

1. Record Nr.	UNINA9910317752203321
Titolo	Adaptive Filtering : Theories and Applications // Lino Garcia Morales, editor
Pubbl/distr/stampa	Rijeka, Croatia : , : IntechOpen, , [2013] ©2013
ISBN	953-51-6308-6
Descrizione fisica	1 online resource (164 pages) : illustrations
Disciplina	621.3815324
Soggetti	Adaptive filters
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references and index.
2. Record Nr.	UNINA9910484162103321
Titolo	Research in Computational Molecular Biology : 13th Annual International Conference, RECOMB 2009, Tucson, Arizona, USA, May 18-21, 2009, Proceedings // edited by Serafim Batzoglou
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2009
ISBN	3-642-02008-9
Edizione	[1st ed. 2009.]
Descrizione fisica	1 online resource (XVI, 534 p.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 5541
Altri autori (Persone)	BatzoglouSerafim
Disciplina	570
Soggetti	Life sciences Computer programming Artificial intelligence Bioinformatics Algorithms Database management Life Sciences Programming Techniques Artificial Intelligence Computational and Systems Biology Database Management

Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di contenuto	<p>Searching Protein 3-D Structures in Linear Time -- Optimization-Based Peptide Mass Fingerprinting for Protein Mixture Identification -- Boosting Protein Threading Accuracy -- New Perspectives on Gene Family Evolution: Losses in Reconciliation and a Link with Supertrees -- A Probabilistic Graphical Model for Ab Initio Folding -- Topology-Free Querying of Protein Interaction Networks -- Cross Species Expression Analysis of Innate Immune Response -- Haplotype Inference in Complex Pedigrees -- Storage and Retrieval of Individual Genomes -- An Online Approach for Mining Collective Behaviors from Molecular Dynamics Simulations -- Parameter Synthesis in Nonlinear Dynamical Systems: Application to Systems Biology -- Spatial Clustering of Multivariate Genomic and Epigenomic Information -- How Many Bootstrap Replicates Are Necessary? -- A Robust Bayesian Two-Sample Test for Detecting Intervals of Differential Gene Expression in Microarray Time Series -- Incorporating Nucleosomes into Thermodynamic Models of Transcription Regulation -- Combinatorial Algorithms for Structural Variation Detection in High Throughput Sequenced Genomes -- Optimizing PCR Assays for DNA Based Cancer Diagnostics -- The Multi-State Perfect Phylogeny Problem with Missing and Removable Data: Solutions via Integer-Programming and Chordal Graph Theory -- COE: A General Approach for Efficient Genome-Wide Two-Locus Epistasis Test in Disease Association Study -- Overlapping Pools for High Throughput Targeted Resequencing -- Deep Sequencing of a Genetically Heterogeneous Sample: Local Haplotype Reconstruction and Read Error Correction -- Lifting Prediction to Alignment of RNA Pseudoknots -- Detection of Locally Over-Represented GO Terms in Protein-Protein Interaction Networks -- Protein Fragment Swapping: A Method for Asymmetric, Selective Site-Directed Recombination -- Simultaneous Alignment and Folding of Protein Sequences -- Shared Peptides in Mass Spectrometry Based Protein Quantification -- Evaluating Between-Pathway Models with Expression Data -- Sorting Signed Permutations by Inversions in <math>O(n \log n)</math> Time -- Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information -- Identification and Frequency Estimation of Inversion Polymorphisms from Haplotype Data -- On the Relationship between DNA Periodicity and Local Chromatin Structure -- Phylogenies without Branch Bounds: Contracting the Short, Pruning the Deep -- Detecting the Presence and Absence of Causal Relationships between Expression of Yeast Genes with Very Few Samples -- An Adaptive and Memory Efficient Algorithm for Genotype Imputation -- A Statistical Framework for the Functional Analysis of Metagenomes -- Learning Models for Aligning Protein Sequences with Predicted Secondary Structure.</p>
Sommario/riassunto	<p>This book constitutes the refereed proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology, RECOMB 2009, held in Tucson, Arizona, USA in May 2009. The 37 revised full papers presented were carefully reviewed and selected from 166 submissions. As the top conference in computational molecular biology, RECOMB addresses all current issues in algorithmic, theoretical, and experimental bioinformatics such as molecular sequence analysis, recognition of genes and regulatory elements,</p>

molecular evolution, protein structure, structural genomics, gene expression, gene networks, drug design, combinatorial libraries, computational proteomics, as well as structural and functional genomics.

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