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Soggetti	Bioinformatics Arithmetic and logic units, Computer Algorithms Artificial intelligence Numerical analysis Computer science—Mathematics Computational Biology/Bioinformatics Arithmetic and Logic Structures Algorithm Analysis and Problem Complexity Artificial Intelligence Numeric Computing Discrete Mathematics in Computer Science
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Nota di contenuto	Invited Talk -- New Divide-and-Conquer Techniques for Large-Scale Phylogenetic Estimation -- Biological Networks and Graph Algorithms -- New Polynomial-Time Algorithm around the Scaffolding Problem -- Enumerating Dominant Pathways in Biological Networks by Information Flow Analysis -- Comparing Different Graphlet Measures for Evaluating Network Model Fits to BioGRID PPI Networks -- Graph-Theoretic Partitioning of RNAs and Classification of Pseudoknots -- PathRacer: Racing Profile HMM Paths on Assembly Graph -- Genome Rearrangement, Assembly and Classification -- A Uniform Theory of

Adequate Subgraphs for the Genome Median, Halving, and Aliquoting Problems -- Lightweight Metagenomic Classification via eBWT -- MULKSG: MULtiple K Simultaneous Graph Assembly -- Counting Sorting Scenarios and Intermediate Genomes for the Rank Distance -- Generalizations of the Genomic Rank Distance to Indels -- Sequence Analysis, Phylogenetics and Other Biological Processes -- Using INC within Divide-and-Conquer Phylogeny Estimation -- Predicting Methylation from Sequence and Gene Expression Using Deep Learning with Attention -- A Mathematical Model for Enhancer Activation Kinetics During Cell Differentiation -- Transcript Abundance Estimation and the Laminar Packing Problem -- Efficient Algorithms for Finding Edit-Distance Based Motifs.

Sommario/riassunto	This book constitutes the proceedings of the 6th InternationalConference on Algorithms for Computational Biology, AlCoB 2019, held in Berkeley, CA, USA, in May 2019. The 15 full papers presented together with 1 invited paper were carefully reviewed and selected from 30 submissions. They are organized in the following topical sections: Biological networks and graph algorithms; genome rearrangement, assembly and classification; sequence analysis, phylogenetics and other biological processes.