TECHSIGHTING
SOFTWARE

e-Grants?

Submitting a grant proposal usually causes anxiety for both principal investigators and their support staff. GrantSlam version 3.1 from Cayuse Software takes some of the pain out of NIH grant submissions [Public Health Service (PHS) 398 and 1250 forms], especially for those who process the grant applications for academic departments as opposed to those who write the main body of the proposal.

GrantSlam
Cayuse, Inc.
Portland, OR.
PC, $279 for PHS 398 or $379 for the Duo (PHS 398 and 2590); Mac, $399 or $499.
503-297-2108
www.cayuse.com

GrantSlam acts as a front-end negotiator to a database of user-entered grant information. Applicants accustomed to word processors will only need to learn how to enter data in the program. The database format simplifies the tracking of different grants as well as the revising of grants for resubmission by reassembling data from earlier applications. Most fields have context-sensitive pop-up windows with program help and information about NIH guidelines, features that make the database entry a bit more manageable.

Most of the information required on NIH forms is formatted automatically by the program as the user enters it. Biographical sketches, for example, are a standard component of many grant applications, so GrantSlam stores this information as a separate file that is available for each new submission. For the main body of the grant proposal, GrantSlam provides document templates for Microsoft Word and Corel WordPerfect with the correct margins, headers, and footers. Another handy template creates shipping labels with the correct addresses.

GrantSlam manages the database workflow fairly effectively, but it lacks some of the standard features of a word processor. For example, the program's lack of a spell checking function and its inability to copy or paste formatted text makes some operations cumbersome. Text formatting and entry of special characters require keystroke combinations that are unique to the program. GrantSlam does not handle graphical material or permit dynamic updating to other programs. NIH does not yet support submitting and receiving forms by e-mail, so printouts are essential; fortunately, the program does print to laser printers, yielding clear copies that comply with NIH formatting guidelines.

GrantSlam manages and balances budgets better than the widely distributed spreadsheet templates, which tend to violate the NIH form-layout requirements after data is entered. The program calculates dollar totals for the detailed and the modular budget pages. Applicants who have incorrectly entered different yearly budget totals on the "Check List" and "Face Page" will appreciate the automation and checking abilities of these forms.

GrantSlam provides excellent contextual guidance, embedded formatting, and simplified budget calculations. Small- to medium-sized departments may be able to justify the cost of the program, but single users will probably prefer the grant templates that are available for free from NIH. GrantSlam will not eliminate the need for expertise in the subtleties of word processing, graphical design, table formatting, and mathematical expressions. Those skills remain in demand until the NIH more fully participates in the use of enterprise software, where paperless forms are more common.

The program is compatible with Windows 3.1 or later and requires a 386 PC, but a Pentium is recommended. Macintosh users must emulate Windows with the Connectix Virtual PC (bundled with the program) to use GrantSlam.

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TECHSIGHTING
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Sequence Analysis Star

As the sequencing of the human genome approaches completion, the task of analyzing and annotating the finished sequence will become increasingly important. Comprehensive sequence analysis products provide alignment of DNA and protein sequences, primer design, sequence editing, secondary structure prediction, mapping, and database homology analysis. One of the most popular and powerful of these has been the Lasergene sequence analysis software suite published by DNASTAR. In recent years, this package has lost ground in the highly competitive market for sequence analysis packages. Last year, an update to this classic program named Lasergene99 was released. The most noticeable change in this update is the integration of Internet capabilities into the seven different modules that compose the Lasergene99 suite, although the user interface and selected modules have also been improved and a number of bugs have been fixed.

Lasergene99
DNASTAR Inc.
Madison, WI.
Pricing available from DNASTAR.
608-258-7420
www.dnastar.com

Despite these changes, the Lasergene99 package is virtually identical in look and feel to the previous version. The entire package retains a modular format, which allows users to select only those modules useful for their work. Rather than the previous bimonthly release that included CD-ROMs with DNA and protein databases, the new version of Lasergene99 is released annually without the accompanying sequence databases. The rapid growth of the public sequence databases, and their availability online, makes the CD-ROMs unnecessary. The individual Lasergene99 modules are accessed through the Navigator, which also allows the user to access help files for the Lasergene99 suite.

Integration of Internet analyses within the various program modules is a major addition to Lasergene. Sequence files can be directly imported into each module, from the National Center for Biotechnology Information (NCBI) Entrez database, either by accession number or by locus name. NCBI, established in 1988 as a national resource for molecular biology information, also provides the Basic Local Alignment Search Tool (BLAST), which is available from every module of Lasergene through a server at NCBI. BLAST can identify similarities between a nucleotide or protein sequence and other such sequences in the public databases. Entrez sequence retrieval and BLAST searches are both configured in Lasergene to use servers at NCBI, although local versions of the programs can be employed if desired. Lasergene is compatible with BLAST versions 1.4 and 2.0 (which allows the introduction of gaps into the sequence alignments and is thus more sensitive, but slower).

EditSeq is a sequence editor module for importing and exporting DNA and protein sequence files. Although the other modules can import from Entrez, as well as from automated sequencer data in the PE Applied Biosystems (ABI) and Standard Chromatogram Format version 3.0 (SCF) file types, other DNA or protein sequence formats must be converted to a DNASTAR configuration before they can be used. EditSeq allows the export