

# BIP: A NEW SOFTWARE APPROACH FOR BATCH ANALYSIS OF BIOLOGICAL IMAGES

Eric Biot, Sandrine Lefranc, Ayoub Ouddah, Philippe Andrey

Université Paris-Saclay, INRAE, AgroParisTech, Institut Jean-Pierre Bourgin (IJPB), 78000, Versailles, France.

## Motivations

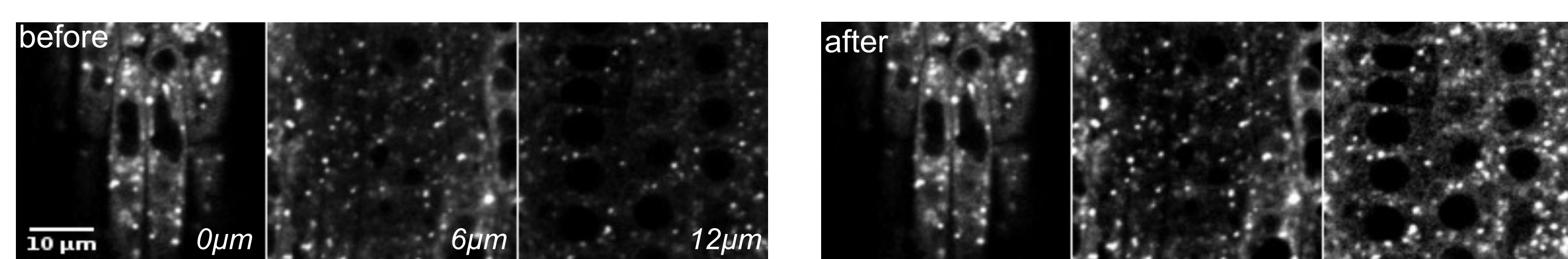
- Overcoming constraints and limitations of existing tools
  - supports all numerical types (from 8-bit to double float precision)
  - supports 2D/3D, multi-channels, time-lapse, and vector images
- Efficient computing and HPC support
  - Generic and optimized operators written in C++
- Easy, reproducible batch processing without programming
  - Minimal, unified syntax to invoke operators and define pipelines
- Simple specification of image sets to be processed
  - Command-line tool benefiting from shell wildcards

```
shell$ bip <operator> *.tif
```

