



GeneJockey: Sequence Processor.

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NEW BIOLOGICAL SOFTWARE

GUEST EDITOR: DR. JUNHYONG KIM

The aim of this section is to evaluate the character, content, cost, and hardware requirements of new software programs in various fields of the biological sciences, and in appropriate related areas. All programs submitted to The Quarterly are given careful consideration, and competent and conscientious reviewers are selected to assess the software for originality, efficacy, and suitability of various applications by our readers. The price of a software program reviewed is the suggested list price of the publisher when the program is released for review.

Authors and publishers of biological software who wish to have their biological software programs considered for review should submit complete programs and documentation to The Editor, Biological Software, The Quarterly Review of Biology, State University of New York, Stony Brook, NY 11794-5275 USA.

GLOSSARY

CGA	IBM Color Graphics Adapter
EGA	Enhanced Graphics Adapter
MCGA	Multi-Color Graphics Array
MDA	Monochrome Display Adapter
VGA	Video Graphics Array
Apple	Includes Apple II, II + , IIe, IIc, and IIGS
MAC	Includes Apple Macintosh Classic and SE
MAC II	Includes Apple Macintosh II
IBM PC	Includes IBM PC, XT, AT, PCJr., PS/1, PS/2, and compatibles
MS	Microsoft

GENEJOCKEY: SEQUENCE PROCESSOR.

By Philip L. Taylor. BIOSOFT, Cambridge. \$499.00 (3½" disk). 1990. [Requirements—MAC: requires system version 4.1 or later, hard disk, manual included.]

GeneJockey is a new member of a small group of DNA (and protein) analysis programs written for personal computers. DNA sequences are accumulating at an ever increasing pace, emphasizing the need and demand for programs like this. Many researchers like to perform some routine chores independent of mainframe computers, for which more powerful sequence analysis software is available. Like other competing programs, e.g., *MacVector* and *GeneWorks*, this program was written for the Macintosh user who might know molecular biology, but not computers. Hierarchical menus make it easy and intuitive to use, like most Macintosh programs. *GeneJockey* has surprising, uncommon and therefore welcome features, like the

capability to design optimized polymerase chain reaction (PCR) primers and to calculate dot-plot matrices. Another nice feature of *GeneJockey* is that it estimates the time required for database searches, and lets the user decide whether he or she really wants to go ahead with the search. It also has most of the usual features of DNA analysis software: searches in databases, simulated restriction analyses, hydrophobicity plots, and searches for open reading frames.

It may not be fair to compare this program with its higher-priced competitors, but with a price tag of "only" \$499, it is a good lower-cost alternative to programs like *MacVector* and *GeneWorks*, which cost much more (around \$2,500); *GeneJockey* fares surprisingly well in this comparison. *GeneJockey* does not have the fancy colors of its competitors, the manual is not as flashy, the voice that reads back entered sequences is scratchy, and one cannot enter DNA sequences into *GeneJockey* through a

digitizer. The manual contains minor typographical errors, but it is well written in a candid and friendly style, and is in some ways more accessible and complete than, e.g., the manual of *MacVector*. Other software exists (similarly priced to *GeneJockey*) that exclusively designs optimized PCR primers. Furthermore, the expensive competing programs do not have the PCR primer feature. It is hoped that *GeneJockey* will find wide acceptance.

When there is a new version of *GeneJockey*, it should include the following useful features: (1) base composition calculated not only for a whole DNA segment, but broken down by positions in codons for protein-coding genes, (2) calculation of genetic distances between two (or more) sequences, also including various corrections for multiple substitutions, and (3) multiple sequence alignment with interleaving sequences.

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GRAFTOOL: GRAPHICAL ANALYSIS SYSTEM. Version 3.3.

3-D Visions, Torrance (California). \$495.00 (two 5¼" disks). 1990. [Requirements—IBM PC: DOS 3.0 or higher, 640K, hard drive, CGA, EGA, VGA, or Hercules, 8087/80287/80387 math coprocessor recommended, manual included.]

This is a comprehensive graphics program oriented toward the production of scientific, rather than just the usual business presentation graphics. Some of the graph types are x-y plots, two-dimensional and three-dimensional scatter plots, contour plots, surface and trajectory plots, parametric graphs (plot with respect to an intrinsic variable), histograms, bar charts, vector field plots, and pie charts. One can also prepare dramatic three-dimensional effects, such as intersecting surfaces, contour plots projected onto planes, and zooming portions of a plot.

While there is a macro capability for automating the production of graphs, most users will use the program interactively. The use of a mouse is optional, but it makes the program much easier to use, since one can just click on the part of the graph to be changed, or point to a color or line texture choice. Some options include different axis scaling, multiple x-axes and/or y-axes, different coordinate systems, choices of sizes of symbols and lettering and of fonts (including Greek and math symbols), line widths, and line textures. Error bars can be plotted. An unlimited number of curves or surfaces can be plotted in a single graph, and an unlimited number of graphs can be plotted on a single page. Three-dimensional graphs can be rotated to the best viewing angle.

There is also a "slide show" feature that allows

one to save groups of screen images as "reels of slides" that can be replayed in rapid succession on the screen.

This program's versatility is greatly enhanced by the built-in spreadsheet (4096 by 4096 entries) that permits the user to generate the data to be plotted (by entering equations) or to manipulate existing data files. The plots can be very complex—the limit is 65,000 points per curve or 268,000,000 points per surface. This program can also compute and plot the results of linear regression and also exponential, Fourier (trigonometric), polynomial, geometric and hyperbolic regressions. Cubic spline interpolation and smoothing can also be performed.

With so many options and features, it takes a while to figure out how to use the program efficiently. I was sometimes frustrated by the fact that I knew the program could create a certain effect (many examples are shown in the manual and in color fliers included with the package), but it was not always obvious from the on-screen menus just how one should select them. The manual, which gives step-by-step descriptions of the sequences of operations required for many of the standard effects, is necessary.

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PROTISTS AS INDICATORS OF POLLUTION.

By John Elberfeld. EduTech, Rochester (New York). \$60.00. 1991. [Requirements—Apple: Apple DOS 3.3 or higher, 48K, 80 column card, backup disk provided, manual included; also available on 3½" disks.]

This program is essentially a specialized database that forms the basis for a class/research project monitoring the water quality of as many locations and samples as one might wish. Test samples of water are brought into the lab and are concentrated. Using a microscope, one scans a drop of water on a microscope slide and records the number of pollution-indicating algal genera (20 total). The program uses these data to calculate Palmer's Index of Pollution (C. M. Palmer, A composite rating of algae tolerating organic pollution. *J. Phycol.*, 5:78-82, 1969). The program is easy enough to be used by high-school or university undergraduate ecology/environmental science classes, but also, it has the capacity to be used in long-term studies by researchers monitoring water quality. The two disks that are provided are double sided; the program is on side 1 of the disk; a sample data set is included on side 2. The program will initialize more data disks—one will need a separate disk side for each location to be monitored.

Each database record allows for a complete description of the microscope and sampling tech-