dedicated servers maintained by the Oak Ridge National Laboratory. Thus, with high-resolution genetic maps in place and the well-advanced state of large-clone and radiation-hybrid–based physical maps, important quantities of mapping information will be preserved and available. What is not clear is the fate of acquisition, interpretation, and annotation of new mapping data. At the moment, there are no plans to continue these activities.

There are quite a few genome databases publicly available on the World Wide Web (*1*). Also, the Human Genome Organization Nomenclature Committee will continue to provide approved symbols for human genes in accordance with its Guidelines for Human Gene Nomenclature and will maintain the Human Gene Nomenclature Database. Thus, new mapping data, often generated in laboratories of institutions hosting databases, will be available on the Internet. In the post-GDB–project world, the user may have to click more often to find mapping information and perform interpretation and editing personally. Problems that might be expected in the absence of GDB coordination include recognizing duplicates of new markers and conflicting map locations from different resources.

Perhaps the community will get by with the available final copy of the GDB and with database "shopping" on the Internet. If not, the international community may have to pull together to arrive at a solution. For instance, database host institutions could form a consortium for the purpose of reviewing new data and maps in a coordinated fashion before release to the public. External expert reviewers might volunteer efforts (similar to those of the "editor" group of scientists that now review and edit GDB data) within the framework of such a consortium, injecting further assurances of quality and coordination. This type of program or something with similar intent could be provided at a minimal cost increase and would continue to support the efforts of many scientists involved in mapping and eventually identifying genes underlying complex disorders.

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Notes

1. These include databases from the National Center for Biotechnology Information (UniGene and Online Mendelian Inheritance in Man, for example), various genome sequencing centers, the Whitehead Institute for Biomedical Research/MIT Center for Genome Research, the European Bioinformatics Institute, the Stanford Human Genome Center, Los Alamos National Laboratory, Centre d"Etude du Polymorphisme Humain, Lawrence Livermore National Laboratory, the Cooperative Human Linkage Center, Généthon, the University of Southampton (the Génétic Location Database), and INFOBIOGEN (GENATLAS).

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NMR Availability

Robert Service, in his News & Comment article "NMR researchers look to the next generation of machines" (20 Feb., p. 1127), states, "For the past 50 years, NMR [nuclear magnetic resonance] machines have been cheap and small enough to allow hundreds of individual investigators to buy and house their own." To be sure, the earlier spectrometers were much cheaper than the new 800- and 900-megahertz (MHz) variety, but they were priced in different dollars and were generally considered too expensive for the funding agencies. When I set up a biological NMR laboratory at Harvard Medical School in 1959, I was first warned by the dean that such an outrageously expensive ($600,000) item would never be funded, and then advised by the National Science Foundation (NSF) that it must be shared, which it was. When Harden McConnell, John Baideschwieler, and I set up the 360-MHz spectrometer at Stanford in 1972 ($360,000), it was set up as a Shared Instrumentation Resource under a joint grant from NSF and the National Institutes of Health. It was a prime example of interagency cooperation and remained the only resource of its kind and the highest field spectrometer in the world for some time—accommodating more than 200 scientists from 24 countries in the first 10 years. Axel Bothner-By's Resource at Pittsburgh, which developed the first 600-MHz spectrometer in 1979, played a similar role. The same principle of sharing applies today to 750- to 800-MHz resources at Oxford, Cambridge, the University of Wisconsin, Harvard, and Stanford. It was not until the late 1980s that 500- and 600-MHz spectrometers were more generously dispensed by the funding agencies and industries alike, lured by the prospects of quick structure determination and rational drug design.

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Eating Cake?

I want to add my support for removing the absurd procedure of withholding coordinates from crystal structures after "publica-