A group of conservation experts emphasizes that "[a] biodiversity conservation database, based on field studies and scientists' notebooks in addition to museum data, is urgently needed..." Chinese proverbs offer sage guidance for international collaborations on bioinformatics projects. And the Wen Ho Lee case has galvanized Asian-American scientists to examine their status in the research community, and on that topic the comment is made that "it is not just a 'glass ceiling,' but it is becoming a more hardened 'diamond ceiling' as more Asian Americans excel in all areas of science and technology."

Databases Tailored for Biodiversity Conservation

We were pleased to see the attention afforded bioinformatics for biodiversity in *Science*'s special issue on the topic (29 Sept., pp. 2305–2314). It is essential that informatics technology be devoted to increasing our understanding of Earth's taxonomic diversity and to developing means to access the vast resources available in the world's scientific collections, and these are indeed the stated goals of the Global Biodiversity Information Facility (GBIF). However, the articles in the special section contain the potentially perilous implication that historical biodiversity data are sufficient to address contemporary issues in conservation. The section's content emphasizes data from natural history collections, as exemplified by a statement in the section's introduction (p. 2305): "These Web resources will be of greatest use if they can be put into a historical context." We see a clear distinction between a biodiversity database (based on historical data from collections) and a biodiversity conservation database (regularly updated with current information and used to support conservation decisions).

Biodiversity is being lost at an alarming rate. The *2000 IUCN Red List of Threatened Species* (*1*) and BirdLife International's *Threatened Birds of the World* (*2*) highlight the recent increase in numbers and severity of change in status of threatened species. Historical data all too frequently reflect long-lost landscapes that are now parking lots or oil palm plantations, or have been otherwise fundamentally altered and are therefore of no use for contemporary analysis or planning. A biodiversity conservation database, based on field studies and scientists' notebooks in addition to museum data, is urgently needed to address the pressing needs for management of what we have left.

In response to this need, the Species Survival Commission (SSC) of the IUCN–World Conservation Union recently announced the development of its Species Information Service (SIS) (*3*), which will link the SSC's network of more than 7000 species specialists in a distributed data management system, integrating modern principles of data custodianship (*4*). The most powerful feature of SIS is that its data will be continuously updated and managed by species experts. This mechanism will link policy-makers with scientists who have first-hand knowledge of the current status of biodiversity. In addition, both scientists and conservationists will have improved access to the data and information they need to assist them in achieving their goals.

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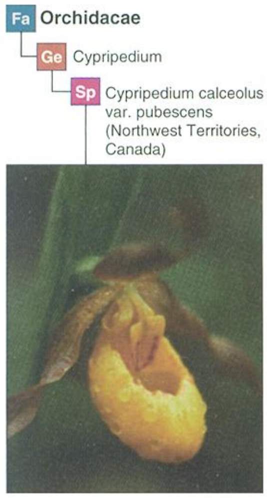
Conservation efforts will be aided by databases that can maintain currency.



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2. BirdLife International, *Threatened Birds of the World* (Lynx Edicions, Barcelona, Spain, 2000).
3. IUCN Species Survival Commission Species Information Service (SIS) (www.iucn.org/themes/ssc/programs/sisbrochure.htm). Six years in development, SIS uses an architecture of complementary modules to ensure maximum flexibility [modules on taxonomic information, population status data, geographic information (at variable scales), IUCN Red List classification (the data source for future IUCN Red Lists of Threatened Species), conservation actions, and resources and documentation]. The completed standalone SIS software is scheduled for release in early 2001; Web access is under development.
4. J. Busby, Ed., *BCIS—Biodiversity Conservation Information System: Framework for Information Sharing* (www.biodiversity.org/Handbooks_eng.htm). BCIS is a consortium of international organizations and networks (Conservation International, Association for Biodiversity Information, Wetlands International, Botanical Gardens Conservation International, TRAFFIC International, BirdLife International, World Conservation Monitoring Centre, International Species Information System, IUCN Environmental Law Programme, IUCN World Commission on Protected Areas, IUCN Species Survival Commission, IUCN Commission on Ecosystem Management) dedicated to the cooperative management and provision of biodiversity information.

Responses

Andrew Smith and colleagues make a valid point: Regularly updated databases are needed to support informed conservation decision-making. Indeed, the GBIF is intended to be a seamless web of such databases. Although the GBIF will be focused on species- and specimen-level data, it will be linked to databases of all

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types, including the nascent SIS and existing repositories like the Nature Conservancy's Natural Heritage Network (www.heritage.tnc.org/), as well as the resources indicated in Fig. 1 of our Viewpoint article in the special issue ("Interoperability of biodiversity databases: biodiversity information on every desktop," p. 2313).

