

indigenous languages of the Americas have a common ancestry) has linguists saying that "it's impossible to trace the family tree of Amerind languages back to one 12,000-year-old ancestor, because written records go back only 5000 years." But tracing linguistic family trees is not based on written records. For most Amerindian languages, there are no such records. Language families are established by systematic comparison of phonetic data from currently spoken languages. Sometimes (although not in Amerindian linguistics), written records have been peripherally relevant to substantiating the validity of the methods used (as when 4000-year-old Hittite inscriptions turned out to confirm certain conclusions about early Indo-European).

What linguists typically disagree with Greenberg about is whether phonetic comparison of present-day languages could ever provide a warrant for suggesting a relationship going back 12,000 years. It is extremely unlikely. Languages appear to change fast enough that over that sort of time scale the phonetic similarities within a group of languages would be irretrievably obscured. That conclusion is (contra Greenberg) fairly secure, and is quite independent of the existence of writing.

The languages of the Americas could, of course, have had a common northeast

Asian ancestor spoken tens of millennia ago. Historical linguists don't dislike that idea; they just feel obliged to point out that linguistic evidence cannot confirm it.

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Response: The article's brief mention of written records was not intended to imply that these were used to trace the origin of American Indian languages, but simply to point out that, even in the best cases, where written records exist, many linguists think that it is impossible to trace languages back to a 12,000-year-old ancestral language.

—Ann Gibbons



Protein Structure Prediction

Elizabeth Pennisi's Research News article "Teams tackle protein prediction" (26 July, p. 426) describes an ongoing project, known as CASP (for Critical Assessment of Techniques for Protein Structure Prediction) (1), to provide researchers who model protein structures with the opportunity to jointly

make bona fide predictions, announced before a structure is determined by experiment. The theme of the article, that collaboration is needed for progress, is indisputable. We do not agree, however, that, among those who participated in the ab initio part of the first prediction contest "nobody really came close to predicting an accurate structure," that "predictions [of secondary structure] were no more accurate than ones made a decade ago with cruder methods," and that the assembly of predicted secondary structural elements into "a complete 3D structure" "didn't work at all," as John Moult alleges.

One advantage of the CASP approach is that the predictions are independently judged and the judges publish their opinions so that they are available to the public. This was so for the ab initio session of CASP1. The evaluations of the predictions published by the judges differed greatly from those reported by Pennisi. "For phospho- β -D-galactosidase," wrote judges DeFay and Cohen (2), "Benner and Sader [both] correctly predicted this protein to be an α/β barrel." The success came from "an exceptionally small number of 'wrong' predictions." Further, the judges wrote, "it . . . would have been unlikely if a prediction was made from the [decade-old, cruder] GOR [method for] secondary structure prediction." For synaptotagmin, the



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judges noted that "both Hubbard and Benner correctly predicted the first six strands," missing only the final secondary structural element. Despite this error, three (out of 196) possible folds were chosen to represent the beta sandwich of this protein (3); one of them was correct. This sounds "close" to us.

Predictions today are not simply contest entries; they are good enough to be applied to solve real biochemical problems. Progress has come in part through the recognition that the protein folding problem is a special example of a much older problem in organic chemistry, conformational analysis. Through this has come the realization that organic chemical approaches have something to contribute to protein folding. *Science* readers should therefore be encouraged to apply prediction tools to their own research problems.

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EMF Report: Is There Consensus?

Although the National Research Council's (NRC's) new report (1) on electromagnetic fields (EMFs) (J. Kaiser, News & Comment, p. 910) makes interesting scientific reading, it falls short as a balanced and informative public communication tool. Like its predecessor committees, the NRC panel chose not to make a prominent display of the true state of scientific uncertainty in their ranks; instead, it issued a carefully worded conclusion that "no conclusive and consistent evidence shows that exposures to residential electric and magnetic fields produce cancer." This presentation is regrettable for two reasons.

First, rational people may choose to take action to eliminate or reduce risk even when the probability that the risk is real is less than that associated with "conclusive

and consistent evidence." The NRC report provides the public with no judgments about how likely or unlikely it is that EMFs really cause cancer. All we can glean from the conclusions is that the panel thinks that there is something less than perhaps a 90% chance that the EMF hazard is real. A more neutral approach, and one that addresses the public's information needs more effectively, would have been for the committee simply to report the range of members' subjective judgments of the probability that EMF exposure is truly hazardous.

Second, those readers unfamiliar with the long-standing scientific uncertainty over EMF health effects may miss the nuances of the NRC committee's conclusions and come to the mistaken belief that scientists have concluded with certainty that EMFs pose no health hazard. Indeed, this inference was the gist of many news stories that followed the release of the report. We might ask how different those news reports would have looked had the committee reported the complementary and equally true conclusion that "no conclusive evidence shows that EMFs are safe."

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