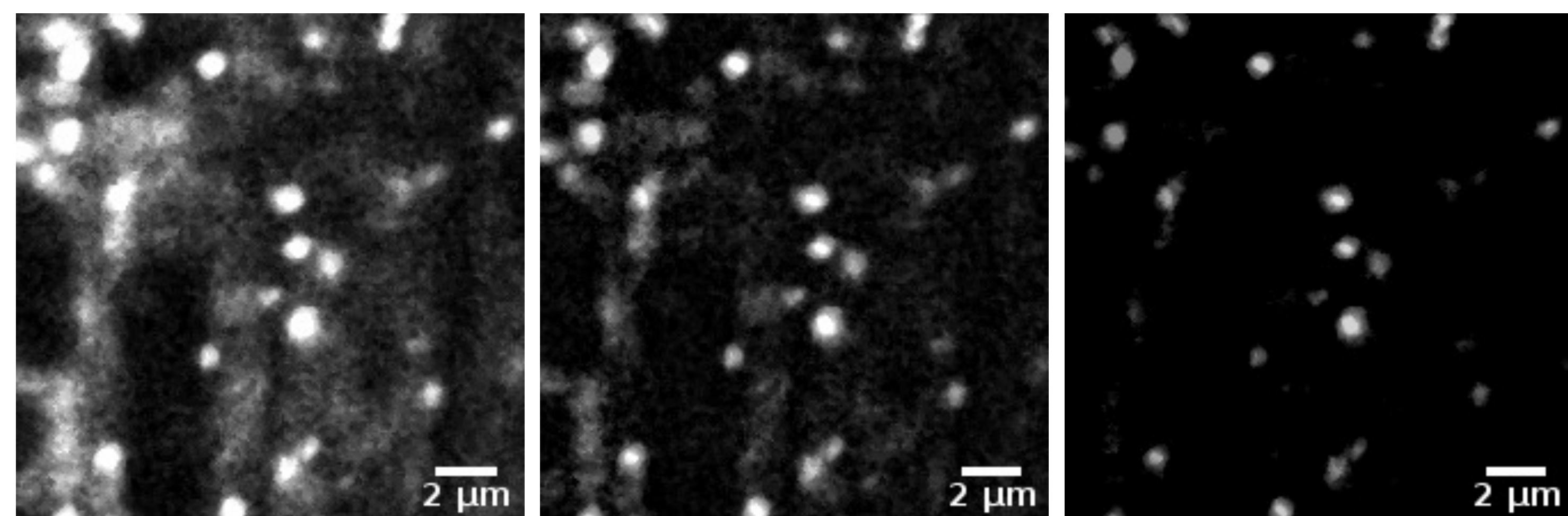
## Image processing

Bip offers classical and original processing operators:

- Pre-processing:** linear, non-linear, and adaptive noise filtering, contrast enhancement, attenuation correction, PlantSeg wrapper, etc.
- Mathematical morphology:** (fast) binary and grey-level operators, standard and attribute top-hats, reconstruction filters, ASFs, etc.
- Segmentation:** classical, marker-based, and auto-seeded watersheds, thresholding (Otsu, Hats, ...), gradients, etc.



