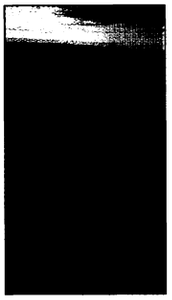
heimer's recent review of the status of understanding of the West Antarctic Ice Sheet (WAIS) and its stability (*1*). According to Kerr, "[Oppenheimer] concluded from the erratic behavior of late that its [the WAIS's] most likely fate is disintegration during the next 500 to 700 years, greatly accelerating sea-level rise beginning in the 22nd century." Kerr suggests that Oppenheimer provided one of several "alarming recent predictions." Oppenheimer discussed three possible future scenarios for the WAIS, and his assessment was that the scenario summarized by Kerr has the highest relative likelihood but, as noted by Oppenheimer, with low confidence. Oppenheimer started the discussion of possible future scenarios with the statement: "It is not possible to place high confidence in any specific prediction about the future of [the] WAIS."



Ross ice shelf: Stay awhile?

C. J. van der Veen
Byrd Polar Research Center, 1090 Carmack Road, Columbus OH 43210–1002, USA. E-mail: vanderveen.1@osu.edu

References
1. M. Oppenheimer, *Nature* **393**, 325 (1998).

Learning from Others

In his article "U.S.–style universities for Germany?" (News & Comment, 19 June, p. 1826), Martin Enserink describes Germany's movement toward infusing private (partially public-supported) universities into its existing traditional higher education structure. This infusion may eventually result in institutions of higher education that operate more like those found in the United States. While the higher education system in Germany may learn from us, our system can also learn from some of Germany's present practices, especially related to teaching strategies emphasized in beginning college-level chemistry or other science courses.

For example, our recent study of teaching behaviors practiced by faculty and teaching assistants in beginning college chemistry education in the United States (*1*) concluded that more than 95% of laboratory instructional time is spent in instructors responding to students' procedural questions. Many students even believe that responding to these kinds of questions is the major role of the instructor. Thus, students spend little time reading and interpreting directions before, during, and after each 3- to 4-hour laboratory class per week. They also spend little time in drawing conclusions from the data collected and virtually no time in addressing the scientific and social significance of the laboratory findings.

We also observed and analyzed the teaching done by "overseers" during beginning college chemistry laboratories in Germany. Examples of effective practices were students spending from 20 to 25 hours per week engaged in laboratory settings planning for and carrying out real investigations. Overseers did not respond to procedural questions, and students met with them and the department chair for oral examinations on knowledge learned from the laboratory experience. On a voluntary basis, these students attended only three or four lectures each semester.

As an example of an ineffective practice, the laboratories were pretty much limited to classical qualitative analysis without the use of analytical instrumentation or computers. These "tools" are left for more advanced courses.

Our recommendation is for German institutions to not "throw out the baby with the bathwater"; that is, they should continue emphasizing active and extensive student participation in scientific investigations, but also adopt some of our more useful instructional laboratory practices.

At the same time, we in the United States need to place more emphasis on student inquiry and involvement in the instructional process. New curricula like MC2 and Modular Chemistry could take chemistry instruction in the United States in this more effective direction (*2*).

Frank X. Sutman
Temple and Rowan Universities, Glassboro, NJ 08028–1701, USA.

References and Notes
1. A. Hilosky, F. Sutman, J. Schmuckler, *J. Chem. Educ.* **75**, 100 (1998).
2. These are two of the five major chemistry curriculum projects supported through the Division of Undergraduate Education of the U.S. National Science Foundation. The two projects joined efforts after initial development at the University of California, Berkeley, and Beloit College in Wisconsin.

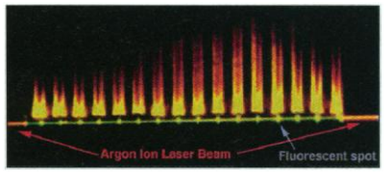
A "Humouse" Project

In their commentary "Shotgun sequencing of the human genome" (*Science*'s Compass, 5 June, p. 1540), J. Craig Venter and his colleagues once more create a sensation by announcing that a new industrial entity is aiming to sequence the whole human genome in 3 years at a cost of $300 million, a small amount in comparison to those of other efforts.

