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	Nota di contenuto	The Trees in the Peaks -- Relating Bisimulations with Attractors in Boolean Network Models -- Neural Network Simulation of Feeding Adaptations of Daphnia -- Generating the Logicome of a Biological Network -- Counting, Generating and Sampling Tree Alignments -- A New Multi-Objective Approach for Molecular Docking Based on RMSD and Binding Energy -- Gibbs/MCMC Sampling for Multiple RNA Interaction with Sub-optimal Solutions -- Accumulated Coalescence Rank and Excess Gene Count for Species Tree Inference -- Bootstrapping Algorithms for Gene Duplication and Speciation Events -- Robustness of the Parsimonious Reconciliation Method in Cophylogeny -- Sorting with Forbidden Intermediates -- Evaluation

	and Improvement of Fast Algorithms for Exact Matching on Genome Sequences -- Identification of Variant Compositions in Related Strains without Reference -- New Error Tolerant Method for Search of Long Repeats in DNA Sequences.
Sommario/riassunto	This book constitutes the proceedings of the Third International Conference on Algorithms for Computational Biology, AlCoB 2016, held in Trujillo, Spain, in June 2016. The 13 full papers presented in this volume were carefully reviewed and selected from 23 submissions. They are organized in the following topical sections: biological networks and modelling; biological structure processing; phylogenetics; and sequence analysis and rearrangement. In addition one invited talk is included.