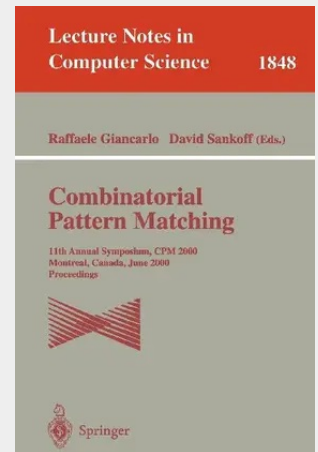


## Combinatorial Pattern Matching

11th Annual Symposium. CPM 2000, Montreal, Canada, June 21-23, 2000, Proceedings

The papers contained in this volume were presented at the 11th Annual Symposium on Combinatorial Pattern Matching, held June 21-23, 2000 at the Université de Montréal. They were selected from 44 abstracts submitted in response to the call for papers. In addition, there were invited lectures by Andrei Broder (AltaVista), Fernando Pereira (AT&T Research Labs), and Ian H. Witten (University of Waikato). The symposium was preceded by a two-day summer school set up to attract and train young researchers. The lecturers at the school were Greg Butler, Clement Lam, and Gus Grahne: BLAST! How do you search sequenced databases?, David Bryant: Phylogeny, Raffaele Giancarlo: Algorithmic aspects of speech recognition, Nadia El-Mabrouk: Genome rearrangement, Laxmi Parida: Flexible pattern discovery, and Ian H. Witten: Adaptive text mining: inferring structure from sequences. Combinatorial Pattern Matching (CPM) addresses issues of searching and matching strings and more complicated patterns such as trees, regular expressions, 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 achieve superior performance for the corresponding computational problems. Over recent years a steady flow of high-quality research on this subject has changed a sparse set of isolated results into a fully-fledged area of algorithmics.

Invited Lectures.- Identifying and Filtering Near-Duplicate Documents.- Machine Learning for Efficient Natural-Language Processing.- Browsing around a Digital Library: Today and Tomorrow.- Summer School Lectures.- Algorithmic Aspects of Speech Recognition: A Synopsis.- Some Results on Flexible-Pattern Discovery.- Contributed Papers.- Explaining and Controlling Ambiguity in Dynamic Programming.- A Dynamic Edit Distance Table.- Parametric Multiple Sequence Alignment and Phylogeny Construction.- Tsukuba BB: A Branch and Bound Algorithm for Local Multiple Sequence Alignment.- A Polynomial Time Approximation Scheme for the Closest Substring Problem.- Approximation Algorithms for Hamming Clustering Problems.- Approximating the Maximum Isomorphic Agreement Subtree Is Hard.- A Faster and Unifying Algorithm for Comparing Trees.- Incomplete Directed Perfect Phylogeny.- The Longest Common Subsequence Problem for Arc-Annotated Sequences.- Boyer-Moore String Matching over Ziv-Lempel Compressed Text.- A Boyer-Moore Type Algorithm for Compressed Pattern Matching.- Approximate String Matching over Ziv-Lempel Compressed Text.- Improving Static Compression Schemes by Alphabet Extension.- Genome Rearrangement by Reversals and Insertions/Deletions of Contiguous Segments.- A Lower Bound for the Breakpoint Phylogeny Problem.- Structural Properties and Tractability Results for Linear Synteny.- Shift Error Detection in Standardized Exams.- An Upper Bound for Number of Contacts in the HP-Model on the Face-Centered-Cubic Lattice (FCC).- The Combinatorial Partitioning Method.- Compact Suffix Array.- Linear Bidirectional On-Line Construction of Affix Trees.- Using Suffix Trees for Gapped Motif Discovery.- Indexing Text with Approximate q-Grams.- Simple Optimal String Matching Algorithm.- Exact and Efficient Computation of the Expected Number of Missing and Common Words in Random Texts.- Periods and Quasiperiods Characterization.- Finding Maximal Quasiperiodicities in Strings.- On the Complexity of Determining the Period of a String.



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