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| 1. Record Nr. | UNINA990003300090403321 |
| Autore | Steiner, George <1929- > |
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| Pubbl/distr/stampa | Oxford ; New York : Oxford University press, 1992 |
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| Titolo | Il canzoniere provenzale estense : riprodotto per il centenario della nascita di Giulio Bertoni / con introduzione di D'Arco Silvio Avalle e Emanuele Casamassima |
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| Collana | Subsidia al Corpus des troubadours
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Nota di contenuto	Calculating the Secrets of Life -- Copyright -- Preface -- Contents -- Calculating the Secrets of Life -- Chapter 1 The Secrets of Life: A Mathematician's Introduction to Molecular Biology -- BIOCHEMISTRY -- CLASSICAL GENETICS -- MOLECULAR BIOLOGY -- THE RECOMBINANT DNA REVOLUTION -- MOLECULAR GENETICS IN THE 1990S -- THE HUMAN GENOME PROJECT -- COMING ATTRACTIONS -- REFERENCES -- Chapter 2 Mapping Heredity: Using Probabilistic Models and Algorithms to Map Genes and Genomes -- GENETIC MAPPING -- The Concept of Genetic Maps -- Challenges of Genetic Mapping: Human Families and Complex Traits -- MAXIMUM LIKELIHOOD ESTIMATION -- Efficient Algorithms -- Statistical Significance -- Excursion:

Susceptibility to Colon Cancer in Mice and the Large Deviation Theory of Diffusion Processes -- PHYSICAL MAPPING -- Assembling Physical Maps by "Fingerprinting" Random Clones -- Excursion: Designing a Strategy to Map the Human Genome -- CONCLUSION -- REFERENCES -- Chapter 3 Seeing Conserved Signals: Using Algorithms to Detect Similarities between Biosequences -- FINDING GLOBAL SIMILARITIES -- Visualizing Alignments: Edit Graphs -- The Basic Dynamic Programming Algorithm -- FINDING LOCAL SIMILARITIES -- VARIATIONS ON SEQUENCE COMPARISON -- Variations in Gap Cost Penalties -- The Duality Between Similarity and Difference Measures -- Aligning More Than Two Sequences at a Time -- K-Best Alignments -- Approximate Pattern Matching -- Parallel Computing -- COMPARING ONE SEQUENCE AGAINST A DATABASE -- Heuristic Algorithms -- Sublinear Similarity Searches -- OPEN PROBLEMS -- REFERENCES -- Chapter 4 Hearing Distant Echoes: Using Extremal Statistics to Probe Evolutionary Origins -- GLOBAL SEQUENCE COMPARISONS -- Sequence Alignment -- Alignment Given -- Alignment Unknown -- LOCAL SEQUENCE COMPARISONS -- Alignment Given -- Alignment Unknown -- APPLICATION TO RNA EVOLUTION. TWO BEHAVIORS SUFFICE -- RNA EVOLUTION REVISITED -- REFERENCES -- Chapter 5 Calibrating the Clock: Using Stochastic Processes to Measure the Rate of Evolution -- OVERVIEW -- THE COALESCENT AND MUTATION -- The Ewens Sampling Formula -- Forwards and Backwards in the Tree -- Top-down -- Bottom-up -- The Infinitely-Many-Sites Model -- K-Allele Models -- The Finitely-Many-Sites Models -- MATHEMATICAL VIGNETTE: APPROXIMATING COMBINATORIAL STRUCTURES -- Approximations for the Ewens Sampling Formula -- Combinatorial Assemblies -- Other Combinatorial Structures -- The Large Components -- WHERE TO NEXT? -- Likelihood Methods -- Discussion -- REFERENCES -- General-Purpose References -- Detailed References -- Chapter 6 Winding the Double Helix: Using Geometry, Topology, and Mechanics of DNA -- DNA GEOMETRY AND TOPOLOGY: LINKING, TWISTING, AND WRITHING -- APPLICATIONS TO DNA TOPOISOMERASE REACTIONS -- DNA ON PROTEIN COMPLEXES -- THE SURFACE LINKING NUMBER -- THE WINDING NUMBER AND HELICAL REPEAT -- RELATIONSHIP BETWEEN LINKING, SURFACE LINKING, AND WINDING -- APPLICATION TO THE STUDY OF THE MINICHROMOSOME -- REFERENCES -- Chapter 7 Unwinding the Double Helix: Using Differential Mechanics to Probe Conformational Changes... -- DNA SUPERHELICITY-MATHEMATICS AND BIOLOGY -- STATEMENT OF THE PROBLEM -- THE ENERGETICS OF A STATE -- ANALYSIS OF SUPERHELICAL EQUILIBRIA -- Evaluation of Free-Energy Parameters -- Accuracy of the Calculated Results -- APPLYING THE METHOD TO STUDY INTERESTING GENES -- DISCUSSION AND OPEN PROBLEMS -- REFERENCES -- Chapter 8 Lifting the Curtain: Using Topology to Probe the Hidden Action of Enzymes -- THE TOPOLOGY OF DNA -- SITE-SPECIFIC RECOMBINATION -- TOPOLOGICAL TOOLS FOR DNA ANALYSIS -- THE TANGLE MODEL FOR SITE-SPECIFIC RECOMBINATION -- THE TOPOLOGY OF TN3 RESOLVASE -- SOME UNSOLVED PROBLEMS -- ANNOTATED BIBLIOGRAPHY -- Knot Theory. Application of Geometry and Topology to Biology -- REFERENCES -- Chapter 9 Folding the Sheets: Using Computational Methods to Predict the Structure of Proteins -- A PRIMER ON PROTEIN STRUCTURE -- BASIC INSIGHTS ABOUT PROTEIN STRUCTURE -- THREADING METHODS -- PREDICTING HIV PROTEASE STRUCTURE:AN EXCURSION -- HIERARCHICAL APPROACHES -- PREDICTING MYOGLOBIN STRUCTURE: AN EXCURSION -- CONCLUSION -- ACKNOWLEDGMENTS -- REFERENCES -- Appendix-Chapter Authors -- Index.

Sommario/riassunto

As researchers have pursued biology's secrets to the molecular level, mathematical and computer sciences have played an increasingly important role--in genome mapping, population genetics, and even the controversial search for "Eve," hypothetical mother of the human race. In this first-ever survey of the partnership between the two fields, leading experts look at how mathematical research and methods have made possible important discoveries in biology. The volume explores how differential geometry, topology, and differential mechanics have allowed researchers to "wind" and "unwind" DNA's double helix to understand the phenomenon of supercoiling. It explains how mathematical tools are revealing the workings of enzymes and proteins. And it describes how mathematicians are detecting echoes from the origin of life by applying stochastic and statistical theory to the study of DNA sequences. This informative and motivational book will be of interest to researchers, research administrators, and educators and students in mathematics, computer sciences, and biology.
