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Titolo	Computational Methods for SNPs and Haplotype Inference [[electronic resource]] : DIMACS/RECOMB Satellite Workshop, Piscataway, NJ, USA, November 21-22, 2002, Revised Papers / / edited by Sorin Istrail, Michael Waterman, Andrew Clark
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Collana	Lecture Notes in Bioinformatics ; ; 2983
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Soggetti	Biochemistry Algorithms Human genetics Computer science—Mathematics Mathematical statistics Database management Biochemistry, general Algorithm Analysis and Problem Complexity Human Genetics Discrete Mathematics in Computer Science Probability and Statistics in Computer Science Database Management
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Nota di bibliografia	Includes bibliographical references at the end of each chapters and index.
Nota di contenuto	Trisomic Phase Inference -- Trisomic Phase Inference -- An Overview of Combinatorial Methods for Haplotype Inference -- A Survey of Computational Methods for Determining Haplotypes -- Haplotype Inference and Its Application in Linkage Disequilibrium Mapping -- Inferring Piecewise Ancestral History from Haploid Sequences --

	Haplotype Blocks in Small Populations -- Simulating a Coalescent Process with Recombination and Ascertainment -- Dynamic Programming Algorithms for Haplotype Block Partitioning and Tag SNP Selection Using Haplotype Data or Genotype Data -- Parametric Bootstrap for Assessment of Goodness of Fit of Models for Block Haplotype Structure -- A Coalescent-Based Approach for Complex Disease Mapping -- Abstracts -- Haplotyping as Perfect Phylogeny -- Exhaustive Enumeration and Bayesian Phase Inference -- How Does Choice of Polymorphism Influence Estimation of LD and Mapping? -- Haplotype Inference in Random Population Samples -- Bayesian Methods for Statistical Reconstruction of Haplotypes -- Combinatorial Approaches to Haplotype Inference -- Large Scale Recovery of Haplotypes from Genotype Data Using Imperfect Phylogeny -- Haplotype Inference and Haplotype Information -- Multi-locus Linkage Disequilibrium and Haplotype-Based Tests of Association -- The Pattern of Polymorphism on Human Chromosome 21 -- Use of a Local Approximation to the Ancestral Recombination Graph for Fine Mapping Disease Genes -- Insights into Recombination from Patterns of Linkage Disequilibrium -- Joint Bayesian Estimation of Mutation Location and Age Using Linkage Disequilibrium -- Evolutionary-Based Association Analysis Using Haplotype Data -- Inferring Piecewise Ancestral History from Haploid Sequences -- Testing for Differences in Haplotype Frequencies in Case-Control Studies -- Haplotypes, Hotspots, and a Multilocus Model for Linkage Disequilibrium -- Dynamic Programming Algorithms for Haplotype Block Partition and Applications to Association Studies -- Genome Sharing in Small Populations -- Patterns of Linkage Disequilibrium across Human Chromosomes 6, 21, AND 22 -- A Software System for Automated and Visual Analysis of Functionally Annotated Haplotypes -- Assessment of Goodness of Fit of Models for Block Haplotype Structure.
Sommario/riassunto	This book constitutes the post-proceedings of the DIMACS/RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotype Inference held in Piscataway, NJ, USA, in November 2002. The book presents ten revised full papers as well as abstracts of the remaining workshop papers. All relevant current issues in computational methods for SNP and haplotype analysis and their applications to disease associations are addressed.