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

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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 tophats, reconstruction filters, ASFs, etc.
- **Segmentation:** classical, marker-based, and auto-seeded watersheds, thresholding (Otsu, Hats, . . .), gradients, etc.
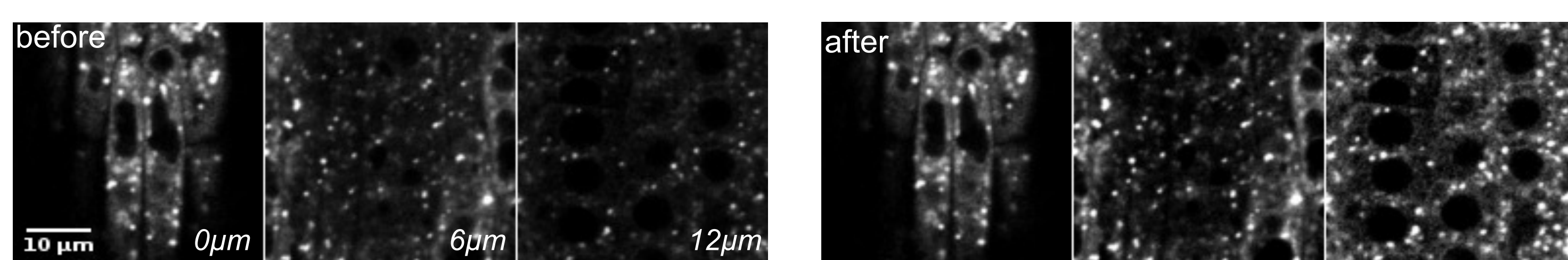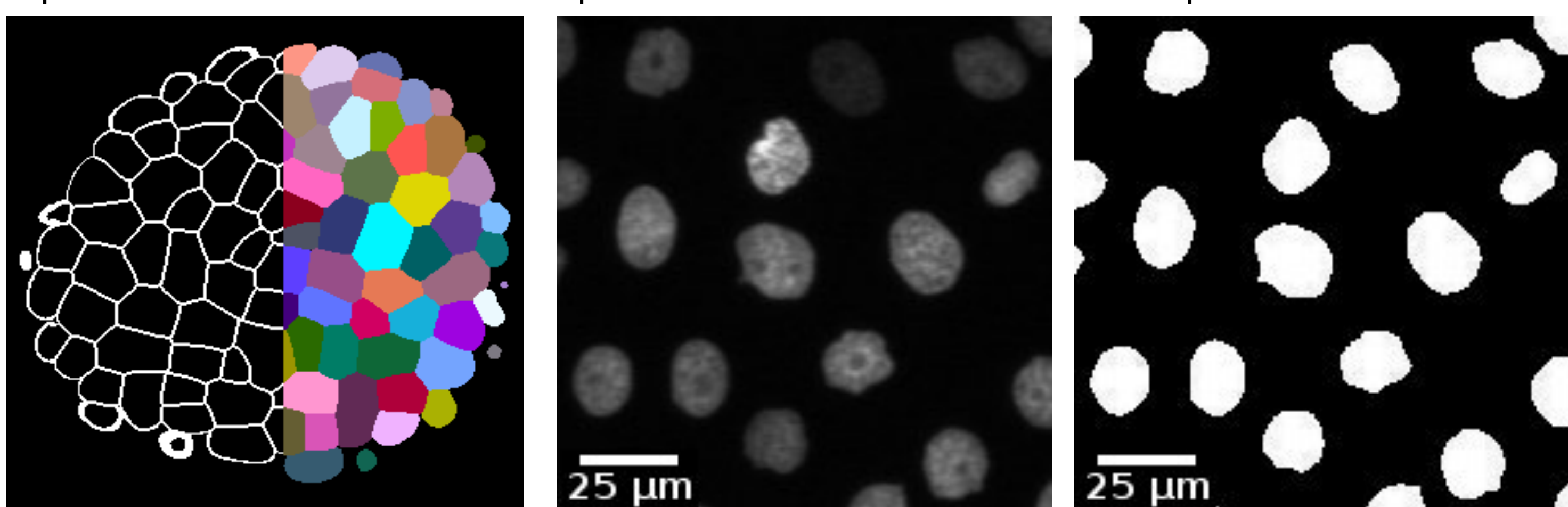

