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 programs 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.

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