



The Book Review Column¹

by William Gasarch

Department of Computer Science
University of Maryland at College Park
College Park, MD, 20742
email: gasarch@cs.umd.edu

Welcome to the Book Reviews Column. We hope to bring you at least three reviews of books every month. In this column three books are reviewed.

1. **Algorithms on strings, trees, and sequences: computer science and computational biology** by Dan Gusfield. Reviewed by Gary Benson. This is an encyclopedic book on algorithms in computer science motivated by biological applications and (gasp!) actually used in such applications.
2. **Verification of Sequential and Concurrent Programs** by Krzysztof R. Apt and Ernst-Rüdiger Olderog. Reviewed by Anish Arora. This is a book on verification that is (according to the review) suitable as a text in a grad course.
3. **Algorithms and Programming: Problems and Solutions** by Alexander Shen. Reviewed by Jerry James. This is a quirky book of, as the title suggests, problems and solutions. The review suggests it might be used by a teacher as a source of problems and to refine ones own skills.

Review of **Algorithms on strings, trees, and sequences: computer science and computational biology**²

Book authored by Dan Gusfield

Publisher: Cambridge University Press, Cambridge, England, 1997

Other Info: \$59.95, Hardcover, 0-521-58519-8, 534 pages

Reviewed by: Gary Benson³

Modern molecular biology, focusing on the hunt for structural and functional information about proteins and genes, has received an enormous boost from the field of computer science. Once it was realized that properties of newly discovered molecules could be inferred from similar, previously analyzed molecules, a boom in the use of databases, comparison algorithms and computer searches commenced. An unfamiliar molecule is first sequenced to determine the order of its DNA or protein subunits – four nucleotides in the case of DNA, 20 amino acids in the case of proteins. The molecule is then represented as a string of letters, one for each subunit, and from this alphabetic proxy much information may be gleaned. Sequence comparison algorithms have been around for less than 30 years and sophisticated methods for database searches were developed only within the last 15, yet today, it is inconceivable to start the analysis of a biological sequence without a BLAST or FASTA search of GenBank or Swiss-Prot or any of the other myriad, annotated, crosslinked databases maintained in research centers and national labs throughout the world.

One of the first cases where biological function was hinted by a database search involved the unexpected near identity between fragments of the Simian sarcoma virus (SSV), which causes

¹© William Gasarch, 1998.

²©Gary Benson. Reprinted from the Bulletin of Mathematical Biology by permission from the Society for Mathematical Biology

³Department of Biomathematical Sciences, Box 1023, Mount Sinai School of Medicine, New York, NY 10029-6574