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Nota di contenuto	Sharper Upper and Lower Bounds for an Approximation Scheme for Consensus-Pattern -- On the Longest Common Rigid Subsequence Problem -- Text Indexing with Errors -- A New Compressed Suffix Tree Supporting Fast Search and Its Construction Algorithm Using Optimal Working Space -- Succinct Suffix Arrays Based on Run-Length Encoding -- Linear-Time Construction of Compressed Suffix Arrays Using o(n log n)-Bit Working Space for Large Alphabets -- Faster Algorithms for ?,?-Matching and Related Problems -- A Fast Algorithm for Approximate String Matching on Gene Sequences -- Approximate Matching in the L 1 Metric -- An Efficient Algorithm for Generating Super Condensed

Neighborhoods -- The Median Problem for the Reversal Distance in Circular Bacterial Genomes -- Using PQ Trees for Comparative Genomics -- Hardness of Optimal Spaced Seed Design -- Weighted Directed Word Graph -- Construction of Aho Corasick Automaton in Linear Time for Integer Alphabets -- An Extension of the Burrows Wheeler Transform and Applications to Sequence Comparison and Data Compression -- DNA Compression Challenge Revisited: A Dynamic Programming Approach -- On the Complexity of Sparse Exon Assembly -- An Upper Bound on the Hardness of Exact Matrix Based Motif Discovery -- Incremental Inference of Relational Motifs with a Degenerate Alphabet -- Speeding up Parsing of Biological Context-Free Grammars -- A New Periodicity Lemma -- Two Dimensional Parameterized Matching -- An Optimal Algorithm for Online Square Detection -- A Simple Fast Hybrid Pattern-Matching Algorithm -- Prefix-Free Regular-Expression Matching -- Reducing the Size of NFAs by Using Equivalences and Preorders -- Regular Expression Constrained Sequence Alignment -- A Linear Tree Edit Distance Algorithm for Similar Ordered Trees -- A Polynomial Time Matching Algorithm of Ordered Tree Patterns Having Height-Constrained Variables -- Assessing the Significance of Sets of Words -- Inferring a Graph from Path Frequency -- Exact and Approximation Algorithms for DNA Tag Set Design -- Parametric Analysis for Ungapped Markov Models of Evolution -- Linear Programming for Phylogenetic Reconstruction Based on Gene Rearrangements -- Identifying Similar Surface Patches on Proteins Using a Spin-Image Surface Representation -- Mass Spectra Alignments and Their Significance.