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Nota di contenuto	ALGORITHMS IN COMPUTATIONAL MOLECULAR BIOLOGY; CONTENTS; PREFACE; CONTRIBUTORS; 1 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 Cases 2.3 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

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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.
