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Soggetti	Biomathematics Bioinformatics Computer networks Computer science - Mathematics Application software Algorithms Mathematical and Computational Biology Computer Communication Networks Mathematics of Computing Computer and Information Systems Applications Design and Analysis of Algorithms Genòmica Bioinformàtica Congressos Llibres electrònics
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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	-- Phylogenetic Networks. -- Statistically Consistent Estimation of Rooted and Unrooted Level-1 Phylogenetic Networks from SNP data. -- Galled Perfect Transfer Networks. -- Homology and Phylogenetic Reconstruction. -- Inferring Transcript Phylogenies from Transcript Ortholog Clusters. -- Gene-Adjacency-Based Phylogenetics under a

Stochastic Gain-Loss Model. -- Tools for Evolution Reconstruction. -- REvolutionH-tl : Reconstruction of Evolutionary Histories tool. -- Gene tree parsimony in the presence of gene duplication, loss, and incomplete lineage sorting. -- Assessing the potential of gene tree parsimony for microbial phylogenomics. -- Genome Rearrangements. -- Maximum Alternating Balanced Cycle Decomposition and Applications in Sorting by Intergenic Operations Problems. -- On the Distribution of Synteny Blocks under a Neutral Model of Genome Dynamics. -- Sampling gene adjacencies and geodesic points of random genomes. -- Genome Evolution. -- Transcription factors across the Escherichia coli pangenome: a 3D perspective. -- Revisiting the effects of MDR1 Variants using computational approaches. -- Evidence of increased adaptation of Omicron SARS-CoV-2 codon to humans.

Sommario/riassunto

This book constitutes the proceedings of the 21st International Conference on Comparative Genomics, RECOMB-CG 2024, which was held in Boston, MA, USA, during April 27–28, 2024. The 13 full papers presented in this book were carefully reviewed and selected from 21 submissions. The papers are divided into the following topical sections: phylogenetic networks; homology and phylogenetic reconstruction; tools for evolution reconstruction; genome rearrangements; and genome evolution. .
