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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 MetabolicNetworks -- 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.
Sommario/riassunto	This book constitutes the refereed proceedings of the Second International Symposium on Computational Life Sciences, CompLife 2006. The 25 revised full papers presented were carefully reviewed and selected from 56 initial submissions. The papers are organized in topical sections on genomics, data mining, molecular simulation, molecular informatics, systems biology, biological networks/metabolism, and computational neuroscience.