Harvey Brooks and I well know, involved more unfounded models). The real critiques that I know of come from outside IIASA, for example, from an independent group in Britain studying "Models of Doom" (*1*).

One essential difficulty with IIASA is that it does not appear to have an adequate critical mechanism, by discipline or by report review. IIASA suffers from its heritage of systems analysis, a field with no disciplinary tradition, from the burden of helping international cooperation (note the enthusiasm for cybernetics in the U.S.S.R.), and from its location in an discarded imperial palace on the outskirts of a city whose intellectual distinction lies well in the past.

SAUNDERS MAC LANE
Department of Mathematics,
University of Chicago,
Chicago, IL 60637

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1. H. S. D. Cole, C. Freeman, M. Jahoda, K. L. R. Pavitt, Eds., *Models of Doom: A Critique of the Limits to Growth* (Universe Books, New York, 1973).

Conflict over the Molecular Clock

We write to comment on Roger Lewin's Research News articles (23 Sept., p. 1598; 30 Sept., p. 1756) describing the recent debate over the DNA hybridization study of hominoids by Charles Sibley and Jon Ahlquist.

The methods and results of DNA hybridization studies have received unusually close scrutiny during the past 5 years. This latest challenge is the most severe and yet the least relevant in terms of evaluating the usefulness of the technique. While it is unfortunate that Sibley and Ahlquist have not explicated their methods of data analysis, this has little to do with evaluating DNA hybridization as a systematic tool. It is crucial to emphasize, as Lewin has done, the distinction among kinds of data, methods of analyzing data, and the behavior of investigators.

The most compelling rationale for using DNA hybridization has been that it indexes a large fraction, if not all, of the genome. We share the systematic community's delight in the elegance of gene sequencing, both for the absolute nature of the data and the opportunity those data afford to apply cladistic analysis. But it is still not possible to sequence efficiently and economically the large numbers of genes from the many species and individuals necessary for serious taxonomic work. Apart from statistical sampling issues, sequencing still tells us more about the evolution of genes than the phylogeny of the organisms bearing them.

As the ratio of experts to armchair critics has slowly increased, a new awareness of the frontiers of DNA hybridization has emerged. Sibley and Ahlquist appear to have done their utmost to facilitate the endeavor. Three basic questions constitute the current methodological research program.

1) Does the technique as currently practiced take adequate account of molecular processes that might bias estimates of genetic relatedness?

2) Can technical modifications improve the precision or extend the range of DNA hybridization, or both?

3) What analytical methods should be employed such that investigators correctly report the evidential meaning of the data?

While all these questions are pertinent, the current debate is mainly with regard to the third. We share the misgivings of Vincent Sarich *et al.* about overinterpreting the meaning of sequences that "might have hybridized," but note that much of their argument turns on confusing what may have been an artifact of tissue-preparations (the low-temperature "bump") with a supposed fundamental flaw in the T50H measure. Nevertheless, the question is not whether one measure discriminates and another does not, but whether two or more statistics give contradictory answers (in systematic terms, distinct rank orders or branching sequences). The espousal by Sarich *et al.* of the "conservative" Tmode is advocacy of a less-discriminating measure, not of one that gives an answer different from that of Sibley and Ahlquist. In our experience, the three measures (TM, T50H, and Tmode—somewhat confused in the caption to "Measures of distance" in Lewin's 23 September article) are rarely if ever inconsistent with each other.

Whichever statistic is chosen, the critical issue is the appropriateness of such corrections as might then be applied to the data. As long as a straightforward and rigorous logic is applied to taking experimental biases into account, we do not see data correction as different in principle from calibrating any laboratory instrument. One such correction [for the compression effect on distances caused by spuriously low homologous melting temperatures (*1*)] derives, ironically enough, from a technique proposed by Sarich and John Cronin (*2*).

There is one more issue of concern. We were alarmed to learn from Lewin's article details about the review of Sibley's latest National Science Foundation proposal. Unless this information came from Sibley himself, its availability seriously compromises the rule of confidentiality that is at the heart of the peer-review system. It is enough that researchers whose contributions will influence systematics for generations to come have been prematurely excoriated outside the normal bounds of reviewed science without the circumstances of their failures to secure grant support becoming a matter of public knowledge.

JOHN A. W. KIRSCH
CAREY KRAJEWSKI
Department of Zoology
and *Zoological Museum,*
University of Wisconsin, Madison, WI 53706

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2. V. M. Sarich and J. E. Cronin, in *Molecular Anthropology: Genes and Proteins in the Evolutionary Ascent of the Primates*, M. Goodman and R. E. Tashian, Eds. (Plenum, New York, 1977), pp. 141–170.

Response: The circumstances of Sibley's NSF proposal were widely known, but the information reported in my article came from Sibley himself.—ROGER LEWIN

Corrections

In our report "Amino acid preferences for specific locations at the ends of α helices" (17 June 1988, p. 1648), the statement in the introduction that "Position-specific preferences have not been compiled for helices or β strands" is not correct. We have since been made aware of a paper by P. Argos and J. Palau [*Int. J. Pep. Protein Res.* **19**, 380 (1982)] which did precisely that. Many of the same trends were observed for helical amino acid preferences.

Also, the reference in the first paragraph of page 1649 to "definitions from (*9*)" should have read "definitions from (*13*)."

JANE RICHARDSON
DAVID RICHARDSON
Department of Biochemistry,
Duke University,
Durham, NC 27710

Erratum: Figure 3 (p. 1310) in the report "A 115-kD polypeptide immunologically related to erythrocyte band 3 is present in Golgi membranes" by S. Kellokumpu *et al.* (2 Dec., p. 1308) was incorrectly printed. The correct figure is reproduced below.