Using Galaxy to interact with OMERO for image analysis

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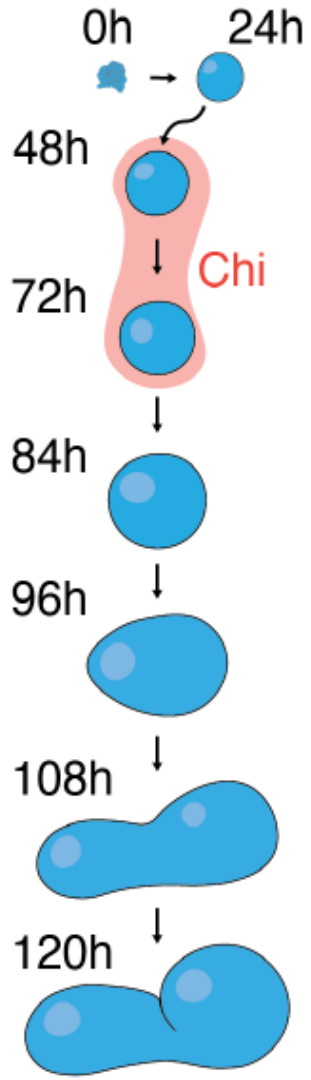
Outline

- Introduction
  - Scientific context
  - OMERO
- Our current setup (not optimal)

Scientific context

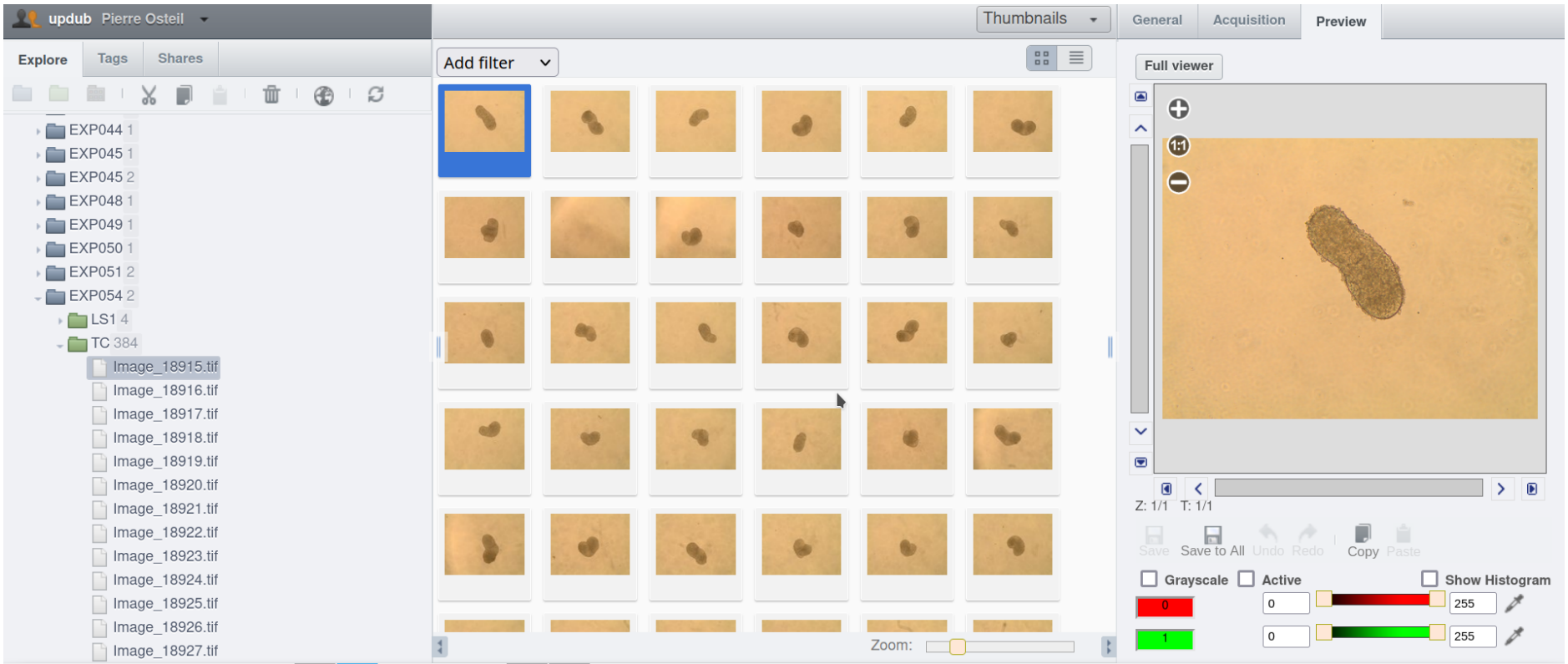
- Study early mouse embryo development with gastruloids
  - Study impact of different treatments (genetic rearrangement, chemical, mechanical) on development and elongation
  - Need an automated 'quantitative' pipeline
    - Beginning of image analysis
    - Get Area of Gastruloids
    - Elongation index
    - Localisation of fluorescent proteins

