

《生物信息学中的算法/会议录 Algori》

图书基本信息

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内容概要

This book constitutes the refereed proceedings of the 6th International Workshop on Algorithms in Bioinformatics, WABI 2006, held in Zurich, Switzerland in September 2006 in the course of the ALGO 2006 conference meetings. The 36 revised full papers presented were carefully reviewed and selected from 100 submissions. All current issues of algorithms in bioinformatics are addressed, ranging from mathematical tools to experimental studies of approximation algorithms and reports on significant computational analyses. Numerous biological problems are dealt with, including genetic mapping, sequence alignment and sequence analysis, phylogeny, comparative genomics, and protein structure. For the first time also machine-learning approaches along with combinatorial optimization are covered.

书籍目录

Measures of Codon Bias in Yeast, the tRNA Pairing Index and Possible DNA Repair Mechanisms
Decomposing Metabolomic Isotope Patterns
A Method to Design Standard HMMs with Desired Length Distribution for
Biological Sequence Analysis
Efficient Model-Based Clustering for LC-MS Data
A Bayesian Algorithm for
Reconstructing Two-Component Signaling Networks
Linear-Time Haplotype Inference on Pedigrees Without
Recombinations
Phylogenetic Network Inferences Through Efficient Haplotyping
Beaches of Islands of Tractability:
Algorithms for Parsimony and Minimum Perfect Phylogeny Haplotyping Problems
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How Many Transcripts Does It Take to Reconstruct the
Splice Graph?
Multiple Structure Alignment and Consensus Identification for Proteins
Procrastination Leads to
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Controlling Size When Aligning Multiple Genomic Sequences
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Reducing Distortion in Phylogenetic Networks
Imputing Supertrees and Supernetworks from
Quartets
A Unifying View of Genome Rearrangements
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Transpositions for Bayesian MCMC
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