IN BRIEF

GENE EXPRESSION

Systematic identification of mammalian regulatory motifs' target genes and functions.

Warner, J. B. *et al. Nature Methods* 2 Mar 2008 (doi:10.1038/nmeth.1188)

Metazoan gene-regulatory sequences can be situated far from transcription start sites, making it hard to assign biological functions to putative *cis*-regulatory elements (CREs). Warner *et al.* tackled this problem by first using an algorithm to predict CREs on the basis of the conservation and clustering of putative transcription-factor binding motifs. A second algorithm then looked for enrichment of these elements in regions surrounding genes with related functions. The authors applied this approach to genes with likely roles in human myogenic differentiation, assigning functions to many predicted regulatory motifs.

CHROMATIN

Dynamic regulation of nucleosome positioning in the human genome.

Schones, D. E. *et al. Cell* **132**, 887–898 (2008)

This paper describes the first genome-wide maps of nucleosome positioning, using human $CD4^+$ T cells. The authors combined micrococcal nuclease-mediated digestion — a traditional means of identifying nucleosome positions — with Solexa high-throughput sequencing, allowing efficient high-resolution mapping. The results provide insights into the dynamics of nucleosome positioning in relation to changes in gene expression programmes, revealing correlations with RNA polymerase II binding, nucleosomal reorganization in promoters and enhancers, and the loss of specific types of nucleosome at crucial positions.

QUANTITATIVE TRAITS

eQED: an efficient method for interpreting eQTL associations using protein networks.

Suthram, S. *et al. Mol. Syst. Biol.* **4**,162 (2008)

In expression QTL (eQTL) analysis, individuals are genotyped across a panel of genetic markers and phenotyped using DNA microarrays. But finely mapping the genes that are responsible for changes in downstream expression can be difficult. These authors describe a method — eQTL electrical diagrams (eQED) — for prioritizing candidate genes at a locus, in which eQTLs and protein-interaction networks are modelled as a wiring diagram of current sources and resistors. The authors demonstrated the efficacy of eQED using regulator–target pairs in yeast.

MODEL ORGANISMS

High-resolution, high-throughput SNP mapping in *Drosophila melanogaster*.

Chen, D. *et al. Nature Methods* 9 Mar 2008 (doi:10.1038/nmeth.1191)

This paper describes the development of resources for fine-scale mapping in *Drosophila melanogaster* using SNPs. The authors generated a map of 27,367 SNPs in widely used *D. melanogaster* stocks, with an average density of one SNP per 6.3 genes, and generated a high-throughput microarray-based genotyping method. An additional resource comprises a set of 62 stocks that enables the generation of recombinants in any region of the genome. Demonstrating the power of these resources, the authors describe the efficient mapping of 14 mutations that perturb muscle patterning in the fruitfly embryo.