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Nota di contenuto	ALGORITHMS INCOMPUTATIONALMOLECULAR BIOLOGY; CONTENTS; PREFACE; CONTRIBUTORS; I STRINGS PROCESSING AND APPLICATION TO BIOLOGICAL SEQUENCES; 1 STRING DATA STRUCTURES FOR COMPUTATIONAL MOLECULAR BIOLOGY; 1.1 Introduction; 1.2 Main String Indexing Data Structures; 1.2.1 Suffix Trees; 1.2.2 Suffix Arrays; 1.3 Index Structures for Weighted Strings; 1.4 Index Structures for Indeterminate Strings; 1.5 String Data Structures in Memory Hierarchies; 1.6 Conclusions; References; 2 EFFICIENT RESTRICTED-CASE ALGORITHMS FOR PROBLEMS IN COMPUTATIONAL BIOLOGY; 2.1 The Need for Special Cases 2.2 Assessing Efficient Solvability Options for General Problems and Special Cases2.3 String and Sequence Problems; 2.4 Shortest Common Superstring; 2.4.1 Solving the General Problem; 2.4.2 Special Case: SCSt for Short Strings Over Small Alphabets; 2.4.3 Discussion; 2.5 Longest Common Subsequence; 2.5.1 Solving the General Problem; 2.5.2 Special Case: LCS of Similar Sequences; 2.5.3 Special Case: LCS Under Symbol-Occurrence Restrictions; 2.5.4 Discussion; 2.6 Common Approximate Substring; 2.6.1 Solving the General Problem; 2.6.2

Special Case: Common Approximate String; 2.6.3 Discussion
2.7 ConclusionReferences; 3 FINITE AUTOMATA IN PATTERN MATCHING; 3.1 Introduction; 3.1.1 Preliminaries; 3.2 Direct Use of DFA in Stringology; 3.2.1 Forward Automata; 3.2.2 Degenerate Strings; 3.2.3 Indexing Automata; 3.2.4 Filtering Automata; 3.2.5 Backward Automata; 3.2.6 Automata with Fail Function; 3.3 NFA Simulation; 3.3.1 Basic Simulation Method; 3.3.2 Bit Parallelism; 3.3.3 Dynamic Programming; 3.3.4 Basic Simulation Method with Deterministic State Cache; 3.4 Finite Automaton as Model of Computation; 3.5 Finite Automata Composition; 3.6 Summary; References
4 NEW DEVELOPMENTS IN PROCESSING OF DEGENERATE SEQUENCES4.1 Introduction; 4.1.1 Degenerate Primer Design Problem; 4.2 Background; 4.3 Basic Definitions; 4.4 Repetitive Structures in Degenerate Strings; 4.4.1 Using the Masking Technique; 4.4.2 Computing the Smallest Cover of the Degenerate String x; 4.4.3 Computing Maximal Local Covers of x; 4.4.4 Computing All Covers of x; 4.4.5 Computing the Seeds of x; 4.5 Conservative String Covering in Degenerate Strings; 4.5.1 Finding Constrained Pattern p in Degenerate String T; 4.5.2 Computing ?-Conservative Covers of Degenerate Strings
4.5.3 Computing ?-Conservative Seeds of Degenerate Strings4.6 Conclusion; References; 5 EXACT SEARCH ALGORITHMS FOR BIOLOGICAL SEQUENCES; 5.1 Introduction; 5.2 Single Pattern Matching Algorithms; 5.2.1 Algorithms for DNA Sequences; 5.2.2 Algorithms for Amino Acids; 5.3 Algorithms for Multiple Patterns; 5.3.1 Trie-Based Algorithms; 5.3.2 Filtering Algorithms; 5.3.3 Other Algorithms; 5.4 Application of Exact Set Pattern Matching for Read Mapping; 5.4.1 MPSCAN: An Efficient Exact Set Pattern Matching Tool for DNA/RNA Sequences; 5.4.2 Other Solutions for Mapping Reads
5.4.3 Comparison of Mapping Solutions

Sommario/riassunto

This book represents the most comprehensive and up-to-date collection of information on the topic of computational molecular biology. Bringing the most recent research into the forefront of discussion, Algorithms in Computational Molecular Biology studies the most important and useful algorithms currently being used in the field, and provides related problems. It also succeeds where other titles have failed, in offering a wide range of information from the introductory fundamentals right up to the latest, most advanced levels of study.