

1. Record Nr.	UNISA996213647903316
Titolo	Advances in Bioinformatics and Computational Biology [[electronic resource]] : 9th Brazilian Symposium on Bioinformatics, BSB 2014, Belo Horizonte, Brazil, October 28-30, 2014, Proceedings / / edited by Sérgio Campos
Pubbl/distr/stampa	Cham : , : Springer International Publishing : , : Imprint : Springer, , 2014
ISBN	3-319-12418-8
Edizione	[1st ed. 2014.]
Descrizione fisica	1 online resource (X, 156 p. 41 illus.)
Collana	Lecture Notes in Bioinformatics ; ; 8826
Disciplina	570.285
Soggetti	Bioinformatics Algorithms Data mining Pattern recognition Application software Computational Biology/Bioinformatics Algorithm Analysis and Problem Complexity Data Mining and Knowledge Discovery Pattern Recognition 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 contenuto	An Extensible Framework for Genomic and Metagenomic Analysis -- On the Multichromosomal Hultman Number -- Towards an Ensemble Learning Strategy for Metagenomic Gene Prediction -- FUNN-MG: A Metagenomic Systems Biology Computational Framework -- FluxMED: An Adaptable and Extensible Electronic Health Record System -- Influence of Sequence Length in Promoter Prediction Performance -- Evolution of Genes Neighborhood within Reconciled Phylogenies: An Ensemble Approach -- Dynamic Programming for Set Data Types -- Using Binary Decision Diagrams (BDDs) for Memory Optimization in Basic Local Alignment Search Tool (BLAST) -- A Multi-Objective Evolutionary Algorithm for Improving Multiple Sequence Alignments --

BION2SEL: An Ontology-Based Approach for the Selection of Molecular Biology Databases -- Structural Comparative Analysis of Secreted NTPDase Models of *Schistosoma mansoni* and *Homo sapiens* -- Length and Symmetry on the Sorting by Weighted Inversions Problem -- Storage Policy for Genomic Data in Hybrid Federated Clouds -- Genome-Wide Identification of Non-coding RNAs in *Komagataella pastoris* str. GS115 -- Multi-scale Simulation of T Helper Lymphocyte Differentiation -- Scaffolding of Ancient Contigs and Ancestral Reconstruction in a Phylogenetic Framework -- Quality Metrics for Benchmarking Sequences Comparison Tools.

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#### Sommario/riassunto

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This book constitutes the refereed proceedings of the 9th Brazilian Symposium on Bioinformatics, BSB 2014, held in Belo Horizonte, Brazil, in October 2014. The 18 revised full papers presented were carefully reviewed and selected from 32 submissions. The papers cover all aspects of bioinformatics and computational biology.

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