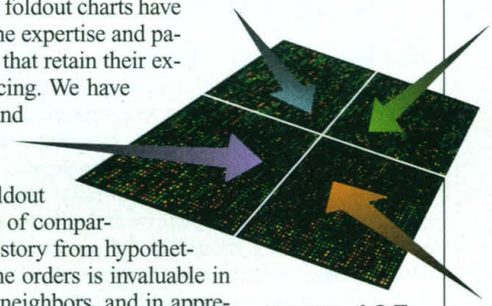
Genome Prospecting



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In the 10 years since *Science* began publishing yearly Genome Issues, the foldout charts have captured the essence of the Genome Project itself. We have witnessed the expertise and patience of investigators who collaborated on the charts and communities that retain their excitement about the science in the midst of the "race" to finish sequencing. We have also experienced the frustrations of coordinating large, disparate, and sometimes competing laboratories, as well as unforgettable moments when passionate authors battled over the raw data.

This year, the Genome Issue focuses on "genome prospecting." The foldout chart and accompanying article from O'Brien *et al.* (p. 458) describe the use of comparative analyses of mammalian genomes to follow the course of evolutionary history from hypothetical rat-sized primordial mammals to humans. Comparison of genes and gene orders is invaluable in identifying animal models for human diseases, in understanding our animal neighbors, and in appreciating our own genetic heritage.

Comparative genomics illuminates not only the path of evolution through epochs but also the path of cultural evolution through human history. Questions thought to be the domain of historians and anthropologists are now approachable with genomics. Owens and King (p. 451) discuss how migration patterns of ancient humans can be reconstructed from traces left in the chromosomal sequences of modern-day descendants. The politics of the sexes, who left home and who moved in with the in-laws, can be traced through the evolution of the X and Y chromosomal sequences.

Much as an architect's blueprint forms the plan of a building, genomic sequence supplies the directions from which a living organism is constructed. However, the blueprint alone cannot tell whether the businesses inside will be successful. As described by Wolffe and Matzke (p. 481), DNA sequence doesn't tell the whole story but must be packaged and managed by epigenetic mechanisms.

Improved tools are needed to extract meaning from genomes. A News story by Eliot Marshall (p. 444) describes cheaper and better microarrays that can track information about expressed genes. Strausberg *et al.* (p. 455) announce an initiative by the National Institutes of Health to support generation of full-length complementary DNA libraries. Both the evidence of shortcomings in the quality of data in genomics databases [see the News story by Elizabeth Pennisi (p. 447)] and Boguski's (p. 453) visions of new systems-based annotations show the directions in which bioinformatics will need to evolve.

One of the most exciting prospects for genomic information is its potential to revolutionize medicine. In a Report, Golub *et al.* (p. 531) demonstrate that gene expression information can be used to categorize human cancers in ways that will support therapeutic decisions. Evans and Relling (p. 487) review the emerging discipline of pharmacogenomics. With knowledge of DNA sequence polymorphisms and their physiological effects, medical treatments may yet be customized for individual patients.

Information without interpretation can be dangerous, particularly when applied to medicine. In his Editorial, Holtzman (p. 409) cautions that genetic tests may offer inflated promises for the technology, especially when they are marketed without the kind of regulation that is in the public's interest. Nevertheless, with appropriate attention to the management and application of genomic information, the results of genome prospecting will be precious to all.

–BARBARA R. JASNY AND PAMELA J. HINES

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See also Editorial, p. 409 and Report, p. 531.

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