the article are evidence of lack of NRC independence, a serious issue has been trivialized. No recommendations were changed in any substantive way, and the small changes that were made in the interest of accuracy were made with the consent of the committee chair and the NRC's Report Review Committee.

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Phylogenetic Analysis

The main thrust of David Hillis's Perspective about historical and current systematic studies (11 Apr., p. 218) appears to be the promotion of the application of statistical procedures to phylogenetic inference, especially those using the maximum likelihood approach. Most empirical systematists, however, use explicitly nonstatistical methods for inferring patterns of phylogenetic relationship. Some reasons for this are as follows.

Morphological data are not amenable to the explicit evolutionary models that underlie the likelihood approach, yet morphology has provided and will continue to provide the basis for our understanding of phylogenetic relationships in most taxa.

The criteria to evaluate models of molecular evolution are poorly defined and extremely unstable, providing a weak basis for building the stable classifications that many consider to be the goal of systematics.

Maximum likelihood is computationally expensive, so it will not find optimal solutions to large taxonomic problems, which, as Hillis notes, are becoming more prevalent.

In many cases where maximum likelihood methods have been applied, such as the gopher-louse data sets reanalyzed and reviewed by Huelsenbeck and Rannala (Reports, 11 Apr., p. 227) (*1*), the same conclusions have already been reached by using strict parsimony methods (*2*).

It is easy for nonsystematists to be seduced by high-profile boosterism of quantitatively oriented methods that appear to provide rigor and reliability. However, many systematists question the philosophical basis of such techniques.

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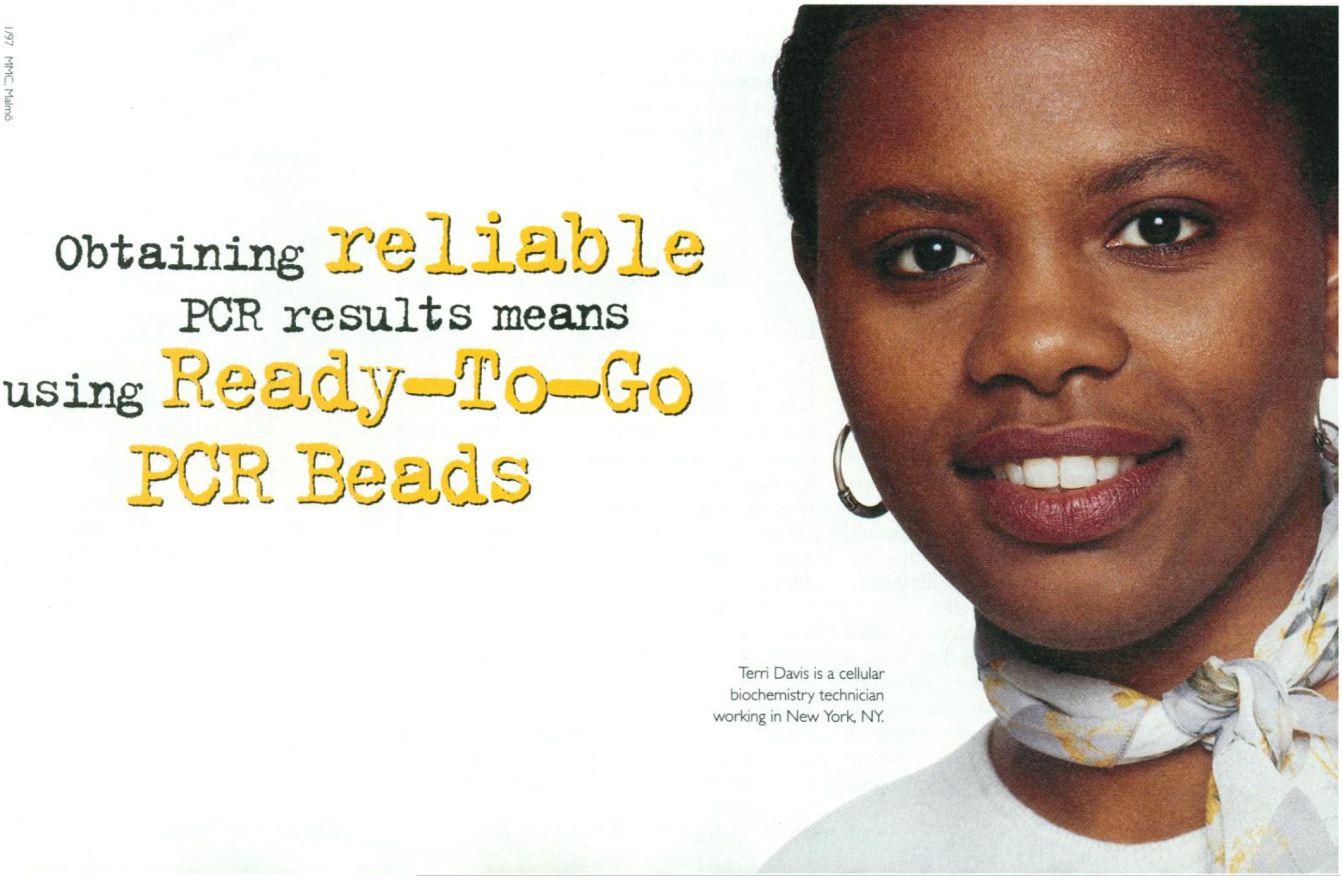
1. J. P. Huelsenbeck, B. Rannala, Z. Yang, *Evolution* **51**, 410 (1997).
2. R. D. M. Page, *Cladistics* **10**, 155 (1994); M. S. Hafner *et al.*, *Science* **265**, 1087 (1994).