BIOP

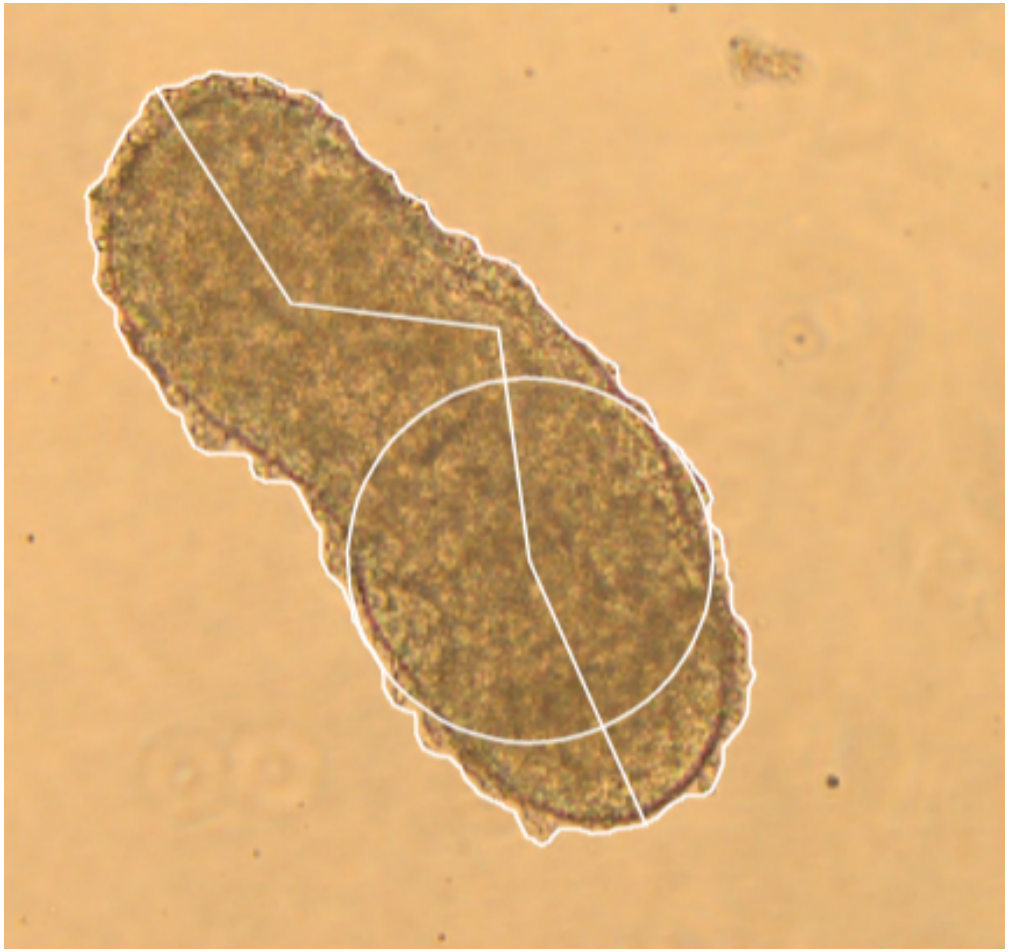


from Rekaik et al. 2022

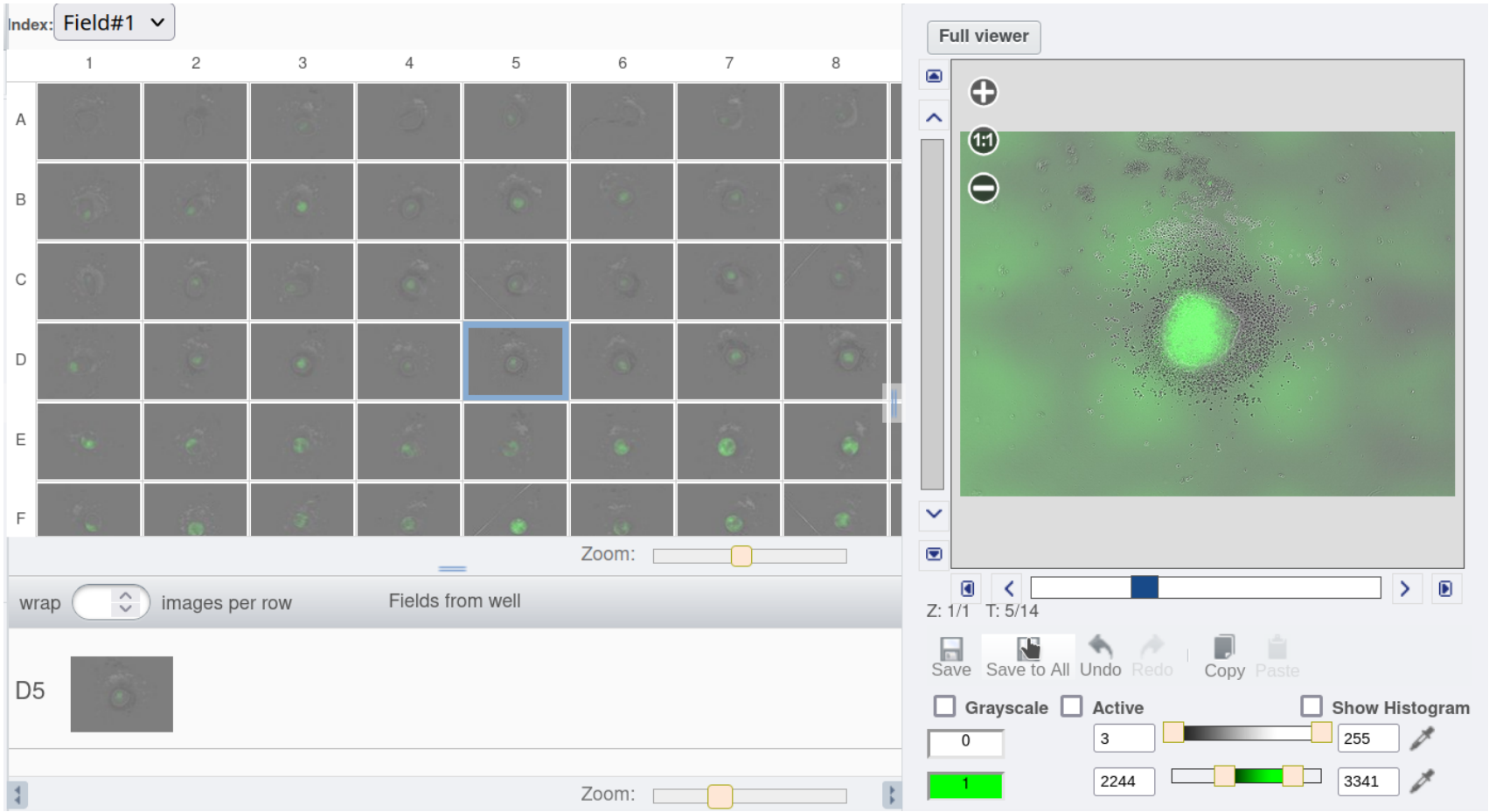
OMERO server at EPFL



