Focus on bioimage informatics

Since the arrival of the digital camera and other computerized equipment, microscopy has increasingly relied on computational tools to acquire, store and analyze images. The grandfather of these tools, NIH Image, is still alive today in the form of ImageJ, but it is now one of an ever-increasing array of bioimage-informatics tools. A special Focus with contributions from leaders in the field highlights this emerging discipline and some of the computational tools that are being developed for biologists. A Review article discusses the role of computational tools at each stage of an imaging experiment, with a focus on open-source solutions. Perspective articles describe three prominent examples of generalist image-analysis tools that each provide biologists with a large selection of different functionalities and facilitate development and delivery of new algorithms to end users. Three Commentaries discuss the opportunities and challenges in bioimage informatics. Finally, original research articles and Correspondences describe new developments in the field of bioimage informatics.

Brief Communications p721, p724, News and Views p655

Catching more with FISH

Single-molecule fluorescence in situ hybridization, or smFISH, uses fluorescently labeled oligonucleotides to image and count individual mRNA transcripts in single cells. Such measurements have previously been limited to imaging transcripts from no more than a few different genes at a time. Lubeck and Cai describe barcoding methods for stochastic optical reconstruction microscopy, a super-resolution imaging method that allows them to greatly increase the multiplexing capability of smFISH. They demonstrate the method by counting the mRNA transcripts for 32 different genes in single Saccharomyces cerevisiae cells. The technique could be extended to larger numbers of different transcripts and to applications besides smFISH.

Article p743

Exploring the zebrafish brain

Mapping gene- and protein-expression patterns to an anatomical brain reference is essential to understand the way the brain is organized and how it develops. Ronneberger, Driever and their colleagues have developed an interactive web tool for virtual exploration of the larval zebrafish (Danio rerio) brain. The Virtual Brain Explorer for Zebrafish, or Vibe-Z, software fuses multiple confocal stacks, aligns three-dimensional gene- or protein-expression patterns of different larvae of a given developmental stage to a common reference and stores the aligned patterns in the Vibe-Z database. An end user can record new expression patterns with any standard confocal microscope, upload the resulting files to the server and download the aligned image for further exploration.

Article p735

Tracking cells in whole embryos

By placing illumination and detection objectives at right angles to one another and illuminating a sample with a thin sheet of light, light-sheet microscopy can achieve fast three-dimensional imaging with low light doses. Unfortunately, because large samples need to be rotated to image all sides, the speeds obtained until now were too slow to track individual rapidly moving cells. Keller and colleagues and Hufnagel and colleagues independently developed a way to increase the imaging speed by adding a second pair of illumination and detection objectives to create two light sheets. Although the solution sounds simple, implementing it turned out to be very challenging. Yet for many applications, it eliminates the requirement for sample rotation, thus greatly increasing the imaging speed. This allowed the researchers to track individual cells in developing fly embryos.

Brief Communication p730, Article p755, News and Views p656

Improved fluorophore localizations

One class of super-resolution microscopy techniques relies on the stochastic activation and imaging of subsets of all the fluorophores in a labeled sample; these techniques require methods for precisely determining fluorophore positions based on the bright spots they create in fluorescence images. Such localization methods have long been used for tracking fluorophores, but the speed of localization and the ability to deal with overlapping image spots are less important for tracking applications. In contrast, speed and spot density are critical in super-resolution imaging. Articles by Huang, Zhu and their colleagues and by Parthasarathy describe two different methods for calculating fluorophore localizations that will be useful for a variety of applications.

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