1.

Record Nr.	UNIORUON00080322
Autore	WENIG, Steffen
Titolo	The catalogue / Steffen Wenig
Pubbl/distr/stampa	366 p., : ill.
ISBN	08-7273-064-6
Disciplina	962.401
Soggetti	Archeologia - Sudan Arte - Nubia - Esposizioni Arte - Sudan - Esposizioni NEW YORK - Musei - Cataloghi
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

2.

Record Nr.	UNINA9910482997403321
Titolo	Algorithms in Bioinformatics : 5th International Workshop, WABI 2005, Mallorca, Spain, October 3-6, 2005, Proceedings / / edited by Rita Casadio, Gene Myers
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2005
Edizione	[1st ed. 2005.]
Descrizione fisica	1 online resource (X, 436 p.)
Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 3692
Altri autori (Persone)	CasadioRita MyersEugene W (Eugene Wimberly)
Disciplina	572.0285
Soggetti	Life sciences Computer programming Algorithms Artificial intelligence - Data processing Computer science Computer science - Mathematics Discrete mathematics Life Sciences Programming Techniques Data Science Theory of Computation

	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 index.
Nota di contenuto	Expression -- Spectral Clustering Gene Ontology Terms to Group Genes by Function -- Dynamic De-Novo Prediction of microRNAs Associated with Cell Conditions: A Search Pruned by Expression -- Clustering Gene Expression Series with Prior Knowledge -- A Linear Time Biclustering Algorithm for Time Series Gene Expression Data -- Time-Window Analysis of Developmental Gene Expression Data with Multiple Genetic Backgrounds -- Phylogeny -- A Lookahead Branch-and-Bound Algorithm for the Maximum Quartet Consistency Problem -- Computing the Quartet Distance Between Trees of Arbitrary Degree -- Using Semi-definite Programming to Enhance Supertree Resolvability -- An Efficient Reduction from Constrained to Unconstrained Maximum Agreement Subtree -- Pattern Identification in Biogeography -- On the Complexity of Several Haplotyping Problems -- A Hidden Markov Technique for Haplotype Reconstruction -- Algorithms for Imperfect Phylogeny Haplotyping (IPPH) with a Single Homoplasy or Recombination Event -- Networks -- A Faster Algorithm for Detecting Network Motifs -- Reaction Motifs in Metabolic Networks -- Reconstructing Metabolic Networks Using Interval Analysis -- Genome Rearrangements -- A 1.375-Approximation Algorithm for Sorting by Transpositions -- A New Tight Upper Bound on the Transposition Distance -- Perfect Sorting by Reversals Is Not Always Difficult -- Minimum Recombination Histories by Branch and Bound -- Sequences -- A Unifying Framework for Seed Sensitivity and Its Application to Subset Seeds -- Generalized Planted (l,d)-Motif Problem with Negative Set -- Alignment of Tandem Repeats with Excision, Duplication, Substitution and Indels (EDSI) -- The Peres-Shields Order Estimator for Fixed and Variable Length Markov Models with Applications to DNA Sequence Similarity -- Multiple Structural RNA Alignmentwith Lagrangian Relaxation -- Faster Algorithms for Optimal Multiple Sequence Alignment Based on Pairwise Comparisons -- Ortholog Clustering on a Multipartite Graph -- Linear Time Algorithm for Parsing RNA Secondary Structure -- A Compressed Format for Collections of Phylogenetic Trees and Improved Consensus Performance -- Structure -- Optimal Protein Threading by Cost-Splitting -- Efficient Parameterized Algorithm for Biopolymer Structure-Sequence Alignment -- Rotamer-Pair Energy Calculations Using a Trie Data Structure -- Improved Maintenance of Molecular Surfaces Using Dynamic Graph Connectivity -- The Main Structural Regularities of the Sandwich Proteins -- Discovery of Protein Substructures in EM Maps.
Sommario/riassunto	We are pleased to present the proceedings of the 5th Workshop on Algorithms in Bioinformatics (WABI 2005) which took place in Mallorca, Spain, October 3-6, 2005. The WABI 2005 workshop was part of the ?ve ALGO 2005 conf- ence meetings, which, in addition to WABI, included ESA, WAOA, IWPEC, and ATMOS. WABI 2005 was sponsored by EATCS (the European Assoc- tion for Theoretical Computer Science), the ISCB (the International Society for Computational Biology), the Universitat Polit` ecnica de Catalunya, the U- versitat de les Illes Balears, and the

Ministerio de Educación y Ciencia. See http://www.lsi.upc.edu/~wabi05/ for more details. The Workshop on Algorithms in Bioinformatics highlights research work specifically developed to address algorithmic problems in biosequence analysis. Theemphasisisthereforeonstatisticalandprobabilisticalgorithmsthataddress important problems in the field of molecular and structural biology. At present, given the enormous scientific and technical efforts in functional and structural genomics, the relevance of the problem is therefore constrained by the need for sound, efficient and specialized algorithms, capable of achieving solutions that can be tested by the biological community. Indeed the ultimate goal is to - plement algorithms capable of extracting real features from real biological data sets. Therefore the workshop aims to present recent research results, including significant work in progress, and to identify and explore directions of future research.