TECHSIGHTING

SOFTWARE

Sequence Analysis

Determining or downloading gene sequences has become common practice for most laboratories, and those sequences must be analyzed. GeneJockey is a program that offers a number of DNA analysis and manipulation tools to accomplish this. Sequences can be entered via the keyboard or imported from text files. GeneJockey can read Applied Biosystems sequencing files directly. When a file is opened, a two-pane window opens with the sequence shown in the lower pane. The upper pane shows comments and sequence features such as open reading frames. Sequences can be checked by a voice read-back of the sequence file. A sequence assembly option aligns any number of sequences and generates a graphical display of the alignment. By selecting the Contig option and clicking the text button, a consensus sequence can be generated.

GeneJockey II
Biosoft

Ferguson, MO
$1000
314-524-8029
www.biosoft.com/mac/genejockeyii.htm

DNA sequences can be reversed, complemented, or saved in many common formats, such as GCG, Staden, and Molgen. Selecting Translate from the Modify menu translates the sequence using all three reading frames. If the Sequence Map option is checked on the pop-up menu, a new window will appear, showing the DNA sequence with the three translations under it. Alternatively, the Reading Frames command can be selected to display a diagram of the sequence file with the possible reading frames marked. An interesting feature of this window is that double-clicking on any arrow (reading frame) generates a new window showing the translation of that segment of the sequence.

One of the most common DNA analyses, and a task at which GeneJockey excels, is restriction digestion. A window allows easy navigation of the restriction process. Selecting the option called Find Enzymes allows GeneJockey to automatically identify enzymes that cut or do not cut a selected sequence. A useful option permits the identification of enzymes that cut only once. Once the analysis is complete, results can be displayed as a simple listing of the enzymes, a graphical map of the DNA fragments, or as a text map showing the sequence marked by the position of each enzyme cut. GeneJockey can identify PCR primers, although it will not allow for advance specification of the region of a DNA sequence to be amplified.

GeneJockey also analyzes protein sequences. These can be manually entered, opened from an existing file, or derived from a translated DNA sequence. Once a protein sequence file is opened or displayed in the front window, the commands of the Analyze menu change from DNA analysis routines to protein-specific routines. Commands allow for pairwise or multiple alignment (Clustal W) of proteins, including an option for matrix analysis of two proteins. In addition, secondary structure prediction plots can be generated by selecting the proper algorithm, such as Chou-Fasman or Hopp-Woods.

Finally, GeneJockey can perform many database searches, although it cannot use the Internet. Although GeneJockey has built-in communications capabilities, they are rooted in the older model of direct phone-line communication and a command-line interface, not standard Internet access. With the myriad of databases currently linked via the Internet, it is hard to see that this model of connecting to databases will be used by many people. This is the major shortcoming of an otherwise good, versatile program.

—**YIANNIS A. IOANNOU**

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TECHSIGHTING

SOFTWARE

Art to Data

Computer software for quantitative analysis of images converts artistic microscopic images to scientific data. SigmaScan Pro 5.0 is a valuable tool for automating repetitive measurements on images.

SigmaScan Pro excels at three tasks: image processing, measurement, and automation. The program processes 27 different image formats, including 12- and 16-bit grayscale images. For analysis or publication, grayscale images can be enhanced with colorization tables. Confocal images can be spliced together into a montage, and uneven background lighting can be fixed. SigmaScan Pro 5.0 introduces one new overlay (for a total of five), which resemble image layers in Adobe Photoshop (www.adobe.com). With the new overlays, an investigator can compare different compartments in a cell, subtract emission spectra from double-labeled tissue slices, or align serial sections from a single organ. Overlays are also useful for comparing shapes and sizes of objects before and after a treatment.

SigmaScan Pro 5.0
SPSS Inc.

Chicago, IL
$1499; $399 (upgrade)
800-543-2185
www.spss.com/software/science/SigmaScan/

Quantitation lies at the heart of SigmaScan Pro. The program calibrates pixel intensity with a simple histogram that can be used to identify a region of an image. Groups of pixels with values within a defined range can be identified as objects by the program (automatically) or by the user with the fill tool (manually). Fifty-five different measurements are available for detecting and defining values of objects, points, and lines. In addition to hue, saturation, density, and location, the program also calculates the volume of filled objects and the slope, length, and angle of lines. Many investigators will appreciate the numbering feature, which labels, counts, and correlates objects with other measured values. For example, a histologist looking for sickle cells in a digitized blood sample can label and identify irregular shapes with a single mouse click. The results of each analysis appear in a spreadsheet. Another worksheet tabulates descriptive statistics for column values in the results, and the data in the spreadsheets can be used to generate rudimentary plots.

Visual Basic macros provide automation functions for SigmaScan Pro. A few come with the program, and more are available at the SPSS Web site. A thorough list of predefined macro functions appears in the program manual.

Image analysis is only as good as the digital information in the picture and the judgment of the analyst. Although SigmaScan Pro eliminates some of the human errors of image analysis, the program has some limitations. It will not control real-time image acquisition or confocal densitometry. It is also limited because it does not cache to a scratch disk that would provide multiple undos or previews of changes. Thus, SigmaScan Pro will be useful in circumstances where programs like MetaMorph (http://www.image1.com/products/metamorph/index.html) are prohibitively expensive to purchase and a comprehensive set of imaging features is not required.

SigmaScan Pro 5.0 requires 16-MB RAM (64 MB recommended), 13-MB

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