icis.unimaas.nl; [2]Global Environment Program, Union of Concerned Scientists, Cambridge, MA 02238, USA. E-mail: smoser@ucsusa.org

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Describing the Release of Sequence Data

RICHARD W. HYMAN'S LETTER ENTITLED "Sequence data: posted vs. published" (2 Feb., p. 827) is not in accord with the data release policies adopted by the National Institutes of Health and the U.S. Department of Energy. That policy statement begins, "[The National Human Genome Research Institute's] policy for release and deposition of DNA sequence data was devised to make sequence data available to the research community as soon as possible for free, unfettered use" (*1*).

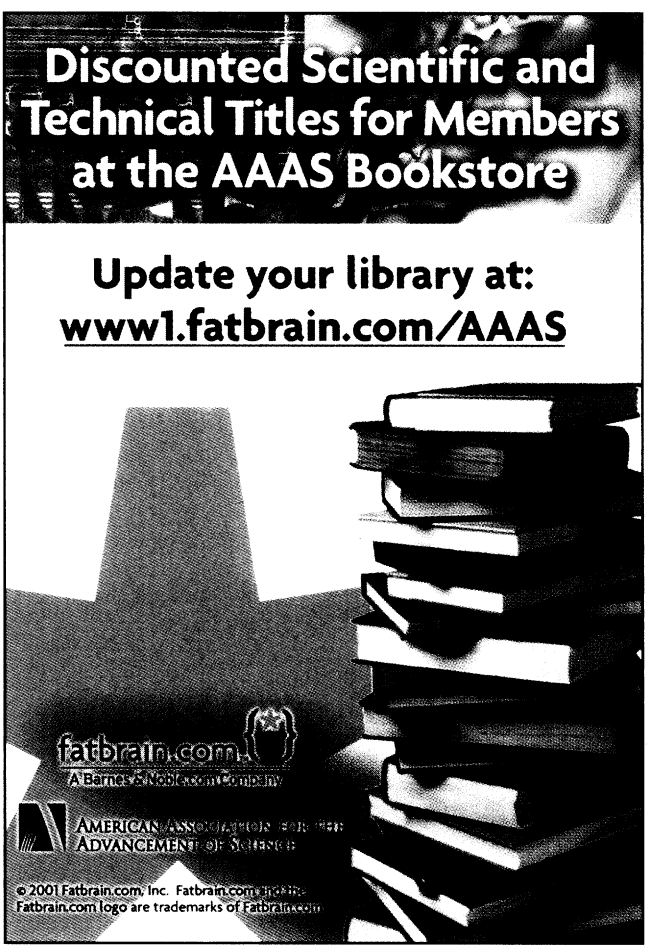
Nowhere in that document is there any implication that sequencing centers would retain veto power over the use of prepublication data in academic publications. Just the opposite. The purpose of prepublication release is to allow the academic community to make full use of genome sequence data in all aspects of research as soon as possible. That such work should result in academic publication is the goal of the data release policy. Sequencing centers uncomfortable with this data release policy were certainly free to seek funding through other sources, and at least one center did just that, with great success.

> **"[P]republication release...allow[s] the academic community to make full use of genome sequence data...as soon as possible."**

I disagree with Hyman's statement that it is easy to recognize prepublication data in GenBank. GenBank policy dictates that only the depositing authors can modify a sequence entry, and many authors fail to update entries to reflect progress in the peer review process. It is difficult for database providers to make these updates because the title, authors, and journal may change in the course of manuscript review and resubmission. Many entries in GenBank are annotated as "unpublished submission," when in fact papers describing the data by the authors who deposited the sequence have appeared in the peer-reviewed literature.

Sequence finishing is an ongoing process, and we will undoubtedly be publishing revisions and additional annotations on the human genome for many years. To delay publication of derivative work until a center signs off on a final version is not feasible, because there will not be a fully finished human genome sequence for many years to come, if ever. Particularly for sequence in the draft phase, the data are a moving target. It is therefore important that publications based on draft sequence cite the source and date of the entry.

Finally, submission of data to GenBank is a form of electronic publication (*2*). Data appear in GenBank only with the consent of a submitting author or through journal scanning. GenBank entries establish publication date for patent purposes, and GenBank accession numbers are routinely used as a mecha-



nism for attribution in the scientific literature. To appropriate a database entry without attribution and imply that the data were generated de novo would be plagiarism, but to use data from a public database as the basis for further analysis is entirely appropriate and widely accepted within the academic community.

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Structured Abstracts for Technical Journals

OUR READING OF THOUSANDS OF technical journal abstracts in myriad disciplines shows substantial information nonuniformity in the nonmedical records' abstracts. They can vary in information volume, information categories, and information clarity. Commonly, research purpose, results achieved, and potential applications are not evident.

We do not find these problems in the bulk of the *medical* literature. Most medical journals require that authors address canonical categories in the abstract and full-text article, based on recommendations made over a decade ago (*1*). The experience of the medical community with these structured abstracts has been well documented (*2*). Structured abstracts are slightly longer than unstructured ones, have slightly longer underlying articles, and have more useful information content. They produce no negative impact on creativity or originality and are widely accepted as a positive improvement.

The advantages of structured abstracts are so obvious, we do not understand why they have not been implemented in the nonmedical journals. The costs are minimal and the potential benefits would be substantial. We recommend that all technical journals require the following generic structured abstract categories for both original research and review articles: Background, Objectives, Approach, Results, and Conclusions. Each journal could also establish subcategories to accentuate information of value to its unique discipline, as many medical journals have done.

CREDIT: LARRY MASTER

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CORRECTIONS AND CLARIFICATIONS

NETWATCH: "Latin America Field Guide" (4 May, p. 815). The bird in the photo accompanying the item is a tufted coquette, not a dark-rumped petrel.

REVIEW: "Genealogical and evolutionary inference with the human Y chromosome" by M. P. H. Stumpf and D. B. Goldstein (2 Mar., p. 1740). In column 3, paragraph 2, headed "Ancestral haplotypes and present variation," the last sentence should have read "...nodes 1 through 4 back to the node at time T_3," not "...at time T_2."