Supplement on visualizing biological data

The increasing amount of scientific data being generated in biology laboratories is taxing the abilities of scientists to make sense of it all and communicate it to others. A special supplement tackles this issue by bringing together a series of papers on visualization approaches and software tools that biologists use to interact with and interpret scientific data. These range from simple stand-alone software programs to complex integrated software packages. The choices of visualization tools available are daunting. Five Reviews by experts in the development and use of visualization tools for a broad range of biological data discuss the challenges faced in each area of biology and the visualization methods available for genomes, alignments and phylogenies, images, macromolecular structures and systems biology data. The Reviews include tables listing the best and most popular data-visualization tools available in each area.

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Tools to tease out neuronal circuits

Peptide toxins present in the venom of several organisms are known to selectively block ion channels and can be used as tools to dissect neuronal circuits. Ibañez-Tallon and colleagues apply optimized membrane-tethered toxins for functional dissection of mammalian circuits in vivo. By targeting the voltage-gated calcium channels that couple presynaptic activity to neurotransmitter release, the researchers demonstrate the use of tethered toxins to block neurotransmission selectively and cell-autonomously in desired cell types, using either lentiviral delivery of the toxins or bacterial artificial chromosome–based transgenesis. They apply the approach to block dopamine release as well as to suppress chronic pain in the mouse, in vivo.

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Mosaic MAZe

Organisms with mosaic tissues—tissues that harbor cells expressing genes not found in the rest of the organism—are useful for analyzing the function of particular transcripts. Zebrafish, with their transparent embryos, are ideally suited for mosaic analysis, but the challenge is the expression of a transgene in a spatially and temporally controlled way. Collins, Lewis and Linker now present a tool that will meet these challenges. Their transgene, dubbed MAZe for mosaic analysis in zebrafish, expresses Cre recombinase from a heat-shock promoter, and the enzyme activates expression of a transcriptional activator that turns on the transgene of choice, either a fluorescent protein for lineage tracing or a gene whose effect on development is to be monitored.

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Autofluorescent tumor-initiating cells

Tumors consist of heterogeneous populations of cells; some cells are more capable than others of initiating new tumors. In this issue of Nature Methods, Radovanovic and colleagues describe an unusual strategy for isolating cancer-initiating cells from human glioma. Instead of using surface markers for this purpose, the authors demonstrate that glioma-initiating cells have a characteristic autofluorescence and morphology, and that they can be isolated from both glioma cultures and fresh glioma by flow cytometric sorting based on these properties. The approach should prove complementary to more traditional strategies for the isolation of glioma-initiating cells for both basic and applied studies.

Article p224

Reprogramming with minicircles

Improved methods for reprogramming human cells are needed. With an eye to the eventual use of induced pluripotent stem cells for therapy, the ideal method would avoid permanent modification of the genome. Wu, Longaker, Kay and colleagues report the use of simple minicircle vectors to deliver the four reprogramming factors to human cells. The vectors are lost from cells over time and do not insert into the genome. Minicircle DNA was used to reprogram adult adipose stem cells, which can be relatively easily obtained from humans; this could prove useful for the preparation of disease-specific cell lines.

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