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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Algorithms for Exploring the Space of Gene Tree/Species Tree Reconciliations -- Limitations of Pseudogenes in Identifying Gene Losses -- Duplication Mechanism and Disruptions in Flanking Regions Influence the Fate of Mammalian Gene Duplicates -- Estimating the Relative Contributions of New Genes from Retrotransposition and Segmental Duplication Events during Mammalian Evolution -- Discovering Local Patterns of Co-evolution -- Ancestral Reconstruction by Asymmetric Wagner Parsimony over Continuous Characters and Squared Parsimony over Distributions -- An Alignment-Free Distance Measure for Closely Related Genomes -- Gene Team Tree: A Compact Representation of All Gene Teams -- Integrating Sequence and Topology for Efficient and Accurate Detection of Horizontal Gene Transfer -- An Evolutionary Study of the Human Papillomavirus Genomes -- An Algorithm for Inferring Mitogenome Rearrangements in

	a Phylogenetic Tree -- Perfect DCJ Rearrangement -- Sorting Genomes with Insertions, Deletions and Duplications by DCJ -- A Fast and Exact Algorithm for the Median of Three Problem—A Graph Decomposition Approach -- A Phylogenetic Approach to Genetic Map Refinement -- Sorting Cancer Karyotypes by Elementary Operations -- On Computing the Breakpoint Reuse Rate in Rearrangement Scenarios -- Hurdles Hardly Have to Be Heeded -- Internal Validation of Ancestral Gene Order Reconstruction in Angiosperm Phylogeny.
Sommario/riassunto	This book constitutes the refereed proceedings of the 6th RECOMB Comparative Genomics Satellite Workshop, RECOMB-CG 2008, held in Paris, France, in October 2008. The 19 revised full papers presented were carefully reviewed and selected from 48 initial 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.