

1. Record Nr.	UNISA996466262703316
Titolo	Computational Life Sciences II [[electronic resource] ] : Second International Symposium, CompLife 2006, Cambridge, UK, September 27-29, 2006, Proceedings // edited by Michael R. Berthold, Robert Glen, Ingrid B. Fischer
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2006
ISBN	3-540-45768-2
Edizione	[1st ed. 2006.]
Descrizione fisica	1 online resource (XIII, 269 p.)
Collana	Lecture Notes in Bioinformatics ; ; 4216
Disciplina	572.80285
Soggetti	Life sciences Computers Information storage and retrieval Health informatics Database management Application software Life Sciences, general Theory of Computation Information Storage and Retrieval Health Informatics Database Management Information Systems Applications (incl. Internet)
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	Genomics -- Improved Robustness in Time Series Analysis of Gene Expression Data by Polynomial Model Based Clustering -- A Hybrid Grid and Its Application to Orthologous Groups Clustering -- Promoter Prediction Using Physico-Chemical Properties of DNA -- Parametric Spectral Analysis of Malaria Gene Expression Time Series Data -- An Efficient Algorithm for Finding Long Conserved Regions Between Genes -- The Reversal Median Problem, Common Intervals, and Mitochondrial Gene Orders -- Data Mining -- Building Structure-Property Predictive

Models Using Data Assimilation -- Set-Oriented Dimension Reduction: Localizing Principal Component Analysis Via Hidden Markov Models -- Relational Subgroup Discovery for Descriptive Analysis of Microarray Data -- Applicability of Loop Recombination in Ciliates Using the Breakpoint Graph -- High-Throughput Identification of Chemistry in Life Science Texts -- Beating the Noise: New Statistical Methods for Detecting Signals in MALDI-TOF Spectra Below Noise Level -- Molecular Simulation -- Dynamic Complexity of Chaotic Transitions in High-Dimensional Classical Dynamics: Leu-Enkephalin Folding -- Solvent Effects and Conformational Stability of a Tripeptide -- Grid Assisted Ensemble Molecular Dynamics Simulations of HIV-1 Proteases Reveal Novel Conformations of the Inhibitor Saquinavir -- Molecular Informatics -- A Structure-Based Analysis of Single Molecule Force Spectroscopy (SMFS) Data for Bacteriorhodopsin and Four Mutants -- Classifying the World Anti-Doping Agency's 2005 Prohibited List Using the Chemistry Development Kit Fingerprint -- A Point-Matching Based Algorithm for 3D Surface Alignment of Drug-Sized Molecules -- Systems Biology -- Adaptive Approach for Modelling Variability in Pharmacokinetics -- A New Approach to Flux Coupling Analysis of Metabolic Networks -- Biological Networks / Metabolism -- Software Supported Modelling in Pharmacokinetics -- On the Interpretation of High Throughput MS Based Metabolomics Fingerprints with Random Forest -- Construction of Correlation Networks with Explicit Time-Slices Using Time-Lagged, Variable Interval Standard and Partial Correlation Coefficients -- Computational Neuroscience -- The Language of Cortical Dynamics -- A Simple Method to Simultaneously Track the Numbers of Expressed Channel Proteins in a Neuron.

---