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	Soggetti	Computers
		Life sciences
		Algorithms
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		Coding theory
		Information theory
		Computer science—Mathematics
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	Nota di contenuto	Speeding Up the DIALIGN Multiple Alignment Program by Using the 'Greedy Alignment of BIOlogical Sequences LIBrary' (GABIOS-LIB) -- GeMCore, a Knowledge Base Dedicated to Mapping Mammalian Genomes -- Optimal Agreement Supertrees -- Segmentation by Maximal Predictive Partitioning According to Composition Biases -- Can We Have Confidence in a Tree Representation? -- Bayesian

Approach to DNA Segmentation into Regions with Different Average Nucleotide Composition -- Exact and Asymptotic Distribution of the Local Score of One i.i.d. Random Sequence -- Phylogenetic Reconstruction Algorithms Based on Weighted 4-Trees -- Computational Complexity of Word Counting -- Eugène: An Eukaryotic Gene Finder That Combines Several Sources of Evidence -- Tree Reconstruction via a Closure Operation on Partial Splits -- InterDB, a Prediction-Oriented Protein Interaction Database for C. elegans -- Application of Regulatory Sequence Analysis and Metabolic Network Analysis to the Interpretation of Gene Expression Data.

Sommario/riassunto	This book presents a selection of revised full papers accepted for presentation at the First International Conference on Biology, Informatics, and Mathematics, JOBIM 2000, held in Montpellier, France, in May 2000. The 13 papers included in the book were selected after two rounds of reviewing and revision from a total of 67 submissions. Among the topics addressed are algorithms, comparative genomics, evolution, phylogeny, databases, knowledge processing, genome anotation, graph theory, combinatorial mathematics, macromolecular structures, RNA and proteins, metabolic pathways and regulatory networks, and statistics and classification.