Letters

Collaboration and Responsibility

I wish to comment on the preposterous suggestion, being seriously advanced in some quarters, that *all* of the authors of a given paper are responsible for *all* of the material that appears in that paper. If that rule were adopted, it would bring multidisciplinary research to a virtual halt.

"Multidisciplinary" means that scientists with very different areas of expertise collaborate to solve a problem. The recent case in my own institution (News & Comment, 4 Nov., p. 659) was typical of such collaboration. Analytical chemists who measured the concentrations of substances in the spinal fluid of psychiatric patients would have been presumptuous, indeed, to "monitor" the assignments of patients to diagnostic categories—just as presumptuous as the clinicians would have been to "monitor" the gas-chromatographic mass-spectrometric procedures.

So let's have more common sense here. Collaboration must continue to rest on trust between colleagues. Yes, sometimes the trust will be misplaced. As in every field of human activity, there will be occasional lapses of judgment, lapses of due care, even lapses of rectitude. But the scientific research establishment and its procedures are fundamentally sound and self-correcting, and such lapses have been very few in relation to the magnitude and productivity of the enterprise. We do need to deal with each occasional problem, always in a manner appropriate to its importance. But we do *not* need new committees to invent new regulations, a new layer of administrative bureaucracy to monitor and enforce them, and yet more mountains of paper to attest to a university's assiduousness.

That approach may sound good to politicians, and it may look good on paper, but it makes no sense to working scientists. Such proposals can hamstring research of just the kinds most likely to serve society by generating the understanding that leads to cure, amelioration, and prevention of disease.

The argument that we must harm our research effort, because otherwise "they" will harm it for us, should be recognized for what it is—the invention of those (especially administrators) who are willing to sacrifice principle for expediency. We scientists should try harder to educate our legislators about how best to nurture scientific research for the benefit of society. Having done that, we will have fulfilled our ethical responsibility. If we fail, and crippling restrictions are nevertheless imposed, it is better not to have participated ourselves in a destructive attack on the scientific enterprise.

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Having recently spent a considerable share of my time as Chair of an investigation which found scientific misconduct on the part of Stephen Breuning, I had an opportunity to ascertain firsthand the importance of the authorship issue. I have concluded that attempting to establish categories of authorship or other arbitrary definitions of "who is an author?" will not work. Modern science, including the relationship of individuals to a scientific work, is too complex.

There is a workable solution, however. Journals should return to the old-fashioned practice in which all authors, or any other participants, designate the role that they played in bringing a study to completion and a paper to publication. In addition to the fair apportionment of credit, this approach would have another benefit. It would help in the evaluation of the work to know, for instance, if the skilled laboratory scientist with his name on a paper actually did the experiments or only served as an adviser or supervisor. Peer reviewers would have access to this information in evaluating a paper and could also determine that the role of each author was not vaguely or ambiguously described.

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Eliminating NO_x

Milton Russell, in his Policy Forum "Ozone pollution: The hard choice" (9 Sept., p. 1275), considers only half the problem when he concludes that there have to be "hard choices." Russell is correct that hydrocarbons reacting with nitrogen oxides (NO_x) in sunlight, after a variety of chemical reactions, produce ozone. However, if unburned hydrocarbons cannot be eliminated, as they cannot because of a fraction coming from natural sources, what about the NO_x?

Two techniques exist for the elimination of NO_x pollution (smog). One way breaks up the NO_x after its formation by means of catalyst-type reactions. Only two materials have been found, and neither is satisfactory. Rhodium is a rare strategic mineral, and we simply do not have enough to do the job. The other material, ammonia, only reacts to eliminate NO_x over a temperature range from about 1650°F to 1725°F.

At present, the only possible approach that appears to work is eliminating nitrogen from the combustion process and recirculating 80% of the exhaust gases, thereby creating a nitrogen-free synthetic atmosphere. The additional fuel cost for electric-generating facilities would be about 1 cent per kilowatt-hour; an increase in utility rates from about 10 cents per kilowatt-hour to about 11 cents per kilowatt-hour is possible with near-zero NO_x. As for vehicles, a mobile air reduction system needs to be developed. No fundamental principles are violated and it may be possible, with concerted effort, to reduce the volumetric requirements to something satisfactory. Needless to say, this synthetic atmosphere approach has not been attempted, even though it appears to be the only possible way to solve the ozone-smog problem and requires no "hard choice."

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IIASA and Modeling

The difficulties in the work of the International Institute for Applied Systems Analysis (IIASA), as discussed in my letter of 2 September, have brought two responses (28 Oct., p. 495). Keyfitz observes correctly that "many of the most difficult problems we have to face" cannot be precisely formulated. I agree that we should tackle these problems and that they require much more than, say, just algebra; but I doubt that they should be tackled by making models "that in the first instance are not verifiable." I saw too much nonsense of this sort in the 8 years I spent as chairman of the report review committee of the National Academy of Sciences (NAS), including, for example, a fictitious model predicting that it would take 100 years to regenerate the mangrove swamps of South Vietnam from the effects of herbicides. Problems are not solved and science is not helped by unfounded speculation about unverifiable models.

Harvey Brooks and Alan McDonald, as guardians of the orphaned IIASA, say that the IIASA "global modeling conferences" helped diminish the initial enthusiasm for the Forrester-Meadows style of system dynamics. They offer no references, except for an unspecified note of some NAS global models of the 1970s (at least one of these, as

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.

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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.

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1. M. S. Springer, thesis, University of California, Riverside (1988).
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*)."

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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.