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Collana	Lecture Notes in Computer Science, , 0302-9743 ; ; 807
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Soggetti	<p>Pattern recognition</p> <p>Discrete mathematics</p> <p>Algorithms</p> <p>Information storage and retrieval</p> <p>Coding theory</p> <p>Information theory</p> <p>Combinatorics</p> <p>Pattern Recognition</p> <p>Discrete Mathematics</p> <p>Algorithm Analysis and Problem Complexity</p> <p>Information Storage and Retrieval</p> <p>Coding and Information Theory</p>
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Formato	Materiale a stampa
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Note generali	Bibliographic Level Mode of Issuance: Monograph
Nota di contenuto	A space efficient algorithm for finding the best non-overlapping alignment score -- The parameterized complexity of sequence alignment and consensus -- Computing all suboptimal alignments in linear space -- Approximation algorithms for multiple sequence alignment -- A context dependent method for comparing sequences -- Fast identification of approximately matching substrings -- Alignment of trees — An alternative to tree edit -- Parametric recomputing in alignment graphs -- A lossy data compression based on string matching: Preliminary analysis and suboptimal algorithms -- A text

compression scheme that allows fast searching directly in the compressed file -- An alphabet-independent optimal parallel search for three dimensional pattern -- Unit route upper bound for string-matching on hypercube -- Computation of squares in a string -- Minimization of sequential transducers -- Shortest common superstrings for strings of random letters -- Maximal common subsequences and minimal common supersequences -- Dictionary-matching on unbounded alphabets: Uniform length dictionaries -- Proximity matching using fixed-queries trees -- Query primitives for tree-structured data -- Multiple matching of parameterized patterns -- Approximate string matching with don't care characters -- Matching with matrix norm minimization -- Approximate string matching and local similarity -- Polynomial-time algorithms for computing characteristic strings -- Recent methods for RNA modeling using stochastic context-free grammars -- Efficient bounds for oriented chromosome inversion distance.

Sommario/riassunto

This volume presents the proceedings of the Fifth Annual Symposium on Combinatorial Pattern Matching, held at Asilomar, California, in June 1994. The 26 selected papers in this volume are organized in chapters on Alignments, Various Matchings, Combinatorial Aspects, and Bio-Informatics. Combinatorial Pattern Matching addresses issues of searching and matching of strings and more complicated patterns, as for example trees. The goal is to derive non-trivial combinatorial properties for such structures and then to exploit these properties in order to achieve superior performance for the corresponding computational problems. In recent years, combinatorial pattern matching has developed into a full-fledged area of algorithmics and is expected to grow even further during the next years.
