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| 1. Record Nr. | UNISA990000760130203316 |
| Autore | Italia : Ragioneria generale dello Stato |
| Titolo | Monti retributivi e monti contributivi : lavoratori dipendenti, settore privato : analisi degli aspetti finanziari : 1993-1994 |
| Pubbl/distr/stampa | [S.l. : s.n.], 1995 |
| Descrizione fisica | IX, 313 p. : 22x32 cm |
| Disciplina | 331.21 |
| Soggetti | Lavoratori dipendenti - Retribuzione - 1994
Contributi di previdenza - 1994 |
| Collocazione | 331.21 ITA 1 (IEP VI 256) |
| Lingua di pubblicazione | Italiano |
| Formato | Materiale a stampa |
| Livello bibliografico | Monografia |
-
- | | |
|--------------------|---|
| 2. Record Nr. | UNINA9910768440603321 |
| Titolo | Research in Computational Molecular Biology : 11th Annunal International Conference, RECOMB 2007, Oakland, CA, USA, April 21-25, 2007, Proceedings // edited by Terry Speed, Haiyan Huang |
| Pubbl/distr/stampa | Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2007 |
| ISBN | 1-280-86487-7
9786610864874
3-540-71681-5 |
| Edizione | [1st ed. 2007.] |
| Descrizione fisica | 1 online resource (XVI, 552 p.) |
| Collana | Lecture Notes in Bioinformatics, , 2366-6331 ; ; 4453 |
| Disciplina | 572.8 |
| Soggetti | Biochemistry
Algorithms
Artificial intelligence - Data processing
Computer science - Mathematics
Discrete mathematics
Database management
Artificial intelligence
Data Science
Discrete Mathematics in Computer Science |

Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di bibliografia	Includes bibliographical references and author index.
Nota di contenuto	QNet: A Tool for Querying Protein Interaction Networks -- Pairwise Global Alignment of Protein Interaction Networks by Matching Neighborhood Topology -- Reconstructing the Topology of Protein Complexes -- Network Legos: Building Blocks of Cellular Wiring Diagrams -- An Efficient Method for Dynamic Analysis of Gene Regulatory Networks and in silico Gene Perturbation Experiments -- A Feature-Based Approach to Modeling Protein-DNA Interactions -- Network Motif Discovery Using Subgraph Enumeration and Symmetry-Breaking -- Nucleosome Occupancy Information Improves de novo Motif Discovery -- Framework for Identifying Common Aberrations in DNA Copy Number Data -- Estimating Genome-Wide Copy Number Using Allele Specific Mixture Models -- GIMscan: A New Statistical Method for Analyzing Whole-Genome Array CGH Data -- Production-Passage-Time Approximation: A New Approximation Method to Accelerate the Simulation Process of Enzymatic Reactions -- Shift-Invariant Adaptive Double Threading: Learning MHC II - Peptide Binding -- Reconstructing the Phylogeny of Mobile Elements -- Beyond Galled Trees - Decomposition and Computation of Galled Networks -- Variational Upper Bounds for Probabilistic Phylogenetic Models -- Heuristics for the Gene-Duplication Problem: A $\Theta(n)$ Speed-Up for the Local Search -- Support Vector Training of Protein Alignment Models -- Tools for Simulating and Analyzing RNA Folding Kinetics -- Multiple Sequence Alignment Based on Profile Alignment of Intermediate Sequences -- Connectedness Profiles in Protein Networks for the Analysis of Gene Expression Data -- Multivariate Segmentation in the Analysis of Transcription Tiling Array Data -- A Bayesian Model That Links Microarray mRNA Measurements to Mass Spectrometry Protein Measurements -- Rearrangements in Genomes with Centromeres Part I: Translocations -- Identification of Deletion Polymorphisms from Haplotypes -- Free Energy Estimates of All-Atom Protein Structures Using Generalized Belief Propagation -- Minimizing and Learning Energy Functions for Side-Chain Prediction -- Protein Conformational Flexibility Analysis with Noisy Data -- Deterministic Pharmacophore Detection Via Multiple Flexible Alignment of Drug-Like Molecules -- Design of Compact, Universal DNA Microarrays for Protein Binding Microarray Experiments -- Improved Ranking Functions for Protein and Modification-Site Identifications -- Peptide Retention Time Prediction Yields Improved Tandem Mass Spectrum Identification for Diverse Chromatography Conditions -- A Fast and Accurate Algorithm for the Quantification of Peptides from Mass Spectrometry Data -- Association Mapping of Complex Diseases with Ancestral Recombination Graphs: Models and Efficient Algorithms -- An Efficient and Accurate Graph-Based Approach to Detect Population Substructure -- RB-Finder: An Improved Distance-Based Sliding Window Method to Detect Recombination Breakpoints -- Comparative Analysis of Spatial Patterns of Gene Expression in <i>Drosophila melanogaster</i> Imaginal Discs.

This book constitutes the refereed proceedings of the 11th Annual International Conference on Research in Computational Molecular Biology, RECOMB 2007, held in Oakland, CA, USA in April 2007. The 37 revised full papers presented were carefully reviewed and selected from just under 170 submissions. As the top conference in computational molecular biology, RECOMB addresses all current issues in algorithmic, theoretical, and experimental bioinformatics.
