fit from both the tutorial and the "assistant" in the online help.

To upgrade or not to upgrade? Although new purchasers of Axon amplifiers or the Digidata 1200B A-D board will certainly opt for the pClamp 7.0 program suite, users of previous pClamp versions will wonder whether to upgrade now. A key consideration is whether the existing data acquisition computer hardware and operating system are compatible with pClamp 7.0. Hardware recommendations are as follows, with minimum requirements in brackets: IBM AT-compatible 133 MHz+ Pentium [80486], Windows 95/98/NT 4.0 [Windows 95], 32 to 128 MB RAM [16 MB RAM], a 1 GB [200 MB] hard drive, a CD-ROM drive [floppy drive], one full-length Industry Standard Architecture (ISA) slot, a parallel port, one free Interrupt Request (IRQ), and two [one] free Direct Memory Access (DMA) channels. In addition, pClamp 7.0 is not compatible with the oldest Digidata board and requires a Digidata 1200 A, AE, or B.

The availability of full-length ISA slots, required not only by the Digidata board, but also by modems, Ethernet, and sound cards, can be a limiting factor in standard computer configurations. Windows resource allocation for other devices may also conflict with the IRQ and DMA settings required for the Digidata acquisition board. To eliminate possible conflicts with the Windows Plug-and-Play utility, the DMA and IRQ settings used by the Digidata board should be reserved as described by the Axon technical support Web page. This site also gives other helpful information for troubleshooting during installation and provides access for downloading the latest debugged versions of pClamp 7.0. Technical support is readily available by e-mail or telephone.

One deciding factor in upgrading to pClamp 7.0 may be whether an experienced electrophysiologist or a novice will be the primary user of the application. The user-friendly, tutorial-based system of pClamp 7.0 makes it an effective teaching tool for electrophysiology.

A possible deterrent to upgrading to pClamp 7.0 is that in its present incarnation, pClamp 7.0 falls short of being a Windows program suite, because it still includes DOS-based data analysis applications. Therefore, it may be worthwhile to wait for improvements.

Overall, the transition to the Windows environment has been done well. The basic design of the data acquisition environment is familiar, and many features were added to make Clampex 7.0 a substantially more versatile application. One hopes that Axon is as successful with upgrading the data analysis components of the pClamp suite—Clampfit, Fetchan, and pStat—to the Windows environment.

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TECHVIEW
SOFTWARE

Protein Structure at Your Desk

Beth Basham

Software that can identify protein function on the basis of amino acid sequence is needed by the biotechnology industry, which is awash in protein sequences of unknown function. The BioTools package, PepTool, integrates many existing, validated algorithms and databases to help identify protein structure and function.

Identification of function from amino acid sequence usually starts with homology searching—identifying sequence similarities between the unknown protein and others of known function. PepTool performs homology searches against the PepTool database, which is an amalgam of public sequence databases. Homologous sequences can be gathered and transferred into PepTool's alignment editor. This program performs multiple sequence alignments and, unlike similar products, allows easy editing of the result. The alignment editor also permits one to color code matches based on chemical similarity, and to create publication-quality output. Sequences may be transferred from one window to another to allow seamless alternation between sequence analysis and sequence alignment.

Peptool

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PepTool recognizes structural domains or amino acid sequence patterns that lead to known secondary structures and uses these to predict biological function in unknown sequences. Many of the programs in PepTool are derived from algorithms that have previously been qualified, documented, and published in the literature by David Wishart and Brian Sykes (*1*). Multiple sequence alignments are done with XALIGN, a modification of the pairwise Needleman-Wunsch algorithm (*2*). Homology searches are done with the SEQSEE algorithm (*3*), called FAST ALIGN in PepTool. PepTool provides flexibility in running these programs, with various options to score similarity and gaps in the alignment. The protein secondary structure prediction algorithms are also standard, such as Chou-Fasman (*4*) and GOR (*5*). PepTool displays the results of analyses graphically and as dot plots and helical wheels.

A strong point of PepTool is the way the databases are implemented. Sequence and annotation information in the public protein sequence databases (SWISS-PROT and PIR) have been compressed by BioTools, making it possible to house the current databases on a desktop computer or CD-ROM. BioTools provides subscription-based updates of the databases on a daily, weekly, or monthly basis. PepTool also includes a protein structure database (formerly called SEQBANK), which contains the secondary structures of the sequences for which three-dimensional configurations are known. This database is a reduced form of the protein structure database (Protein Data Bank) and contains only sequences that are not more than 50% identical to one another. These databases are searchable by sequence homology, keyword, or patterns. PepTool also permits users to import their own databases.

The documentation and online help are thoughtfully designed. All technical terms are described in detail, and some are hyperlinked to relevant references or, in some cases, to the abstract of the original paper. The computational methods are clearly described and include a summary of the method, its strengths, when it is most accurate, and its general predictive ability. With this information, the scientist can evaluate the results of PepTool's calculations to determine whether the outcome is biologically meaningful.

PepTool is available for Windows 95/98/NT, Power Macintosh, Sun, Solaris, and SGI. For some of these operating systems, a network version is available. A network parallelism option may be purchased for UNIX platforms, which allows for computationally intensive calculations to be distributed over a computer network.

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