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Nota di contenuto	Sorting by Reversals in Subquadratic Time -- Computational Problems in Perfect Phylogeny Haplotyping: Xor-Genotypes and Tag SNPs -- Sorting by Length-Weighted Reversals: Dealing with Signs and Circularity -- Optimizing Multiple Spaced Seeds for Homology Search -- Approximate Labelled Subtree Homeomorphism -- On the Average Sequence Complexity -- Approximate Point Set Pattern Matching on Sequences and Planes -- Finding Biclusters by Random Projections -- Real-Time String Matching in Sublinear Space -- On the k-Closest Substring and k-Consensus Pattern Problems -- A Trie-Based

Approach for Compacting Automata -- A Simple Optimal Representation for Balanced Parentheses -- Two Algorithms for LCS Consecutive Suffix Alignment -- Efficient Algorithms for Finding Submasses in Weighted Strings -- Maximum Agreement and Compatible Supertrees -- Polynomial-Time Algorithms for the Ordered Maximum Agreement Subtree Problem -- Small Phylogeny Problem: Character Evolution Trees -- The Protein Sequence Design Problem in Canonical Model on 2D and 3D Lattices -- A Computational Model for RNA Multiple Structural Alignment -- Computational Design of New and Recombinant Selenoproteins -- A Combinatorial Shape Matching Algorithm for Rigid Protein Docking -- Multi-seed Lossless Filtration -- New Results for the 2-Interval Pattern Problem -- A Linear-Time Algorithm for Computing Translocation Distance between Signed Genomes -- Sparse Normalized Local Alignment -- Quadratic Time Algorithms for Finding Common Intervals in Two and More Sequences -- Maximal Common Connected Sets of Interval Graphs -- Performing Local Similarity Searches with Variable Length Seeds -- Reversal Distance without Hurdles and Fortresses -- A Fast Set Intersection Algorithm for Sorted Sequences -- Faster Two Dimensional Pattern Matching with Rotations -- Compressed Compact Suffix Arrays -- Approximate String Matching Using Compressed Suffix Arrays -- Compressed Index for a Dynamic Collection of Texts -- Improved Single and Multiple Approximate String Matching -- Average-Case Analysis of Approximate Trie Search.