TOOLS IN BRIEF

GENOMICS

De novo short read assembler

No longer limited by technology to generate DNA sequences, researchers now run into computational challenges when trying to make sense of up to hundreds of gigabases of fragmented information from a single genome. For certain applications, such as assessing the individual differences in human genomes or the analysis of genomes without a reference, *de novo* assembly is the only way forward. Simpson & Durbin now lower memory requirements by using compressed data structures in their string graph assembler (SGA). After filtering low-quality reads, SGA creates a compressed read index of intact reads and queries it to create a graph from the overlap between reads. These graphs are the basis for longer contiguous sequences (also known as contigs), which in turn are used to construct larger scaffolds. The researchers use SGA on a human genome and cover 95% of the reference genome.

Simpson, J.T. & Durbin, R. *Genome Res.* advance online publication (7 December 2011).

CHEMICAL BIOLOGY

Watching protein synthesis

The regulation of protein translation has a role in several aspects of biology; tools to study it are therefore in demand. Salic and colleagues report that an alkyne analog of the aminonucleoside antibiotic puromycin can be incorporated into translating polypeptide chains and can be used to label them for fluorescence detection or affinity purification. Like puromycin, the O-propargyl puromycin analog blocks protein synthesis by generating covalent conjugates to the growing nascent chain; the terminal alkyne is then available for labeling via click chemistry. The approach is rapid, does not require methionine-free medium and is compatible with monitoring protein synthesis in cells and in whole organisms.

Liu, J. *et al. Proc. Natl. Acad. Sci. USA* advance online publication (12 December 2011).

GENETICS

A database of yeast mutant phenotypes

Performing genetic analysis in budding yeast is often hard given the fact that about one-fifth of its genes are essential for the viability of the organism. To overcome this, researchers use strains expressing temperature-sensitive alleles of essential genes, and large collections of such yeast strains have been generated. Using genetically engineered fluorescent markers and high-throughput microscopy Jin and colleagues analyzed the phenotypes of many cells with these mutations and put this information to the service of the community. They announce an online database—called PhenoM for 'phenomics of yeast mutants'—that contains quantitative single-cell measurements extracted from micrographs of almost two million cells and for 775 temperature-sensitive mutants spanning 491 different essential genes. PhenoM can be used to store, retrieve, visualize and data-mine this dataset, and it is freely available at http://phenom.ccbr.utoronto.ca/.

Jin, K. *et al. Nucleic Acids Res.* **40**, 687–694 (2012).

SENSORS AND PROBES

Switchable infrared dyes

Near-infrared light is highly advantageous for biological imaging thanks to its minimal photodamage, its capacity for deep tissue penetration and the minimal background autofluorescence that is produced by living tissue at this wavelength. Fluorescent dyes that absorb and emit in the infrared range exist, but often it is hard to design functional near-infrared sensors that switch on or off their fluorescence in response to a given metabolite. Yuan and colleagues describe a new type of near-infrared functional dyes called Changsha, which are hybrids of merocyanine A and benzoic acid. These compounds have a fluorescence on-off switching mechanism similar to that of rhodamine dyes, making them good candidates for near-infrared functional sensor design. The authors synthesized six Changsha dyes with slightly different photophysical characteristics and used one of them to develop a near-infrared sensor that turns on its fluorescence upon binding to endogenously produced HClO in living cells and mice.

Yuan, L. *et al. J. Am. Chem. Soc.* advance online publication (6 January 2012).