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IN BRIEF

GENE REGULATION

A chromatin landmark and transcription initiation at most promoters in human cells.

Guenther, M. G. *et al. Cell* **130**, 77–88 (2007)

In a genome-wide analysis of human cells, this study found that the promoter regions of most protein-coding genes are occupied by RNA polymerase II, and by nucleosomes with histone H3 modifications that are associated with transcription initiation. However, only a subset of these genes produced full-length transcripts or showed histone modifications that are characteristic of transcriptional elongation. These findings suggest that, for most genes, regulation is not at the level of transcription initiation, but occurs at a later stage.

NETWORK BIOLOGY

Spontaneous emergence of modularity in cellular networks.

Solé, R. V. & Valverde, S. *J. R. Soc. Interface* 11 July 2007 (doi 10.1098/rsif.2007.1108)

Many cellular components are organized into functional networks, be they genes, proteins or metabolites. The modular topology of many networks is functionally adaptive, and is therefore thought to arise by selection. By running a computational model in which the emergence of modularity is monitored when genes duplicate and diverge, the authors show that modules in cellular networks emerge inevitably as a result of the intrinsic way in which networks develop, rather than as the direct outcome of selection.

GENOME EVOLUTION

Evolutionary history of mammalian transposons determined by genome-wide defragmentation.

Giordano, J. *et al. PLoS Comp. Biol.* **3**, e127 (2007)

Transposable elements (TEs) constitute 45% of the human genome and have had an important influence on the evolution of mammalian genomes. Traditionally, the age of TEs has been studied using sequence-based methods that assume the existence of a constant molecular clock. In this study, the authors have estimated the age and chronological order of transposition of four main classes of mammalian TEs, solely on the basis of their pattern of transposition into existing TEs. This allowed them to estimate the relative age of TEs spanning 100 million years within and between classes, and to build TE phylogenies.

MOUSE GENETICS

A sequence-based variation map of 8.27 million SNPs in inbred mouse strains.

Fraser, K. A. *et al. Nature* 29 July 2007 (doi:10.1038/nature06067)

A genome-wide haplotype map for the mouse has now been published. Frazer *et al.* resequenced 15 mouse strains and identified 8.27 million high-quality SNPs. The data were used to identify regions of shared ancestry among strains, which in turn were used to construct a haplotype map consisting of 40,898 segments that range from 1 kb to 3 Mb in size. The map, which covers 90% of the mouse genome, should shed light on the basis of genotypic and phenotypic differences between mouse strains, and on the evolutionary history of this species.