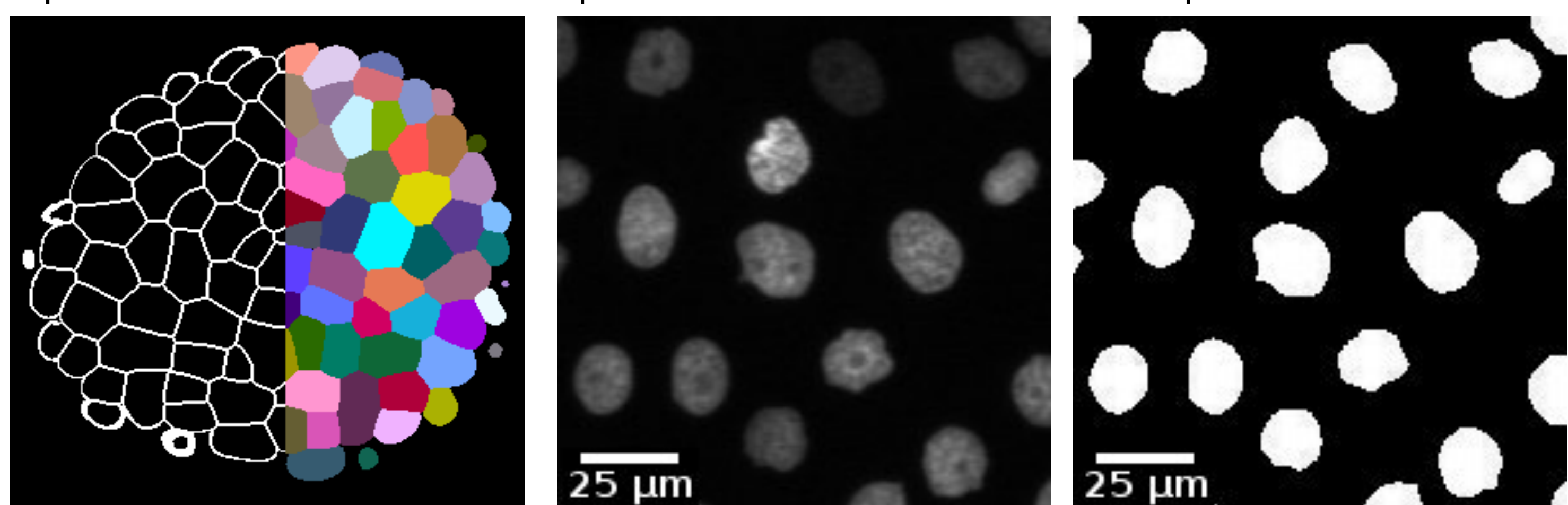
Attenuation correction



Input

Top Hat

Size Top Hat



Watershed

Homogeneous Attribute Threshold Selection

## Conclusion

- Batch processing of large numbers of multi-dimensional images
- Combines simplicity, efficiency, robustness and reproducibility
- Algorithmic processes and data are completely separated
- Large number of operators (>130) in constant evolution

