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.

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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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hard disk space, a Pentium processor running at least Windows 95, and a monitor with a minimum resolution of 800 x 600 pixels and 8-bit (256) color, although true color mode (24-bit) is recommended.

—**J. BRUCE MCCALLUM**

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TECHSIGHTING
SOFTWARE

Pretty Plasmids

Recombinant plasmids are commonly constructed in molecular biology laboratories. The Gene Construction Kit 2 (GCK2) simplifies the design, manipulation, and presentation of plasmid maps. Previously, this program was only available for use on Macintosh systems, but now it is available to Windows 95, 98, and NT users. Files created by Macintosh and Windows GCK2 versions are interchangeable, simplifying collaborations between colleagues with different computers.

Gene Construction Kit 2
Textco, Inc.

West Lebanon, NH
$999, academic;
$1499, commercial
603-643-1471
www.textco.com

Twelve short tutorials provide step-by-step directions to help experienced or new users to rapidly learn program features and increase productivity. More advanced program functions are logically organized and presented in a paperback user's manual, a virtual manual (installed with the program), and at the Textco, Inc. Web site. The tutorials, which require several hours to complete, are highly recommended.

Plasmid map construction in GCK2 begins with entry of the sequence(s) of a parental plasmid or any other DNA molecules. This may be accomplished manually via the keyboard or by importing sequences in a variety of formats (DNA Inspector, GenBank, Intelligenetics, FASTA, NBRF, text, GCG, EMBL, Staden, and Gene Inspector). DNA segments are viewed as either text (sequence) or as a graphic. Once imported, DNA sequences can be cut from one plasmid and pasted into another construct, edited, and annotated with restriction sites and icons. GCK2 can create color illustrations containing multiple constructs, sequences, text, and legends. The program can also manipulate much larger and more complex plasmids, such as the *Agrobacterium tumefaciens* Ti plasmid (~200 kb).

GCK2 will automatically track and document the parent-descendant connection for any given DNA segment within a construct. Students and professionals no longer need to labor over handwritten notes to describe complex plasmid designs. Users can assign keywords to specific DNA segments and place them in defined subdatabases to make future access more efficient.

GCK2 offers a DNA sequence manipulation package combined with basic graphic illustration features that allow rapid production of professional-quality presentations. Graphics may be exported as illustrations, PICT, or JPEG images for editing in more powerful graphic applications.

Other useful features of the program include identification of silent mutations that create or remove restriction sites in coding sequences, agarose gel simulations for single-, partial-, or multiple-enzyme digests, and an open reading frame finder with translation capability. GCK2 also contains a ligation dialogue feature that disallows DNA segment insertions with incompatible ends.

GCK2 supplies a user-friendly and affordable graphic interface to manipulate complex plasmids and produce professional color illustrations. To add to the program's attractiveness, the company offers a technical support telephone line and a Web site. GCK2 is an especially good choice for labs with students because it is an easy-to-learn program that documents each step of plasmid construction. This program would be an excellent addition to any molecular biology lab.

GCK2 is supplied on a single CD-ROM and requires a system with a Windows 95, 98, or NT platform and at least 8.5-MB hard disk space. Some Windows 95 users will need to download a free driver directly from Microsoft.

—**ORIN C. SHANKS , LAURIE BISSONETTE, WALT REAM**

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TECHSIGHTING
SOFTWARE

Manage Your Microbes

Researchers performing investigations in microbial genetics create many modified strains of microbes in a relatively short time, and many find it difficult to keep the information organized and accessible. Recently, Caesar Software launched their first software product, StrainMan (version 1.0), to ease this problem. StrainMan is a predefined database application for tracking and logging information about bacterial strains. It not only keeps track of where a vial is stored, it also gives essential data about the genetics of the microbe, its growth needs, and other information. Only basic computer skills are required to run the program. Help is supplied through tutorials and on the company Web site.

StrainMan provides blank database records for the user to fill in information describing their bacterial stocks. The entries include genotype, phenotype, genetic modifications, growth requirements, mutations, and notes. The developers estimate that 1500 strain records occupy about 6 MB of hard disk space. Maneuvering in the program is simple and convenient. StrainMan uses numerous options that reduce typographical errors upon data entry. The attention paid to detail is noteworthy.

Filling in a new strain record is easy. After selecting the Genus window, a pop-up window with over 50 entries beginning with the letter "a" appears. To view a genus beginning with a different letter, one only needs to enter that letter. Clicking on the desired genus in the list selects it for entry into the record. This intuitive, simple design is also available for other records, such as antibiotic resistance, genetic makeup, nutrients, plasmids, transposons, and sources. The last category consists of a catalog of 1309 vendors with their complete contact information.

StrainMan users will spend little time searching for strains after entering relevant information into their records because all the microbes will be cataloged. User-specified parameters combined with Boolean logic search capabilities enable rapid retrieval of desired information. Users may also publish their strain database on a Web site, thus providing wider access to collaborators. Password protection allows control over who may view and search the library.

StrainMan
Caesar Software, LLC

Portsmouth, NH
$495; $395, academic
Fax, 603-436-7984
www.caesarsoftware.com

StrainMan is well-suited for its task. A downloadable trial version is available on the Web for those who wish to browse through the program before purchase. StrainMan version 1.0 is available on both Macintosh and Windows platforms.

—**FRANK HOOVER**

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