Attenuation correction
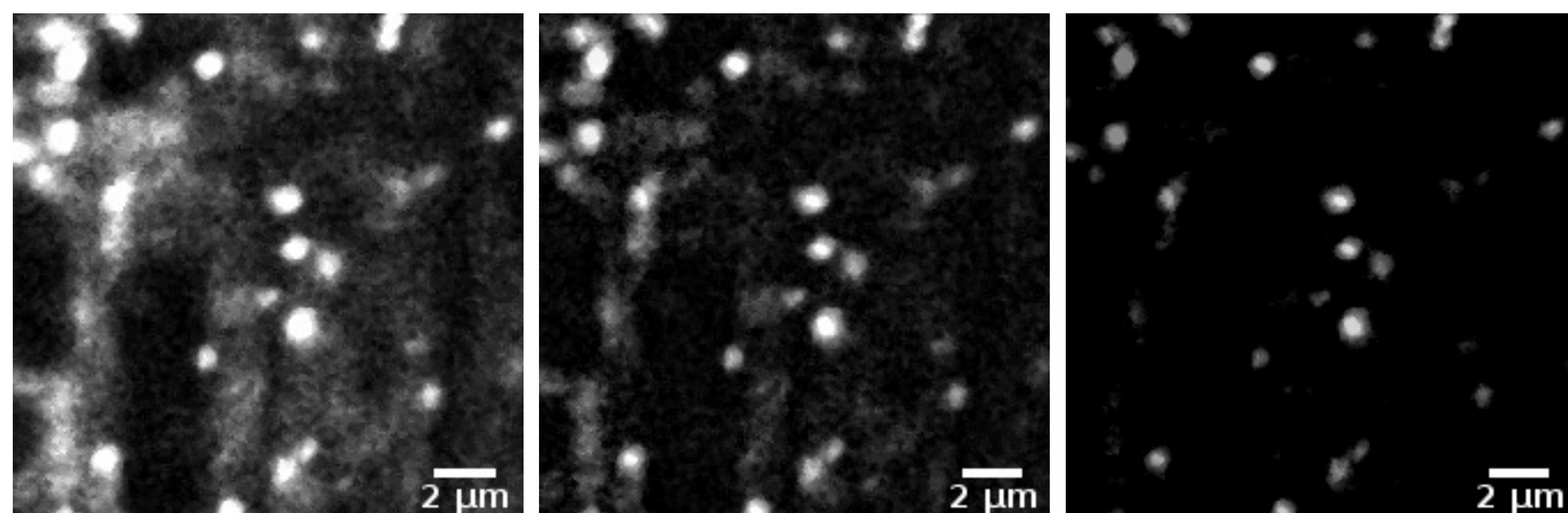
Input   Top Hat   Size Top Hat

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
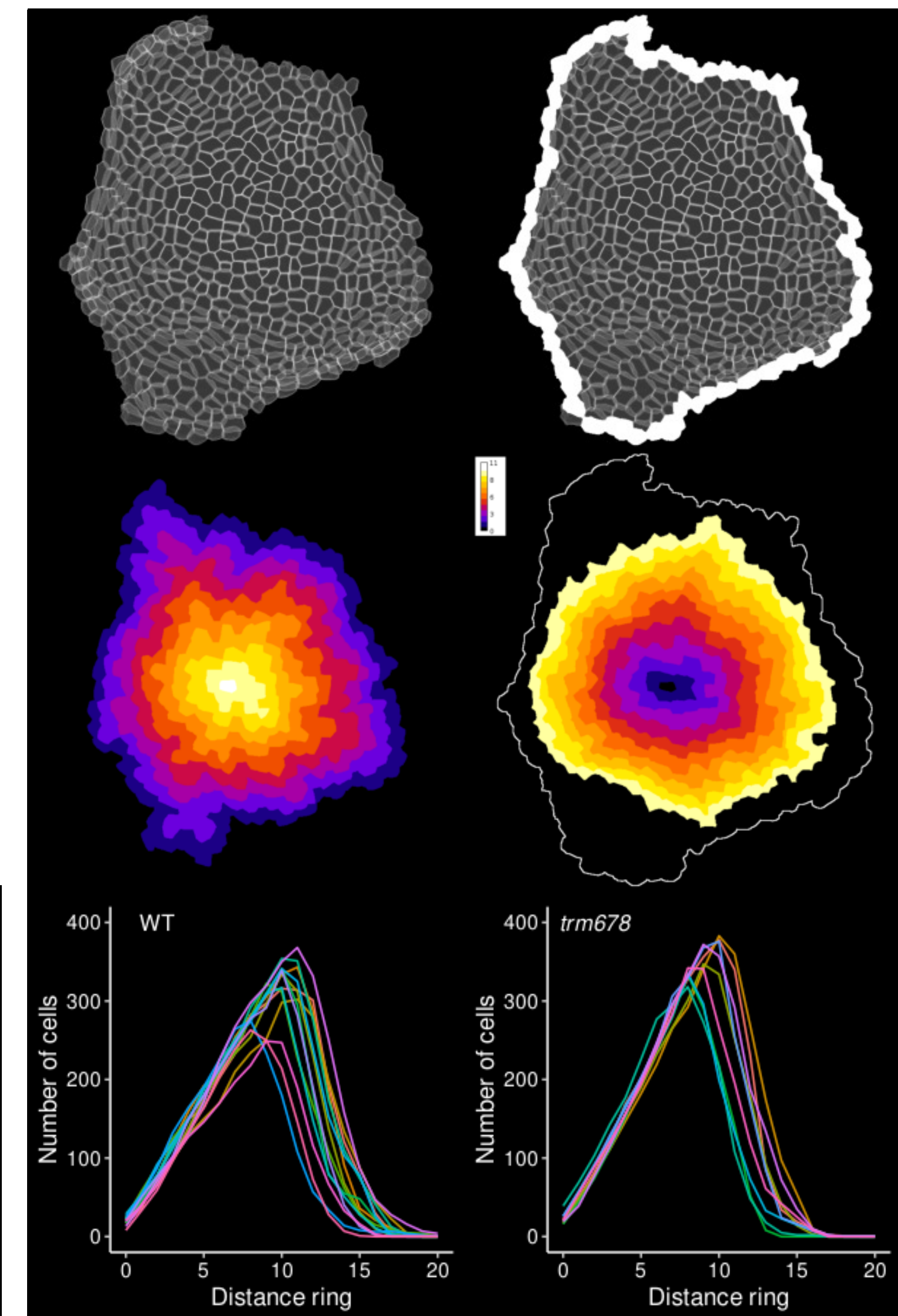
Acknowledgements

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.

Globularity:

$$\sqrt{\frac{3}{5}\frac{R_{equiv}}{R_{gyr}}}$$

with

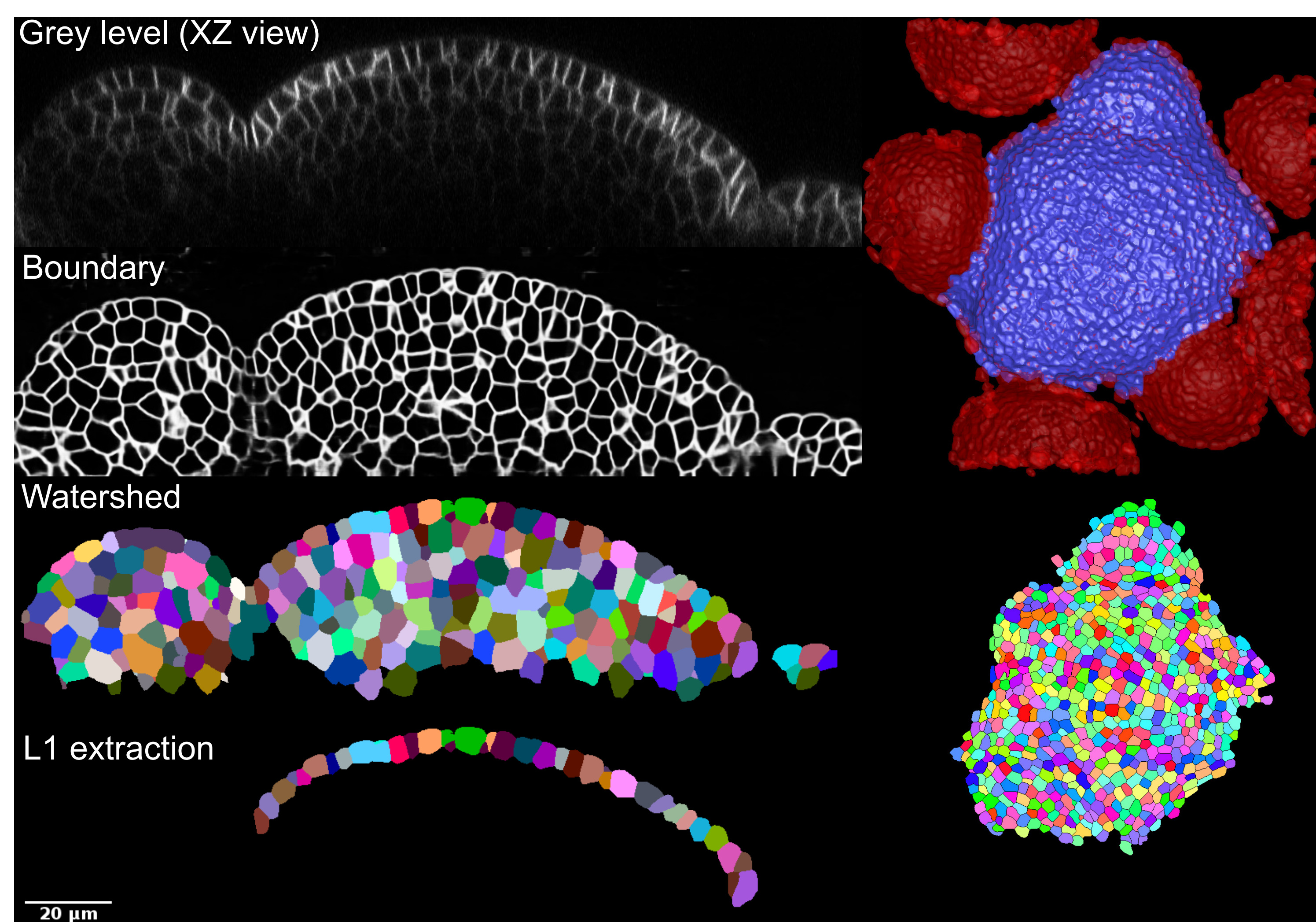$$R_{gyr} = \sqrt{\frac{1}{N}\sum \|\mathbf{x}_i - \bar{\mathbf{x}}\|^2}$$
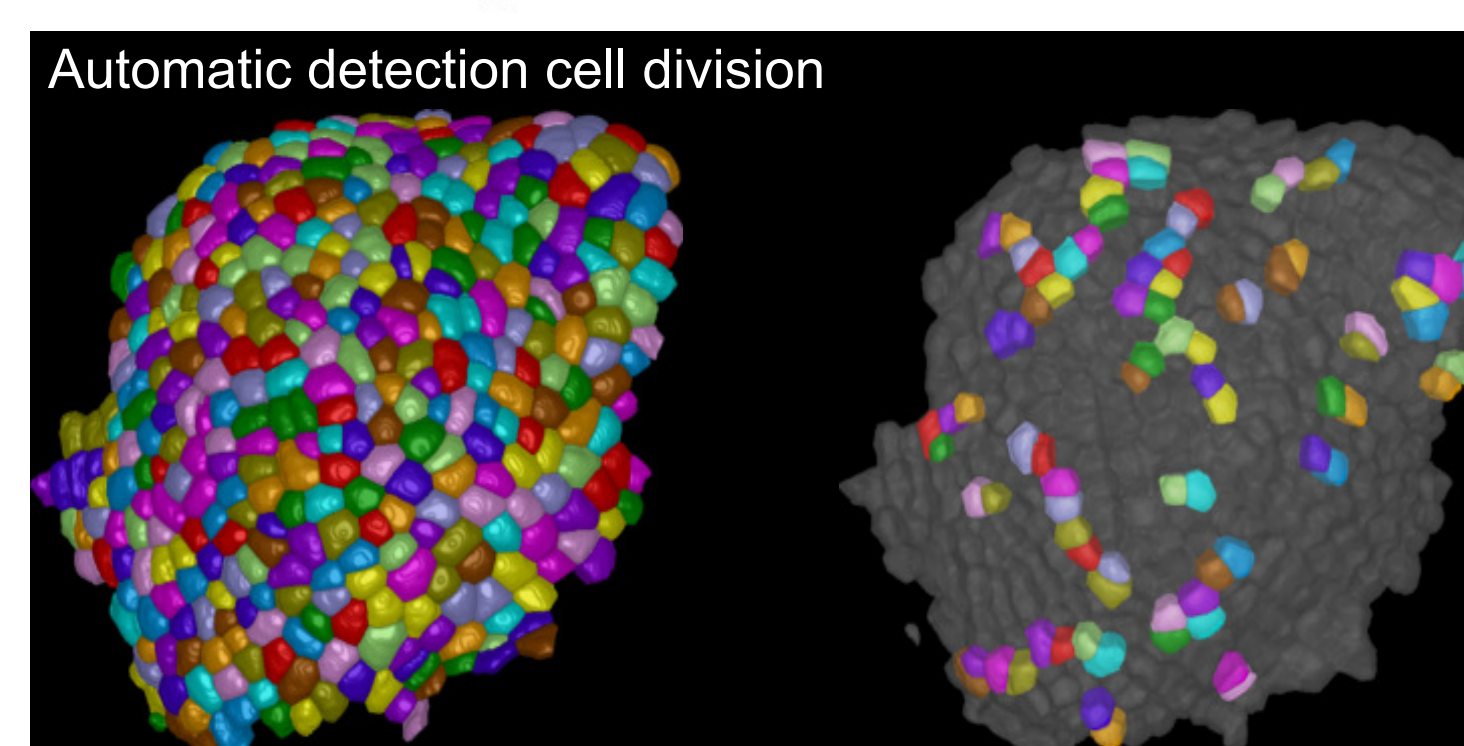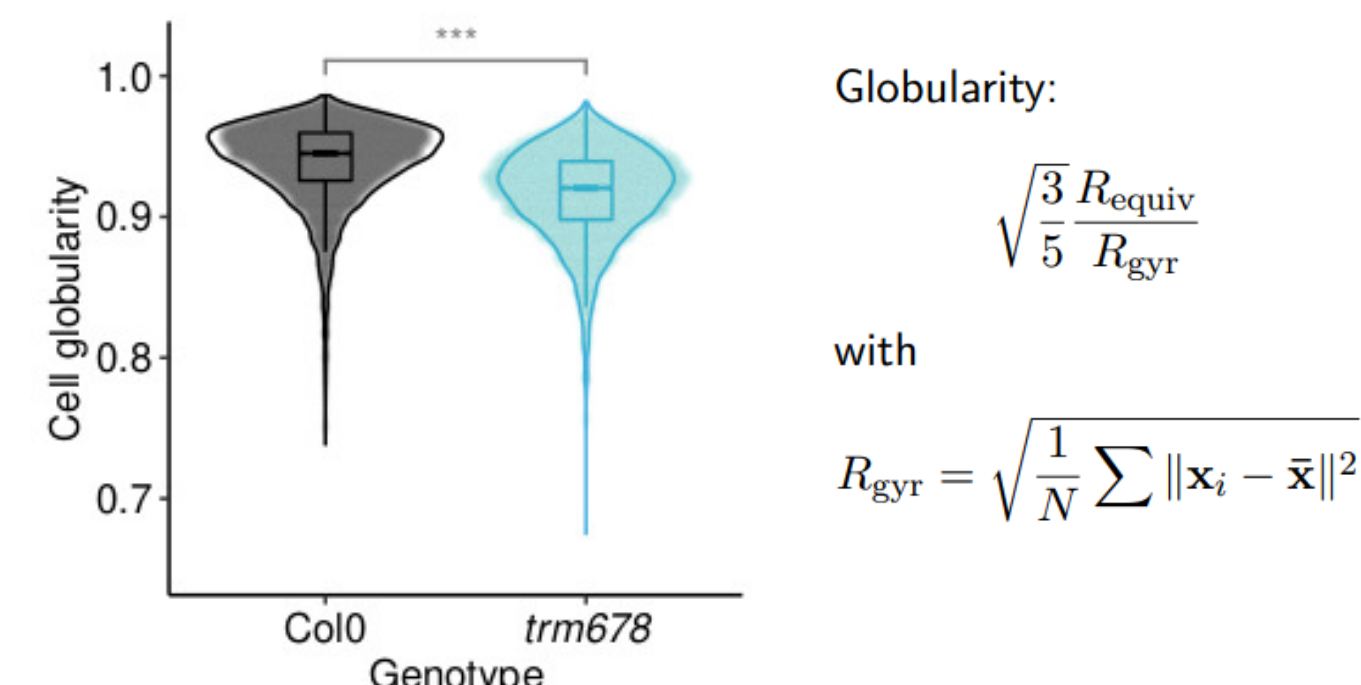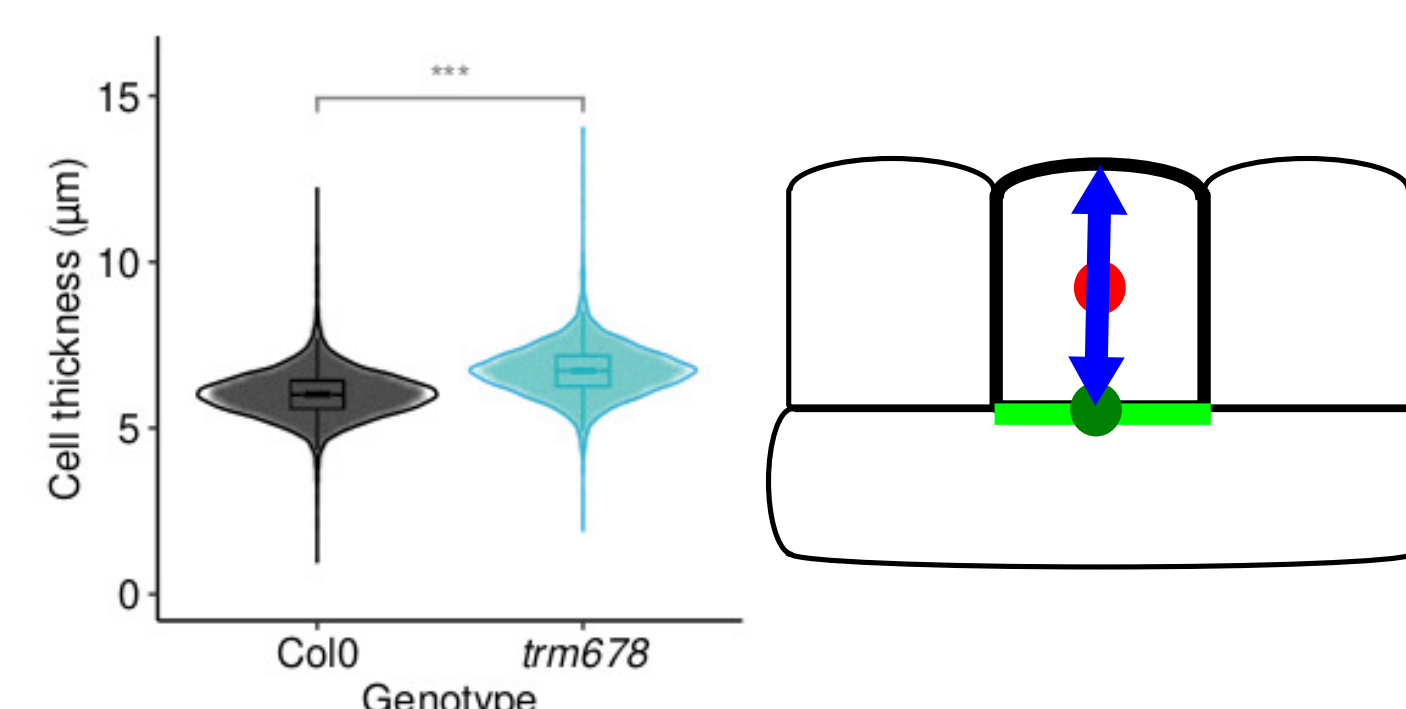
Automatic detection cell division

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

Batch processing

Automated extraction of meristematic dome layer 1

Text file *dome.txt*:

```
plant-seg
h-watershed 0.12
store %image
zmap
store %zimage
h-watershed 12
select largest
store %largest
recall %zimage
mask %largest
store %ref
recall %image
izmap %ref
label-reconstruction %image
```

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

Benchmarking