top terminal and get the results back without ever having to visit the center.

In the first phase, which is now under way, Jennings is trying to establish links to existing, special-purpose national networks such as Livermore's Magnetic Fusion network and the defense department's ARPANET. In the second phase, which will be under way by 1986, the supercomputer project will establish its own national network linking to local area networks on individual campuses. Possibilities include renting a transponder on a communications satellite, or renting access on the transcontinental fiber-optics cables being planned by AT&T, GTE, and others.

"Ultimately," says Jennings, "if you design the supercomputer network properly, a general network falls right out." It would be a "National Science and Engineering Network" linking every scientist and engineer in the United States, much as the Joint Academic Network ("JANET") does in the United Kingdom. "And once you get that, the international dimension will come very quickly," he adds, "because many of our major users—the particle physics community, the atmospherics community, the astrophysics community—are already international."

Officially, NSF has committed to support the supercomputer initiative for 5 years. Unofficially, however, agency officials clearly see the centers as a permanent part of the NSF program. In fact, the system is already being expanded. A fifth center will be announced soon and outfitted with the Cray 1 from NASA's Lewis Research Center in Cleveland. Ultimately, says Connolly, he hopes to fulfill Bardon-Curtis recommendations by establishing at least seven centers.

Meanwhile, the agency is working through the Federal Coordinating Committee on Science, Engineering, and Technology—"Fixit"—to achieve greater cooperation with the other federal supercomputer facilities. If nothing else, NSF hopes to work out a quid pro quo with national laboratories for training and for widespread dissemination of the treasure trove of supercomputer software already available in the laboratories.—**M. Mitchell Waldrop**

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Molecular Clocks Scrutinized

When Emil Zuckerkandl and Linus Pauling suggested in 1962 that the phylogenetic distance between species might be read directly through a measure of genetic difference, they initiated a revolution that was to transform an important segment of evolutionary biology. But, like all revolutions, this one has been turbulent, and many uncertainties remain in the minds of some protagonists. Specifically, how accurate is the "molecular evolutionary clock?" as Zuckerkandl and Pauling called it. Does it tick regularly, and therefore, keep good time? Or is it something of an erratic, sloppy clock? Two recent papers point potential problems for would-be users of the clock.

The first is by Francisco Ayala and his colleagues Young Moo Lee and David J. Friedman at the University of California, Davis (*1*). They recently obtained the complete amino acid sequence of the enzyme superoxide dismutase in *Drosophila melanogaster* and compared it with data for the enzyme in humans, horse, cow, and the yeast *Saccharomyces cerevisiae*. Counting the number of amino acid substitutions per million years, they obtained rates of change that varied fivefold, from 30.9 to 5.8, depending on the nature of the phylogenetic comparison being made. The very reasonable conclusion is that "using the primary structure of a single gene or protein to time evolutionary events or to reconstruct phylogenetic relationships is potentially fraught with error." Vincent Sarich of the University of California, Berkeley, has always conceded that some proteins change in a distinctly un-clocklike manner, and practitioners must be sure to demonstrate metronomic change (using the relative rate test) before drawing evolutionary inferences from protein data.

The second paper, by Chung-I Wu and Wen-Hsiung Li at the University of Texas, Houston, is a reminder that there is no such thing as *the* molecular clock: there are several, each with different attributes. Wu and Li scrutinized the DNA sequence clock, in which they are able to see nucleotide changes that cause amino acid substitutions in the encoded protein (called nonsynonymous changes) and others that are redundant and do not (synonymous changes). A comparison of the coding regions of 11 genes in rodents (rat or mouse) and humans reveals, they conclude, a faster rate of nucleotide substitutions in rodents. Rats and mice appear to accumulate synonymous changes twice as fast as humans do, whereas the comparison for nonsynonymous substitutions is 1.3 times faster in rodents. (Natural selection appears to keep substitutions that cause protein sequence changes under a tighter rein.) Comparisons within the family of globin genes in rodents and humans produce similar conclusions: rodent genes change faster than human genes.

Wu and Li suggest that the difference might be the result of differences in generation times, thus resurrecting an argument that has come and gone several times in debates over the molecular clocks. Generation times for humans is some 100 times longer than in rodents, making the difference in substitution rates of 2.0 and 1.3 look a little meager. As others have pointed out before, Wu and Li note that mutation is more likely to be linked to cell cycle times rather than to generation times: here, rodents are sevenfold faster than humans, which is still a long way from the observed substitution differences. For a good deal of their history, the ancestors of rodents and humans would of course have been much closer in size, and therefore generation time, and the substitution rate difference observed today is an average of the history of the lineages, with the difference presumably increasing with the passage of time.

The analysis by Wu and Li does appear to reveal a faster mutation rate in rodents than in humans, but whether generation time is the cause remains an open question, one that could be tested by looking at data for other short-generation-time species. A higher replication error rate or lower DNA repair efficiency in rodents are other possibilities.—**Roger Lewin**

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