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Disciplina	004.0151
Soggetti	Computers Pattern perception Algorithms Information storage and retrieval Computer science—Mathematics Combinatorial analysis Theory of Computation Pattern Recognition Algorithm Analysis and Problem Complexity Information Storage and Retrieval Discrete Mathematics in Computer Science Combinatorics
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Nota di contenuto	An improved pattern matching algorithm for strings in terms of straight-line programs -- Episode matching -- Efficient algorithms for approximate string matching with swaps -- On the complexity of pattern matching for highly compressed two-dimensional texts -- Estimating the probability of approximate matches -- Space- and time-efficient decoding with canonical huffman trees -- On weak circular squares in binary words -- An easy case of sorting by reversals -- External inverse pattern matching -- Distributed generation of suffix arrays -- Direct construction of compact directed acyclic word graphs

-- Approximation algorithms for the fixed-topology phylogenetic number problem -- A new algorithm for the ordered tree inclusion problem -- On incremental computation of transitive closure and greedy alignment -- Aligning coding DNA in the presence of frame-shift errors -- A filter method for the weighted local similarity search problem -- Trie-based data structures for sequence assembly -- Flexible identification of structural objects in nucleic acid sequences: Palindromes, mirror repeats, pseudoknots and triple helices -- Banishing bias from consensus sequences -- On the Nadeau-Taylor theory of conserved chromosome segments -- Iterative versus simultaneous multiple sequence alignment -- Modern comparative lexicostatistics.

Sommario/riassunto

This book constitutes the refereed proceedings of the Eighth Annual Symposium on Combinatorial Pattern Matching, CPM 97, held in Aarhus, Denmark, in June/July 1997. The volume presents 20 revised full papers carefully selected from 32 submissions received; also included are abstracts of two invited contributions. The volume is devoted to the issue of searching and matching strings and more complicated patterns, such as trees, regular expressions, graphs, point sets and arrays. The results presented are particularly relevant to molecular biology, but also to information retrieval, pattern recognition, compiling, data compression and program analysis.
