Communicator browsers (version 4.0 or newer). Users load each software package within their browsers by clicking on the name of the program on a palette at the site. This organizational scheme is a bit confusing because the palette also contains links to other spacecraft-specific information, such as the locations of MIR, the Space Station, and the Shuttle. (When the Shuttle was not flying, clicking on its name gave an error message about a broken link, instead of simply saying the shuttle was on the ground.)

Of the three software products, J-Track 3D is the most impressive. Providing the user a viewpoint beyond the position of geosynchronous orbiting satellites (22,000 miles), the program shows a hemisphere of Earth with the satellites around it as points of light (see the figure). Users can either click on a point to learn more about it (such as the satellite's orbit, ground tracking, launch, or data collecting information) or select a satellite by name from the Satellite menu option. Simple controls allow one to rotate the planet in any direction. Satellite positions are updated at user-specified intervals of real time as short as 0.25 seconds.

[redacted]

Our world. View of Earth and man-made satellites in J-Track 3D.

J-Track illustrates the track of satellites superimposed on a two-dimensional (2D) map of the earth, similar to plots one might see on NASA television. Though the information overlaps with that available in J-Track 3D, the advantages of J-Track are that users can specify which spacecraft to follow instead of seeing all of them and that the 2D map of J-Track is easier to view than the globe of J-Track 3D.

J-Pass is a tool for anyone interested in watching satellites overhead. It provides users with a list of satellites with time plots and sky maps of when and where each one can be viewed. Users define their location on Earth by specifying longitude and latitude or, in the United States, by using their ZIP code. This clever feature works well and simplifies user interaction with the program.

On the downside, the results of having the roots of each program in Java are interfaces that are not exactly cutting edge. Menus appear in different places depending on whether one uses Netscape or Internet Explorer. Each program contained several bugs that were annoying. Ideally, visitors to the site should have a network connection that is faster than a 56K modem to avoid slow downloads, although each program can be used on a modem, if one is patient.

—KEVIN AHERN

Department of Biochemistry and Biophysics, Oregon State University, Corvallis, OR 97331, USA. E-mail: ahernk@ucs.orst.edu

TECHSIGHTING

SOFTWARE

Genomics Made Easy

This is an era in which molecular biologists can often obtain gene sequences of interest by searching databases rather than by screening libraries of cloned DNA fragments. Thus, instead of wandering around labs with tubes of radioactive probes, scientists are often found at their desks, peering hopefully at their computer screens. As whole genomes find their way into the databases, the probability is ever greater that a sequence of interest is only a BLAST search away.

Although the power of the Internet makes enormous amounts of sequence data readily accessible, molecular biologists still need tools to help them with routine sequence analysis tasks such as restriction mapping, identifying protein coding regions or special sequence motifs, and carrying out sequence similarity searches. There are, of course, numerous shareware programs on the Web, but most of these will perform a single type of analysis (e.g., identifying restriction enzyme recognition sites) and each has a different user interface. This variability can be frustrating if one needs to carry out a variety of analyses fairly often. A convenient if more expensive alternative is to buy a comprehensive sequence analysis program designed to perform the most commonly used analyses with a single, user-friendly interface. One such software package is called MacVector, the latest release of which provides the molecular biologist with a wide variety of tools for analyzing nucleic acid and protein sequences. MacVector is designed to be used on Macintosh computers, and has a well-deserved reputation for being swift, powerful, and amazingly easy to use. A short, but by no means complete, list of nucleic acid analyses available includes restriction mapping, open reading frame searches to identify protein coding regions within a sequence, base composition and codon usage analyses, nucleic acid subsequence motif searches, primer design for PCR (polymerase chain reaction), multiple sequence alignments, and translation of open reading frames to the corresponding amino acid sequences. Protein sequences may be analyzed to determine (among other things) the molecular weight and pI (isoelectric pH) of the protein of interest and to obtain profiles of hydrophilicity, antigenicity, and secondary structure along the length of the protein. MacVector will also retrieve protein or nucleic acid sequences of interest from databases by conducting an Internet search, which is trivial to set up as well as extremely fast. Another useful feature is the ability to perform BLAST searches, where a query sequence is compared with sequences in databases accessible through the Internet, without leaving the program. Such features offer an improvement over version 6.5 [see the review of version 6.5 in (*1*)].

MacVector 7.0
Genetics Computer Group

Campbell, CA
$2950
800-876-9994
www.gcg.com

New in version 7.0 is the ability to generate true phylogenetic trees with the use of distance matrix methods. Other notable features in version 7.0 include additional algorithms for identifying coding regions, and an improved multiple sequence alignment editor. BLAST searches done through MacVector are now carried out with NCBI's enhanced BLAST 2.0 programs, which permit gapped alignments. A number of small, but thoughtful, changes in the interface make the program easier to use than ever. As with earlier versions, this one is a winner. One complaint, however, concerns the Keyserver used in the network-licensed version of the program. Though the MacVector software itself is easy to use, the network installation of it is overly complicated.

—INDIRA RAJAGOPAL

Department of Biochemistry and Biophysics, Oregon State University, Corvallis, OR 97331, USA. E-mail: rajagopi@ucs.orst.edu

References

1. I. Rajagopal, *Science* **283**, 652 (1999).