METHODS IN BRIEF

BIOINFORMATICS

Membrane proteins in 3D

About one-quarter of all our proteins protrude through a membrane. This makes them important communicators both in cellular compartments and outside the cell, but it also makes their structure more difficult to determine, which in turn makes their precise mode of action harder to understand. Several experimental and computational structure prediction tools have been used to estimate the three-dimensional structure of membrane proteins, but these tools are limited by the number of transmembrane helices they can incorporate. Hopf *et al*. used maximum-entropy analysis to calculate amino-acid changes in protein families across their evolution, which allowed them to determine the proximity of residues in three dimensions and their fold. The authors' EVfold_membrane algorithm predicts *de novo* structures of transmembrane proteins. When they benchmarked the tool against known crystal structures, the researchers found very high agreement, particularly in functionally important regions and substrate-binding pockets.

Hopf, T.A. *et al. Cell* advance online publication (10 May 2012).

MOLECULAR BIOLOGY

The synaptic transcriptome

There is no question that the localization of mRNAs in the cell matters. In neurons, for example, local protein synthesis at the dendrites is required for certain forms of learning and memory. However, documentation of the local transcriptome in neurons has been somewhat limited. Microarray analysis and high-throughput *in situ* hybridization approaches have identified hundreds of mRNAs specifically localized to dendrites and their synapses, but this number could be higher. Cajigas *et al.* screened the full complement of mRNAs present in synaptic regions by deep RNA sequencing and bioinformatic analysis. The group microdissected segments of neuropil (areas composed of mostly neuronal and glial processes without cell bodies) from the mouse hippocampus and identified over 2,000 mRNAs associated with dendrites and/or axons in this region.

Cajigas, I.J. *et al. Neuron* **74**, 453–466 (2012).

IMAGING

Exciting fluorescence with luminescence

Under the right conditions, nonradiative energy transfer occurs between a bioluminescent donor and a fluorescent acceptor molecule. This phenomenon, termed bioluminescence resonant energy transfer (BRET), requires that the participating molecules have spectral overlap and that they are in close proximity (10 nanometers apart or less). Dragavon *et al.* show that bioluminescent light can also excite fluorescence in a radiative process in which the excitation light travels over distances too large to be compatible with BRET. They demonstrated this phenomenon *in vitro* and *in vivo* using bacteria expressing the *lux* operon from *Photorhabdus luminescens* (donor) and red-emitting quantum dots (receptor). Although the applications of this approach remain to be fully realized, the results suggest that additional controls may be needed to interpret BRET data.

Dragavon, J. *et al. Proc. Natl. Acad. Sci. USA* **109**, 8890–8895 (2012).

NEUROSCIENCE

Virtual swimmers

Our movements often adapt to what we see in complex ways. Fish, for example, adjust their swimming speed according to the visual perception of how fast their surroundings move. To study how this is achieved at the cellular level, Ahrens *et al.* captured the activity of individual neurons throughout the brain of paralyzed zebrafish larvae using two-photon imaging of a genetically encoded calcium sensor. The group then linked brain activity and behavior by developing a 'swim simulator' in which they controlled the rate at which the virtual world seemed to move while simultaneously measuring the fish's motor intentions via electrophysiological recordings from the relevant motor nerves. This fictively driven virtual-reality setup allowed them to study neural dynamics during visually guided motor adaptation.

Ahrens, M.B. *et al. Nature* **485**, 471–477 (2012).