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| Soggetti                | <p>Pattern perception</p> <p>Algorithms</p> <p>Data structures (Computer science)</p> <p>Computer science—Mathematics</p> <p>Information storage and retrieval</p> <p>Natural language processing (Computer science)</p> <p>Pattern Recognition</p> <p>Algorithm Analysis and Problem Complexity</p> <p>Data Structures</p> <p>Discrete Mathematics in Computer Science</p> <p>Information Storage and Retrieval</p> <p>Natural Language Processing (NLP)</p>   |
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| Nota di bibliografia    | Includes bibliographical references at the end of each chapters and index.  |
| Nota di contenuto       | <p>Sorting by Reversals in Subquadratic Time -- Computational Problems in Perfect Phylogeny Haplotyping: Xor-Genotypes and Tag SNPs --</p> <p>Sorting by Length-Weighted Reversals: Dealing with Signs and Circularity -- Optimizing Multiple Spaced Seeds for Homology Search -- Approximate Labelled Subtree Homeomorphism -- On the Average Sequence Complexity -- Approximate Point Set Pattern Matching on Sequences and Planes -- Finding Biclusters by Random Projections -- Real-Time String Matching in Sublinear Space -- On the k-Closest Substring and k-Consensus Pattern Problems -- A Trie-Based</p> |

Approach for Compacting Automata -- A Simple Optimal Representation for Balanced Parentheses -- Two Algorithms for LCS Consecutive Suffix Alignment -- Efficient Algorithms for Finding Submasses in Weighted Strings -- Maximum Agreement and Compatible Supertrees -- Polynomial-Time Algorithms for the Ordered Maximum Agreement Subtree Problem -- Small Phylogeny Problem: Character Evolution Trees -- The Protein Sequence Design Problem in Canonical Model on 2D and 3D Lattices -- A Computational Model for RNA Multiple Structural Alignment -- Computational Design of New and Recombinant Selenoproteins -- A Combinatorial Shape Matching Algorithm for Rigid Protein Docking -- Multi-seed Lossless Filtration -- New Results for the 2-Interval Pattern Problem -- A Linear-Time Algorithm for Computing Translocation Distance between Signed Genomes -- Sparse Normalized Local Alignment -- Quadratic Time Algorithms for Finding Common Intervals in Two and More Sequences -- Maximal Common Connected Sets of Interval Graphs -- Performing Local Similarity Searches with Variable Length Seeds -- Reversal Distance without Hurdles and Fortresses -- A Fast Set Intersection Algorithm for Sorted Sequences -- Faster Two Dimensional Pattern Matching with Rotations -- Compressed Compact Suffix Arrays -- Approximate String Matching Using Compressed Suffix Arrays -- Compressed Index for a Dynamic Collection of Texts -- Improved Single and Multiple Approximate String Matching -- Average-Case Analysis of Approximate Trie Search.

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#### Sommario/riassunto

The 15th Annual Symposium on Combinatorial Pattern Matching was held in Ciragan Palace Hotel, Istanbul, Turkey during July 5-7, 2004. CPM 2004 - peated the success of its predecessors; it even surpassed them in terms of the numberofinvitedspeakers, thenumberofsubmissions,andthenumberofpapers accepted and presented at the conference. In response to the call for papers, CPM 2004 received a record number of 79 high-quality submissions. Each submission was reviewed by at least three program committee members and the comments were returned to the authors. Following an extensive electronic discussion period, the Program Committee accepted36ofthesubmissionstobepresentedattheconference. Theyconstitute originalresearchcontributionsincombinatorialpatternmatchingalgorithm sand datastructures,molecularsequenceanalysis, phylogenetictreeconstruction,and RNA and protein structure analysis and prediction. CPM 2004 had 7ve invited speakers. In alphabetical order they were: Evan Eichler from the University of Washington, USA, Martin Farach-Colton from Rutgers University, USA, Paolo Ferragina from the University of Pisa, Italy, Piotr Indyk from MIT, USA, and Gene Myers from the University of California, Berkeley, USA. It is impossible to organize such a successful program without the help of many individuals. We would like to express our appreciation to the authors of the submitted papers and to the program committee members and external referees, who provided timely and signi'cant reviews. July 2004 S.C. Sahinalp, S. Muthukrishnan, U. Dogrusoz Organization CPM 2004 was locally organized by Bilkent University, Ankara, Turkey. Within Bilkent University, the Center for Bioinformatics (BCBI) and the Computer Engineering Department cooperated.

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