Response: The main point of my Perspective was that phylogeny has once again become central to biology and that phylogenies are being used in many new and interesting ways. The papers I discussed were not about phylogenetic inference per se; they were about how to evaluate, compare, and incorporate phylogenies into analyses after they have been inferred (by whatever means). Only one of the papers I discussed used the maximum likelihood approach (the report by Huelsenbeck and Rannala). Although I supported that report, I also explicitly pointed out that the specific procedures the authors were using with maximum likelihood could also be extended to other methods, including parsimony (the method promoted by Brower



et al.). The other two papers I discussed used phylogenies derived from parsimony analyses, and one of them (by Pierce and Crawford) used a phylogeny derived from morphological data.

However, I know of no recent paper that uses "explicitly nonstatistical methods for inferring patterns of phylogenetic relationship." Apparently, Brower *et al.* are referring to parsimony analyses, which are in no sense "nonstatistical," because inferences are justified and compared with objective optimality criteria. Furthermore, it is difficult to find any recent parsimony analyses that do not assess the relative support for the preferred solution, whether with bootstrapping, jackknifing, likelihood-ratio tests, decay indices, or one of many other methods. It is true that I support this nearly universal standard in science.

If Brower *et al.* are concerned that the criteria to evaluate models of molecular evolution have been poorly defined, then they should welcome the report by Huelsenbeck and Rannala, whose goal was to make criteria for evaluating models of evolution objective and well defined.

I disagree with Brower *et al.* that stable classifications are the only goal of systematics, although that is certainly one important goal. That is why, in addition to pointing out some of the newer uses of phylogeny, I stated, "At the same time, phylogeny has solidified its more traditional role as the criterion for organizing and classifying life."

Not only did I note that large taxonomic problems are becoming more prevalent, I also said that methods besides maximum likelihood were necessary "to relieve the computational burden that prevents the application of likelihood-ratio tests to highly complex phylogenetic problems."

I do not think that "high-profile boosterism" (or even a piece clearly labeled a Perspective) is necessary to "seduce" either nonsystematists or systematists into being attracted to quantitatively oriented methods that provide rigor and reliability. It is common among scientists in general (and systematists in particular) to favor explicit, quantitative assessments over unsupported qualitative assertions. The latter approach (appeal to authority, with no explicit criteria for favoring one tree over another) was what led to the demise of phylogenetics earlier this century. The explicit, quantitative approaches in phylogenetics (including parsimony, maximum-likelihood, and minimum-evolution methods) developed over the past several decades are a major reason for the recent resurgence and success of phylogenetics.

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Evaluating Biologics

I should like to comment on the problems faced by the Food and Drug Administration (FDA) and more particularly on the Center for Biologics Evaluation and Research (CBER) (ScienceScope, 14 Feb., p. 915; Letters, 11 Apr., p. 183). I was on the staff of the National Institutes of Health (NIH) for some years, eight of them as deputy director for intramural research; as such, I became familiar with the work of the CBER. The scientists in this center, which is on the campus of the NIH, were on a par with the rest of the scientists at NIH and were completely integrated into that community. It has been the good fortune of the country that the CBER has been able to attract first-class scientists who spend approximately half of their time in regulatory affairs and the rest of the time doing research. I should note that the evaluation of