OMERO server at EPFL



OMERO server at EPFL



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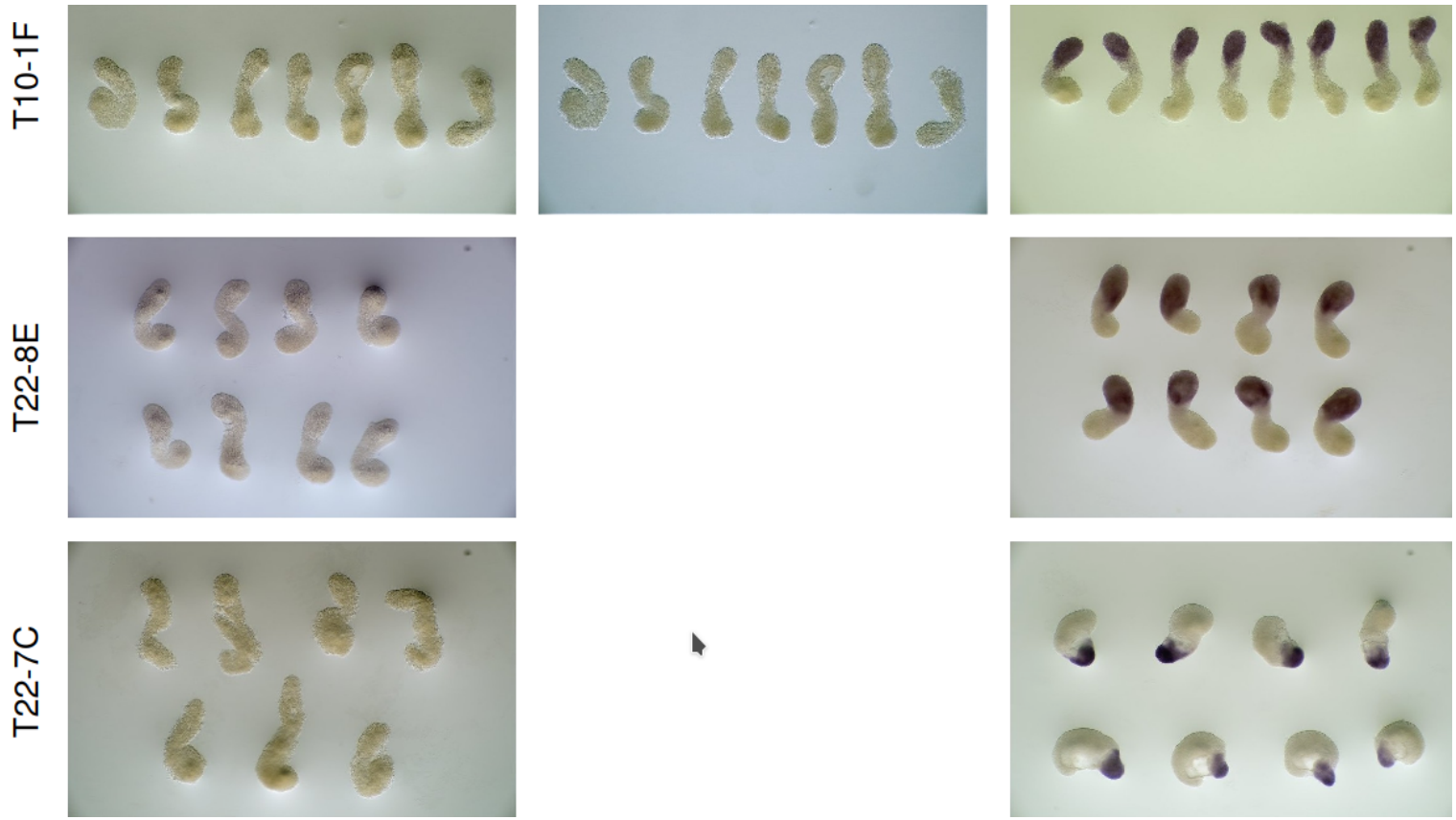

Duboule's lab setup
1. Backup and put to OMERO

High throughput images
(whole plates, time-course)
A lot of metadata are in filename
One file per channel per time-point

