

## IN BRIEF

**GENOME BIOLOGY**

The fine-scale and complex architecture of human copy-number variation.

Perry, G. H. *et al. Am. J. Hum. Genet.* 24 January 2008 (doi:10.1016/j.ajhg.2007.12.010)

Copy-number variants (CNVs) have received much attention owing to their high prevalence and functional consequences. This paper describes a fine-scale (1 kb resolution) analysis of human CNVs by applying array-based comparative genomic hybridization to 30 individuals drawn from the HapMap population. The analysis revealed that 88% of CNV regions are smaller than previously thought, and that 8% have architectures that vary among individuals. This newly found complexity should be incorporated into the design of future association studies.

**EPIGENETICS**

High resolution mapping of epigenetic modifications of the rice genome uncovers interplay between DNA methylation, histone methylation and gene expression.

Li, X. *et al. Plant Cell* 8 February 2008 (doi:10.1105/tpc.107.056879)

This paper describes the mapping of three important epigenetic modifications — di- and trimethylation at histone H3 lysine 4, and DNA methylation — at high resolution for two entire rice chromosomes. The authors explore correlations between combinations of these modifications, chromatin structure and gene expression, and identify epigenomic differences between two developmental states. The mapping included large stretches of heterochromatin and completely sequenced centromeres, providing a novel epigenomics resource.

**SYSTEMS BIOLOGY**

Gene expression dynamics in the macrophage exhibit criticality.

Nykter, M. *et al. Proc. Natl Acad. Sci. USA* 4 February 2008 (doi:10.1073/pnas.0711525105)

Many self-organized systems show criticality — a state in which perturbations are maintained temporally and spatially, rather than being dampened or amplified. This property allows systems to maintain a balance between stability and the ability to adapt to change. By applying an information theory analysis of expression data for almost 10,000 genes, this study showed that gene expression dynamics in macrophages show criticality in response to stimulation of cell-surface receptors — the strongest evidence provided to date for criticality in biological systems.

**POPULATION GENETICS**

Data and theory point to mainly additive genetic variance for complex traits.

Hill, W. B. W. *et al. PLoS Genet.* 1 February 2008 (doi:10.1371/journal.pgen.1000008.eor)

Although studies of gene networks and biological pathways indicate that epistasis should have an important role in complex traits, many empirical studies have suggested that most genetic variation is additive. The authors analysed previously published empirical data and found that additive variance generally comprises over 50% of total genetic variance, and often almost 100%. They go on to show that this high contribution of additive variance is expected under a neutral population genetic model.