

1. Record Nr.	UNINA9910143870803321
Titolo	Combinatorial pattern matching : 14th annual symposium, CPM 2003, Morelia, Michoacan, Mexico, June 25-27, 2003 : proceedings. // Ricardo Baeza-Yates, Edgar Chavez, Maxime Crochemore (editors)
Pubbl/distr/stampa	Berlin : , : Springer, , [2003] 2003
ISBN	1-280-80486-6 9786610804863 3-540-44888-8
Edizione	[1st ed. 2003.]
Descrizione fisica	1 online resource (411 p.)
Collana	Lecture notes in computer science ; ; 2676
Disciplina	005.1
Soggetti	Computer algorithms
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Multiple Genome Alignment: Chaining Algorithms Revisited -- Two-Dimensional Pattern Matching with Rotations -- An Improved Algorithm for Generalized Comparison of Minisatellites -- Optimal Spaced Seeds for Hidden Markov Models, with Application to Homologous Coding Regions -- Fast Lightweight Suffix Array Construction and Checking -- Distributed and Paged Suffix Trees for Large Genetic Databases -- Analysis of Tree Edit Distance Algorithms -- An Exact and Polynomial Distance-Based Algorithm to Reconstruct Single Copy Tandem Duplication Trees -- Average-Optimal Multiple Approximate String Matching -- Optimal Partitions of Strings: A New Class of Burrows-Wheeler Compression Algorithms -- Haplotype Inference by Pure Parsimony -- A Simpler 1.5-Approximation Algorithm for Sorting by Transpositions -- Efficient Data Structures and a New Randomized Approach for Sorting Signed Permutations by Reversals -- Linear-Time Construction of Suffix Arrays -- Space Efficient Linear Time Construction of Suffix Arrays -- Tuning String Matching for Huge Pattern Sets -- Sparse LCS Common Substring Alignment -- On Minimizing Pattern Splitting in Multi-track String Matching -- Alignment between Two Multiple Alignments -- An Effective Algorithm for the Peptide De Novo Sequencing from MS/MS Spectrum -- Pattern

Discovery in RNA Secondary Structure Using Affix Trees -- More
Efficient Left-to-Right Pattern Matching in Non-sequential Equational
Programs -- Complexities of the Centre and Median String Problems --
Extracting Approximate Patterns -- A Fully Linear-Time Approximation
Algorithm for Grammar-Based Compression -- Constrained Tree
Inclusion -- Working on the Problem of Sorting by Transpositions on
Genome Rearrangements -- Efficient Selection of Unique and Popular
Oligos for Large EST Databases.