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→ Backup Server

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Backup
Server

Galaxy

Stack Incucyte Plate And upload to omero

Omero-py
CLI

OMERO

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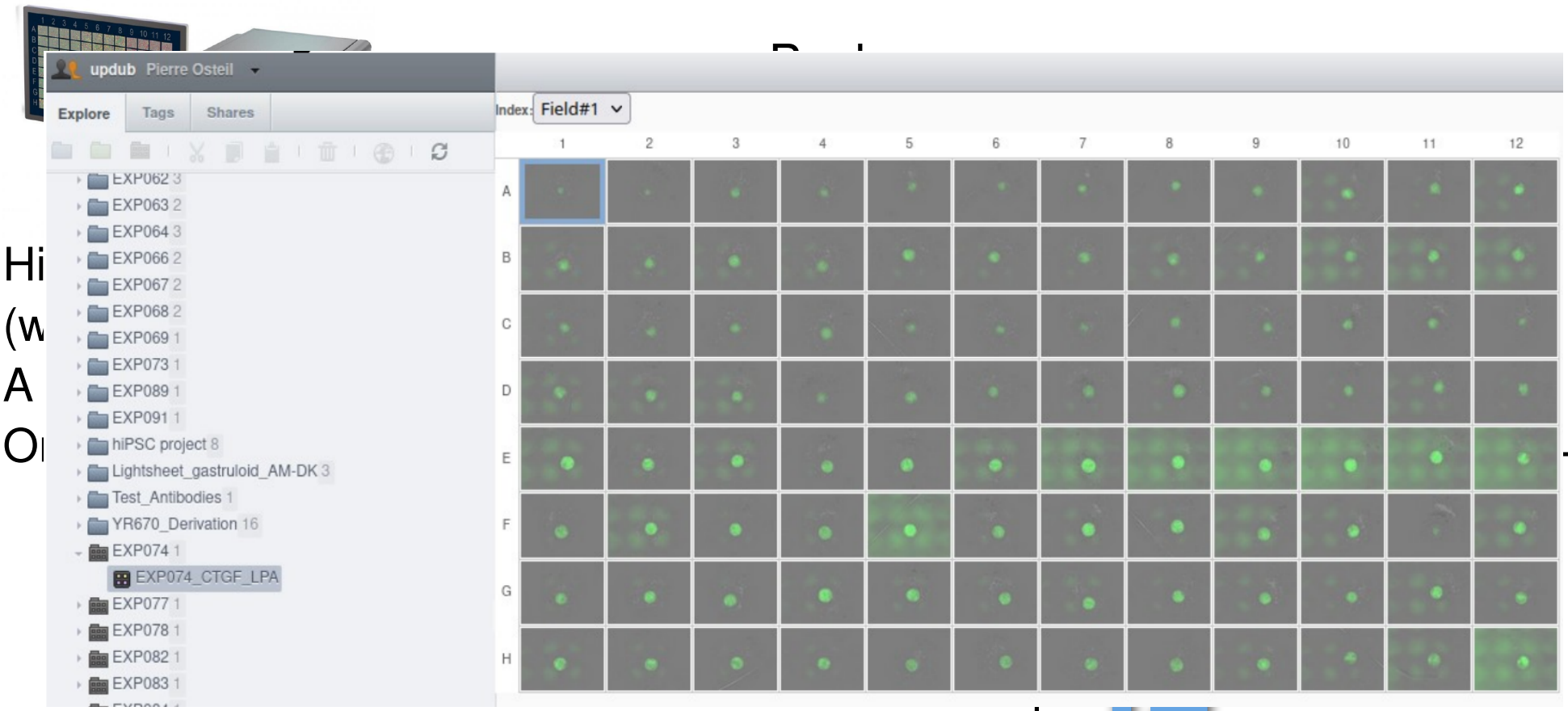
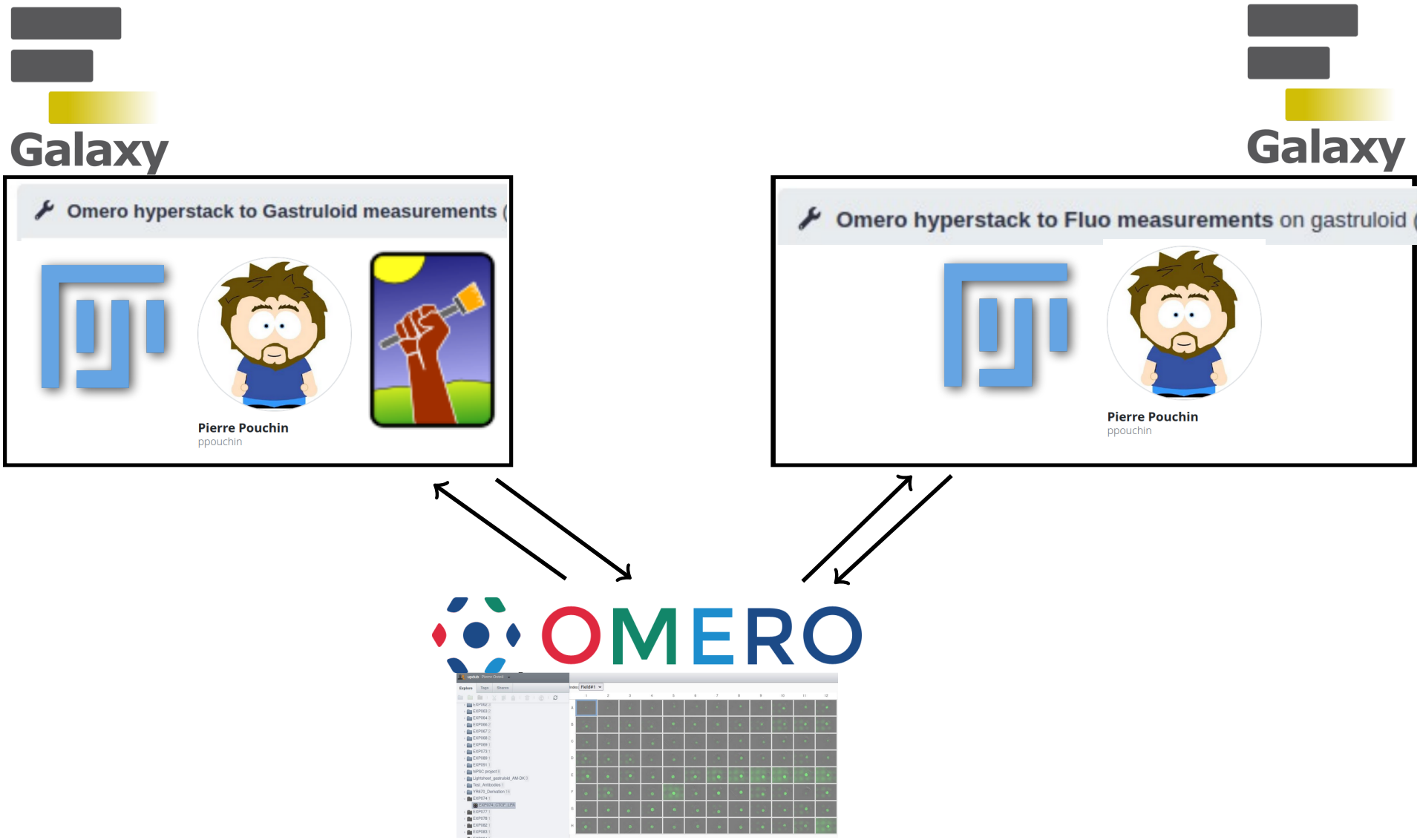


