IN THIS ISSUE

Computational genomics tools
As the whole-genome sequences of more model organisms become available, they can be scrutinized in silico to find genetic regulatory elements. In this issue, we present protocols for the two computational methods most commonly used for such analyses. The first method, described by Dmitri Papatsenko and Michael Levine, relies on prior knowledge of specific transcription factor binding sites. The authors describe how to deduce candidate regulatory elements by clustering the binding site sequence motifs with various algorithms. The second method, described by David Haussler’s group, does not require prior knowledge of transcription binding sites. Instead, these authors show how to use the conservation of sequences across different species as indication of potential regulatory function, using the popular UCSC Genome Browser.
Protocols p529, p535

Mapping bacterial adhesion domains
Adhesin molecules on pathogenic bacteria mediate binding of the bacteria to specific receptors on host cells in the process of infection. Unfortunately, the details of these interactions are still largely unknown. Dufrêne, Menozzi and colleagues report that atomic force microscopy with tips bearing either adhesin or receptor molecules can be used to measure the specific binding forces of individual adhesins and map their distribution on the surface of living bacteria. They demonstrate that the adhesin molecules on Mycobacterium tuberculosis are not randomly distributed over the surface of the bacteria but are concentrated into nanodomains.
Article p515

The alpha and omega of protein translocation
Precise localization of a protein in response to a stimulus is crucial for a cell’s ability to function. Whereas previous assays to determine protein translocation were largely qualitative, Helen Blau and colleagues now introduce an enzymatic assay that allows quantitative assessment of protein localization. They split β-galactosidase into a short N-terminal α fragment, attached to a protein of interest, and a C-terminal ω fragment, targeted to the cellular region of interest. Only if α and ω are in close proximity, that is, if the protein has translocated to the region of interest, is full enzymatic activity of β-galactosidase restored. Optimal length and mutations in the α fragment, which lower its affinity for ω, allowed the use of this assay even to study protein translocations in the same cellular compartment.
Article p521

Unraveling the mystery of the genome
Genome researchers have made great strides with the sequencing of more whole genomes; hand in hand with these advances goes the need for a through annotation of transcribed regions. In their review of current methods for transcriptome analysis, Matthias Harbers and Piero Carninci compare present state-of-the-art techniques that are used for quantitative analysis of gene expression, identification of gene boundaries and promoter regions, and genome annotation. In addition to explaining the technical underpinnings behind less familiar acronyms such as SAGE, CAGE and GIS, the authors discuss the applications each technique is best suited for.
Review p495

Super-sized tissue microarrays
As most screening technologies used in biomedical research have steadily increased in throughput, tissue arrays have seen much less improvement in this regard. Now, using nothing more than common laboratory equipment, Rui and colleagues present a technique they call cutting edge matrix assembly, or CEMA. This method can be used to produce high density arrays of almost any solid sample. Arrays with over 10,000 unique samples can be easily made using their sectioning and bonding technology. To aid in sample identification, color-coded identifiers can also be added. Technology will not speed up the current bottleneck in tissue array screening—the pathologist; but it may provide an impetus to automate image analyses.
Brief Communication p511, News and Views p492