



Computer Center

A Population Biology Software Review

Timothy A. Mousseau

Guest Author

- Title:** *Populus: Simulations of Population Biology*
- Authors:** Don Alstad, Jim Curtsinger, Peter Abrams and Dave Tilman
- Source:** Don Alstad, department of ecology, evolution, and behavior, University of Minnesota, 318 Church St. SE, Minneapolis, MN 55455-0302. DNA@UMNACVX.bitnet.
- Price:** \$10 for costs of duplication and postage.
- Computer Requirements:** IBM PC or compatible with 500 kb RAM, video graphics board (hercules, CGA, EGA, VGA or 8514), 1.44 MB 3.5 inch floppy disc drive.

Population biology is a vast field incorporating elements of ecology, mathematics, statistics and genetics to explain patterns of population growth, regulation and evolution through space and time. *Populus*, a package of 30 simulation models developed by Don Alstad et al. and underwritten by IBM, the University of Minnesota and the National Science Foundation, is an excellent teaching tool to help illustrate the dynamics of many complex theories associated with the study of population biology. This program is directed at senior undergraduate and graduate students. However, inspired and highly motivated novices might also be seduced by *Populus'* magnificent graphics and simplicity of use, and in so doing gain great appreciation of a few of the fundamental processes in biology. The program is entirely menu-driven with informative help screens liberally interspersed,

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making it a breeze to use even for the uninitiated and/or computer-phobic student (or instructor!).

Populus opens with a Main Menu listing the three major categories of simulation models used: Ecological, Evolutionary and Hybrid (i.e. evolutionary ecology). Within the ecological category are models investigating population growth (including logistic and age-structured), multispecies interactions (Lotka-Volterra competition and predator-prey, mutualism, etc.) and optimal diet choice based on energy content. The evolutionary simulations include models investigating the effects of autosomal and sex-linked selection, genetic drift with and without selection, inter- and intrademe group selection, differentiation in structured environments (including clines) and a series of quantitative genetic models examining the interactions between selection, heritability and phenotypic evolution. The "hybrid" models include a simulation of density-dependent selection with genetic variation for carrying capacity (k) and growth rate (r), and two very appealing models investigating host-parasite coevolution. Each simulation opens with a title screen giving a brief introduction to the operation of the model. This is followed by an optional detailed description of the equations used and a short bibliography for further reading on the subject. Next comes a screen on which the parameters are entered. Parameters can be changed to examine the influence of each on the outcome of the model. When the parameters have been set (students can use the defaults to examine typical situations), the model runs and the output is plotted to a graph on the computer monitor. Output can be printed to dot matrix or laserjet printers, although the Hewlett Packard DeskJet printer is not supported. This process can be repeated ad infinitum to investigate the full range of possible outcomes.

As an instructor, I found this program to be complete, easy to use and extremely informative. The program is logically organized, thorough in its documentation, and its graphical output is very attractive. The program ran quickly and without glitches on my 486 and 386 machines with VGA graphics, although I suspect some of the models incorporating Monte Carlo methods might run quite slowly on machines with a smaller configuration, and many of the graphics screens could be ambiguous or messy on monochrome monitors.

I asked several of my students (especially Alex Olvido and Renee Flinchum) to evaluate *Populus* on their own, and all agreed it was a "fun," useful and user friendly program. There was unanimous agreement that this software helped them understand several difficult concepts in ecology and evolution. On the down side, students felt that the introductory help screens were insufficient. They also would have preferred more information about the interpretation of the graphical output from the models. Despite these deficiencies (which could easily be overcome by consulting the bibliography provided for each model), students and instructor alike were very impressed by this program.

In summary, *Populus* is a superb teaching tool for population biology. Its interactive format and graphical output permit easy demonstration of

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many important concepts in ecology and evolution. It is not totally self-contained, however, and students will need to consult their textbooks for a better understanding of the material and its interpretation. Nonetheless, this computer program is the ideal complement to any course in population biology. It is without question the best computer software of its kind.

