Tools for mapping interactomes

In this issue a series of papers describe complementary advances in high-throughput protein-protein interaction (PPI) methods to decipher the interactomes of various organisms. Two Articles by Vidal and colleagues, in collaboration with members of several other laboratories, present methods to assess the quality and coverage of PPI datasets from large-scale screens and assign quality scores to individual protein-protein interactions. A Resource by Vidal and colleagues uses some of these methods to assess the quality of the largest Caenorhabditis elegans interactome assembled so far and estimate its full size. In an Analysis, Ideker and colleagues assess the performance of different experimental designs for completing interactome mapping efforts. All of these efforts point to the need for complementary high-throughput PPI screens that have little overlap with existing techniques. In a Brief Communication, Quake and colleagues describe a promising microfluidic platform that will help fill this need.

Articles p83, p91, Resource p47, Analysis p55, Brief Communication p71

Addressing issues in PPI curation

Large-scale curation of biological data from the primary literature has become a potentially powerful method for analyzing PPI networks. In a Perspective, Vidal and colleagues discuss their efforts to assess the completeness and reproducibility of literature-curated PPI datasets and evaluate their quality. This assessment includes recuration of small randomly chosen subsets of PPIs from three organisms. The results suggest that literature-curated PPI dataset quality is lower than often believed. Wu and colleagues discovered similar problems in PPI data integrated from six databases. They describe a web-based analysis platform that simplifies manual recuration and provides tools specifically designed to filter these data and analyze medium-sized PPI networks.

Perspective p39, Brief Communication p75

In vivo knockdown of microRNAs

Studying the phenotype of a cell or animal with a gene of interest knocked out is a popular approach to glean functional information. Lately it has been applied not only to genes that encode proteins but also to regulatory microRNAs. Knock out approaches are elegant but time-consuming. Naldini and colleagues now present an alternative for studying microRNA function in mice. By stably expressing a lentiviral vector containing the target sequence for a particular microRNA, the researchers can sequester the microRNA away from its endogenous target, which is consequently derepressed. This allows them to replicate the phenotype of a mouse that had its microRNA knocked out.

Brief Communication p63, News and Views p37

Software for ‘next-gen’ data analysis

The main power of next-generation sequencing is in the ability to rapidly generate millions of short DNA sequence reads; its main challenge is the conversion of these reads into valuable biological information. Enter bioinformatics experts. In this issue, Lander and colleagues present an algorithm to detect copy-number changes in genomic DNA and to map the chromosomal breakpoints at one-kilobase resolution. Jaffe and colleagues introduce a computational tool that discovers differences in bacterial genomes with unprecedented sensitivity and accuracy.

Article p99, Brief Communication p67

Method of the Year 2008

We continue our annual celebration of the methods that drive biological research with a special feature on super-resolution fluorescence microscopy, our Method of the Year 2008. Techniques for using fluorescence to visualize cellular structures with nanometer-scale resolution have been developing rapidly in the past years and are poised for widespread biological application. In our special feature, a news piece describes the development of these methods, and a Commentary describes their potential for understanding cellular biology. In addition, the founder of the methodology presents his Perspective on its implementation, and, for those who are not familiar with the basic principles of super-resolution, we provide a Primer. For a taste of things to come, we have also included a selection of Methods to Watch.

Special feature starting on p15