METHODS IN BRIEF

BIOINFORMATICS

Deep learning to predict sequence specificity

To understand the role of DNA- and RNA-binding proteins in gene regulation, it is essential to characterize their sequence specificities. Experimental evidence for sequence specificity comes in many different formats, including the output from protein binding microarrays, chromatin immunoprecipitation and high-throughput SELEX (systematic evolution of ligands by exponential enrichment). To analyze such disparate data types in very large data sets, Alipanahi *et al.* introduce DeepBind, a software tool based on deep convolutional neural networks. Sequence specificities can be visualized as a 'mutation map' that shows the effect of variations on binding. The authors applied DeepBind to study the role of RNA-binding proteins in regulating alternative splicing and to analyze how disease-associated variants affect transcription factor binding and gene expression.

Alipanahi, B. *et al. Nat. Biotechnol.* **33**, 831–838 (2015).

SYNTHETIC BIOLOGY

Universal parts

Complex genetic circuits and pathways are engineered in a particular host and cannot usually be transferred to a different organism without laborious optimization. Kushwaha and Salis sought to simplify biological engineering and expand its reach by developing regulatory genetic parts that function independently of their host. Their Universal Bacterial Expression Resource (UBER; not related to the car service) achieves T7 polymerase autoactivation and self-limitation by using positive and negative feedback loops, respectively, and does not rely on host-specific promoters. The researchers showed that they could easily transfer a functional multienzyme pathway between *Bacillus subtilis*, *Pseudomonas putida* and *Escherichia coli*.

Kushwaha, M. & Salis, H. *Nat. Commun.* **6**,7832 (2015).

STEM CELLS

Cardiovascular progenitors from human stem cells

Multipotent cardiovascular progenitor cells (CPCs) can give rise to cells of the circulatory system, including cardiomyocytes and vascular precursors. When derived from human pluripotent stem cells (hPSCs), CPCs can be powerful tools to understand cardiovascular development, study toxicology and treat disease. However, CPCs cannot be robustly expanded in culture. Birket *et al.* now use controlled *MYC* expression to slow the appearance of CPCs marked by an NKX2-5–GFP cardiac lineage marker in differentiating hPSC culture. The pure CPC populations that are generated can be expanded over more than 40 population doublings in the presence of insulin-like growth factor 1. By modulating fibroblast growth factor and bone morphogenetic protein signaling, as in normal heart development, the authors recapitulate features of cardiogenic mesoderm known as the early heart field and go on to generate a number of mature cardiovascular cell types.

Birket, M.J. *et al. Nat. Biotechnol.* doi:10.1038/nbt.3271 (20 July 2015).

NEUROSCIENCE

Wireless pharmacology and optogenetics

Pharmacological and optogenetic manipulations of neurons are two approaches for interrogating circuit function in the brain that are usually performed in separate experiments. Jeong *et al.* have now developed a device that can deliver both light and fluids *in vivo*. The device consists of an array of inorganic light-emitting diodes (μ-ILEDs) and four fluid-delivery channels connected to independent reservoirs. The device is wirelessly controlled by an infrared sensor that enables light delivery or a heating element that triggers fluid pumping via heat-sensitive expandable microspheres. The researchers used these devices to optogenetically activate and pharmacologically inhibit dopamine neurons in the ventral tegmental area of mice, causing a modulation of place preference behavior in freely moving animals.

Jeong, J.-W. *et al. Cell* **162**, 662–674 (2015).