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	Nota di contenuto	Sorting -Permutations by -Operations -- Super Short Reversals on Both Gene Order and Intergenic Sizes -- Identifying Maximal Perfect Haplotype Blocks -- Sorting by Weighted Reversals and Transpositions -- Graph databases in Molecular Biology -- ViMT - Development of a Web-based Vivarium Management Tool -- An argumentation theory-based multiagent model to annotate proteins -- AutoModel: a client-server tool for intuitive and interactive homology modeling of protein-ligand complexes -- Detecting Acute Lymphoblastic Leukemia in Down

	Syndrome Patients using Convolutional Neural Networks on Preprocessed Mutated Datasets -- S2FS: Single score feature selection applied to the problem of distinguishing long non-coding RNAs from protein coding transcripts -- A Genetic Algorithm for Character State Live Phylogeny -- A workflow for predicting microRNAs targets via accessibility in Flavivirus genomes -- Parallel solution based on collective communication operations for phylogenetic bootstrapping in PhyML 3.0.
Sommario/riassunto	This book constitutes the refereed proceedings of the 11th Brazilian Symposium on Bioinformatics, BSB 2018, held in Rio de Janeiro, Brazil, in October/November 2018. The 13 revised full papers presented were carefully reviewed and selected from 26 submissions. The papers cover all aspects of bioinformatics and computational biology.