

vants, the subjects included in our study exhibited average or above average intelligence and exceptional musical skills, with no apparent deficits in other cognitive functions. Furthermore, our subjects did not exhibit either of the two poles of aberrant social behavior, such as the extreme sociability of Williams syndrome patients or the withdrawal of autistic savants. Also, savants are more compulsive in pursuing their special abilities than are normal musicians. Thus, savants demonstrate patterns of psychosocial functions that are different from those of the musicians we studied, making a comparison difficult.

Nevertheless, a thought-provoking hypothesis implicit in Sacks's comment would be that special talents may be a result of the asymmetrical development of specialized "neuromodules." This hypothesis, which is compatible with our study and with the work of others (2), is intriguing and testable, at least in the case of perfect pitch.

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World Wide Web and Molecular Biology

Bruce R. Schatz and Joseph B. Hardin (Articles, 12 Aug. 1994, p. 895) write, "The revolution of the Net is just beginning." This may be so, but of critical importance to many researchers—especially biologists—is the fact that the Net, and the World Wide Web (WWW) set of protocols in particular, are of immense utility now. For example, every molecular biologist could make fruitful use of the WWW GenBank/Entrez (1). A collection of nearly all biosciences WWW information servers is maintained by Keith Robison at Harvard (2).

At a most fundamental level, these net-

work resources are equivalent to storing current databases locally, but without consuming resources. In addition, most facilities provide additional features; for example, WWW Entrez includes links to images and coordinates of proteins whose structures have been solved. A single Web viewer can provide a simple interface that embodies many of the complex features of sophisticated database access and analysis systems. Moreover, the WWW is indeed worldwide and encourages links between databases. The paragon of this connectivity is the Sequence Retrieval System (SRS) (3), which interlinks some two dozen databases. It has, in essence, merged many of the major biological databases of the world into one comprehensive structure.

Another major feature of the WWW is the ease with which complex, hierarchical data structures can be made accessible and intelligible. The ability to separate different levels of information has caused the network version of FlyBase (4) to virtually supplant the Red Book (5). Similarly, a number of model organism databases using ACEDB (6) have been made available on the WWW (7). Although WWW implementations currently lack ACEDB's powerful visualization tools (for example, for viewing and modifying sequences), stan-

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dardized protocols and display systems can work surprisingly well, even with specialized information. One is not always tied to the generic viewers, though; for example, a server at the National Institutes of Health (8) will rotate a protein structure into a preferred conformation and send it to an interactive molecular viewer on a user's personal computer.

The convenience and utility of micro-centrifuges, thermocyclers, and other molecular biology tools are greatly enhanced by standard size tubes. Information resources will soon become as crucial to biological research as those devices are today. Likewise, they need common access standards. Networked databases with complex, independent annotation are already beginning to provide students and researchers with previously unimaginable fingertip access to comprehensive and coherent views of known biology.

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Response: We thank Brenner for his excellent brief summary of how the Net has revolutionized molecular biology. The speed with which biology databases simply "came up," first with Gopher and then with Mosaic/WWW, is perhaps the most striking illustration of the power of the new computer tools. An earlier version of our paper contained a section with biology examples but, because of space limitations, the published version only mentioned how research systems such as the Worm Community System (WCS) might lead to a new branch of science where analysis environments make possible using the Net as a "dry lab."

It should also be noted that new features of Mosaic mentioned in our paper illustrate the forthcoming era. The Common Client Interface (CCI) complements the Common

Gateway Interface (CGI) and enables external viewers (visualization tools) to be not only invoked but interacted with. For example, the Net database federation prototype ENQUIRE (1) uses Mosaic to emulate such WCS functionality as following a link from a literature document to a gene description to a separate genetic map display to a sequence record. Finally, digital library technology is developing new architectures that will fully support analysis environments, with such features as recording navigation paths [see the Illinois Digital Library project (2) and, in particular, the next-generation system called the "Interspace" (3)]. Since the realization of these architectures lies in the (near) future, the revolution of the Net is indeed just beginning.

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