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Collana	Lecture Notes in Bioinformatics, , 2366-6331 ; ; 12715
Disciplina	570.285
Soggetti	Data structures (Computer science) Information theory Artificial intelligence Image processing - Digital techniques Computer vision Computer science - Mathematics Mathematical statistics Discrete mathematics Numerical analysis Data Structures and Information Theory Artificial Intelligence Computer Imaging, Vision, Pattern Recognition and Graphics Probability and Statistics in Computer Science Discrete Mathematics in Computer Science Numerical Analysis
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Nota di contenuto	Learning Molecular Classes from Small Numbers of Positive Examples Using Graph Grammars -- Can We Replace Reads by Numeric Signatures? Lyndon Fingerprints as Representations of Sequencing Reads for Machine Learning -- Exploiting Variable Sparsity in Computing Equilibria of Biological Dynamical Systems by Triangular

Decomposition -- A Recovery Algorithm and Pooling Designs for One-Stage Noisy Group Testing Under the Probabilistic Framework -- Novel Phylogenetic Network Distances Based on Cherry Picking -- Best Match Graphs with Binary Trees -- Scalable and Accurate Phylogenetic Placement Using pplacer-XR -- Comparing Methods for Species Tree Estimation with Gene Duplication and Loss -- Reversal Distance on Genomes with Different Gene Content and Intergenic Regions Information -- Reversals Distance Considering Flexible Intergenic Regions Sizes -- Improved DNA-versus-Protein Homology Search for Protein Fossils -- The Maximum Weight Trace Alignment Merging Problem.

Sommario/riassunto

This book constitutes the proceedings of the 8th International Conference on Algorithms for Computational Biology, AlCoB 2020, was planned to be held in Missoula, MT, USA in June 2021. Due to the Covid-19 pandemic, AlCoB 2020 and AlCoB 2021 were merged and held on these dates together. AlCoB 2020 proceedings were published as LNBI 12099. The 12 full papers included in this volume were carefully reviewed and selected from 22 submissions. They were organized in topical sections on genomics, phylogenetics, and RNA-Seq and other biological processes. The scope of AlCoB includes topics of either theoretical or applied interest, namely: sequence analysis; sequence alignment; sequence assembly; genome rearrangement; regulatory motif finding; phylogeny reconstruction; phylogeny comparison; structure prediction; compressive genomics; proteomics: molecular pathways, interaction networks, mass spectrometry analysis; transcriptomics: splicing variants, isoform inference and quantification, differential analysis; next-generation sequencing: population genomics, metagenomics, metatranscriptomics, epigenomics; genome CD architecture; microbiome analysis; cancer computational biology; and systems biology.
