1.

Record Nr.	UNINA9910298561103321
Titolo	Parallel Computational Fluid Dynamics : 25th International Conference, ParCFD 2013, Changsha, China, May 20-24, 2013. Revised Selected Papers / / edited by Kenli Li, Zheng Xiao, Yan Wang, Jiayi Du, Keqin Li
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2014
ISBN	3-642-53962-9
Edizione	[1st ed. 2014.]
Descrizione fisica	1 online resource (XIV, 614 p. 384 illus.)
Collana	Communications in Computer and Information Science, , 1865-0937 ; ; 405
Disciplina	004.6
Soggetti	Computer simulation Computer systems Microprocessors Computer architecture Electronic digital computers - Evaluation Computer science Application software Computer Modelling Computer System Implementation Processor Architectures System Performance and Evaluation Models of Computation Computer and Information Systems Applications
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di contenuto	Parallel algorithms -- Developments in software tools and environments -- Unstructured adaptive mesh applications -- Industrial applications -- Atmospheric and oceanic global simulation -- Interdisciplinary applications -- Evaluation of computer architectures and software environments.
Sommario/riassunto	This book constitutes the refereed proceedings of the 25th International Conference on Parallel Computational Fluid Dynamics,

ParCFD 2013, held in Changsha, China, in May 2013. The 35 revised full papers presented were carefully reviewed and selected from more than 240 submissions. The papers address issues such as parallel algorithms, developments in software tools and environments, unstructured adaptive mesh applications, industrial applications, atmospheric and oceanic global simulation, interdisciplinary applications and evaluation of computer architectures and software environments.

2.

Record Nr.	UNINA9910768441203321
Titolo	Evolutionary Computation, Machine Learning and Data Mining in Bioinformatics : 8th European Conference, EvoBIO 2010, Istanbul, Turkey, April 7-9, 2010, Proceedings / / edited by Clara Pizzuti, Marylyn D. Ritchie, Mario Giacobini
Pubbl/distr/stampa	Berlin, Heidelberg : , : Springer Berlin Heidelberg : , : Imprint : Springer, , 2010
ISBN	1-280-38605-3 9786613563972 3-642-12211-6
Edizione	[1st ed. 2010.]
Descrizione fisica	1 online resource (XII, 249 p. 63 illus.)
Collana	Theoretical Computer Science and General Issues, , 2512-2029 ; ; 6023
Classificazione	BIO 110f DAT 708f MAT 919f SS 4800 WC 7700
Altri autori (Persone)	PizzutiClara RitchieMarylyn DeRiggi GiacobiniMario
Disciplina	006.3
Soggetti	Bioinformatics Algorithms Database management Artificial intelligence Computer science Artificial intelligence - Data processing Computational and Systems Biology Database Management Artificial Intelligence Theory of Computation Data Science

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	Variable Genetic Operator Search for the Molecular Docking Problem -- Variable Genetic Operator Search for the Molecular Docking Problem -- Role of Centrality in Network-Based Prioritization of Disease Genes -- Parallel Multi-Objective Approaches for Inferring Phylogenies -- An Evolutionary Model Based on Hill-Climbing Search Operators for Protein Structure Prediction -- Finding Gapped Motifs by a Novel Evolutionary Algorithm -- Top-Down Induction of Phylogenetic Trees -- A Model Free Method to Generate Human Genetics Datasets with Complex Gene-Disease Relationships -- Grammatical Evolution of Neural Networks for Discovering Epistasis among Quantitative Trait Loci -- Grammatical Evolution Decision Trees for Detecting Gene-Gene Interactions -- Identification of Individualized Feature Combinations for Survival Prediction in Breast Cancer: A Comparison of Machine Learning Techniques -- Correlation–Based Scatter Search for Discovering Biclusters from Gene Expression Data -- A Local Search Appproach for Transmembrane Segment and Signal Peptide Discrimination -- A Replica Exchange Monte Carlo Algorithm for the Optimization of Secondary Structure Packing in Proteins -- Improving Multi-Relief for Detecting Specificity Residues from Multiple Sequence Alignments -- Using Probabilistic Dependencies Improves the Search of Conductance-Based Compartmental Neuron Models -- Posters -- The Informative Extremes: Using Both Nearest and Farthest Individuals Can Improve Relief Algorithms in the Domain of Human Genetics -- Artificial Immune Systems for Epistasis Analysis in Human Genetics -- Metaheuristics for Strain Optimization Using Transcriptional Information Enriched Metabolic Models -- Using Rotation Forest for Protein Fold Prediction Problem: An Empirical Study -- Towards Automatic Detecting ofOverlapping Genes - Clustered BLAST Analysis of Viral Genomes -- Investigating Populational Evolutionary Algorithms to Add Vertical Meaning in Phylogenetic Trees.
Sommario/riassunto	The ?eld of bioinformatics has two main objectives: the creation and main- nance of biological databases, and the discovery of knowledge from life sciences datainordertounravelthemysteriesofbiologicalfunction, leadingtonewdrugs andtherapiesforhumandisease. Life sciencesdatacomeinthe formofbiological sequences, structures, pathways, or literature. One major aspect of discovering biological knowledge is to search, predict, or model speci'c information in a given dataset in order to generate new interesting knowledge. Computer science methods such as evolutionary computation, machine learning, and data mining all have a great deal to o'er the ?eld of bioinformatics. The goal of the 8th - ropean Conference on Evolutionary Computation, Machine Learning, and Data Mining in Bioinformatics (EvoBIO 2010) was to bring together experts in these ?elds in order to discuss new and novel methods for tackling complex biological problems. The 8th EvoBIO conference was held in Istanbul, Turkey during April 7-9, 2010attheIstanbulTechnicalUniversity. EvoBIO2010washeldjointlywiththe 13th European Conference on Genetic Programming (EuroGP 2010), the 10th European Conference on Evolutionary Computation in Combinatorial Opti- sation (EvoCOP 2010), and the conference on the applications of evolutionary

computation,EvoApplications. Collectively,the conferences areorganizedunder the name Evo* (www. evostar. org). EvoBIO, held annually as a workshop since 2003, became a conference in 2007 and it is now the premiere European event for those interested in the interface between evolutionary computation, machine learning, data mining, bioinformatics, and computational biology.