Integrated methods for network inference

A variety of methods are used to infer gene regulatory networks from gene expression data sets. Stolovitzky and colleagues present the results of the DREAM5 challenge for 35 such methods, using in silico data and gold-standard data sets from Escherichia coli and Saccharomyces cerevisiae as benchmarks. No single approach was found to be the best for all data sets, and integrating the predictions of multiple methods resulted in good performance across many data sets. Importantly, integrated methods were robust to the inclusion of poorly performing methods. The researchers used integrated methods to infer consensus networks for E. coli and Staphylococcus aureus, and they present a web resource through which other researchers can generate consensus networks.

Analysis p796

Zinc-finger nucleases cross membranes

Zinc-finger nucleases (ZFNs) can be used to make targeted changes in the genomes of many species. They are typically delivered to cells as DNA or RNA, but Barbas and colleagues now report that ZFNs can cross the cell membrane of several mammalian cell types as proteins. They do so at a high enough level to generate targeted genomic changes as efficiently as via DNA delivery. ZFN protein delivery results in transient rather than sustained nuclease activity in the cell; a ZFN targeting the CCR5 locus generates fewer off-target effects. Delivery of ZFNs as proteins will enable applications in which the genomic integrity of modified cells is important.

Brief Communication p805

Seeing SVs for the Forest

Structural variants (SV) are major contributors to differences in our genomes and can confer an increased risk of disease. A plethora of computational tools exists to detect these insertions, deletions, inversions and translocations from the short reads produced by high-throughput sequencing technologies. Still, for optimal results, one needs to merge the results of several tools. As an alternative to this time- and resource-intensive task, Sebat and Michaelson used a machine learning approach and trained a Random Forest classifier on known features of SVs. ForestSV performed well on real data and had the added strength of finding rare variants in a single genome without the need for supporting data from several related samples. ForestSV will improve as new SVs are added to the training data.

Brief Communication p819

Tools to study microRNA function

microRNAs have the potential to regulate a large fraction of the human transcriptome. Their expression level is often used to predict their effect on targets, but a complicated relationship between concentration and activity demands tools to test function on a large scale. Brown and colleagues have generated a library of vectors that can be used to ‘sense’ the activity of most human microRNAs. Their Sensor-seq assay uses the library to provide a snapshot of microRNA activity in a given cell type in a single rapid experiment. The researchers find that the majority of detected microRNAs have no effect on their targets because the microRNAs exist below a threshold required for activity. They also provide a series of ‘decoy’ vectors, each of which can bind a specific microRNA and inhibit its activity so that its function can be understood.

Article p840

The Metatron: studying animal dispersal

Animals disperse from their habitats for many reasons, including environmental change or habitat fragmentation due to human activity. Studying this process experimentally is not trivial; existing setups trade off scale with experimental control. Here Clobert and colleagues introduce the Metatron: an experimental infrastructure that meets the need for a large-scale, controlled system to study animal dispersal. The Metatron consists of 48 habitat patches on 4 hectares of land, in which temperature, light and humidity can be controlled. The patches are flexibly connected by corridors presenting varying degrees of difficulty to a dispersing animal. Clobert and colleagues demonstrate the use of the Metatron to study lizard and butterfly dispersal. Other researchers may apply to use the Metatron. It should enable previously infeasible experiments in ecology and conservation biology.

Article p828, News and Views p794