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Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	Invited Talks (Abstracts) -- A Combinatorial Approach to Genome-Wide Ortholog Assignment: Beyond Sequence Similarity Search -- Stringology: Some Classic and Some Modern Problems -- Algorithmic Problems in Scheduling Jobs on Variable-Speed Processors -- Session 1: Alogirthmic Techniques I -- Speeding Up HMM Decoding and Training by Exploiting Sequence Repetitions -- On Demand String Sorting over Unbounded Alphabets -- Session 2: Approximate Pattern Matching -- Finding Witnesses by Peeling -- Cache-Oblivious Index for Approximate String Matching -- Improved Approximate String Matching and Regular Expression Matching on Ziv-Lempel Compressed Texts -- Self-normalised Distance with Don’t Cares -- Session 3: Data

Compression I -- Move-to-Front, Distance Coding, and Inversion Frequencies Revisited -- A Lempel-Ziv Text Index on Secondary Storage -- Dynamic Rank-Select Structures with Applications to Run-Length Encoded Texts -- Most Burrows-Wheeler Based Compressors Are Not Optimal -- Session 4: Computational Biology I -- Non-breaking Similarity of Genomes with Gene Repetitions -- A New and Faster Method of Sorting by Transpositions -- Finding Compact Structural Motifs -- Session 5: Computational Biology II -- Improved Algorithms for Inferring the Minimum Mosaic of a Set of Recombinants -- Computing Exact p-Value for Structured Motif -- Session 6: Algorithmic Techniques II -- Improved Sketching of Hamming Distance with Error Correcting -- Deterministic Length Reduction: Fast Convolution in Sparse Data and Applications -- Guided Forest Edit Distance: Better Structure Comparisons by Using Domain-knowledge -- Space-Efficient Algorithms for Document Retrieval -- Session 7: Data Compression II -- Compressed Text Indexes with Fast Locate -- Processing Compressed Texts: A Tractability Border -- Session 8: Computational Biology III -- Common Structured Patterns in Linear Graphs: Approximation and Combinatorics -- Identification of Distinguishing Motifs -- Algorithms for Computing the Longest Parameterized Common Subsequence -- Fixed-Parameter Tractability of the Maximum Agreement Supertree Problem -- Session 9: Pattern Analysis -- Two-Dimensional Range Minimum Queries -- Tiling Periodicity -- Fast and Practical Algorithms for Computing All the Runs in a String -- Longest Common Separable Pattern Among Permutations -- Session 10: Suffix Arrays and Trees -- Suffix Arrays on Words -- Efficient Computation of Substring Equivalence Classes with Suffix Arrays -- A Simple Construction of Two-Dimensional Suffix Trees in Linear Time.

Sommario/riassunto

The papers contained in this volume were presented at the 18th Annual S- posium on Combinatorial Pattern Matching (CPM 2007) held at the University of Western Ontario, in London, Ontario, Canada from July 9 to 11, 2007. All the papers presented at the conference are original research contri- tions on computational pattern matching and analysis, data compression and compressed text processing, su?x arrays and trees, and computational biology. They were selected from 64 submissions. Each submission was reviewed by at least three reviewers. The committee decided to accept 32 papers. The p- gramme also included three invited talks by Tao Jiang from the University of California, Riverside, USA, S. Muthukrishnan from Rutgers University, USA, and Frances Yao from City University of Hong Kong, Hong Kong. Combinatorial Pattern Matching addresses issues of searching and matching stringsandmorecomplicatedpatternssuchastrees, regularexpressions,graphs, point sets, and arrays.The goal is to derive non-trivial combinatorial properties of such structures and to exploit these properties in order to either achieve superior performance for the corresponding computational problems or pinpoint conditions under which searches cannot be performed e?ciently.