Duboule's lab setup

2. Analysis (segmentation + measurement)



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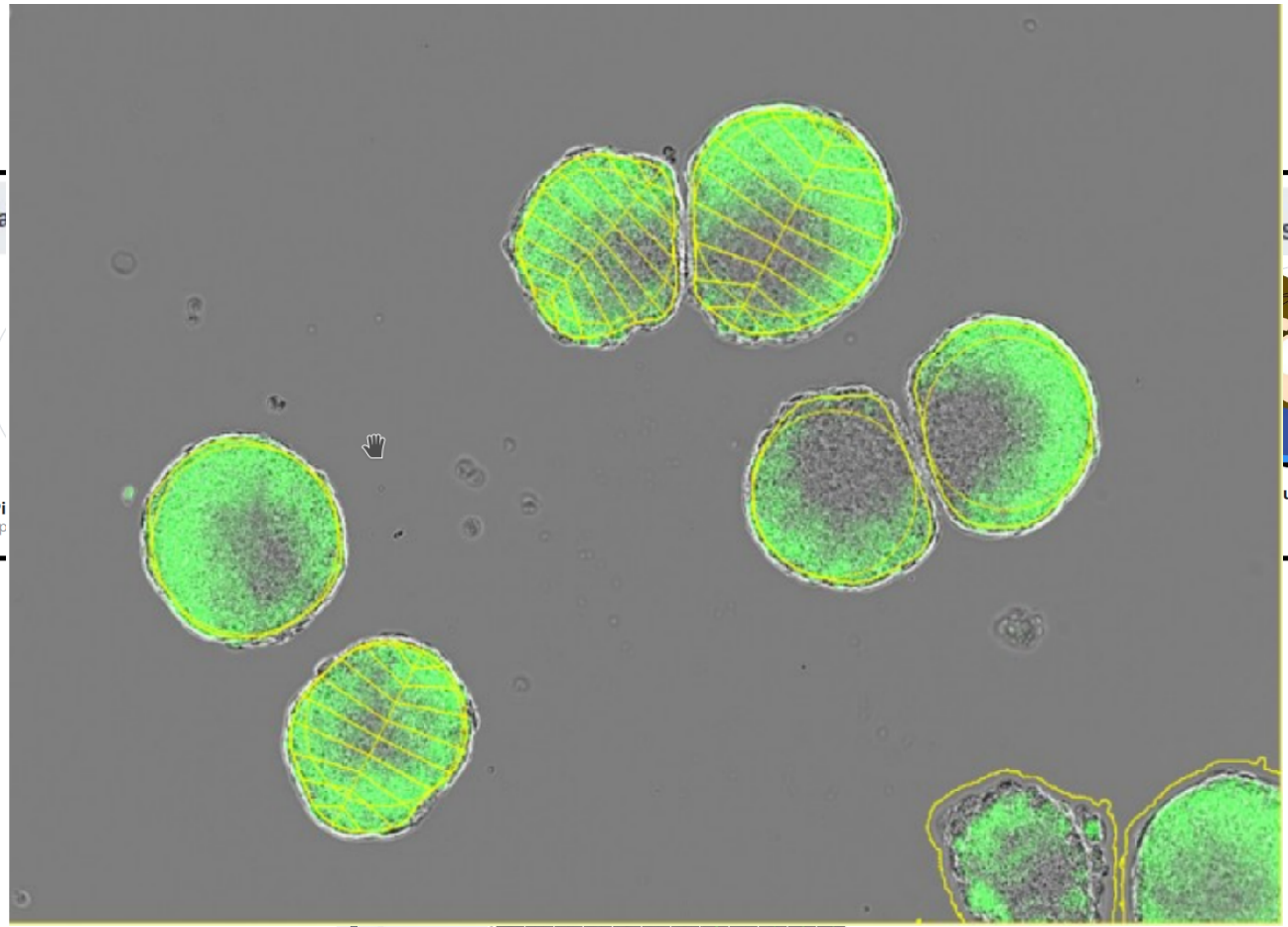

Conclusion

- Galaxy enables to run the macros without GUI, keeping trace of what have been done.
- lldelisle-tools do not follow the 'galaxy spirit' (cut a pipeline into very small pieces)
  - To avoid read and write
  - To make sure what is sent back to OMERO comes from the same image.
- Everything is available on my github, tools are available on testtoolshed (unless you think they can be used by more people than my lab).

Acknowledgements

- Duboule's lab (Pierre)
- BIOP (Romain & Rémy)
- Pierre Pouchin