TOOLS IN BRIEF

NEUROSCIENCE

Electrophysiology at a massive scale

So far, extracellular recording electrodes have been limited to a few recording sites per shank. In a large collaborative effort across several labs with the backing of major funding organizations, Jun *et al.* have developed high-performance electrodes that harbor almost a thousand recording sites. 384 of these sites can be used simultaneously. Because of their length, the Neuropixels probes can record from several brain regions, which the team demonstrated by recording from the mouse cortex, hippocampus and thalamus using a single probe. When inserting two probes into the brain of a mouse, the researchers could measure the activity of almost 750 neurons. Finally, the Neuropixels probes are compatible with chronic recordings over weeks.

Jun, J.J. *et al. Nature* **551**, 232–236 (2017).

GENOMICS

Annotating full-length long noncoding RNAs

To begin to understand the function of a cell's large repertoire of long noncoding RNAs (lncRNAs), one must start with their detailed annotation. Current resources are either based on automated annotation and are therefore large but have incomplete transcript structures, such as the 101,700 genes in NONCODE, or they are manually annotated and therefore accurate but small, such as ENCODE's 15,767 lncRNA genes. Lagarde *et al.* seek to increase the number of lncRNAs in the ENCODE resource by a combination of targeted RNA capture and PacBio single-molecule real-time sequencing. They profile full-length lncRNAs in human and mouse tissues and present new transcript models for over 3,000 human and over 500 mouse genes.

Lagarde, J. *et al. Nat. Genet.* **49**, 1731–1740 (2017).

IMAGING

Imaging 3D enzyme dynamics in 2D

Enzyme dynamics and function are directly correlated in a variety of biological processes, but imaging the dynamics of a high number of single enzymes in real time is challenging. Sun *et al.* translated 3D movements that are difficult to track with TIRF microscopy into 2D movements on a supported lipid bilayer that is fixed on a coverslip. The researchers used cholesterol-bound DNA that integrates into this bilayer and forms stationary cholesterol–DNA origami rafts. One of the enzymes of interest is statically bound to this DNA origami raft, while the second enzyme of interest is tethered to individual cholesterol molecules and therefore remains freely diffusive within the membrane. This enables enzyme colocalization detection via FRET analysis. The researchers applied this tool to visualize the glucose oxidase–catalase cascade.

Sun, L. *et al. J. Am. Chem. Soc.* **139**, 17525–17532 (2017).

BIOINFORMATICS

Fast curve fitting on a graphics processing unit

Curve fitting is ubiquitous in the analysis of biological data. For example, super-resolution images reconstructed during image analysis in single-molecule localization microscopy (SMLM) can require data fitting for millions, or possibly even more, molecular localizations. Particularly for real-time experiments or for those involving very large data sets, analysis time can be a bottleneck. Pryzybylski *et al.* now present Gpufit, with which a general curve-fitting algorithm (the Levenberg–Marquardt algorithm) can be implemented on a graphical processing unit (GPU), speeding up data analysis substantially. The software is open source and modular and in its present version includes both least-squares and maximum-likelihood estimators. The authors report that data analysis is about 42-fold faster than equivalent analysis on a central processing unit (CPU); they reach up to 4.5 million fits per second with no compromise on accuracy. They illustrate the power of their approach on STORM data, again showing 45-fold faster analysis with Gpufit than with standard processing, with no loss of fit precision.

Przybylski, A. *et al. Sci. Rep.* **7**, 15722 (2017).