(http://www.tigr.org). This step in the analysis, while relatively stable, evolves with time as more closely related sequences appear in the databases. The assignment of function to genes is less direct (and often less certain). It requires synthesis of much data, including the spectrum of functions represented by related sequences (which in turn relies on the availability and accuracy of annotated functions for these related sequences), information about the presence (or absence) of genes for other functions, and information about the organism itself. The functional interpretation of genomic sequences therefore improves with time and with the input and suggestions of diverse researchers.

With regard to nitrogen fixation and *M. jannaschii*, Haselkorn and Buikema are probably correct. However, the *M. jannaschii* genome contains a large percentage of genes new to biology that are of unknown function. Bioinformatics and sequence comparisons can lead to the generation of many hypothesis, including our own, that must be tested and verified experimentally. We applaud the interest taken by our colleagues and encourage further constructive comment. A large number of other useful contributions have been made through the TIGR Internet site. Our goal is to provide an environment in which this information can be collected in a coherent manner, updated, and made available to the world.

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Whose Genes Are They and How Can We Identify Them?

The new policy of the National Center for Human Genome Research (NCHGR) on informed consent for DNA sources for the Human Genome Project (E. Marshall, News & Comment, 27 Sept., p. 1788) may protect the identity of donors at a high price for the image of human genetic research. The need for detailed informed consent for DNA sources cannot be questioned. The issue is how the research effort manages the identity of the new sources and the justification for anonymity. Anonymity should not be required for donor protection if the NCHGR collaborates with consenting DNA donors who are at low risk of adverse psychosocial effects [for example, those of a mature age (say, 75) with no children or who are retired and on Medicare].

The problem with strict anonymity is the message it broadcasts about the nature of genetic information. The Human Genome Project will be an important landmark in the history of science and medicine. There is a public fascination with this effort that will only increase as "the sequence" is completed. Yet secrecy surrounding the often-asked question about the identity of the source will raise troubling questions. Why are the donors being hidden? What kind of threat does genetic analysis pose? Is this information about which we should be afraid or ashamed? Why are we paying billions for this information? Ironically, the elaborate mechanisms developed to protect the identity of the DNA sources through the new policy may foster the very social stigmas that the NCHGR seeks to avoid. While great care must be taken in the conduct of clinical genetic testing (*1*), overstating the risks will hinder the beneficial applications that justify the project and augment the psychosocial risks. Also, the NCHGR would make a strong

political statement about "genetic elitism" by openly accepting donors from traditionally disenfranchised groups.

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References

1. J. Botkin *et al.*, *J. Natl. Cancer Inst.* **88**, 872 (1996).

On reading Marshall's article "Whose genome is it, anyway?," it occurred to me that this entire issue could be handled in an entirely different manner. Why not auction off the right to sequence chromosomes or parts of chromosomes? The highest bidder would get his or her DNA sequenced. This would provide additional funding, diversity, and the question of consent, and anonymity would be obsolete. Admittedly, it would lead to an elitist genome being sequenced first—the genome of the financially potent. But didn't certain qualities determine who was the first man to walk on the moon? The Human Genome Project would make it into history books, and surely many people would like to have their names (DNA) associated with it.

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Evolution Teaching

In Karen Schmidt's News & Comment article "Creationists evolve new strategy" (26 July, p. 420), Eugenie Scott of the National Center for Science Education is said to discourage individual scientists from debating creationists. Schmidt further suggests that scientists who have engaged in such debates say Scott is right. I have had several formal debates with creationists, I have experienced that feeling of having "been in a boxing match," and I think Scott is flat wrong.

No evolutionist should ever plan on converting the faithful to our view of the planet's history in a debate or even in a semester-long class. True believers are not swayed by logical interpretations of loads of evidence. The pious, however, are not the ones for whom we present our counterarguments to creationists' interpretations. We are there for those who would like to learn how to deal with that purveyor of creationism on the doorstep, that biblical literalist in the cafeteria, that roommate who believes in Noah's ark, or even that schoolteacher who presents "both models" and lets students choose the preferred alternative.

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Paul R. Gross (Letters, 6 Sept., p. 1321) is quite right: not only is it not "demeaning" for scientists to enter public debates to question claims about "facts" (his quotes) offered by creationists, but it is usually their duty to do so, and such interventions are not without their effects. What, however, *is* demeaning is for scientists to treat their disputants with contempt and derision and to try to counter what scientists may see as misconceived parodies of scholarship with "a willful strategy of distortion and demonization" (*1*) of their own, abandoning all pretense of trust and respect among academic colleagues. To do so is to squander one priceless asset of scientific practice, namely, eschewing ad hominem argument and engaging in open, fair, honest, and well-informed disputation. To behave otherwise is to demean (and will eventually destroy) the very science and reason that we all are so anxious to conserve and extend. Whom the cap fits. . . .

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References

1. M. N. Wise, *Iris* **87**, 323 (June 1996).

Judy Harvey writes (Letters, 6 Sept., p. 1321) that after significant experimental support is gathered, a hypothesis becomes a theory. This much is true. She then writes that if, after further testing, the theory "proves true in all circumstances, then it becomes a law." This should be restated. A law is a concise verbal or mathematical statement of a relationship between experimentally observed parameters that is always the same under the same conditions. A theory does not become a law; rather, a theory explains a pre-existing law and the body of facts upon which that law is based.

Hypotheses explain laws, and well-tested, corroborated hypotheses become theories. Harvey states, "there is a Law of Gravity and the Laws of Thermodynamics, but there is not a Law of Evolution. . . ." This mixes apples with oranges. The laws of gravity and thermodynamics are mathematical equations. There is no Law of Evolution because the facts explained by the theory of evolution cannot for the most part be pre-