There are two key elements to this project. First, a new generation of sequencers will be launched by Perkin-Elmer Corp., a partner in the project. Second, a global "shotgun" approach to sequencing will be attempted.

Can this project succeed? The goal of sequencing 5×10^{10} nucleotides can likely be reached, but assembling these raw data is another story. The main problem lies in the presence of regions difficult to sequence—with an increasing load of poor base identification and of the repeat sequences that literally stuff the human genome—that will eventually (and erroneously) associate raw sequences that originate in regions remote from one another. A correcting move would be to sequence both ends of recombinant clones and, at the time of assembly, impose a constraint such that the two sequences are positioned at a given distance calculated from the size of the clones.

These difficulties have not been overlooked by Venter *et al.* Their objective is not to get a perfect human sequence, but to get 99% of the genome sequence in some 5000 fragments—which is adequate for the purpose, namely, the discovery of human genes and their control elements. The strategy is industrial and is intended for economic purposes. In contrast, the motivation of the publicly founded sequencing centers is primarily academic. Only a complete, overall view of the human genome will allow researchers to grasp its complexity, internal consistency, and phylogenic relations.



N. DOVICHI, UNIV. OF ALBERTA

Sixteen fast lanes: DNA sequencing

Venter's expertise in the field of sequencing is tremendous. The scientific community should take his proposal seriously and integrate it into the larger strategy. Doubling the financial effort while sticking to present-day technology, as recently advised at a meeting in Warrenton, Virginia ("Sequence, sequence, sequence," ScienceScope, 5 June, p. 1515), would not be enough.

What is really needed is a demarche complementary to that proposed by Venter *et al.* It should be established at the outset is that (i) the number of species for which a sequenced genome is useful is large, (ii) the full significance of a sequence can only be grasped if it can be compared with other sequences, and (iii) a complete sequence of the human genome would be the most useful of all. From these considerations, the following three proposals might appeal to the scientific community and its sponsors.

First, we should strive to analyze complete complementary DNAs. A large number of tags have been described, but complete sequencing of all complementary DNAs is essential. Predicting the location and exon structure of genes from the bare sequence data remains a hard task. Second, we should commit ourselves to finishing up other ongoing efforts to sequence the human genome. Third, we should increase efforts to analyze mouse DNA. Mouse is the model *par excellence* for understanding the significance of the human genome. By comparison with the latter, knowledge of the mouse genome will enable us to spot the genes and their most conserved parts—namely, the exons—and to mutagenize genes at will, to disrupt or simply modify them, and to study their function. Also, knowledge of the mouse genome sequence should facilitate the finishing of the human genome.

Drawing inspiration from the centralized organization of Venter *et al.*, we could combine the energy and competence of many scientists into a decentralized network of laboratories dedicated to performing the sequencing reactions and migrations while bringing back the raw sequences for analysis in a unique information center.

Many in the scientific community are uneasy about the conditions in which the sequences produced by this private consortium are to be released and kept accessible to all. Venter *et al.* advocate collaboration, not confrontation. Their associate, Applied Biosystems of Perkin-Elmer (ABI), is not a pharmaceutical company, but one known for its reagents and sequencing machines. Availability of the mouse and human sequences will provide a fantastic interpretative tool to all, including Venter *et al.* It is my belief that both sound emulation and efficient cooperation can be founded on this ground.

Francis Galibert
Head, Centre National de la Recherche Scientifique (CNRS) Genome Program, 35043 Rennes Cedex, France. E-mail: galibert@univ-rennes1.fr

DRD2 Gene and Alcoholism

The article "New clues to alcoholism risk" by Constance Holden (Research News, 29 May, p. 1348) includes statements attributed to "the COGA [Collaborative Study on The Genetics of Alcoholism] people" with which I disagree. The statement that their study leads to "debunking" the D2 dopamine receptor gene (*DRD2*) as an "alcoholism gene" runs counter to the growing body of evidence implicating this gene not only in alcoholism but in other drug addictions.

A number of studies both in the United States and abroad have ascertained the association of the *DRD2 A1* allele with alcoholism. At least seven independent meta-analyses of ethnically matched (non-Hispanic) Caucasians found the prevalence