

1. Record Nr.	UNISA996465910803316
Titolo	Bioinformatics Research and Applications [[electronic resource]] : 6th International Symposium, ISBRA 2010, Storrs, CT, USA, May 23-26, 2010. Proceedings // edited by Mark Borodovsky, J. Peter Gogarten, Teresa M. Przytycka, Sanguthevar Rajasekaran
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	1-280-38658-4 9786613564504 3-642-13078-X
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (XII, 253 p. 80 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 6053
Disciplina	572.80285
Soggetti	Life sciences Database management Application software Information storage and retrieval Algorithms Data mining Life Sciences, general Database Management Information Systems Applications (incl. Internet) Information Storage and Retrieval Algorithm Analysis and Problem Complexity Data Mining and Knowledge Discovery
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	Tracing the Early Cell Divisions of Mouse Embryos by Single Cell RNA-Seq -- Successes and Failures of Elegant Algorithms in Computational Biology -- Modeling without Borders: Creating and Annotating VCell Models Using the Web -- Touring Protein Space with Matt -- Fixed-Parameter Algorithm for General Pedigrees with a Single Pair of Sites -- Analysis of Temporal-spatial Co-variation within Gene Expression

Microarray Data in an Organogenesis Model -- Human Genome Annotation -- Extensions and Improvements to the Chordal Graph Approach to the Multi-state Perfect Phylogeny Problem -- Analysis of Gene Interactions Using Restricted Boolean Networks and Time-Series Data -- Residue Contexts: Non-sequential Protein Structure Alignment Using Structural and Biochemical Features -- Essential Proteins Discovery from Weighted Protein Interaction Networks -- Identifying Differentially Abundant Metabolic Pathways in Metagenomic Datasets -- A Novel Approach for Compressing Phylogenetic Trees -- Structure of Proximal and Distant Regulatory Elements in the Human Genome -- Combinatorics in Recombinational Population Genomics -- Uncovering Hidden Phylogenetic Consensus -- An Agglomerate Algorithm for Mining Overlapping and Hierarchical Functional Modules in Protein Interaction Networks -- Fast Protein Structure Alignment -- Predicting and Analyzing Cellular Networks -- A Consensus Tree Approach for Reconstructing Human Evolutionary History and Detecting Population Substructure -- Inferring Evolutionary Scenarios for Protein Domain Compositions -- Local Structural Alignment of RNA with Affine Gap Model -- Fast Computation of the Exact Hybridization Number of Two Phylogenetic Trees -- "Master-Slave" Biological Network Alignment -- Deciphering Transcription Factor Binding Patterns from Genome-Wide High Density ChIP-chip Tiling Array Data -- The Expected Fitness Cost of a Mutation Fixation under the One-Dimensional Fisher Model.

2. Record Nr.	UNISALENTO991001315729707536
Autore	Meriggi, Piero
Titolo	Grammatica / Piero Meriggi
Pubbl/distr/stampa	Roma : Edizioni dell'Ateneo, 1966
Descrizione fisica	112 p. ; 27 cm
Collana	Manuale di eteo geroglifico ; 1 Incunabula Graeca ; 13
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia