# MorphoLibJ: an integrated library for morphological filtering, segmentation and analysis of plant tissues

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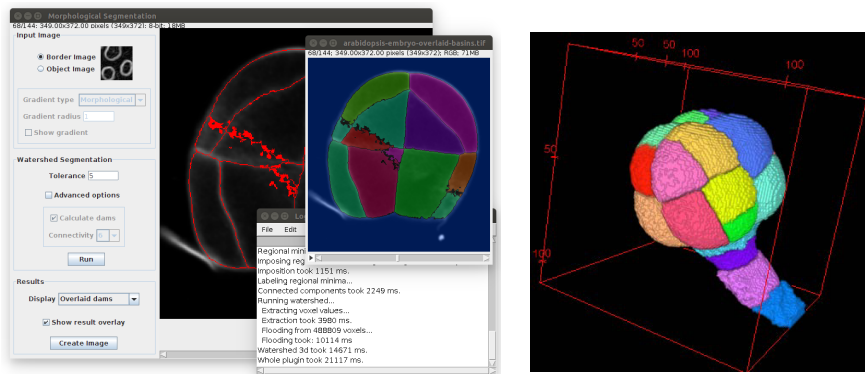[d] Sorbonne Universités, UPMC Univ Paris 06, UFR927, F-75005, Paris, France

## Context: analysis of the morphology and organisation of cells in plant organs and tissues

Understanding the cellular bases of complex phenomena such as plant development and morphogenesis requires the precise determination and quantification of cellular morphology and of tissular organization. Imaging techniques such as 3D confocal microscopy constantly gain in spatial resolution, signal quality and throughput, thus allowing 3D imaging of several dozens or hundreds of cells and of their spatial organization. However, the automated analysis of plant tissues still remains challenging.

The MorphoLibJ library therefore proposes a collection of tools that facilitate the exploitation of 3D images of plant cells. These tools are mostly based on mathematical morphology, including powerful algorithms such as 3D watershed and 3D geodesic reconstruction. Moreover, these algorithms were integrated into user-friendly interfaces to facilitate their appropriation by biologists.

## 1. Image Processing



A large collection of morphological filters have been implemented both for 2D and 3D images. Available operators range from base operations (dilation, erosions) and their compositions (opening, closing, gradient, top-hat…) to more elaborate algorithms such as geodesic reconstruction or H-minima and H-maxima transforms.
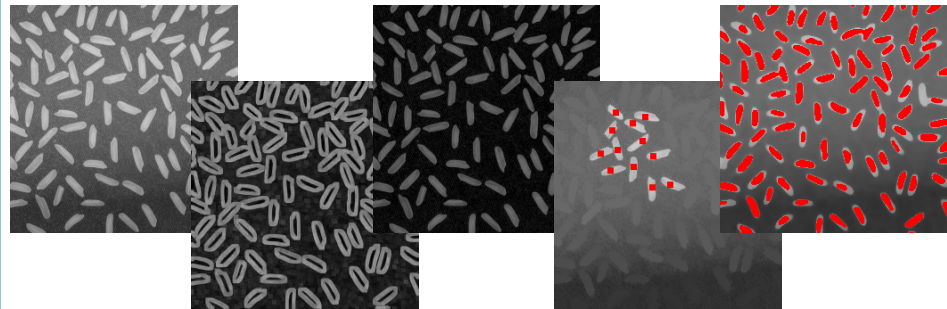
## 2. Semi-Automated 3D Watershed Segmentation



The morphological segmentation plugin allows to quickly segment 2D or 3D plant tissues composed of many cells. It is based on a powerful watershed implementation, packed together with a semi-automated detection of extended minima. Only a single parameter needs to be adjusted. Direct visualization of the result in a user friendly graphical interface greatly improves the time spent for segmentation of 3D images.

## 4. Application: Quantitative description of arabidospsis early embryo



The MorphoLibJ library was applied to the analysis and modeling of cellular division in *arabidopsis thaliana* early embryo. 3D gray scale images were acquired with confocal microscopy. The computation of extended minima imposed allows rough detection of cells, that was used in conjunction with the watershed algorithm to obtain accurate 3D segmentation of all cells in the embryo. The quantification of cells and the application of clustering algorithms could reveal homogeneous populations of cells corresponding to distinct tissues.
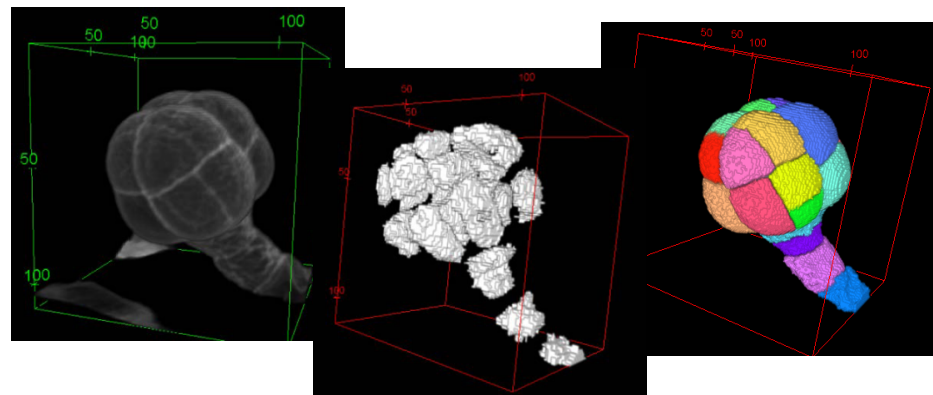
## 3. 3D Morphometry analysis

Several measurements of cell morphology (volume, surface area, mean breadth, equivalent ellipsoid…) or spatial organization (region adjacency graph) allow quantitative exploitation of images. When possible, the spatial resolution of images is taken into account for measurements.

## Conclusion & Perspectives

MorphoLibJ is implemented as a plugin for the ImageJ/Fiji platform. The software is distributed freely. The sources are available on the GitHub platform:
http://github.com/ijpb/MorphoLibJ