

1. Record Nr.	UNINA9910784004403321
Titolo	Proceedings of the 5th Asia-Pacific bioinformatics conference [[electronic resource]] : Hong Kong, 15-17 January 2007 // editors, David Sankoff, Lusheng Wang, Francis Chin
Pubbl/distr/stampa	London, : Imperial College Press, c2007
ISBN	1-281-12066-9 9786611120665 1-86094-799-9
Descrizione fisica	1 online resource (391 p.)
Collana	Series on advances in bioinformatics and computational biology ; ; v. 5
Altri autori (Persone)	SankoffDavid WangLusheng <1962-> ChinFrancis <1948->
Disciplina	572.80285
Soggetti	Bioinformatics Biology - Data processing
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Preface; APBC 2007 Organization; CONTENTS; Keynote Papers; Contributed Papers; Exploring Genomes of Distantly Related Mammals J.A. Marshall Graves; Bugs, Guts and Fat - A Systems Approach to the Metabolic 'Axis of Evil' J. Nadeau; Protein Identification via Spectral Networks Analysis P. Pevzner; Metagenome Analysis using MEGAN D.H. Huson, A.F. Auch, J. Qi, and S.C. Schuster; Algorithmic Approaches to Selecting Control Clones in DNA Array Hybridization Experiments Q. Fu, E. Bent, J . Borneman, M. Chrobak, and N. Young Subtle Motif Discovery for Detection of DNA Regulatory Sites M. Comin, and L. ParidaAn Effective Promoter Detection Method using the Adaboost Algorithm X . Xze, S. Wu, K.-M. Lam, and H. Yan; A New Strategy of Geometrical Biclustering for Microarray Data Analysis H. Zhao, A. W.C. Liew, and H. Yan; Using Formal Concept Analysis for Microarray Data Comparison V. Choi, Y. Huang, V. Lam, D. Potter, R. Laubenbacher, and K. Duca; An Efficient Biclustering Algorithm for Finding Genes with Similar Patterns in Time-series Expression Data S.C. Madeira, and A.L. Oliveira

Selecting Genes with Dissimilar Discrimination Strength for Sample Class Prediction Z. Cai, R. Goebel, M.R. Salavatipour, Y. Shi, L. Xu, and G. Lin; Computing the All-Pairs Quartet Distance on a Set of Evolutionary Trees M. Stissing, T. Mailund, C.N.S. Pedersen, G.S. Brodal, and R. Fagerberg; Computing the Quartet Distance Between Evolutionary Trees of Bounded Degree M. Stissing, C.N.S. Pedersen, T. Mailund, G.S. Brodal, and R. Fagerberg; A Global Maximum Likelihood Super-Quartet Phylogeny Method P. Wang, B.B. Zhou, M. Taraeneh, D. Chu, C. Wang, A. Y. Zomaya, and R.P. Brent

A Randomized Algorithm for Comparing Sets of Phylogenetic Trees S.-J. Sul, and T.L. Williams; Protein Structure-Structure Alignment with Discrete Frkchet Distance M. Jiang, Y. Xu, and B. Zhu; Deriving Protein Structure Topology from the Helix Skeleton in Low Resolution Density Map using Rosetta Y. Lu, J. He, and C.E.M. Strauss; Fitting Protein Chains to Cubic Lattice is NP-complete J. Mafiuch, and D.R. Gaur; Inferring a Chemical Structure from a Feature Vector Based on Frequency of Labeled Paths and Small Fragments T. Alcutsu, and D. Fukagawa

Exact and Heuristic Approaches for Identifying Disease-Associated SNP Motifs G. Huang, P. Jeavons, and D. Kwiatkowski; Genotype-Based Case-Control Analysis, Violation of Hardy-Weinberg Equilibrium, and Phase Diagrams Y.J. Suh, and W. L i; A Probabilistic Method to Identify Compensatory Substitutions for Pathogenic Mutations B.C. Easton, A. V. Isaev, G.A. Huttley, and P. Maxwell; Exploring Genome Rearrangements using Virtual Hybridization M. Belcaid, A. Bergeron, A. Chateau, C. Chauve, Y. Gingras, G. Poisson, and M. Vendette

Two Plus Two Does not Equal Three: Statistical Tests for Multiple Genome Comparison N. Raghupathy, R. Hoberman, and D. Durand

Sommario/riassunto

High-throughput sequencing and functional genomics technologies have given us the human genome sequence as well as those of other experimentally, medically, and agriculturally important species, and have enabled large-scale genotyping and gene expression profiling of human populations. Databases containing large numbers of sequences, polymorphisms, structures, and gene expression profiles of normal and diseased tissues are being rapidly generated for human and model organisms. Bioinformatics is thus rapidly growing in importance in the annotation of genomic sequences; the understanding of the
