TOOLS IN BRIEF

GENOMICS

Juicer and Juicebox for chromatin conformation analysis

Chromatin ligation followed by sequencing is the bedrock underlying methods for analyzing genomic architecture, but getting from short sequence reads that represent DNA segments in close physical proximity to a 3D chromatin structure requires complex computational analysis. Erez Lieberman Aiden and colleagues now present two pipelines for automated analysis. Juicer converts sequence reads into contact maps at different resolutions. It normalizes for contact probability and annotates features such as loops and contact domains. Juicebox lets a user visualize the data and zoom in and out to explore regions of interest and view them in the context of transcription and epigenetic marks.

Durand, N.C. *et al. Cell Syst.* **3**, 95–98 (2016).
Durand, N.C. *et al. Cell Syst.* **3**, 99–101 (2016).

NEUROSCIENCE

Wireless recording of neural activity with ultrasound

Implanted devices that record neural activity in model organisms such as rats ideally should be as small as possible, remotely powered and able to transduce information wirelessly. Seo *et al*. aim for all of these features by using neural dust to record from peripheral neurons in the mouse. Neural dust is a tiny recording system that consists mainly of electrodes and a piezoelectric crystal. The crystal reflects ultrasonic energy (sent from an external transducer) after neural activity picked up with the electrodes modulates the ultrasonic signal. Electrical activity can thus be inferred from the difference in emitted and received ultrasound signal. The researchers applied their technology *in vivo* to obtain electroneurographic and electromyographic recordings from rat sciatic nerve and skeletal muscles, respectively.

Seo, D. *et al. Neuron* **91**, 529–539 (2016).

GENOMICS

Expanding known viral diversity

More than 2,000 viral genomes have been sequenced, but the vast majority of viruses are unknown. Paez-Espino *et al*. provide a glimpse of the viral universe beyond the small snapshot of previously known viruses. The researchers explored thousands of publicly available metagenomic data sets that were acquired by untargeted sequencing of samples from various habitats all over the world. Using their analysis pipeline, they expanded the number of known viral groups or singletons by two orders of magnitude. For many of the identified viruses, they were able to identify host species, for example, by analyzing remnants in the viral genomes that were left by CRISPR–Cas-based immune responses. The newly identified viral genomes promise to be a useful resource for studies into viral ecology as well as a source of previously unknown gene families.

Paez-Espino, D. *et al. Nature* **536**, 425–430 (2016).

IMMUNOLOGY

Antigen-receptor sequences captured from single T cells

The antigen receptor on a T lymphocyte consists of an α- and a β-chain, which together dictate the specificity of the cell's adaptive immune response. Single-cell RNA sequencing can be used to explore the diversity of T cell receptor sequences in an individual, but many high-throughput methods, including those that prime reverse transcription off of beads in microdroplets, sequence only transcript 3′ ends. Hanson *et al*. have now developed a way to synthesize two different barcoded primers on a single bead, using a mixture of 5′ phosphoramidite monomers with two different protecting groups at the 3′ position. Deprotection and chain extension of one barcoded primer can be followed by a second deprotection and primer synthesis step, thus enabling the capture and sequencing of full-length α- and β-chain RNA sequences from the same receptor at high throughput.

Hanson, W.M. *et al. J. Am. Chem. Soc.* **138**, 11073–11076 (2016).