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Open software tools for microscopy image processing

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Recent advances in microscope technology combined with new digital tools now provide outstanding images (3D, time-lapse, multichannel, fluorescence), allowing us to address fundamental questions in developmental biology, molecular biology and neuroscience. The analysis of this unprecedented flow of imaging data requires the development of sophisticated software packages to numerically reconstruct images and to automatically perform segmentation, quantification and tracking of structures of interest. This has led to the emergence of a new field of research, "bioimage informatics," which aims to develop computational procedures to process, analyze, and visualize images coming from various light microscopy techniques.

Here, we report our experience in the development of open-source software tools. These tools are written as Java plugins for the popular software suites: ImageJ, Fiji or Icy. In particular, we are focusing on the reconstruction of images from incomplete data measurements. This is often a challenging image-processing task in terms of algorithmic tuning and computational runtime. In this context, we show the importance of carefully identifying the image formation model in properly designing algorithms. We describe bioimaging applications such as restoration of details with deconvolution methods, recovery of shape from phase images, segmentation of cellular compartments from the photobleaching decay, reconstruction of nanoscale images by applying super-resolution localization microscopy, and generation of theoretical point-spread functions.

Often overlooked in software development, the validation and usability are finally what counts for the end-users. In this respect, we report our effort to propose reference datasets and quantitative benchmarks of software through the organization of Grand Challenges.