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Nota di contenuto	Intro -- Preface -- Organization -- Contents -- Efficient Alignment Free Sequence Comparison with Bounded Mismatches -- 1 Introduction -- 2 Key Concepts and Properties -- 3 An Overview of Our Algorithm -- 4 Constructing Sk -- 4.1 Analysis -- 5 Processing Sk -- 5.1 Proof of Lemma 6 -- 6 Conclusions -- A Ordering of Pairs -- References -- DockStar: A Novel ILP Based Integrative Method for Structural Modelling of Multimolecular Protein Complexes (Extended Abstract) -- References -- CRISPR Detection from Short Reads Using Partial Overlap Graphs -- 1 Introduction -- 2 Methods -- 2.1 Algorithm Overview -- 2.2 Identifying Frequent k-Mers -- 2.3 Analysis of Frequent k-Mers: Basic Observation -- 2.4 Data Indexing -- 2.5 Partial Construction of Overlap Graph -- 2.6 k-Mer Clustering -- 2.7 Repeat Consensus Derivation -- 3 Results -- 3.1 Simulated Reads Data -- 3.2 Real Reads Data -- 4 Conclusions and Future Work -- References -- HapTree-X: An Integrative Bayesian Framework for Haplotype Reconstruction from

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Sommario/riassunto	This book constitutes the refereed proceedings of the 19th Annual International Conference on Research in Computational Molecular Biology, RECOMB 2015, held in Warsaw, Poland, in April 2015. The 36 extended abstracts were carefully reviewed and selected from 170 submissions. They report on original research in all areas of computational molecular biology and bioinformatics.