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Nota di contenuto	Systems Biology -- Structural Protein Interactions Predict Kinase-Inhibitor Interactions in Upregulated Pancreas Tumour Genes Expression Data -- Biochemical Pathway Analysis via Signature Mining -- Recurrent Neuro-fuzzy Network Models for Reverse Engineering Gene Regulatory Interactions -- Data Analysis and Integration -- Some Applications of Dummy Point Scatterers for Phasing in Macromolecular X-Ray Crystallography -- BioRegistry: A Structured Metadata Repository for Bioinformatic Databases -- Robust Perron Cluster Analysis for

Various Applications in Computational Life Science -- Structural Biology -- Multiple Alignment of Protein Structures in Three Dimensions -- Protein Annotation by Secondary Structure Based Alignments (PASSTA) -- MAPPIS: Multiple 3D Alignment of Protein-Protein Interfaces -- Genomics -- Frequent Itemsets for Genomic Profiling -- Gene Selection Through Sensitivity Analysis of Support Vector Machines -- The Breakpoint Graph in Ciliates -- Computational Proteomics -- ProSpect: An R Package for Analyzing SELDI Measurements Identifying Protein Biomarkers -- Algorithms for the Automated Absolute Quantification of Diagnostic Markers in Complex Proteomics Samples -- Detection of Protein Assemblies in Crystals -- Molecular Informatics -- Molecular Similarity Searching Using COSMO Screening Charges (COSMO/3PP) -- Increasing Diversity in In-silico Screening with Target Flexibility -- Multiple Semi-flexible 3D Superposition of Drug-Sized Molecules -- Molecular Structure Determination and Simulation -- Efficiency Considerations in Solving Smoluchowski Equations for Rough Potentials -- Fast and Accurate Structural RNA Alignment by Progressive Lagrangian Optimization -- Visual Analysis of Molecular Conformations by Means of a Dynamic Density Mixture Model -- Distributed Data Mining -- Distributed BLAST in a Grid Computing Context -- Parallel Tuning of Support Vector Machine Learning Parameters for Large and Unbalanced Data Sets -- The Architecture of a Proteomic Network in the Yeast.

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