TECHSIGHTING

SOFTWARE

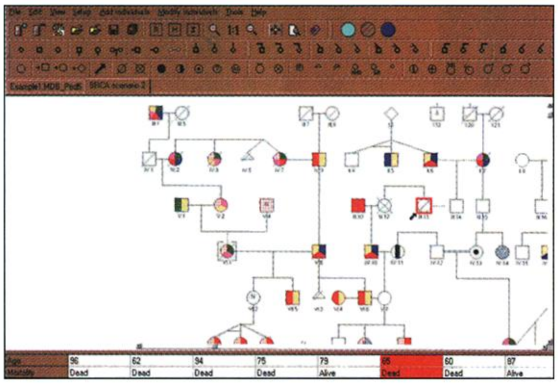
Prime Pedigrees

Genetic counselors, investigators, and physicians who need to maintain pedigrees for genetic analysis will find a friend in Cyrillic 3. The software is simple to use and makes drawing pedigrees by hand a thing of the past. Retrieving and updating pedigree databases are also uncomplicated, thanks to useful tools in Cyrillic 3. With little practice, one can create, download, and analyze pedigrees easily.

Cyrillic 3
Cherwell Scientific, Ltd.

Acton, MA.
$769; $299 (upgrade).
888-257-6652, ext. 203
www.cyrillicsoftware.com

The software boots up to a working window for importing databases and pedigree diagrams. A previously saved database or pedigree can be accessed easily with toolbar options. Database files must be retrieved in Microsoft Access or Paradox file formats. Cyrillic 3 imports and stores database files in these formats without requiring the corresponding software on the computer. A search feature allows information in pedigrees to be retrieved by name, genetic characteristic, or other identifier information.



Age	96	62	94	75	79	65	60	87
Mortality	Dead	Dead	Dead	Dead	Alive	Dead	Dead	Alive

Drawing pedigrees. A genetic pedigree produced with Cyrillic 3.

Pedigrees are simple to draw and modify with toolbar icons and mouse drag-and-click operations (see figure). Markers and other information about individuals can be added in the database window. Creating new databases is simple by first setting up a data table and then adding database characteristics with the New Database Dialogue Window.

Database information appears in two windows. The main window presents the pedigree drawing. Individuals in the pedigree window can be identified by gender, name, age, sibling age, and other criteria. Below the main window is the database table window that organizes information in a spreadsheet format. Clicking on an individual in the pedigree diagram highlights their information in the database window.

Cyrillic 3's capacity to read and analyze information is impressive. It tracks up to 10,000 individuals per family and can manage 150 alleles per genetic marker, as well as up to 150 markers per chromosome. The program can also calculate kinship coefficients and automatically identify consanguineous matings.

Cyrillic 3 imports genetic data from popular gene bank Internet sites, such as those at the Center for Genome Research at the Whitehead Institute for Biomedical Research and the Human Genome Database from John Hopkins University. Other databases supported by Cyrillic 3 include the Online Mendelian Inheritance in Man, the UK Medical Research Council Human Genome Mapping Project, and the database of the European Bioinformatics Institute.

Genetic risk analysis calculations can be performed with the feature MENDEL, which generates likelihood calculations with age-dependent penetrance. Another feature of Cyrillic 3, BRCAPRO, tracks the risk of inherited breast cancer.

The software has a detailed help option that is accessible from the toolbar, and documentation is available in printed or electronic form and online at www.cherwell.com.

Cyrillic 3 possesses easy-to-use drawing tools and superior printing options to produce publication-quality pedigree diagrams. Database retrieval and development are simple and are supported by commonly available software.

Cyrillic 3 runs on Windows 98 and NT systems with a CPU at the Pentium level or higher and 16 MB of RAM. The program uses 20 MB of hard disk space and requires Internet browser software to download online databases. —**BRIAN R. SHMAEFSKY**

Tech.Sight is published in the third issue of each month. Contributing editor: Kevin Ahern, Department of Biochemistry and Biophysics, Oregon State University. Send your comments by e-mail to techsight@aaas.org

Department of Biology/Biotechnology, Kingwood College, Kingwood, TX 77339, USA. E-mail: -Bshmaefs@nhmccd.edu

---

TECHSIGHTING

SOFTWARE

An Improved Tool for Molecular Biology

In 1998, Oxford Molecular Group released a comprehensive nucleic acid and protein sequence analysis package for the Windows platform. This package provided a significant resource for investigators who wished to have sequence analysis capabilities on their own PC. In its latest release, OMIGA 2.0, a number of new features have been included along with several fixes and improvements. The program runs under Windows 95, 98, or NT, and it represents a powerful tool for molecular biology. The application requires about 50 MB of disk space and runs well on a Pentium II machine with 32 MB of memory. Some sequence database searches require an Internet connection, through either modem or network. All of the features of the first release of the program are retained; added are several capabilities to enhance both nucleic acid and protein sequences. The 2.0 version is provided on a single CD ROM, which also contains updated versions of databases for protein motifs (PROSITE), restriction enzyme sites (REBASE), protein cleavage sites (PABASE), and nucleic acid motifs (NASITE). RasMol 2.6 is included to facilitate visualization of data from Protein Data Bank (PDB) files. A database of sequences for use in OMIGA, Vecbank, is also provided.

OMIGA 2.0
Genetics Computer Group, an Oxford Molecular Company

Madison, WI.
$1995 commercial,
$1495 academic/
government.
800-876-9994
www.gcg.com

This software can perform sequence composition analysis; search sequences for digestion sites, coding regions, and specific sequence motifs. It contains functions useful for using the polymerase chain reaction, such as identifying primer pairs, predicting primer properties, and also identifying DNA sequencing primers. Algorithms for identifying sequence similarity include BLAST searches of the National Center for Biotechnology Information (NCBI) and Entrez databases; multiple alignments (protein and nucleic acid sequences); and dot plot alignments. OMIGA 2 also contains numerous modules for protein analysis, including prediction of protein secondary structure; calculation of hydropathy and antigenicity profiles; translation; and reverse translation.