TECHSIGHTING
SOFTWARE

Mega Stats

Stat-200 is a general-purpose statistical analysis program for Windows 95, 98, NT, or 2000 with high-performance features suitable for large biostatistical data sets. The program can manipulate very large data sets with more analysis tools than are typically found in spreadsheet programs. An easy-to-use graphical interface and a help window that includes literature citations for statistical methods make Stat-200 a valuable program.

Stat-200
BioSoft

Ferguson, MO
$399
314-524-8029
www.biosoft.com

Stat-200 is supplied on three diskettes and registration is required for first time use. Sending BioSoft an installation-generated serial number by e-mail generates a return password to use the program. The Stat-200 main window opens with a menu bar, a toolbar, and a tree-type display of data functions. Data in Microsoft Excel file format and from network-based queries of ODBC (open database connectivity) databases can be imported into the Stat-200. Data is placed in the Stat-200 spreadsheet, which is called a grid.

The Stat-200 workbook is a collection of data grids organized as pages in a book. A significant advantage for users of large data sets is that the grid size is only limited by the computer's RAM storage. Arrays of one half-million cells can be manipulated and analyzed, a vast improvement over Excel and other Windows-based statistical analysis programs. Although it is somewhat time-consuming, analysis of such large data sets can be accomplished on a personal computer instead of on a UNIX workstation.

The program incorporates most of the descriptive statistics, parametric and nonparametric statistical methods, graphics, and data transforms needed for research projects. There are 60 parametric tests, which are based on an underlying distribution in the data, 66 nonparametric tests and procedures, and 30 different descriptive statistics. Analysis of variance is available and includes general *N* factor analysis. All tests have associated informational windows, which usually provide recent literature references that may be helpful for citing in written reports.

Graphing in Stat-200 includes all the usual types for statistical data presentation such as line, pie, bar, scatter, and box-whisker charts together with three-dimensional plotting options. A wide variety of graph styles is available, including fits to polynomial, logarithmic, exponential and power functions, and plots of moving averages, as well as graphs of raw data, means, and data frequencies. In addition, many specialized graph types such as Kaplan-Meier, Weibull, Pareto, Shewart, or Polar can be plotted. Templates of frequently used graph styles can be created and saved.

Tables of numeric summaries of tests can be printed directly from Stat-200, copied to the clipboard, or saved. Graphs can be printed or saved and may be exported as Windows Bitmaps or Windows Metafiles. Integration with the Web is enhanced by optional output of text results in HTML and graphical results in .jpg and .png file formats.

An embedded high-level language (Python) enables any data transformation to be programmed by the user. Like Visual Basic in Excel, Python is an interpreted language that supports a wide range of data types and functions. Powerful string operators could be used, if needed, to transform DNA or protein sequences, for example, to numeric values for a statistical analysis in bioinformatics.

In summary, Stat-200 is a powerful statistical analysis and graphing tool. Its wide range of analysis functions and transforms should cover the needs of most research projects.

—WILLIAM SEFFENS

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TECHSIGHTING
SOFTWARE

New Primer Predictor

It was appreciated early on, during the polymerase chain reaction (PCR) revolution, that the proper design of oligonucleotides was probably the most critical variable for a successful reaction. However, visual inspection of oligonucleotide sequences was not sufficient, as it was necessary to determine whether primers would form secondary structures such as hairpin loops or primer dimers. To complicate things, other parameters, such as the individuality of the primer's 3′ end, as well as each primer's melting temperature were also important, making visual inspection of oligonucleotide sequences inefficient. Then came computer programs, which could consider all of these parameters and find, in seconds, the optimal primer pair for a given sequence to be amplified.

iOligo
Caesar Software

Portsmouth, NH
$499.00;
$99.00 (academic)
www.caesarsoftware.com

iOligo is a newcomer in the primer design software arena, a program that excels in its simplicity and ease of use. Sequences can be typed into the iOligo sequence editor window or imported from another file via a cut and paste command. Unfortunately, iOligo seems unable to open text files containing DNA sequences. However, the application makes up for this little nuisance by providing a powerful search and download function that uses an Internet connection to access the National Center for Biotechnology Information database. The database can be searched for DNA or protein sequences, and the desired sequence can be imported directly into the iOligo sequence editor, where it can be manipulated.

The sequence under analysis can also be viewed as a graph. In this view, the display window is split in half, with the 5′ end of the sequence in the left panel and the 3′ end of the sequence in the right panel, to simplify scrolling back and forth through a long sequence. In addition, in this mode a graph is displayed under the sequence, which can show the melting temperature, free energy, or pentamer free energy of pairing (for the last five base pairs) of the oligonucleotide.

The simple design of iOligo allows setting of the upper and lower values of the parameters that are important for designing functional oligonucleotides through a single dialog box. In this box, the user can set the location of the forward and reverse oligonucleotides, their lengths, melting temperature, and free energy (ΔG). Finally, the length (number of base pairs) and ΔG allowed for hairpin and dimer formation can be specified, including the length of unique 3′ end sequence desired. Like other programs, iOligo calculates the nearest-neighbor thermodynamic data, which provide accurate melting temperature predictions. On the basis of the above parameters, the sequence is searched and a list of forward and reverse primers is instantly presented. From this list, a forward and/or reverse primer pair can be selected and analyzed to determine whether the two primers form primer dimers.

iOligo is a simple, compact application that effectively accomplishes its task of identifying the optimal oligonucleotides for PCR and sequencing reactions. Undoubtedly, its simplicity will make it indispensable for most molecular biology labs.

—YIANNIS A. IOANNOU

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