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	Altri autori (Persone)	MiyanoSatoru
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	Lingua di pubblicazione	Inglese
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	Livello bibliografico	Monografia
	Note generali	"This volume contains the papers presented at the 9th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005)"--Pref.
	Nota di bibliografia	Includes bibliographical references and index.
	Nota di contenuto	Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks -- Efficient Algorithms for Detecting Signaling Pathways in Protein Interaction Networks -- Towards an Integrated Protein-Protein Interaction Network -- The Factor Graph Network Model for Biological Systems -- Pairwise Local Alignment of Protein Interaction Networks Guided by Models of Evolution -- Finding Novel Transcripts in High-Resolution Genome-Wide Microarray Data Using the GenRate Model -- Efficient Calculation of Interval Scores for DNA

Copy Number Data Analysis -- Keynote -- A Regulatory Network Controlling Drosophila Development -- Keynote -- Yeast Cells as a Discovery Platform for Neurodegenerative Disease -- RIBRA–An Error-Tolerant Algorithm for the NMR Backbone Assignment Problem -- Avoiding Local Optima in Single Particle Reconstruction -- A High-Throughput Approach for Associating microRNAs with Their Activity Conditions -- RNA-RNA Interaction Prediction and Antisense RNA Target Search -- Consensus Folding of Unaligned RNA Sequences Revisited -- Keynote -- Discovery and Annotation of Genetic Modules -- Efficient q-Gram Filters for Finding All ?-Matches over a Given Length -- A Polynomial Time Solvable Formulation of Multiple Sequence Alignment -- A Fundamental Decomposition Theory for Phylogenetic Networks and Incompatible Characters -- Reconstruction of Reticulate Networks from Gene Trees -- A Hybrid Micro-Macroevolutionary Approach to Gene Tree Reconstruction -- Constructing a Smallest Refining Galled Phylogenetic Network -- Keynote -- Mapping Molecular Landscapes Inside Cells -- Information Theoretic Approaches to Whole Genome Phylogenies -- Maximum Likelihood of Evolutionary Trees Is Hard -- Graph Theoretical Insights into Evolution of Multidomain Proteins -- Peptide Sequence Tags for FastDatabase Search in Mass-Spectrometry -- A Hidden Markov Model Based Scoring Function for Mass Spectrometry Database Search -- EigenMS: De Novo Analysis of Peptide Tandem Mass Spectra by Spectral Graph Partitioning -- Keynote -- Biology as Information -- Using Multiple Alignments to Improve Gene Prediction -- Learning Interpretable SVMs for Biological Sequence Classification -- Segmentation Conditional Random Fields (SCRFs): A New Approach for Protein Fold Recognition -- Rapid Protein Side-Chain Packing via Tree Decomposition -- Recognition of Binding Patterns Common to a Set of Protein Structures -- Predicting Protein-Peptide Binding Affinity by Learning Peptide-Peptide Distance Functions -- Keynote -- Amino Acid Sequence Control of the Folding of the Parallel ?-Helix, the Simplest ?-Sheet Fold -- A Practical Approach to Significance Assessment in Alignment with Gaps -- Alignment of Optical Maps -- Keynote -- Engineering Gene Regulatory Networks: A Reductionist Approach to Systems Biology -- Modeling the Combinatorial Functions of Multiple Transcription Factors -- Predicting Transcription Factor Binding Sites Using Structural Knowledge -- Motif Discovery Through Predictive Modeling of Gene Regulation -- HAPLOFREQ – Estimating Haplotype Frequencies Efficiently -- Improved Recombination Lower Bounds for Haplotype Data -- A Linear-Time Algorithm for the Perfect Phylogeny Haplotyping (PPH) Problem -- Keynote -- Human Genome Sequence Variation and the Inherited Basis of Common Disease -- Stability of Rearrangement Measures in the Comparison of Genome Sequences -- On Sorting by Translocations.

Sommario/riassunto	This volume contains the papers presented at the 9th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005), which was held in Cambridge, Massachusetts, on May 14–18, 2005. The RECOMB conference series was started in 1997 by Sorin Istrail, Pavel Pevzner and Michael Waterman. The list of previous meetings is shown below in the s- tion “Previous RECOMB Meetings. ” RECOMB 2005 was hosted by the Broad Institute of MIT and Harvard, and Boston University’s Center for Advanced - nomic Technology, and was excellently organized by the Organizing Committee Co-chairs Jill Mesirov and Simon Kasif. This year, 217 papers were submitted, of which the Program Committee - lected 39 for presentation at the meeting and inclusion in this proceedings. Each submission was refereed by at least three members of the Program

Committee. After the completion of the referees' reports, an extensive Web-based discussion took place for making decisions. From RECOMB 2005, the Steering Committee decided to publish the proceedings as a volume of Lecture Notes in Bioinf- matics (LNBI) for which the founders of RECOMB are also the editors. The prominent volume number LNBI 3500 was assigned to this proceedings. The RECOMB conference series is closely associated with the Journal of Compu- tional Biology which traditionally publishes special issues devoted to presenting full versions of selected conference papers. The RECOMB Program Committee consistedof42members,aslistedonaseparatepage. Iwouldliketothank the RECOMB 2005 Program Committee members for their dedication and hard work.