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Autore	Song Giltae
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Altri autori (Persone)	Song
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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
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di contenuto	Cancer genomics -- Novel Driver Mutations in GCB Lymphoma Patients That Affect Transcription Factors Binding. -- Inferring Phylogenetic Trees of Cancer Evolution from Longitudinal Single-Cell Copy Number Profiles. Homology and Reconciliation -- Tree decomposition for reconstructing ancestral RNA sequences of multiple families. -- Whole-genome duplication detection with phylogenomics reconciliation: a scalable approach. -- A Sankoff-Rousseau-like Algorithm for Minimizing Lateral Gene Transfers and Losses on Single Origin Characters. -- tMHG-Finder: Tree-guided Maximal Homologous Group Finder for Bacterial Genomes. Phylogenetics -- Phylogenetic Network Diversity Parameterized by Reticulation Number and Beyond.

-- On the robustness to gene tree rooting (or lack thereof) of triplet-based species tree estimation methods. -- Exact Counts of Binary Phylogenetic Networks with Two and Three Reticulation Events. -- Ancestral pangenomes and their phylogenetic reconstruction. -- QT-WEAVER: Correcting quartet distribution improves phylogenomic analyses despite gene tree estimation error. -- Fast calculation of cherry distance on level-1 orchard networks: optimization, heuristic and implementation. Sequence analysis -- Detecting and Mapping Local Model Violations During Biomolecular Sequence Analysis: a RE sampling and Visual EvALuation Approach. -- A simple way to find related sequences with position-specific probabilities. -- Position Specific Scoring Is All You Need? Revisiting Protein Sequence Classification Tasks. Epidemiology -- Residual immunity and seasonality of an epidemic. -- Adapting the cov2clusters tool for clustering MPOXV whole genome sequences. Genome evolution -- Probability-based sequence comparison finds the oldest ever nuclear mitochondrial DNA segments in mammalian genomes. -- Unraveling Insect Immunity: A Cross-Order Comparative Genomic Analysis of Key Immune Proteins. -- Analyzing Sequence Similarity Distributions in Salmonidae: A Branching Process Approach. -- Evolutionary Reconstruction of Hormone-bHLH Regulatory Networks in Solanaceae: Phylogenomic Insights from PSTVd-Tomato Interactions.

Sommario/riassunto

This book constitutes the proceedings of the 22nd International Conference on Comparative Genomics, RECOMB-CG 2025, which was held in Seoul, South Korea, during April 24–25, 2025. The 21 full papers presented in this book were carefully reviewed and selected from 27 submissions. The papers are divided into the following topical sections: Cancer Genomics; Homology and Reconciliation; Phylogenetics; Sequence Analysis; Epidemiology and Genome Evolution.
