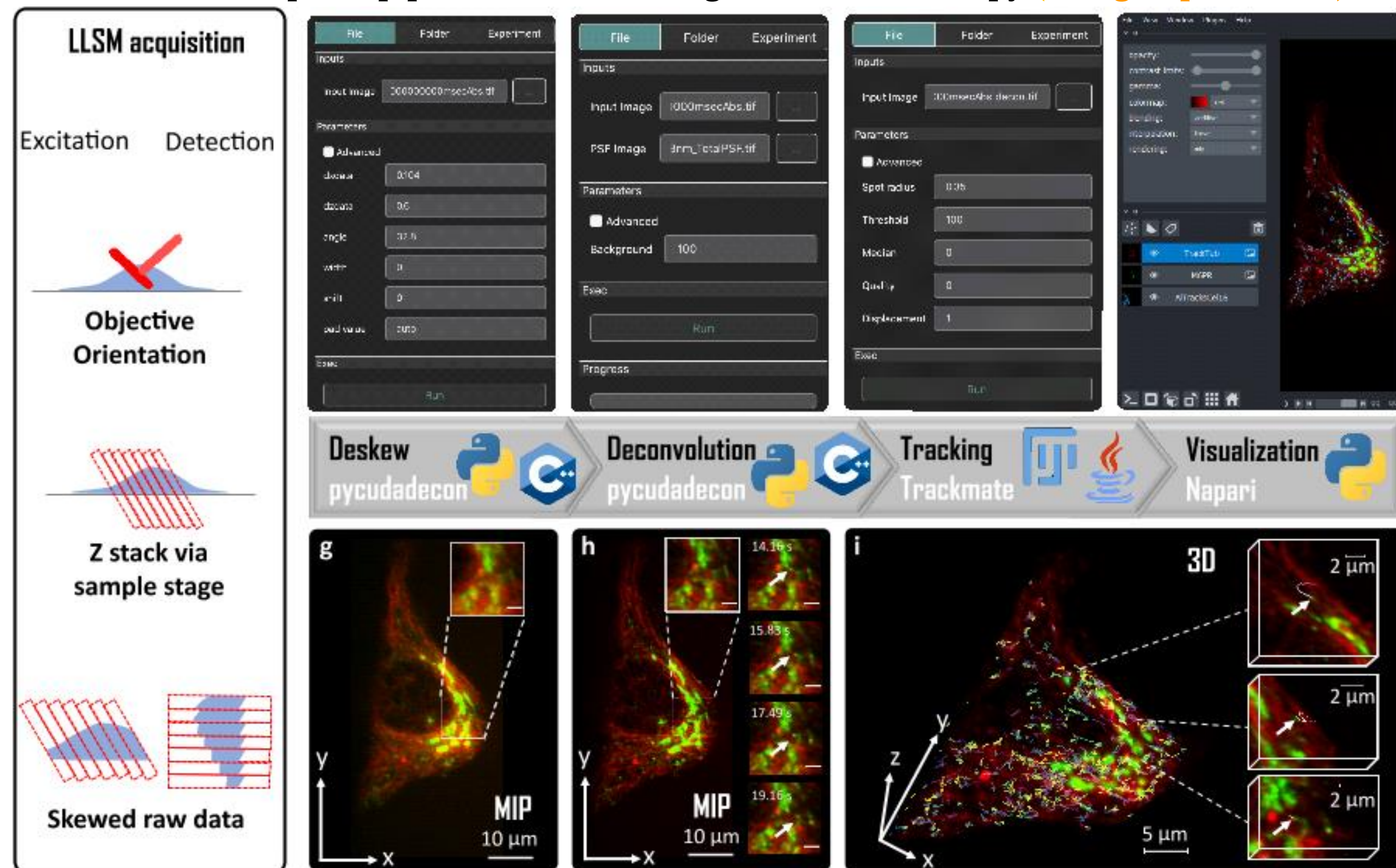
process2 = pipeline.add_process(threshold_particles)
process2.set_parameters('threshold', 'Default dark')
process2.set_dataset_name('particles')
process2.add_input('deconv')
process2.run()

process3 = pipeline.add_process(ProcessAccess().get('Wilcoxon_v1.0.0'))
process3.set_dataset_name('Wilcoxon')
process3.add_input('particles')
process3.add_input('y', 'particles', 'Population=population1', 'count')
process3.add_input('y', 'particles', 'Population=population2', 'count')
process3.run()
```

Integrate your own tools



Example of pipeline for Lattice Light Sheet Microscopy (Using Expert Mode)



Conclusion

- Usable for regular users of image tools and for expert Analystist
- Very easy to integrate data management tools (omero, json...) for data tracking
- Integrate your own tools
- Viewing data via Napari

Ressources and website

[Installation and view tutorials](#)

