

# 《生物信息学中的算法/会议录 Algori》

## 图书基本信息

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作者：Moret, Bernard M. E. 编

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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  
On the Complexity of SNP Block Partitioning Under the Perfect Phylogeny Model  
How Many Transcripts Does It Take to Reconstruct the Splice Graph?  
Multiple Structure Alignment and Consensus Identification for Proteins  
Procrastination Leads to Efficient Filtration for Local Multiple Alignment  
Controlling Size When Aligning Multiple Genomic Sequences with Duplications  
Reducing Distortion in Phylogenetic Networks  
Imputing Supertrees and Supernetworks from Quartets  
A Unifying View of Genome Rearrangements  
Efficient Sampling of Transpositions and Inverted Transpositions for Bayesian MCMC  
Alignment with Non-overlapping Inversions in  $o(na)$ -Time  
Accelerating Motif Discovery: Motif Matching on Parallel Hardware  
Segmenting Motifs in Protein-Protein Interface Surfaces  
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