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Nota di contenuto	Title Page; Copyright; Table of Contents; Preface; Chapter 1: Introduction; 1.1 Motivation; 1.2 The Organization of this Book; 1.3 Sequence Fundamentals; Chapter 2: Protein/DNA/RNA Pairwise Sequence Alignment; 2.1 Sequence Alignment Fundamentals; 2.2 Dot-Plot Matrix; 2.3 Dynamic Programming; 2.4 Word Method; 2.5 Searching Sequence Databases; References; Chapter 3: Quantifying Sequence Alignments; 3.1 Evolution and Measuring Evolution; 3.2 Substitution Matrices and Scoring Matrices; 3.3 GAPS; 3.4 Scoring Multiple Sequence Alignments; 3.5 Circular Sum Score; 3.6 Conservation Score Schemes 3.7 Diversity Scoring Schemes 3.8 Stereochemical Property Methods; 3.9 Hierarchical Expected Matching Probability Scoring Metric (HEP); Chapter 4: Sequence Clustering; 4.1 Unweighted Pair Group Method with Arithmetic Mean - UPGMA; 4.2 Neighborhood-Joining Method - NJ; 4.3 Overlapping Sequence Clustering; Chapter 5: Multiple Sequences Alignment Algorithms; 5.1 Dynamic Programming; 5.2 Progressive Alignment; 5.3 Consistency and Probabilistic MSA; 5.4 Genetic Algorithms; 5.5 New Development in Multiple Sequence Alignment Algorithms; 5.6 Test Data and Alignment Methods; 5.7 Results Chapter 6: Phylogeny in Multiple Sequence Alignments 6.1 The Tree of

Life; 6.2 Phylogeny Construction; 6.3 Inferring Phylogeny from Multiple Sequence Alignments; Chapter 7: Multiple Sequence Alignment on High-Performance Computing Models; 7.1 Parallel Systems; 7.2 Exiting Parallel Multiple Sequence Alignment; 7.3 Reconfigurable-Mesh Computing Models - (R-Mesh); 7.4 Pairwise Dynamic Programming Algorithms; 7.5 Progressive Multiple Sequence Alignment ON R-Mesh; Chapter 8: Sequence Analysis Services; 8.1 EMBL-EBI: European Bioinformatics Institute
8.2 NCBI: National Center for Biotechnology Information
8.3 GenomeNet and Data Bank of Japan; 8.4 Other Sequence Analysis and Alignment Web Servers; 8.5 SeqAna: Multiple Sequence Alignment with Quality Ranking; 8.6 Pairwise Sequence Alignment and Other Analysis Tools; 8.7 Tool Evaluation; Chapter 9: Multiple Sequence for Next-Generation Sequences; 9.1 Introduction; 9.2 Overview of Next Generation Sequence Alignment Algorithms; Chapter 10: Multiple Sequence Alignment for Variations Detection; 10.1 Introduction; 10.2 Genetic Variants; 10.3 Variation Detection Methods Based on MSA
10.4 Evaluation Methodology
10.5 Conclusion and Future Work; Chapter 11: Multiple Sequence Alignment for Structure Detection; 11.1 Introduction; 11.2 RNA Secondary Structure Prediction Based on MSA; 11.3 Protein Secondary Structure Prediction Based on MSA; 11.4 Conclusion and Future Work; References; Index; End User License Agreement
