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| 1. Record Nr.           | UNINA9910337806103321  |
| Autore                  | Blazewicz Jacek  |
| Titolo                  | Handbook on Scheduling : From Theory to Practice // by Jacek Blazewicz, Klaus H. Ecker, Erwin Pesch, Günter Schmidt, Malgorzata Sterna, Jan Weglarz  |
| Pubbl/distr/stampa      | Cham : , : Springer International Publishing : , : Imprint : Springer, , 2019  |
| ISBN                    | 3-319-99849-8  |
| Edizione                | [2nd ed. 2019.]  |
| Descrizione fisica      | 1 online resource (839 pages)  |
| Collana                 | International Handbooks on Information Systems   |
| Disciplina              | 343.73078624   |
| Soggetti                | Production management<br>Information technology<br>Business—Data processing<br>Application software<br>Industrial engineering<br>Production engineering<br>Operations Management<br>IT in Business<br>Information Systems Applications (incl. Internet)<br>Industrial and Production Engineering   |
| Lingua di pubblicazione | Inglese  |
| Formato                 | Materiale a stampa   |
| Livello bibliografico   | Monografia   |
| Nota di contenuto       | Introduction -- Basics -- Definition, Analysis and Classification of Scheduling Problems -- Scheduling on One Processor -- Scheduling on Parallel Processors -- Communication Delays and Multiprocessor Tasks -- Scheduling in Hard Real-Time Systems -- Flow Shop Scheduling -- Open Shop Scheduling -- Scheduling in Job Shops -- Scheduling with Limited Processor Availability -- Time-Dependent Scheduling -- Scheduling under Resource Constraints -- Scheduling Imprecise Computations -- Online Scheduling -- Constraint Programming and Disjunctive Scheduling -- Scheduling in flexible Manufacturing Systems -- Computer Integrated Production Scheduling -- Scheduling in Logistics. . |

This handbook provides a comprehensive introduction to the theory and applications of scheduling in advanced planning and computer systems. It addresses a broad audience including practitioners and researchers interested in scheduling, as well as graduate and advanced undergraduate students in the fields of computer science and computer engineering, operations research, industrial and real-time engineering, management science, business administration and information systems, and applied mathematics. The book begins by providing an introduction to and basic concepts from discrete mathematics. Single and multiple processor systems are covered, with a focus on multiprocessor tasks and hard real-time systems. Flow shop and open shop scheduling, as well as scheduling in job shops, are explained in detail. Issues like limited processor availability, time-dependence, resource constraints and imprecise computations are dealt with in dedicated chapters. Special attention is given to online scheduling, constraint programming and disjunctive scheduling. The book also features applications and cases involving flexible manufacturing systems, computer integrated production scheduling and logistics. In particular it presents case studies on optimization procedures for the production of acrylic glass and of helicopter parts in a flexible manufacturing system, an efficient decision support system for airport gate scheduling, concrete delivery planning, and berth and quay crane allocation at seaports.

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| 2. Record Nr.           | UNINA9910957259103321   |
| Titolo                  | Calculating the secrets of life : applications of the mathematical sciences in molecular biology / / Eric S. Lander and Michael S. Waterman, editors  |
| Pubbl/distr/stampa      | Washington, D.C., : National Academy Press, 1995  |
| ISBN                    | 9786610211388<br>9781280211386<br>1280211385<br>9780309556163<br>0309556163<br>9780585037233<br>058503723X  |
| Edizione                | [1st ed.]   |
| Descrizione fisica      | 1 online resource (299 p.)  |
| Altri autori (Persone)  | LanderEric S<br>WatermanMichael S   |
| Disciplina              | 574.8/8/0151  |
| Soggetti                | Genetics - Mathematical models<br>Genetics - Statistical methods<br>Molecular biology - Mathematical models<br>Molecular biology - Statistical methods  |
| Lingua di pubblicazione | Inglese   |
| Formato                 | Materiale a stampa  |
| Livello bibliografico   | Monografia  |
| Note generali           | Bibliographic Level Mode of Issuance: Monograph   |
| Nota di bibliografia    | Includes bibliographical references and index.  |
| 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.

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