METHODS IN BRIEF

MICROBIOLOGY

Buckets of bacterial genomes

The power of metagenomics is that it can identify microbes on the basis of pooled sequences recovered from any sample. But it is difficult to assign every sequence fragment to the organism it came from, which limits taxonomic accuracy and the amount of functional information that can be gleaned. Lan *et al*. use the latest mantra of high-throughput genomics—compartmentalize, barcode, pool and sequence—to perform single-cell genomic sequencing (SiC-seq) on microbial communities. SiC-seq is a microfluidic approach that traps single cells in oligo-barcoded agarose microspheres and carries out enzymatic lysis and pooled library prep on over 50,000 cells in a single run. Because many sequence reads are linked to each genome, the researchers were able to classify microbes and identify patterns of antibiotic resistance, virulence factors and viral transduction potential in tens of thousands of microbes from San Francisco seawater.

Lan, F. *et al*. *Nat. Biotechnol.* http://dx.doi.org/10.1038/nbt.3880 (2017).

NEUROSCIENCE

Reconciling small and large scales with FIB-SEM

Focused ion beam scanning electron microscopy (FIB-SEM) offers high axial resolution while maintaining image registration. However, the technology has so far been limited to relatively small samples, as the imaging process destroys the sample, and system errors or disruptions lead to low image quality or data loss. Xu *et al.* have tweaked several components of the FIB-SEM system, and together their changes amount to a substantial improvement in system stability. These modifications allow an increase in imaging speed as well as better recovery from interruptions, translating into larger imaging volumes or higher-resolution data sets. The researchers demonstrated their system by imaging large chunks of mammalian or *Drosophila* brain as well as by acquiring a high-resolution data set for the green alga *Chlamydomonas reinhardtii*.

Xu, C.S. *et al. Elife* http://dx.doi.org/10.7554/eLife.25916 (2017).

NANOBIOTECHNOLOGY

Ultrafast thermal cycling

The polymerase chain reaction (PCR) is ubiquitous in biological research laboratories, and substantial technological advances have improved our ability to control the speed and accuracy of this important process. The majority of PCRs are carried out on devices with heating blocks that heat and cool the reactions over multiple cycles. Although these devices work well, the time they take to heat and cool samples can be substantial. Lee *et al.* present an alternative approach for cost-effective, ultrafast thermal cycling. In their approach, gold bipyramidal nanoparticles are included in reaction mixtures and illuminated with infrared-light-emitting diodes. Upon illumination, the nanoparticles generate heat that rapidly increases the reaction temperature, enabling robust and rapid PCR. This ultrafast thermal cycling is also fully compatible with quantitative PCR methods.

Lee, J. *et al*. *J. Am. Chem. Soc*. http://dx.doi.org/10.1021/jacs.7b01779 (2017).

IMAGING

Single-protein detection by cryo-EM

The ability to see where proteins are located in a cell and how they are oriented would be highly useful to biologists. Toward this goal, Rickgauer *et al.* report a method to determine protein location and orientation in cryo-EM images. At high resolution, an electron wave passing through a sample is imprinted with projection patterns of phase shifts that are unique to each protein and each orientation. Rickgauer *et al.* describe an algorithm that simulates such projection patterns for varying orientations of a given protein and then scans the cryo-EM image for targets that match the patterns. Though the method has not yet been tested in biological slices, the data highlight the potential of the approach for detecting single proteins and their orientations in the crowded environment of the cell.

Rickgauer, J.P. *et al. eLife* **6**, e25648 (2017).

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