IN BRIEF

PHYLOGENETICS

Rapid and accurate large-scale coestimation of sequence alignments and phylogenetic trees

Liu, K. *et al. Science* **324**, 1561–1564 (2009)

Current methods to estimate the evolutionary relatedness between sequence data sets are imprecise and slow, as typically they involve inferring homologies followed by tree assembly. The authors present an automated method that infers phylogenetic relationships by combining the sequence alignment and tree building steps into a single, iterative operation. The new program (SATé, simultaneous alignment and tree estimation), which uses a maximum likelihood approach, outperforms existing two-stage methods in speed and accuracy, and can analyse data sets of up to 1,000 sequences.

TECHNOLOGY

Chromosomal translocations induced at specified loci in human stem cells

Brunet, E. *et al. Proc. Natl Acad. Sci. USA* **106**, 10620–10625 (2009)

Recurrent chromosomal rearrangements underlie many malignancies, but the insights into their causes and consequences gleaned from mouse studies are not entirely applicable to humans. To study such rearrangements in humans, a method using engineered zinc-finger nucleases was devised to induce double-stranded breaks at precise points at two loci. The method was tested in three embryonic stem cell lines or their derivatives, and translocations were assayed by PCR. Although rearrangements occur less frequently than repair, the technique can be easily transferred to primary human cells.

EPIGENETICS

Shifts in replication timing actively affect histone acetylation during nucleosome reassembly

Lande-Diner, L. *et al. Mol. Cell* **34**, 767–774 (2009)

Although a relationship between replication timing and gene expression is well established, the mechanistic basis of this link is poorly understood. By adapting a previously developed nuclear microinjection method these authors showed that changes in replication timing, as occur in development, result in the repackaging of DNA into nucleosomes carrying altered histone modifications. A switch from late to early replication resulted in repackaging into acetylated nucleosomes (typical of active genes), whereas a switch from early to late replication caused repackaging into deacetylated (inactive) nucleosomes.

TRANSCRIPTOMICS

Quantification of the yeast transcriptome by single-molecule sequencing

Lipson, D. *et al. Nature Biotechnol.* 5 Jul 2009 (doi:10.1038/nbt.1551)

Transcriptome sequencing using high-throughput short-read methods (RNA-Seq) can be used to quantify transcript levels. However, the variable number of reads per mRNA means that the whole transcriptome must be assessed to obtain a normalized quantification for each transcript. This paper reports a quantitative transcriptomics method based on single-molecule sequencing. Because no amplification is required, sequence read counts are directly proportional to transcript abundance and very high throughput can be achieved, providing an efficient and accurate method for quantitative transcriptomics.