IN BRIEF

PHYLOGENETICS

Efficient method for estimating divergence times

Methods for estimating the timing of species divergences are widely used but require a large amount of computational time for even a modest number of genomes. Current methods also rely on calibrations of the molecular clock, including modelling differences in the rate of the molecular clock across lineages, which has many uncertainties. To overcome these difficulties, Tamura *et al.* present a method called RelTime, which estimates relative divergence times for each branch point on a phylogenetic tree, thus overcoming the need for calibrations. It is much faster than existing Bayesian methods.

ORIGINAL RESEARCH PAPER Tamura, K. *et al.* Estimating divergence times in large molecular phylogenies. *Proc. Natl. Acad. Sci. USA* **109**, 19333–19338 (2012)

TRANSLATIONAL GENOMICS

Sequencing to detect tumour DNA in circulation

The authors explore the feasibility of using whole-genome sequencing to detect chromosomal alterations in tumour DNA that is found in the circulating blood of cancer patients. Leary *et al.* show that detecting structural alterations can clearly distinguish samples from patients with colorectal cancer or breast cancer from controls, making this a promising avenue for non-invasive diagnosis. However, the sensitivity of the method depends on the amount of DNA in the circulation, and the cost of sequencing would need to be further reduced for such an approach to be implemented.

ORIGINAL RESEARCH PAPER Leary R. J. *et al.* Detection of chromosomal alterations in the circulation of cancer patients with whole-genome sequencing. *Sci. Transl. Med.* **4**, 162ra154 (2012)

MOLECULAR PROFILING

mRNA profiling of activated neurons

Understanding which of the many classes of neuron are involved in particular mammalian brain functions is a major challenge in neuroscience. This study shows that the ribosomal protein S6 is phosphorylated in mouse neurons in response to a wide range of stimuli. By exposing mice to a stimulus, such as fasting or altered salt balance, and then immunoprecipitating phosphorylated S6 from brain homogenates, the authors were able to detect associated mRNAs that are expressed in response to the stimulus. Some of these mRNAs are cell-type-specific, allowing identification of the activated neuronal types.

ORIGINAL RESEARCH PAPER Knight, Z. A. *et al.* Molecular profiling of activated neurons by phosphorylated ribosome capture. *Cell* **151**, 1126–1137.

MOUSE MODELS

Uncovering the unexpected for Cre

A common way to manipulate and to study a gene of interest *in vivo* uses a tissue-specific promoter to drive the expression of the Cre recombinase. Heffner *et al.* used a *LacZ* colourimetric reporter to characterize the tissue distribution of Cre activity in 40 mouse Cre strains during embryogenesis and adulthood. They found various features indicating that caution is required when interpreting phenotypes from these strains: off-target Cre activity in multiple tissues, variability in expression between littermates and differential activities of maternally versus paternally inherited Cre alleles. The authors plan to extend these analyses to more of the 365 strains in The Jackson Laboratory Cre repository.

ORIGINAL RESEARCH PAPER Heffner, C. S. *et al.* Supporting conditional mouse mutagenesis with a comprehensive Cre characterization resource. *Nature Commun.* **3**, 1218 (2012)

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