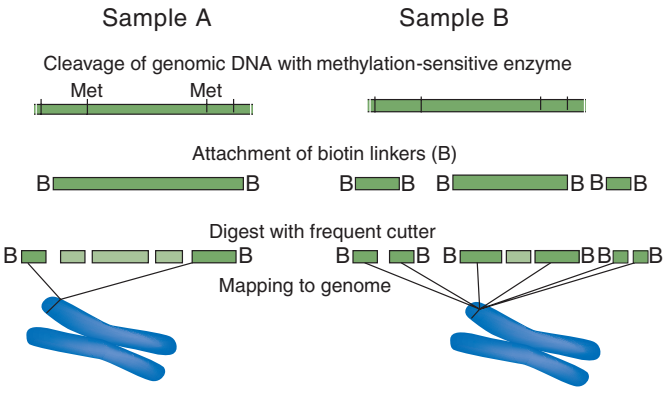

Figure 1 In methylation-sensitive digital karyotyping the number of tags obtained from genomic DNA depends on the methylation status of the DNA (Met). A high number of tags mapping to a chromosomal location indicates that this location is hypomethylated.

Polyak's work will bring important insights into the driving force behind regulation of gene expression in all the factors involved in tumor progression. These findings will be invaluable for new therapies aimed to deal a strong blow against a tumor and its supporting network.

Nicole Rusk

RESEARCH PAPERS
Hu, M. *et al.* Distinct epigenetic changes in the stromal cells of breast cancers. *Nat. Genet.* **37**, 899–905 (2005).

years). The team then moved on to the brain, hoping to shed light on the controversy over neurogenesis in the cerebral cortex. After fluorescent sorting of cortical cells, analysis revealed that although the glia were quite young, the neurons were essentially the age of their donors, suggesting an absence of significant neurogenesis.

The present sensitivity of the technique allows age estimates within two years, but Frisén indicates that this could soon improve considerably, and his group shortly hopes to follow up their initial experiments with a more ambitious project: "We want to create a map of the normal brain in terms of turnover of cells, to understand in which regions there might be neuronal turnover and to what extent." They also intend to look at the relationship between cell turnover and disease in various tissues, a task for which Frisén sees abundant resources. "You can do this just as well with frozen tissue," he says. "There's so much tissue in bio-banks already—I think pretty much any tissue or disease that we may want to study… there's probably tissue enough collected already to get whatever we want."

Michael Eisenstein

RESEARCH PAPERS
Spalding, K.L. *et al.* Retrospective birth dating of cells in humans. *Cell* **122**, 133–143 (2005).

NEWS IN BRIEF

BIOINFORMATICS

Effective function annotation through catalytic residue conservation

Although comparative sequence analysis can be useful for determining function of unknown proteins, the reliability of prediction drops dramatically as the extent of sequence identity decreases. George *et al.* show that the inclusion of strict active site–based analysis, using data from the Catalytic Site Atlas, greatly improves the accuracy of functional analysis.

George, R.A. *et al. Proc. Natl. Acad. Sci. USA*; published online 21 July, 2005.

SPECTROSCOPY

Multidimensional NMR spectroscopy for protein characterization and assignment inside cells

Reardon and Spicer have taken advantage of new advances in nuclear magnetic resonance (NMR) to develop a heteronuclear, three-dimensional spectroscopy strategy capable of providing full backbone assignments for any protein in-cell. As proof of concept, the authors successfully assign the backbone for the *Escherichia coli* protein GB-1 with three rapid NMR experiments.

Reardon, P.N. & Spicer, L.D. *J. Am. Chem. Soc.* **127**, 10848–10849 (2005).

MOLECULAR LIBRARIES

Functional dissection of sRNA translational regulators by nonhomologous random recombination and *in vivo* selection

Nonhomologous random recombination has been previously demonstrated as a useful strategy for the directed evolution of DNA aptamers and functionally modified enzymes. Now, Liu *et al.* use this technique to identify the key structural determinants that allow a pair of small, nontranslated RNAs (sRNAs) to regulate translation of a stress response gene in *Escherichia coli*.

Liu, J.M. *et al. Chem. Biol.* **12**, 757–767 (2005).

GENE DELIVERY

Organically modified silica nanoparticles: a nonviral vector for *in vivo* gene delivery and expression in the brain

Finding safe and effective methods for the delivery of therapeutic genes to the brain has proven to be a challenging task. Bharali *et al.* present a new strategy for the delivery of DNA via organically modified silica particles, permitting efficient transfection of neurons after ventricular injection, without the inherent risks of retroviral or other delivery systems.

Bharali, D.J. *et al. Proc. Natl. Acad. Sci. USA* **102**, 11539–11544 (2005).

CHEMINFORMATICS

High-throughput assays for promiscuous inhibitors

Several different mechanisms have been suggested to explain why certain chemical compounds act as reduced-specificity, or promiscuous, inhibitors. Feng *et al.* suggest that aggregation may be a major cause for promiscuity and present two rapid assays developed specifically to assess the extent of aggregation by compounds contained in chemical libraries.

Feng, B.Y. *et al. Nat. Chem. Biol.* **1**, 146–148 (2005).