

Access to Genetic Sequence Data

In Leslie Roberts' News & Comment article "MRC denies blocking access to genome data" (13 Dec., p. 1583), the head of the British Medical Research Council (MRC) Human Genome Mapping Resource Center, Tony Vickers, is reported as saying he does not know why researchers might want to scan through and download genetic sequence data freely. He says that the MRC possesses analytic software that small labs could not easily have access to otherwise.

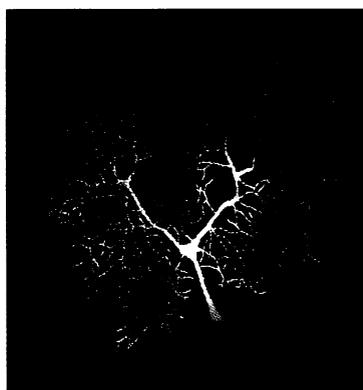
This attitude is wrong and disappointing. One of the main aims of the Human Genome Project should be to develop innovative new software for analyzing sequence data and collating it with other biological data. My colleagues and I are now working on artificial intelligence techniques that we intend to apply to learning to recognize structure in sequence data. This work has funding from the National Institutes of Health, and teams at a number of other universities are doing similar research. Free access to primary data will be essential for testing the methods that are developed.

Computer science and artificial intelligence promise to make available tools for performing sequence analyses far deeper than simple recognitions of homology. It would be a grave mistake if the MRC, or any other database custodian, adopted as a standard any particular existing analytic software.

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Chronic Fatigue Syndrome

I would like to address Joseph Palca's Research News article "On the track of an elusive disease" (20 Dec., p. 1726). I have used the polymerase chain reaction, under conditions of reduced stringency, to seek out viral sequences related to either herpes viruses or retroviruses in patients with the chronic fatigue syndrome (CFS). This work led to the culturing of a virus that appeared to contain sequences of both herpes virus and retrovirus. I notified the Centers for Disease Control (CDC) early in 1991 that an atypical virus had been repeatedly cul-



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Photo of intracellular calcium concentration in a guinea pig cerebellar Purkinje cell taken using Photometrics Series 200 CCD system. Courtesy of Dr. D.W. Tank, Molecular Biophysics Research Department, AT&T Bell Laboratories.

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tured from a CFS patient. The cytopathic effect (CPE) seen in culture was characterized by foamy cell changes. A virus inducing a similar CPE was isolated from a patient with an unexplained severe encephalopathy. Many additional patients have also tested positive by culture. CDC officials were invited to visit my laboratory and review the culture findings, but declined to do so.

A meeting sponsored by the California Department of Health in San Francisco and a National CFS Advisory Council Meeting held at CDC in September 1991 provided additional opportunities to present ongoing research and to show photomicrographs of the CPE and electron micrographs of the viral particles. At each meeting, I emphasized the importance of obtaining additional sequence data to characterize the type of virus involved. Contrary to Palca's account, I did not consider the audience at either San Francisco or at CDC to be "hostile."

A brief report describing the culture and electron micrographic findings in the initial CFS patient was submitted for publication and was rejected. I consider a reviewer's comment to Palca that most of the data were "negative or uninterpretable" to be a breach of the confidentiality of peer review that may reflect the type of personal bias that has continually led to questioning of even the

existence of CFS. The best response to this type of skepticism is to continue to perform careful science and to obtain conclusive sequence data on the viruses we have isolated. My laboratory is actively engaged in this research.

I trust that the publicity associated with our work will encourage the efforts of others to investigate CFS patients for evidence of viral infection.

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*Response:* Martin's concern that the confidentiality of the peer review was breached by my report is understandable but unfounded. In the course of interviews for this story, one expert in the field criticized Martin's work and explained that he knew its details because he had been asked to peer review a paper Martin had submitted for publication. The scientist did not share his review or the paper with me, nor even say to which journal it had been submitted. I mentioned his role as a reviewer simply to give the reader some indication of his credibility as a critic, and to protect his confidentiality, I did not name him.—JOSEPH PALCA