We offer three additional observations. First, databases of natural history collections are not static but are constantly updated, as species identifications and phylogenetic relationships are improved and as new specimens are added to the collections. Second, one of the GBIF's major goals is to catalyze the completion of the Catalog of Names of Known Organisms. The catalog will serve biological databases of every type, enabling the SSC's specialist network to make linkages among their own and other databases. And third, it is precisely the long time series and the large samples present in many collections that allow historical trends and population variability to be studied and brought to bear on conservation decision-making. Even if some previous collection sites have disappeared, fuller understanding of historical ranges and habitats can be gleaned from collections. Such insights contribute to wise decisions on how to manage species or habitats.

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Specimen data alone are insufficient for making informed conservation decisions. Estimates of current conditions are also needed. Given this proviso, specimen data in large quantities are tremendously useful for making all kinds of biodiversity-related decisions, as evidenced by several recent papers (*1*).

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2. We thank J. Soberon for comments and suggestions.

Smith and his coauthors are right. The interoperability frameworks being developed in biodiversity informatics can link all manner of biodiversity record types and should be available to serve a wide range of biodiversity disciplines, including those of the conservation community. Indeed, applications ranging from germplasm resources to agroforestry and marine biota are already in process, and bringing together information from different sectors within the biodiversity community is itself an important goal. Several programs mentioned in my Viewpoint article ("The quiet revolution: biodiversity informatics and the Internet," p. 2309) and in other articles in the special issue are already under way. One program, Species Analyst, is experimenting with observational and museum records. Another program, Species 2000, will link the conservation, publishing, and germplasm worlds. Such programs will assure that applications will not just focus on historical data. A good example of cross-discipline interoperability is the network of botanic garden, gene bank, wild flora, genetic, and ecological resource systems within the big network of the German agency ZADI (Centre for Documentation and Information in Agriculture).

Smith *et al.* emphasize that a dynamic biodiversity information system on the Internet needs to synthesize information from resources that are themselves kept current and dynamic. Time scales may vary, but it is easy to envision moments when conservation alert systems, germplasm stock catalogs, and museum accessions databases all need to be updated on an immediate day-to-day basis. In other cases, even where the underlying information changes daily, users may not wish for reference systems and standards to be reissued too frequently. Several taxonomic systems are experimenting with fixed annual editions. Whatever the time scale, expectations that "living" systems in all sectors will be continuously updated are important.

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Collaborations Tailored for Bioinformatics Projects

As long-term participants in international collaborative research projects related to biodiversity informatics, we strongly support the activities described in *Science*'s special issue of 29 September and believe that they should be carried out worldwide and that all data should be shared by all countries. Moreover, the collaborations under way should receive more attention, not only technologically, but also conceptually.

The conventional pattern of collaboration—funds come from mainly developed countries and raw data from mainly developing countries—is in need of reform. Many developing countries are willing to contribute to global data systems, but they may also be concerned that without foreign technical assistance their own data systems could not be maintained after completion of the collaborative projects. As an ancient Chinese proverb says, "Give a man a fish and he will eat for a day; teach him how to fish and he will eat for the rest of his days." The availability of core technology and advice rather than money is more important for a successful collaboration between developed and developing countries. We believe that the biodiversity data "fishing expedition" would benefit from attention to this issue.

At present, the establishment of close collaborations between biodiversity scientists in developing countries and more highly trained computer scientists and engineers from developed countries is still a necessary and valuable step during the development phase of biodiversity informatics systems, for, as another Chinese proverb suggests, "It is better to go back and make a net than to stand by the pond and long for fish."

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Tools of the Trade in Vaccine Design

Michael Hagmann provides a good account in his News article "Computers aid vaccine design" of the potential that computer algorithms and computer modeling have for predicting what parts of an antigen (what epitopes) would be most likely to elicit a strong immunological response and hence be well suited as a target for vaccines (special issue, Frontiers in Cellular Immunology, 6 Oct., p. 80). This exciting technology will undoubtedly yield important immunotherapeutics for both cancer and infectious diseases. In the article, however, there are a few inaccuracies that we wish to clarify.

First, Hagmann says that Hans-Georg Rammensee at the University of Tübingen, Germany, defined motifs for major histocompatibility complex (MHC) class I proteins, and our group did the same for epitopes for MHC class II proteins. But, in fact, both groups defined both types of motifs and compiled class I and class II databases.

Second, it is stated that we use a matrix-based algorithm similar to the one developed by J. Hammer and F. Sinigaglia's group at Hoffmann-La Roche, which suggests that their method was developed first. Without detracting from the outstanding