## Acknowledgements

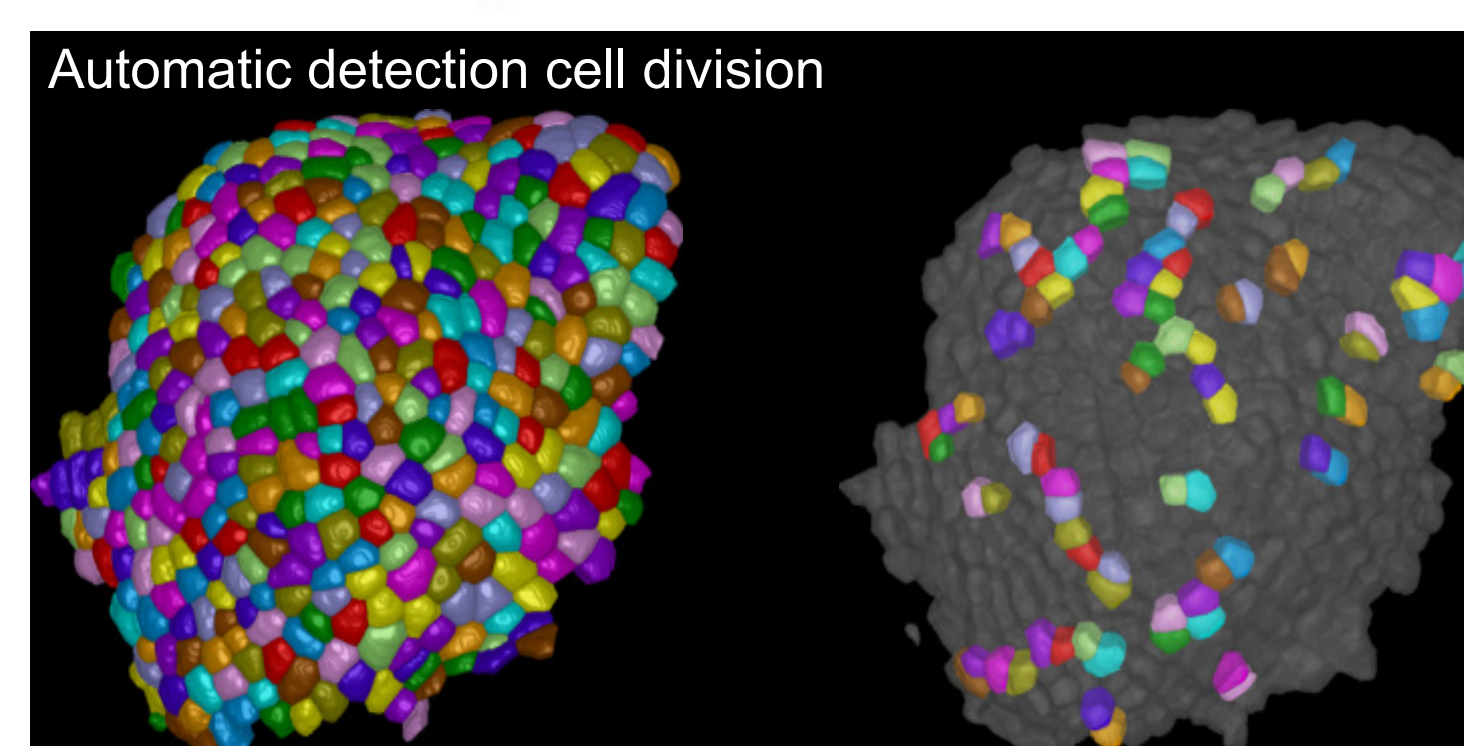
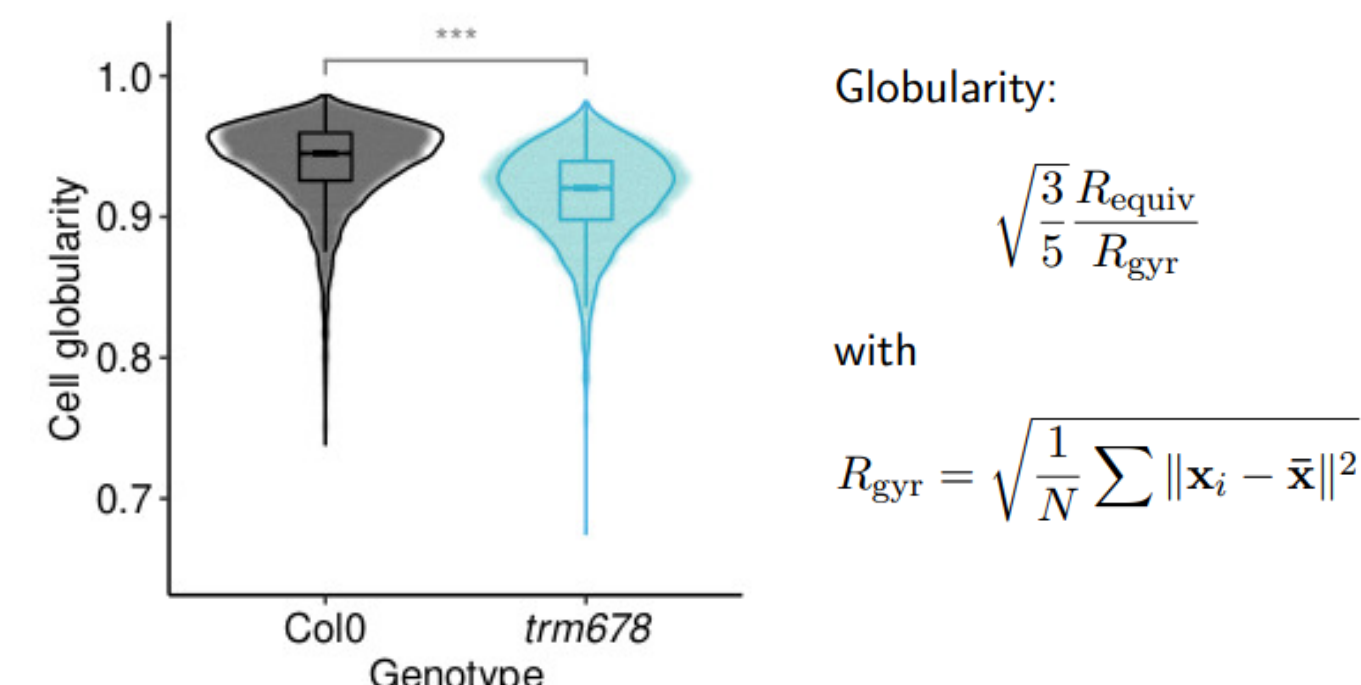
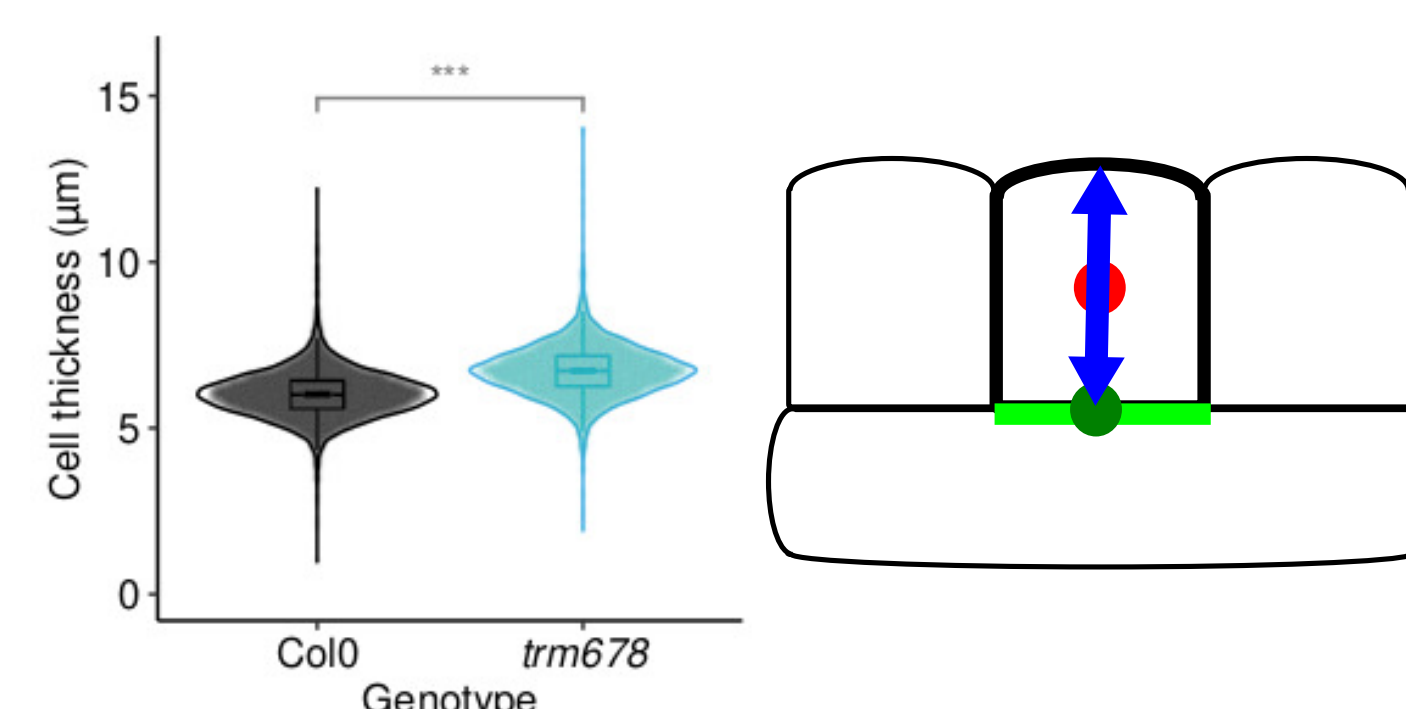
We thank Chie Kodera, Magalie Uyttewaal and David Bouchez (IJPB, INRAE Versailles) for providing time-lapse 3D confocal images of *Arabidopsis thaliana* meristems.



