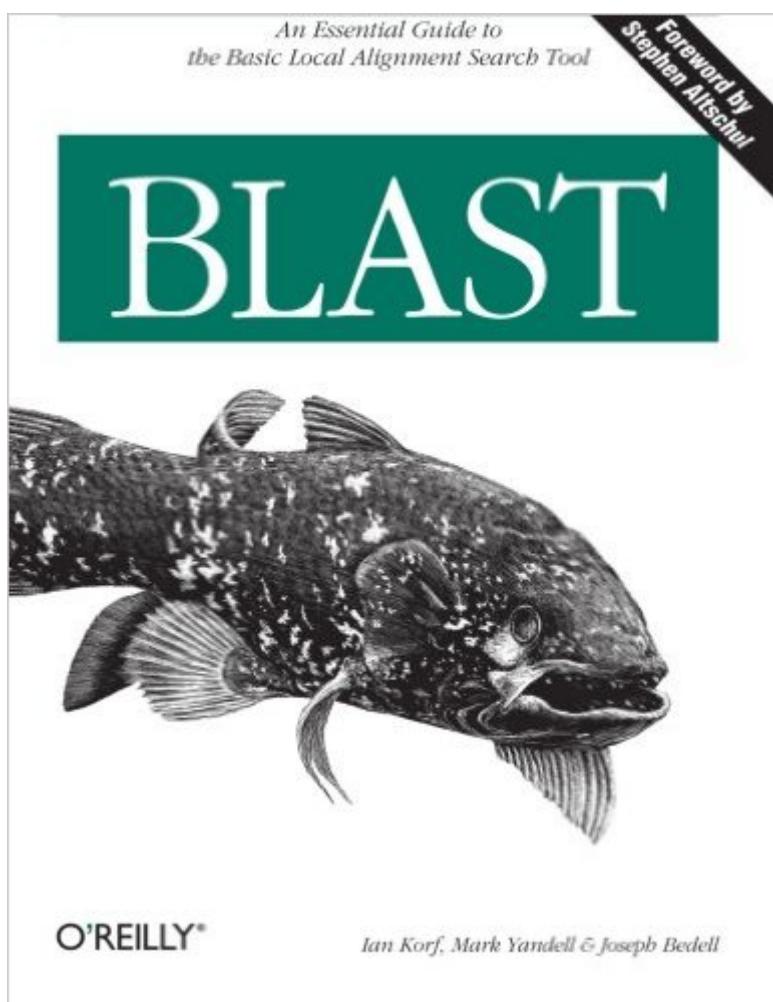


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Synopsis

Sequence similarity is a powerful tool for discovering biological function. Just as the ancient Greeks used comparative anatomy to understand the human body and linguists used the Rosetta stone to decipher Egyptian hieroglyphs, today we can use comparative sequence analysis to understand genomes. BLAST (Basic Local Alignment Search Tool), is a sophisticated software package for rapid searching of nucleotide and protein databases. It is one of the most important software packages used in sequence analysis and bioinformatics. Most users of BLAST, however, seldom move beyond the program's default parameters, and never take advantage of its full power. BLAST is the only book completely devoted to this popular suite of tools. It offers biologists, computational biology students, and bioinformatics professionals a clear understanding of BLAST as well as the science it supports. This book shows you how to move beyond the default parameters, get specific answers using BLAST, and how to interpret your results. The book also contains tutorial and reference sections covering NCBI-BLAST and WU-BLAST, background material to help you understand the statistics behind BLAST, Perl scripts to help you prepare your data and analyze your results, and a wealth of tips and tricks for configuring BLAST to meet your own research needs. Some of the topics covered include: BLAST basics and the NCBI web interface How to select appropriate search parameters BLAST programs: BLASTN, BLASTP, BLASTX, TBLASTN, TBLASTX, PHI-BLAST, and PSI BLAST Detailed BLAST references, including NCBI-BLAST and WU-BLAST Understanding biological sequences Sequence similarity, homology, scoring matrices, scores, and evolution Sequence Alignment Calculating BLAST statistics Industrial-strength BLAST, including developing applications with Perl and BLAST BLAST is the only comprehensive reference with detailed, accurate information on optimizing BLAST searches for high-throughput sequence analysis. This is a book that any biologist should own.

Book Information

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Customer Reviews

If you want to understand the nuts and bolts of how sequence alignment works, then this is the book for you. It will be especially useful for BLAST users who want to understand how it actually works and also for developers who don't know much biology, struggle with the math, but have no problem reading a perl script. The book is basically divided into:

0. A Foreword by Stephen Altschul (the co-creator of BLAST)
1. A quick web intro to a BLAST search
2. Sequence alignment and how the algorithms work
3. Blast and how the Blast statistics are calculated
4. The different types of Blast e.g. WU-Blast
5. Approaches to Performance speedup
6. Reference sections on BLAST parameters

The real key is that this book neatly splits the difference between academic texts and papers which are quite often too difficult to read without sufficient background (and they are not precise about the implementation anyway) and the user-manual type texts which don't discuss the theory at all. One of the best chapters (in my view) is chapter three, where they explain and illustrate the workings of the Needleman-Wunsch and Smith-Waterman algorithms for global and local alignment. If you read the text, then study and run the included perl code, you WILL understand how they work, but be prepared to spend several hours trying different examples. The real advantage of this approach is that you get a deep, practical understanding of how alignment actually works, that you just can't get from reading a mathematical treatment of the subject. Once you understand this chapter, you are actually sufficiently expert to get inside alignment code and modify it for your own purposes.

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