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Collana	Lecture Notes in Bioinformatics ; ; 6044
Disciplina	570
Soggetti	Life sciences Computer programming Data structures (Computer science) Algorithms Bioinformatics Database management Life Sciences, general Programming Techniques Data Structures and Information Theory Algorithm Analysis and Problem Complexity Computational Biology/Bioinformatics Database Management
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	An Algorithmic Framework for Predicting Side-Effects of Drugs -- SubMAP: Aligning Metabolic Pathways with Subnetwork Mappings -- Admixture Aberration Analysis: Application to Mapping in Admixed Population Using Pooled DNA -- Pathway-Based Functional Analysis of Metagenomes -- Hierarchical Generative Biclustering for MicroRNA Expression Analysis -- Subnetwork State Functions Define Dysregulated Subnetworks in Cancer -- Proteome Coverage Prediction for Integrated

Proteomics Datasets -- Discovering Regulatory Overlapping RNA Transcripts -- Alignment-Free Phylogenetic Reconstruction -- Inference of Isoforms from Short Sequence Reads -- The Clark Phaseable Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS -- A New Algorithm for Improving the Resolution of Cryo-EM Density Maps -- Towards Automated Structure-Based NMR Resonance Assignment -- Gapped Spectral Dictionaries and Their Applications for Database Searches of Tandem Mass Spectra -- naiveBayesCall: An Efficient Model-Based Base-Calling Algorithm for High-Throughput Sequencing -- Extracting Between-Pathway Models from E-MAP Interactions Using Expected Graph Compression -- Simultaneous Identification of Causal Genes and Dys-Regulated Pathways in Complex Diseases -- Incremental Signaling Pathway Modeling by Data Integration -- The Poisson Margin Test for Normalisation Free Significance Analysis of NGS Data -- Compressing Genomic Sequence Fragments Using SlimGene -- On the Genealogy of Asexual Diploids -- Genovo: De Novo Assembly for Metagenomes -- MoGUL: Detecting Common Insertions and Deletions in a Population -- Generalized Buneman Pruning for Inferring the Most Parsimonious Multi-state Phylogeny -- Seed Design Framework for Mapping SOLiD Reads -- Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments -- Cactus Graphs for Genome Comparisons -- IDBA – A Practical Iterative de Bruijn Graph De Novo Assembler -- Predicting Nucleosome Positioning Using Multiple Evidence Tracks -- Dense Subgraphs with Restrictions and Applications to Gene Annotation Graphs -- Time and Space Efficient RNA-RNA Interaction Prediction via Sparse Folding -- HLA Type Inference via Haplotypes Identical by Descent -- Algorithms for Detecting Significantly Mutated Pathways in Cancer -- Leveraging Sequence Classification by Taxonomy-Based Multitask Learning -- A Novel Abundance-Based Algorithm for Binning Metagenomic Sequences Using l-Tuples -- A Markov Random Field Framework for Protein Side-Chain Resonance Assignment -- Genomic DNA k-mer Spectra: Models and Modalities -- Deciphering the Swine-Flu Pandemics of 1918 and 2009 -- Distinguishing Direct versus Indirect Transcription Factor-DNA Interactions -- A Self-regulatory System of Interlinked Signaling Feedback Loops Controls Mouse Limb Patterning -- Automated High-Dimensional Flow Cytometric Data Analysis -- Discovering Transcriptional Modules by Combined Analysis of Expression Profiles and Regulatory Sequences.

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### Sommario/riassunto

This volume contains the papers presented at RECOMB 2010: the 14th Annual International Conference on Research in Computational Molecular Biology held in Lisbon, Portugal, during April 25–28, 2010. The RECOMB conference series was started in 1997 by Sorin Istrail, Pavel Pevzner, and Michael Waterman. RECOMB 2010 was hosted by INESC-ID and Instituto Superior Tecnico, organized by a committee chaired by Arlindo Oliveira and took place at the International Fair of Lisbon Meeting Centre. This year, 36 papers were accepted for presentation out of 176 submissions. The papers presented were selected by the Program Committee (PC) assisted by a number of external reviewers. Each paper was reviewed by three members of the PC, or by external reviewers, and there was an extensive Web-based discussion over a period of two weeks, leading to the final decisions. RECOMB 2010 also introduced a Highlights Track, in which six additional presentations by senior authors were chosen from papers published in 2009. The RECOMB conference series is closely associated with the Journal of Computational Biology, which traditionally publishes special issues devoted to

presenting full versions of selected conference papers.

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