salmon fishing. According to Wynn, these studies highlight three nonlinguistic characteristics of technology.

First, a series of tasks involved in achieving a particular goal is based on what the study's authors describe as "constellations of knowledge." These, explains Wynn, are made up of "images and impressions, not words, that are tied to a particular task." To put it formally, "technology is not performed within a lexically conceived realm."

Second, technology is truly a sequential operation whereas language is only superficially so. The author of the salmon-fishing study describes technology as being based upon a string-of-beads organization. "First I do job 1, then I do job 2, then I do job 3 . . ., then I am finished." Wynn concludes that "learning technology appears to be more a matter of rote, sequential programming than a hierarchically conceived understanding like that of syntax."

Third, the overall structure of a specific technological task may vary from individual, even within a closely communicating group. Language structures within groups, by contrast, are common. "Languages are shared. Technologies apparently are not."

Wynn concludes from this survey of technological behavior that "technology and language may lie in separate cognitive domains." The two, he suggests, "are only superficially similar in that the products—tool behavior and utterances—must be performed sequentially in time. They are neither conceived nor learned in the same manner."

There is by now a good deal of information in the scientific literature on prelinguistic behavior of infants. Perhaps the most striking component of such behavior is imitation, which begins very early. As the child gets older the degree and complexity of imitation grows, but its essential character remains the same. Wynn is intrigued by scientific descriptions of infants' prelinguistic behavior and notes that "they resemble the accounts of modern technological behavior." In particular, "they share an emphasis on contiguous behavior, sequential behavior, and rote routines."

This simple imitative behavior, at which the great apes are also relatively accomplished, would be quite adequate for learning the first forms of tool technology, argues Wynn. "Nonlinguistic hominids could well have made Oldowan tools and Early Acheulean tools." Language must have arisen at some point of course. And there is no reason to assert that it did not arise in concert with an increasing technological facility. Wynn's point is simply that "we cannot make the facile assumption that stone tools can *inform* us about language. ■ ROGER LEWIN

*Briefing:*

## DNA Sequencing Goes Automatic

Leroy Hood and his colleagues at the California Institute of Technology have developed the first automated DNA sequencing machine. Their DNA sequenator can read off nucleotides at a rate that may soon approach 8000 bases a day, which is at least tenfold higher than is currently achieved manually and at a small fraction of the current cost per base.

DNA sequencing has of course become a routine part of life in molecular biology laboratories, but it remains a time-consuming and technically demanding exercise. By making the task largely automatic and by boosting the rate at least an order of magnitude, molecular biologists will be tempted to shift their thoughts to projects currently too ambitious to attempt, such as sequencing the entire human genome (*Science*, 27 June, page 1598).

The DNA sequenator joins three other instruments developed by the Caltech team—a protein sequenator, a DNA synthesizer, and a protein synthesizer—to form what Hood describes as a microchemical facility. Instrumented thus, molecular biology has the potential to move into the realm of Big Science, he says. Hood described the new machine at the recent Cold Spring Harbor summer symposium, which was entitled "Molecular Biology of *Homo sapiens*."

Currently there are two approaches to sequencing DNA: the enzymic method, developed by Frederick Sanger and his colleagues in Cambridge, England; and the chemical method, invented by Allan Maxam and Walter Gilbert of Harvard University. Sanger and Gilbert shared the 1980 Nobel Prize for chemistry for their work.

The Caltech team's DNA sequenator is based on the enzymic method, at least partly because it represented a more promising prospect in the face of the chemistry that would be involved. Hood and his colleagues, Stephen Kent, Lloyd Smith, Jane Sanders, and Robert Kaiser, are already beginning to explore the possibilities of automating the Maxam/Gilbert method.

The Sanger technique involves generating a series of DNA fragments of different length, just as if the strand being analyzed had been nibbled away, nucleotide by nucleotide, from one end. Separated on a gel, the fragments form a ladder-like pattern of bands, each one being one base longer than the band in front and and one base shorter than the one behind. The trick is to be able to identify which of the four bases—adenine, thymidine, cytosine, and guanosine—is represented at each band.

This identification is achieved by carrying out four separate, but identical, enzymic reactions. In each a small oligonucleotide primer is used to initiate synthesis of the complementary chain of the DNA sequence being analyzed. In addition to the normal reaction constituents, however, there is in each a small quantity of the di-deoxy form of one of the four bases. Once a di-deoxy nucleotide becomes incorporated into the growing chain, the elongation process is stopped. The balance of normal and modified nucleotides in the reaction mixtures is such that there is a small but finite chance that the di-deoxy form will become incorporated at any one of its appropriate positions. This means that in the reaction mixture that contains, for instance, di-deoxy-thymidine, there will be a series of complementary DNA fragments of increasing length that represents every single position of adenosine in the original strand. The same principle holds for each of the four reactions.

The products of each of the four reactions are kept separate and are run on an electrophoresis gel. The positions of the various bands are detected by autoradiography, as the oligonucleotide primers used are radioactively tagged. The sequence of the entire chain is then read off by looking at the positions of the bands representing the four different nucleotides in their respective lanes.

Instead of using radioactive tags on the primers in their system, the Caltech team substituted fluorescent labels, one color for each of the four bases. Once the DNA synthesis is completed in the normal way, the four separate products are combined and run down a gel. At the bottom an argon laser beam illuminates the bands as they pass by, a detector identifies the wave band of the resultant fluorescence, and the DNA sequence is thus read off by a computer. Simple.

In fact, there is a series of problems that makes the reading not quite straight forward. For instance, the fluorescence of the four dyes overlaps to a significant extent. And the presence of the dyes on the primers affects their mobility on the gel, and to different extents. Nevertheless, these various wobbles can be accounted for by the computer, giving a sequence accuracy of about 1%. ■ ROGER LEWIN

ADDITIONAL READING

L. M. Smith *et al.*, "Fluorescence detection in automated DNA sequence analysis," *Nature (London)* **321**, 674 (1986).