TOOLS IN BRIEF

MICROBIOLOGY

Extracting microbial function from phylogeny

Researchers performing microbial community sampling ask the question: "Who is there?" Single marker–gene sequencing has proven cost-effective for microbe identification, but it cannot reveal what the microbes in a community are capable of doing. To bridge the gap, Langille *et al*. serve up PICRUSt (phylogenetic investigation of communities by reconstruction of unobserved states), a computational tool that predicts functions from marker-gene profiling data. PICRUSt first extracts gene content from every microbe with a genome sequence in a reference phylogenetic tree; then it predicts the gene content and corresponding traits of related unsequenced microbes using an adaptation of ancestral state reconstruction methods. From 16S ribosomal DNA marker sequences, it can reproduce a large share of the functional information found by shotgun metagenomic sequencing in the Human Microbiome Project and other data sets.

Langille, M.G.I. *et al. Nat. Biotechnol.* doi:10.1038/nbt.2676 (25 August 2013).

PROTEOMICS

The NCI-60 proteomes

The 59 cancer cell lines of the US National Cancer Institute's Developmental Therapeutics Program are widely used in cancer research, from efforts to understand mechanism to developing chemotherapeutic drugs. Gholami *et al*. present a quantitative global proteome analysis of these cell lines by mass spectrometry profiling, covering a total of 10,350 proteins including 375 protein kinases. The study revealed a core cancer proteome of nearly 6,000 proteins and showed that cell-line proteomes tended to cluster by tissue type. The results also showed a strong correlation of proteomic results with transcriptome data, and integration with cancer drug profiles yielded potentially novel biomarkers for drug resistance or sensitivity. The data are publicly available at http://wzw.tum.de/proteomics/nci60/.

Gholami, A.M. *et al. Cell Rep.* **4**, 609–620 (2013).

NEUROSCIENCE

Anterograde rabies neural tracers

To study neural circuits, one needs to identify the neurons that make synaptic contacts with a cell of interest (input connections) as well as where the axon terminal of that cell projects to (output connection). For the former, one can use viral tracers that are transported retrogradely, from the synapse of a target cell to the soma of the presynaptic partner. Rabies virus shows this type of tropism and has been engineered into a popular neuronal tracer. In new work, Wickersham *et al*. engineer rabies viruses that are transported in the opposite direction: from the soma of the target cell to its axon terminal, or anterogradely. The authors accomplish this by coating the rabies virus with the envelope glycoprotein of vesicular stomatitis virus. They show several new capabilities for neuronal tracing that are enabled by the combination of retrograde and anterograde rabies vectors, such as labeling a brain region's inputs and outputs simultaneously.

Wickersham, I.R. *et al. Nat. Commun.* **4**, 2332 (2013).

MASS SPECTROMETRY

Highly multiplexed proteome analysis

Earlier this year, *Nature Methods* published a paper describing a neutron-encoding (NeuCode) stable-isotope labeling by amino acids in cell culture (SILAC) method that extended the number of possible quantitative proteomics comparisons by SILAC from a standard 3 to up to a theoretical 39 (Hebert *et al*., *Nat. Methods*). In this approach, different combinations of stable-isotope labels are encoded into an amino acid and decoded by high-resolution mass spectrometry; the method exploits subtle mass differences in atoms due to varying nuclear binding energies. Practically speaking, however, the approach is limited to a handful of comparisons because of limited reagent availability. Hebert *et al*. (*Mol. Cell. Proteomics*) now report the design and synthesis of additional NeuCode reagents to allow practical 12-plex quantitative proteome comparisons.

Hebert, A.S. *et al. Mol. Cell. Proteomics* doi:10.1074/mcp.M113.032011 (23 July 2013).

Hebert, A.S. *et al. Nat. Methods* **10**, 332–334 (2013).