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.

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).

James L. Edwards
Directorate for Biological Sciences, National Science Foundation, Arlington, VA 22230, USA. E-mail: jledward@nsf.gov

Meredith A. Lane
Academy of Natural Sciences, Philadelphia, PA 19103, USA. E-mail: lane@acnatsci.org

Ebbe S. Nielsen
Australian National Insect Collection, CSIRO, Canberra 2601, Australia. E-mail: ebbe.nielsen@ento.csiro.au

References and Notes
1. A. T. Peterson, S. L. Egbert, V. Sanchez-Cordero, K. P. Price, Biol. Conserv. 93, 95 (2000); V. Sanchez-Cordero, E. Martinez-Meyer, Proc. Natl. Acad. Sci. U.S.A. 97, 7074 (2000); J. Soberon, J. Llorente, L. Onate, Biodivers. Conserv. 9, 1441 (2000).
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.

Frank A. Bisby
Centre for Plant Diversity and Systematics, School of Plant Sciences, The University of Reading, Reading RG6 6AS, UK. E-mail: f.a.bisby@reading.ac.uk

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."

Yang Zhong, Liang Zhang,* Deming Su
The Key Laboratory of Biodiversity Science and Ecological Engineering, Chinese Ministry of Education, and School of Life Sciences, Fudan University, Shanghai 200433, People's Republic of China. E-mail: yangzhong@fudan.edu.cn and zhangl@fudan.edu.cn
* Also in the Department of Computer Science

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

Fa **Ericaceae**
└ Ge Cassiope
  └ Sp Cassiope mertensiana
    (Sierra Nevada, California)