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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

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-- 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.