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Soggetti	<p>Pattern recognition</p> <p>Algorithms</p> <p>Natural language processing (Computer science)</p> <p>Information storage and retrieval</p> <p>Coding theory</p> <p>Information theory</p> <p>Combinatorics</p> <p>Pattern Recognition</p> <p>Algorithm Analysis and Problem Complexity</p> <p>Natural Language Processing (NLP)</p> <p>Information Storage and Retrieval</p> <p>Coding and Information Theory</p>
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Nota di contenuto	A linear time pattern matching algorithm between a string and a tree -- Tight comparison bounds for the string prefix-matching problem -- 3-D docking of protein molecules -- Minimal separators of two words -- Covering a string -- On the worst-case behaviour of some approximation algorithms for the shortest common supersequence of k strings -- An algorithm for locating non-overlapping regions of maximum alignment score -- Exact and approximation algorithms for the inversion distance between two chromosomes -- The maximum

weight trace problem in multiple sequence alignment -- An algorithm for approximate tandem repeats -- Two dimensional pattern matching in a digitized image -- Analysis of a string edit problem in a probabilistic framework -- Detecting false matches in string matching algorithms -- On suboptimal alignments of biological sequences -- A fast filtration algorithm for the substring matching problem -- A unifying look at d-dimensional periodicities and space coverings -- Approximate string-matching over suffix trees -- Multiple sequence comparison and n-dimensional image reconstruction -- A new editing based distance between unordered labeled trees.

Sommario/riassunto

The papers contained in this volume were presented at the Fourth Annual Symposium on Combinatorial Pattern Matching, held in Padova, Italy, in June 1993. Combinatorial pattern matching addresses issues of searching and matching of strings and more complicated patterns such as trees, regular expressions, extended expressions, etc. The goal is to derive nontrivial 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, a steady flow of high-quality scientific studies of this subject has changed a sparse set of isolated results into a full-fledged area of algorithmics. The area is expected to grow even further due to the increasing demand for speed and efficiency that comes especially from molecular biology and the Genome project, but also from other diverse areas such as information retrieval, pattern recognition, compilers, data compression, and program analysis.
