

## Blast

*Ian Korf, Mark Yandell, Joseph Bedell*  
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#574971 in Books Ian Korf 2003-08-08 2003-08-05Ingredients: Example IngredientsOriginal language:EnglishPDF # 1 9.19 x .82 x 7.00l, 1.30 #File Name: 0596002998339 pagesBlast | File size: 67.Mb

**Ian Korf, Mark Yandell, Joseph Bedell : Blast** before purchasing it in order to gage whether or not it would be worth my time, and all praised Blast:

2 of 2 people found the following review helpful. Very Practical Useful Users GuideBy Elliot KleimanFrom a users-perspective this book serves its purpose well - it explains what it is that BLAST is doing "under-the-hood" so that one may better customize Blast's search behavior. All I know is that I really learned a lot of basic fundamental core concepts here that I previously just took for granted.The book discusses the biology, statistics, algorithms, and computer science issues involved in explaining blast. I liked this approach because it does not head super far into any one core area but rather sticks to a strong fundamental overview of each topic. The other strong aspect of this book is that the author thoroughly compares NCBI and WU Blast throughout, characterizing instances where one may choose one over the other and/or how to tweak the parameters for both in those situations.I orginally bought the book b/c I wanted an overview on PAM and BLOSUM matrices and to understand how Blast Statistics work. It really served as

an informative contextual tutorial that has definitely raised my overall understanding on not only Blast, but to better grasp the very interdisciplinary nature concerning sequence alignment for in-silico biological research. 0 of 0 people found the following review helpful. good quality, good service. By Rogelio Prieto A. It's a good introductory book. Good explanation. Materials quality is excellent, soft cover, good price, it's a O'Reilly book!. Good job! thanks ! 0 of 0 people found the following review helpful. I liked it, I loved it, and I want more! By Eldritch Psychomancer I liked it, I loved it, and I want more! It's all about the Bioinformatics Tool, BLAST.

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.

About the Author Ian Korf received his B.A. from Cornell University and his Ph.D from Indiana University. His formal training is in molecular biology but he has had a fondness for computer programming since his early teens. His post-doctoral research at Washington University in St. Louis and at The Wellcome Trust Sanger Institute in the U.K. has focused on genomic sequence analysis with an emphasis on comparative genomics and gene prediction. His goal in life is to follow genomes, wherever they happen to take him.