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| | Nota di contenuto | Yeast Ancestral Genome Reconstructions: The Possibilities of Computational Methods -- Natural Parameter Values for Generalized Gene Adjacency -- Parking Functions, Labeled Trees and DCJ Sorting Scenarios -- Counting All DCJ Sorting Scenarios -- Minimal Conflicting Sets for the Consecutive Ones Property in Ancestral Genome Reconstruction -- Finding Nested Common Intervals Efficiently -- DCJ Median Problems on Linear Multichromosomal Genomes: Graph |

Representation and Fast Exact Solutions -- Rearrangement Models and Single-Cut Operations -- Aligning Two Genomic Sequences That Contain Duplications -- Inferring the Recent Duplication History of a Gene Cluster -- Pseudo Boolean Programming for Partially Ordered Genomes -- Computing the Summed Adjacency Disruption Number between Two Genomes with Duplicate Genes Using Pseudo-Boolean Optimization -- Reconstructing Histories of Complex Gene Clusters on a Phylogeny -- Co-evolutionary Models for Reconstructing Ancestral Genomic Sequences: Computational Issues and Biological Examples -- Whole-Genome Analysis of Gene Conversion Events -- A Statistically Fair Comparison of Ancestral Genome Reconstructions, Based on Breakpoint and Rearrangement Distances -- Comparative Genomics and Extensive Recombinations in Phage Communities -- Properties of Sequence Conservation in Upstream Regulatory and Protein Coding Sequences among Paralogs in Arabidopsis thaliana -- Transcription Factor Binding Probabilities in Orthologous Promoters: An Alignment-Free Approach to the Inference of Functional Regulatory Targets.

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| Sommario/riassunto | This book constitutes the proceedings of the 7th RECOMB International Satellite Workshop on Comparative Genomics, RECOMB-CG 2009, Budapest, Hungary, in September 2009. This workshop is devoted to bringing together scientists working on all aspects of comparative genomics, from computer scientists, mathematicians and statisticians working on novel computational approaches for genome analysis and comparison, to biologists applying these computational tools to study the structure and the evolution of prokaryotic and eukaryotic genomes. The 19 papers presented were carefully reviewed and selected from 31 submissions. The papers illustrate the crucial role of comparative genomics in understanding genome function and address a broad variety of aspects, ranging from the inference of evolution in genetic regulatory networks to the divergent fates of gene and genome duplication events and to the importance of new computational approaches to unraveling the structural evolution of genomes. |