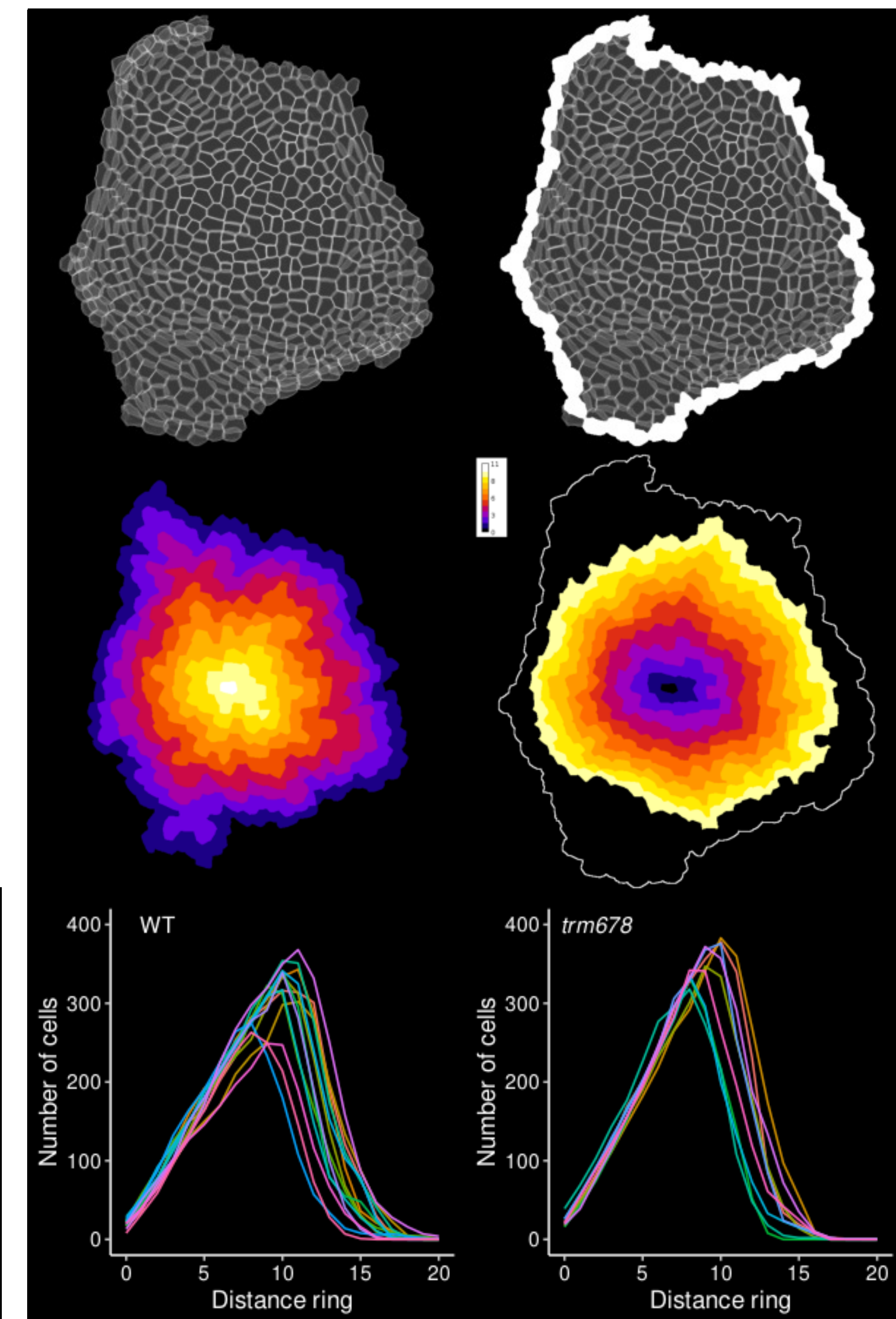
## Analysis

Bip offers classical and original analysis operators:

- Photometry:** object intensity histogram descriptors
- Morphology:** size (volume, area, principal axes) and shape (elongation, globularity, thickness, etc.) measures, interfaces, etc.
- Topology:** connectivity, cell to cell distances, automated detection of external and fringe labels, division/lineage reconstruction, etc.

