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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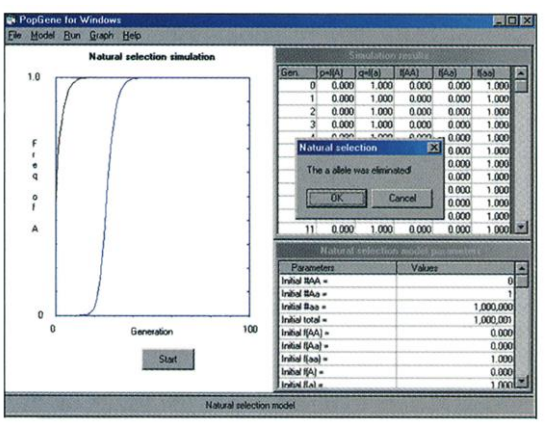
TECHSIGHTING

SOFTWARE

Modeling Population Genetics

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).

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

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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