# METHODS IN BRIEF

GENOMICS

## Single-cell DNA amplification gets even

Recovering a genome sequence from the tiny quantity of DNA in a single cell requires considerable amplification, which leads to strong biases. Multiple-displacement amplification (MDA) is a method chosen often for its robust amplification, but many sequences are amplified either preferentially or not at all, skewing genetic interpretation. Fu *et al*. have designed a simple way around uneven amplification that involves isolating single-cell DNA fragments into individual oil droplets and using each droplet as a separate reaction chamber. Amplifying in an emulsion allows each genomic region to reach saturation regardless of amplification kinetics. The authors show that emulsion whole-genome amplification (eWGA) provides sensitive detection of copy-number variation and single-nucleotide polymorphisms in single human cells. The approach works with commercial emulsion generators.

Fu, Y. *et al. Proc. Natl. Acad. Sci. USA* **112**, 11923–11928 (2015).

BIOINFORMATICS

## Improving correlated mutation analysis

Correlated mutation analysis is an increasingly powerful approach used to help predict protein and protein-complex structures. The premise behind such methods is that mutations that occur at a given position in a protein are compensated by other mutations of residues close in space; such coevolving residues can be identified by multiple sequence alignments. However, the approach is subject to false positives stemming from indirect interactions or common ancestry. Jacob *et al.* report a clever way to help reduce such false positives by also considering codon-level multiple sequence alignments. They show that if the correlation is strong at the amino-acid level but weak at the codon level, it is more likely to reflect selection for a true, direct interaction, and not an indirect interaction or common ancestry. The approach can be implemented in a variety of tools to enhance their performance.

Jacob, E. *et al. eLife* 10.7554/eLife.08932 (15 September 2015).

MICROBIOLOGY

## Growth signatures in bacterial sequence data

Korem *et al*. have shown that it is possible to extract information about population growth dynamics from static sequence data. Most bacterial chromosomes are circular, with a single origin that initiates bidirectional replication toward a single terminus. Using chemostat experiments, the authors found that the proportion of DNA copies near the origin to those near the terminus (peak-to-trough ratio (PTR)) can give a quantitative readout of the population growth rate. They extended their approach to metagenomic sequence data and developed a computational pipeline to determine ratios in large cohorts. They measured PTRs to detect the bacteriostatic effects of antibiotics in the mouse gut, to identify human gut bacteria that oscillate in growth or respond to diet changes, to profile growth rates on human body sites and to identify bacterial growth associated with bowel disease.

Korem, T. *et al. Science* **349**, 1101–1106 (2015).

NANOBIOTECHNOLOGY

## Designing protein-DNA nanowires

Self-assembled DNA nanostructures are increasingly being used to solve problems across scientific disciplines. However, assemblies based on one type of building block are inherently limited in terms of the structural diversity possible and the spatiotemporal control over self-assembly. Mou *et al.* now report a computational design method to create protein-DNA coassembling nanostructures, driven by noncovalent interactions between protein and DNA. As proof of principle of their approach, they engineered a homodimerization interface into the *Drosophila engrailed* homeodomain, which enables it to bind to two dsDNA molecules. They show that protein-binding sites on dsDNA molecules can be varied to enable the self-assembly of a nanowire structure, which they confirmed with fluorescence microscopy, crystallography and atomic force microscopy. This noncovalent self-assembly approach shows promise for expanding the toolbox of nanobiotechnology.

Mou, Y. *et al. Nature* **525**, 230–233 (2015).