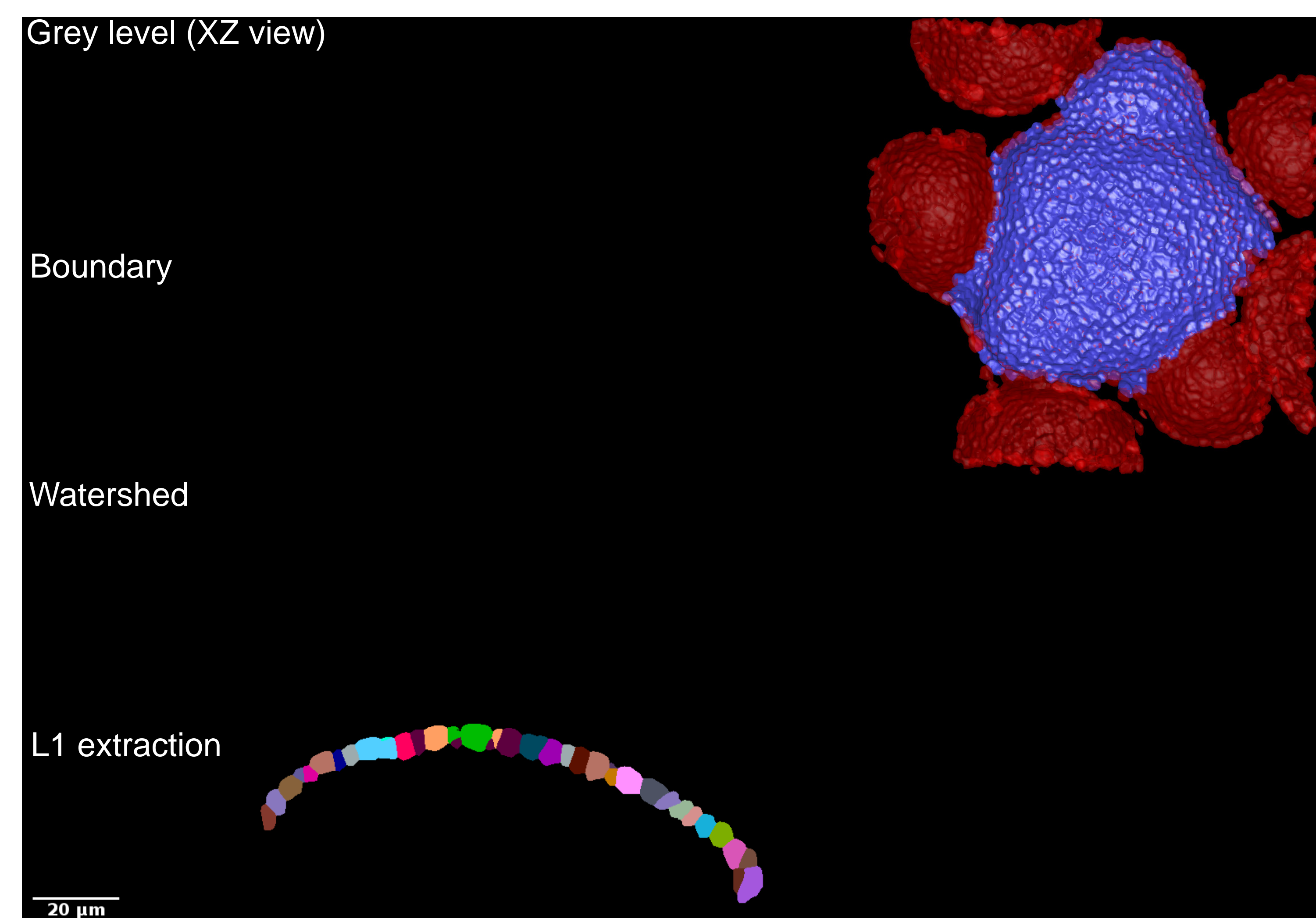


Automatic detection cell division



- Available on N images, 2D/3D, with K channels, T timepoints
- Results can be directly imported into R, Excel, etc.

## Batch processing



Grey level (XZ view)

Boundary

Watershed

L1 extraction

Automated extraction of meristem dome layer 1

Text file *dome.txt*:

```
plant-seg
h-watershed 0.12
store %i mage
zmap
store %zi mage
h-watershed 12
select largest
store %largest
recall %zi mage
mask %largest
store %ref
recall %i mage
izmap %ref
label -reconstruction %i mage
```

```
shell$ bip pipeline dome.txt *.tif
```

## Benchmarking