

<<Computational Biolog>>

图书基本信息

书名：<<Computational Biology: First International Conference on Biology, Informatics, and Mathematics, JOBIM 2000 Montpellier, France, May 3-5, 2000 Selected Papers (平装)>>

13位ISBN编号：9783540422426

10位ISBN编号：3540422420

出版时间：2001-12

出版时间：1 edition (2001年6月1日)

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页数：163

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内容概要

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

书籍目录

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 EUGENE: An Eukaryotic Gene Finder That Combines Several Sources of Evidence Tree Reconstruction via a Closure Operation on Partial Splits InterDB, a Prediction-Oriented for C. elegans Protein Interaction Database Application of Regulatory Sequence Analysis and Metabolic Network Analysis to the Interpretation of Gene Exprtession Data Author Index

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