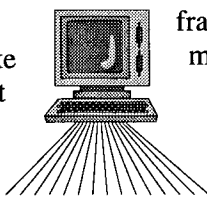## RLDB2 Information System

Many of the current tools like gopher, archie, and wais that are used to retrieve information from the Internet cannot be used to work interactively with graphical information or to provide an integrated view of information from more than one data source. The Reference Library Data-Base (RLDB2) uses the World Wide Web (WWW) to link data stored at different locations. A graphical user interface is provided by XMosaic together with external viewer programs. RLDB2 returns all information as hypertext documents, which can contain text, graphics, and sound, as well as links to other documents. RLDB2 contains data from the Reference Library System at the Imperial Cancer Research Fund, London, results from the YAC Screening Centre, Leiden, The Netherlands, and data from the Human Genome Project. The system allows participating scientists to combine and compare results of experiments. Contact: Günther Zehetner. E-mail: genome@icrf.ac.uk.

## Mass Spectrometry and Sequence Databases

Mass spectrometry (MS) is increasingly being used to characterize proteins by virtue of their mass. This provides a fingerprint of the protein in question, which can then be used to scan the sequence databanks. Searches using MS data are being developed at EMBL in collaboration with Peter Roepstorff in Denmark; at Genentech, USA, and at other sites. New programs and searching methods will in the future offer a method of correlating proteins to randomly sequenced DNA fragments. Contact: Mathias Mann. mann@embl.heidelberg.de.

## GeneWorks 2.3

IntelliGenetics have recently released GeneWorks 2.3, the newest version of their popular sequence analysis software for the Macintosh. This release allows scientists to generate circular maps. The maps can be in full color, and there is a capability to generate circular maps of multiple nucleic acid analyses. Contact: IntelliGenetics, 700 East El Camino Real, Ste. 300, Mountain View, CA 94040. Fax: 415-962-7302. E-mail: kate@presto.ig.com.

## DeCypher

Time Logic has produced the DeCypher Sequence Similarity Search System for performing fast DNA sequence data bank similarity searches. This is an integrated hardware and software system that claims to achieve processing rates equivalent to those of supercomputers. DeCypher runs Microsoft Windows 3.1. Contact: Time Logic, 11992 Challenger Ct., Moorpark, CA 93021. E-mail: 73311, 1777@compuserve.com.

## Seqnet

Seqnet is the UK national node of EMBnet, the molecular biology network established six years ago to link European laboratories using biocomputing and bioinformatics in molecular biology research, is run by manager Alan Bleasby and based at Daresbury Laboratory. EMBnet has published a brochure to explain its major role is to ensure that the updated central nucleotide and protein sequence databases are made available to users.