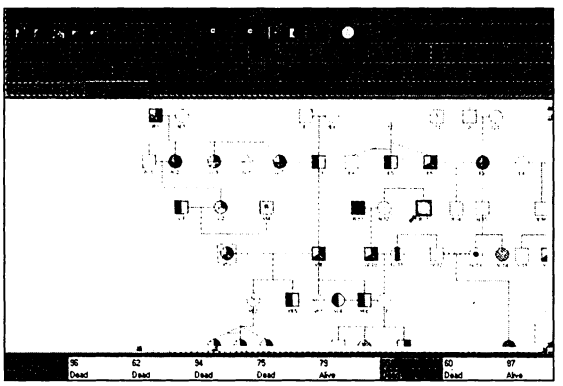
TECHSIGHTING
SOFTWARE

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.



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**

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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.

This release contains an enhanced ability to utilize BLAST algorithms to compare local sequences with the NCBI database; increased flexibility in searching and retrieving sequences from the NCBI and Entrez databases; and a new feature for sequence comparison display as dot plots. In addition, an increased capacity to search for and evaluate primers, including your own test primers in a selected sequence, is provided. New protein analysis features include an option to calculate the isoelectric point and the charge of a peptide sequence at neutral pH and an enhanced display of secondary structural features in a variety of sequence views. Consensus cutoff value selection is now available in both DNA and protein sequence comparisons. A flexible user selection of display color schemes has also been added.

User friendliness has been improved with a startup dialog box, which allows the user to select a new project, work on an already existing project in OMIGA, or open a project from a location outside the OMIGA folder or directory. The program retains the File Manager/Windows Explorer format for file and project organization. A simple command for recalculations is provided for searches, which can be edited and then recalculated on the fly. Printing formats have been improved as well to address problems in previous versions of the program. The file import capability has been enhanced. The zoom command in the features view now allows a user to enlarge sequence regions so that individual bases can be seen on screen. Another program enhancement allows the user to move between consecutive features at the residue level in the map view.

The excellent documentation and online help provided with OMIGA 1.1 has been retained and further improved.

Although some problems with the earlier release of OMIGA have been addressed in this new version, several still remain. These include alerting the user erroneously with messages of file attribute problems when limited free space remains on the hard drive, requiring the user to delete file types manually from a temp folder, requiring files to be deleted files from within the program to avoid corruption of projects, and limiting the number of files that can be selected within some modes. Some problems also remain with outputting maps to Windows metafiles. The publisher provides work-arounds for most of these problems, and they represent only minor inconveniences when run on a PC with sufficient disk space.

This release of OMIGA improves the software product, which should continue to serve as a valuable resource to laboratories that require rapid sequence analyses and definition of strategies for such procedures as cloning and PCR primer design, as well as analysis of peptide and protein sequence properties.

—ALLEN B. RAWITCH

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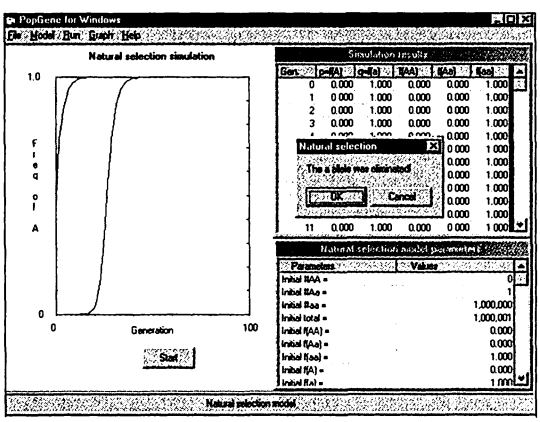
TECHSIGHTING
SOFTWARE

Modeling Population Genetics

PopGene
Trinity Software, Inc.
Plymouth, NH.
$95.00;
$39.95, college students.
800-352-1282
www.trinitysoftware.com

Population genetics relies heavily on mathematical modeling to make quantitative predictions about the behavior of genes in populations. These models are based on the principles of classic Mendelian gene inheritance; the Hardy-Weinberg equilibrium law, which predicts the gene frequency in a population; and Darwin's theory of natural selection.

PopGene version 1 is a simulation program that explores the parameters that affect the behavior of alternative forms of a gene (alleles) in a population. The program window is composed of three smaller windows specifying the parameters used, the calculated allele frequencies through each generation, and the graphical output of the calculations.



Popgene Simulation. Graph showing result of natural selection simulation.

PopGene provides simulations for both basic and more advanced models in population genetics. The simplest model demonstrates the principles of the Hardy-Weinberg equilibrium law for the case of a single gene with two alleles. Increasingly complex examples based on the assumptions of the Hardy-Weinberg equilibrium law demonstrate the effect of multiple alleles of a gene and multiple gene loci on the genotype of all the individuals in a population.

Default parameters for each model are built into the program, but users may also enter their own values. The simulation results, parameters, and graphs may be saved or printed. Up to 15 simulations may be run for a particular model with the results plotted on a single graph for easy comparison (see figure).

Natural selection and inbreeding can be studied with the program. Natural selection of a gene with two alleles occurs when the fitness of each genotype is not equal. The program permits users to examine the outcomes of several scenarios—selection of an allele that exhibits dominance over another, alleles that combine to produce an intermediate (semidominant) phenotype, an allele that is recessive to another, or selection against a recessive allele because of its lethality.

The model for inbreeding explores the consequence of nonrandom mating between individuals on the genotype frequencies of that population. Mating pairings are included to demonstrate self-fertilization (the most extreme form of nonrandom mating), as well as matings between parent and offspring; matings between siblings, first cousins, and second cousins; and random mating. PopGene also provides simulations for genetic drift, mutation, and migration—factors that contribute to evolutionary changes in a population that have long-term effects and are more difficult to study.

In summary, PopGene is a valuable tool to use in conjunction with traditional textbook-based teaching of an introductory population genetics course. It provides students with illustrations of the principles they have learned. The program is straightforward, easy to use, and is available for Macintosh and Windows platforms. No preprinted manual is available for PopGene; however, a concise and well-written one is supplied as a PDF file that is readable with Adobe Acrobat. It covers the specifics of using the program and provides a step-by-step tutorial. A brief summary of population genetics, mathematical modeling, and the value and limitations of computer simulations is also discussed.

The system requires a PC with a 486 or Pentium processor that uses Windows 3.1, 95, 98, or NT with 8 MB RAM or any Macintosh with 4 MB RAM, a 1.4-MB disk drive, and a hard drive.

—ELLEN QUARDOKUS

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