

TableCurve™

**One step fits
221 equations to
your X-Y data.
Automatically.
In less than
7 seconds.***

With TableCurve™ finding the best formula to fit your data couldn't be simpler...or faster.

- **Flexible Data Input** – input from Lotus®, dBase®, ASCII and many other file formats, or manually from the keyboard.
- **Data Manipulation** – smooth data, weight data, or apply standard math calculations.
- **Curve Fitting** – 221 candidate equations including Gaussian, log-normal, sigmoidal, sine, and user-defined—ranked by best fit and interactively displayed.



- **Speed*** – an 8MHz PC AT, with math coprocessor, will process 221 equations (50 data points) in 6.8 seconds. More powerful systems are much faster.
- **Output** – supports most dot-matrix and LaserJet® printers. Output directly to SigmaPlot 4.0®, Lotus, ASCII, and other formats.
- **Quality Interface** – pull down menus, mouse support and more.

To find out more about TableCurve or other scientific and engineering software from Jandel, just give us a call.

800-874-1888
415-924-8640

SCIENTIFIC

Circle No. 62 on Readers' Service Card

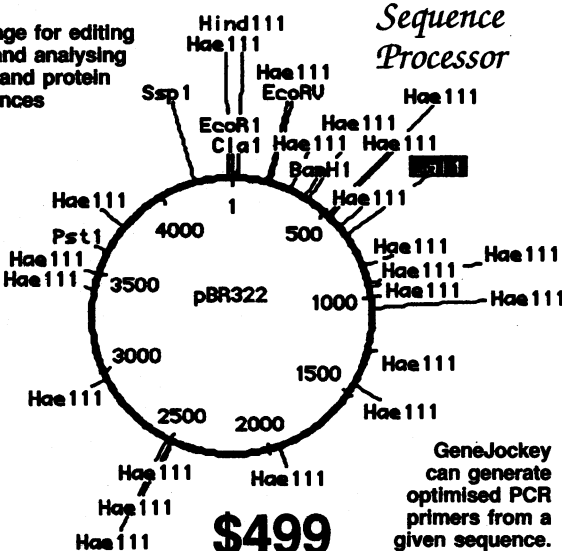
New! for Apple
Macintosh

GeneJockey

*Multi-window
Sequence
Processor*

A superb package for editing
manipulating and analysing
nucleic acid and protein
sequences

GeneJockey makes full use of the Macintosh environment. It is a fine example of the principle that a program does not have to be difficult to use in order to be powerful. It has superb facilities for sequence alignment and concatenation. Searches can be made in the GenBank, EMBL and other libraries, as well as GeneJockey's own files. Sequences can easily be imported from or exported to other programs. Restriction Analysis can be performed, with recognition sequences given for over 400 restriction enzymes, and more can easily be added. Built-in communications routines enable on-line access to databases from within the GeneJockey environment. Perhaps the most appealing feature of GeneJockey is the comprehensive tutorial module which makes the program rapidly accessible to new users.



\$499

GeneJockey
can generate
optimised PCR
primers from a
given sequence.

BIOSOFT

PO Box 580, Milltown, NJ 08850.
Tel 201 613 9013 Fax 201 613 8860

WRITE OR CALL FOR FREE DEMO DISK.

Circle No. 34 on Readers' Service Card

chastic in that the time-varying, random dynamics of the three cell populations are modeled, providing outputs that also are probabilistic. An attractive feature of discrete-time models is that the underlying mathematical expressions have a recursive form that makes for computational simplicity on digital computers. If analog computers were the norm, continuous-time simulation models would be more practical. As it is, these models require numerical integration schemes that are based on discrete-time analogs.

SAMUEL M. COHEN

LEON B. ELLWEIN

University of Nebraska Medical Center,
600 South 42nd Street,
Omaha, NE 68198-6545

REFERENCES

1. R. E. Greenfield, L. B. Ellwein, S. M. Cohen, *Carcinogenesis* 5, 437 (1984).

Asians and UCLA Admission

The headline "Anti-Asian bias seen at UCLA" (Briefings, 12 Oct., p. 204) is more than a small stretch of the truth. During some 30 months of detailed investigation, the Office for Civil Rights of the Department of Education looked at "84 separate graduate programs with 95 separate admissions processes." The office found "a statistical disparity" in one case, thereby clearing the university of the charge of "anti-Asian bias" in 99% of the cases. Even the single deviant case is dubious, since the admission process in any university department involves warranted judgments on qualities not readily quantified. The overall record is clear: the University of California at Los Angeles is a national leader in Asian-American access to higher education.

BURTON R. CLARK

Department of Education,
University of California,
Los Angeles, CA 90024-1521

Erratum: The last sentence of David Hamilton's 21 December News & Comment article "Space program: Blueprint for ambiguity" (p. 1654) should have read, "It [the Augustine Commission] will reconvene in 6 months to assess NASA's progress."

Erratum: The first sentence of the abstract of the report "Control of yeast mating signal transduction by a mammalian β_2 -adrenergic receptor and G_s α subunit" by K. King *et al.* (5 Oct., p. 121) was incorrectly printed. It should have read, "To facilitate functional and mechanistic studies of receptor-G protein interactions, the human β_2 -adrenergic receptor (h β -AR) has been expressed in *Saccharomyces cerevisiae*."

Erratum: The last name of the eleventh author of the report "Inhibition of HIV-1 replication by a nonnucleoside reverse transcriptase inhibitor" by V. J. Merluzzi *et al.* (7 Dec., p. 1411) was incorrectly printed. That author