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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Multi-break Rearrangements: From Circular to Linear Genomes -- A Pseudo-boolean Programming Approach for Computing the Breakpoint Distance Between Two Genomes with Duplicate Genes -- Improving Inversion Median Computation Using Commuting Reversals and Cycle Information -- Inferring a Duplication, Speciation and Loss History from a Gene Tree (Extended Abstract) -- How to Achieve an Equivalent Simple Permutation in Linear Time -- Baculovirus Phylogeny Based on Genome Rearrangements -- Learning Gene Regulatory Networks via Globally Regularized Risk Minimization -- Evolution of Tandemly Arrayed Genes in Multiple Species -- Selecting Genomes for Reconstruction of Ancestral Genomes -- A Heuristic Algorithm for Reconstructing Ancestral Gene Orders with Duplications -- Reconstructing an Inversion History in the Anopheles Gambiae Complex -- Recovering True Rearrangement Events on Phylogenetic Trees -- Parts of the Problem of Polyploids in Rearrangement Phylogeny -- A Rigorous Analysis of the Pattern of Intron Conservation Supports the

Coelomata Clade of Animals.
