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	Nota di contenuto	Asynchronous Pattern Matching -- Asynchronous Pattern Matching -- SNP and Haplotype Analysis – Algorithms and Applications -- Identifying Co-referential Names Across Large Corpora -- Session 1. Data Structures -- Adaptive Searching in Succinctly Encoded Binary Relations and Tree-Structured Documents -- Theoretical and Practical Improvements on the RMQ-Problem, with Applications to LCA and LCE -- Session 2. Indexing Data Structures -- A Linear Size Index for Approximate Pattern Matching -- On-Line Linear-Time Construction of Word Suffix Trees -- Obtaining Provably Good Performance from Suffix Trees in Secondary Storage -- Geometric Suffix Tree: A New Index Structure for Protein 3-D Structures -- Session 3. Probabilistic and

Algebraic Techniques -- New Bounds for Motif Finding in Strong Instances -- Fingerprint Clustering with Bounded Number of Missing Values -- Tiling an Interval of the Discrete Line -- Common Substrings in Random Strings -- Session 4. Applications in Molecular Biology I -- On the Repeat-Annotated Phylogenetic Tree Reconstruction Problem -- Subsequence Combinatorics and Applications to Microarray Production, DNA Sequencing and Chaining Algorithms -- Solving the Maximum Agreement SubTree and the Maximum Compatible Tree Problems on Many Bounded Degree Trees -- An Improved Algorithm for the Macro-evolutionary Phylogeny Problem -- Session 5. String Matching I -- Property Matching and Weighted Matching -- Faster Two Dimensional Scaled Matching -- Session 6. Applications in Molecular Biology II -- Approximation of RNA Multiple Structural Alignment -- Finding Common RNA Pseudoknot Structures in Polynomial Time -- A Compact Mathematical Programming Formulation for DNA Motif Finding -- Local Alignment of RNA Sequences with Arbitrary Scoring Schemes -- Session 7. Applications in MolecularBiology III -- An Algorithm for Sorting by Reciprocal Translocations -- Longest Common Subsequences in Permutations and Maximum Cliques in Circle Graphs -- Session 8. Data Compression -- A Simpler Analysis of Burrows-Wheeler Based Compression -- Statistical Encoding of Succinct Data Structures -- Dynamic Entropy-Compressed Sequences and Full-Text Indexes -- Reducing the Space Requirement of LZ-Index -- Session 9. String Matching II -- Faster Algorithms for Computing Longest Common Increasing Subsequences -- New Algorithms for Text Fingerprinting -- Sublinear Algorithms for Parameterized Matching -- Approximate Matching in Weighted Sequences -- Session 10. Dynamic Programming -- Algorithms for Finding a Most Similar Subforest -- Efficient Algorithms for Regular Expression Constrained Sequence Alignment -- Large Scale Matching for Position Weight Matrices.

Sommario/riassunto

This book constitutes the refereed proceedings of the 17th Annual Symposium on Combinatorial Pattern Matching, CPM 2006, held in Barcelona, Spain, July 2006. The book presents 33 revised full papers together with 3 invited talks, organized in topical sections on data structures, indexing data structures, probabilistic and algebraic techniques, applications in molecular biology, string matching, data compression, and dynamic programming.