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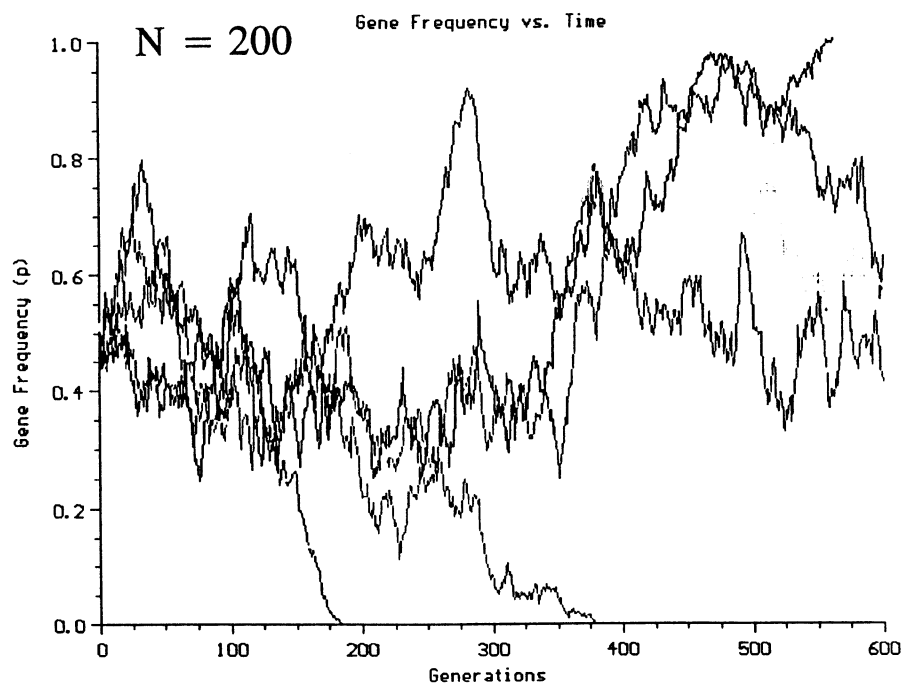
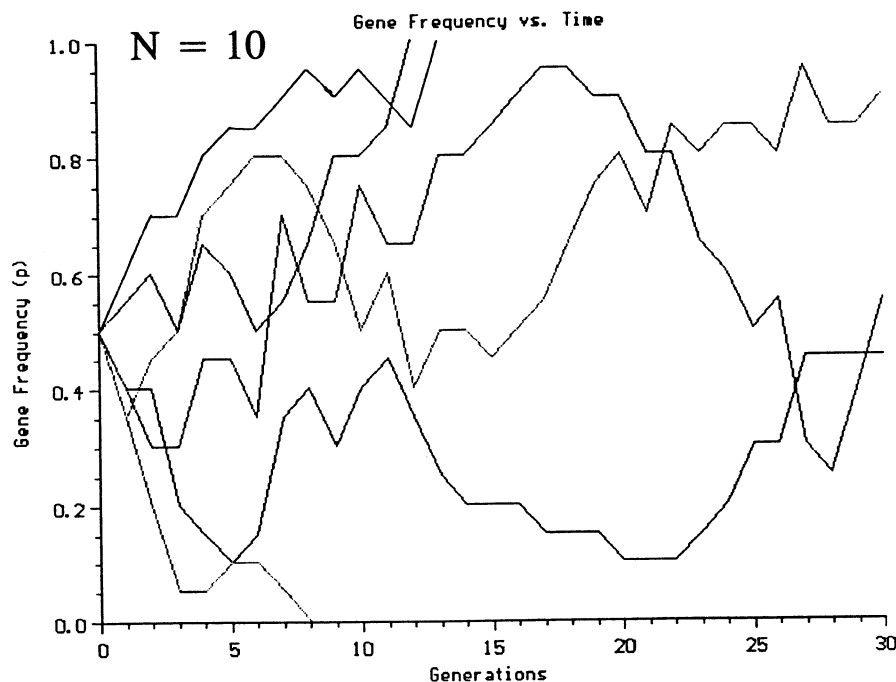


Figure 1. Two graphics screens dumped from *Populus* illustrating the effects of population size on genetic drift. In the top figure population size is 10, while the bottom figure shows the result for a population size of 200. The model uses Monte Carlo methods to randomly sample populations. Six loci are plotted.