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Autore	Raghavarao Damaraju
Titolo	Block designs [[electronic resource]] : analysis, combinatorics, and applications / / Damaraju Raghavarao, Lakshmi V. Padgett
Pubbl/distr/stampa	New Jersey, : World Scientific, 2005
ISBN	1-281-88125-2 9786611881252 981-270-109-5
Descrizione fisica	1 online resource (224 p.)
Collana	Series on applied mathematics ; ; v. 17
Altri autori (Persone)	PadgettLakshmi V
Disciplina	519.5/7
Soggetti	Block designs Experimental design
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and indexes.
Nota di contenuto	Contents; Preface; 1. Linear Estimation and Tests for Linear Hypotheses; 2. General Analysis of Block Designs; 3. Randomized Block Designs; 4. Balanced Incomplete Block Designs- Analysis and Combinatorics; 5. Balanced Incomplete Block Designs- Applications; 6. t-Designs; 7. Linked Block Designs; 8. Partially Balanced Incomplete Block Designs; 9. Lattice Designs; 10. Miscellaneous Designs; References and Selected Bibliography; Author Index; Subject Index
Sommario/riassunto	Combinatorial mathematicians and statisticians have made a wide range of contributions to the development of block designs, and this book brings together much of that work. The designs developed for a specific problem are used in a variety of different settings. Applications include controlled sampling, randomized response, validation and valuation studies, intercropping experiments, brand cross-effect designs, lotto and tournaments. The intra- and inter- block, nonparametric and covariance analysis are discussed for general block designs, and the concepts of connectedness, orthogonality, and

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Titolo	Algorithms in computational molecular biology : techniques, approaches and applications / / edited by Mourad Elloumi, Albert Y. Zomaya
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ISBN	9786612939631 9781282939639 1282939637 9780470892091 0470892099 9780470892107 0470892102
Descrizione fisica	1 online resource (1085 p.)
Collana	Wiley series on bioinformatics
Altri autori (Persone)	ElloumiMourad ZomayaAlbert Y
Disciplina	572.80285
Soggetti	Biophysics - Mathematical models
Lingua di pubblicazione	Inglese
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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.