Book Review

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Sequence Analysis in a Nutshell: A Guide to Common Tools and Databases. By Scott Markel and Darryl León. Sebastopol, CA: O'Reilly Press, 2003. Pp. 286. $29.95.

Like other books in the Nutshell series, *Sequence Analysis in a Nutshell* is a quick-reference source for bioinformatics laboratories. This book is not intended as an introduction to sequence analysis or a tutorial for beginners. Nor is this book a dense reference manual like those found in the standard O'Reilly reference book series. Rather, the book is intended as a compendium for users familiar with sequence-analysis tools on UNIX systems. *Sequence Analysis in a Nutshell* provides a compact compilation of all the manual pages and help pages for commonly used sequence-analysis tools. This information is presented in a comfortable format with readable, informative fonts and a useful index. Experienced users of sequence-analysis tools will find that this book provides a convenient source of information about command-line options and sequence-data formats.

The first section of the book contains the field definitions for common file formats used in a number of sequence databases. In addition to the nucleotide and protein databases, such as GenBank, EMBL, and SWISS-PROT, motif and pattern databases, such as PROSITE and Pfam, are included. The second section of the book contains descriptions of common tools that are used for sequence analysis. There are sections on the most important sequence-analysis tools (Readseq, BLAST, BLAT, ClustalW, HMMER, and MEME/MAST) and a large section on the EMBOSS package of sequence-analysis tools that includes about 150 tools in all. All of the tools described in this book are available in the public domain, and many are available on the World Wide Web. The final section of the book is an appendix with nucleic acid and amino acid codes and properties.

Most if not all of the information included in the book is readily available from the programs themselves, through menu options or from the manual pages or help pages. However, for readers who have trouble finding or remembering how to call up the help pages or for those who would like to have menu options at hand instead of clicking through the deep menu trees of programs like ClustalW, *Sequence Analysis in a Nutshell* is a very useful book. For readers who frequently refer to the manual pages or help pages, having this information available in a book on one's lap in a pleasant, readable font is a nice improvement.

As a desktop reference, the Nutshell book does not provide an introduction to the general topics and issues in sequence analysis and does little to provide better descriptions of the programs and program options. Readers looking for help in choosing sequence-analysis programs or selecting program options and those seeking better descriptions of the general issues in sequence analysis and a background into the methods that the programs use to produce the analyses should consider *Bioinformatics* by David Mount (Cold Spring Harbor, NY: Cold Spring Harbor Laboratory Press, 2001).

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