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Nota di contenuto	Cover; Contents; Preface to the French edition; Preface to the English edition; 1: Genome sequencing; 1.1 Automatic sequencing; 1.2 Sequencing strategies; 1.3 Fragmentation strategies; 1.4 Sequence assembly; 1.5 Filling gaps; 1.6 Obstacles to reconstruction; 1.7 Utilizing a complementary 'large'1 clone library; 1.8 The first large- scale sequencing project: The Haemophilus influenzae genome; 1.9 cDNA and EST; 2: Sequence comparisons; 2.1 Introduction: Comparison as a sequence prediction method; 2.2 A sample molecule: the human androsterone receptor 2.3 Sequence homologies - functional homologies2.4 Comparison matrices; 2.5 The problem of insertions and deletions; 2.6 Optimal alignment: the dynamic programming method; 2.7 Fast heuristic methods; 2.8 Sensitivity, specificity, and confidence level; 2.9 Multiple alignments; 3: Comparative genomics; 3.1 General properties of

genomes; 3.2 Genome comparisons; 3.3 Gene evolution and phylogeny: applications to annotation; 4: Genetic information and biological sequences; 4.1 Introduction: Coding levels; 4.2 Genes and the genetic code; 4.3 Expression signals; 4.4 Specific sites 4.5 Sites located on DNA 4.6 Sites present on RNA; 4.7 Pattern detection methods; 5: Statistics and sequences; 5.1 Introduction; 5.2 Nucleotide base and amino acid distribution; 5.3 The biological basis of codon bias; 5.4 Using statistical bias for prediction; 5.5 Modeling DNA sequences; 5.6 Complex models; 5.7 Sequencing errors and hidden Markov models; 5.8 Hidden Markov processes: a general sequence analysis tool; 5.9 The search for genes - a difficult art; 6: Structure prediction; 6.1 The structure of RNA; 6.2 Properties of the RNA molecule; 6.3 Secondary RNA structures 6.4 Thermodynamic stability of RNA structures 6.5 Finding the most stable structure; 6.6 Validation of predicted secondary structures; 6.7 Using chemical and enzymatic probing to analyze folding; 6.8 Long-distance interactions and three-dimensional structure prediction; 6.9 Protein structure; 6.10 Secondary structure prediction; 6.11 Three-dimensional modeling based on homologous protein structure; 6.12 Predicting folding; 7: Transcriptome and proteome: macromolecular networks; 7.1 Introduction; 7.2 Post-genomic methods; 7.3 Macromolecular networks; 7.4 Topology of macromolecular networks 7.5 Modularity and dynamics of macromolecular networks 7.6 Inference of regulatory networks; 8: Simulation of biological processes in the genome context; 8.1 Types of simulations; 8.2 Prediction and explanation; 8.3 Simulation of molecular networks; 8.4 Generic post-genomic simulators; Index

Sommario/riassunto

This book is an excellent introductory text describing the use of bioinformatics to analyze genomic and post-genomic data. It has been translated from the original popular French edition, which was based on a course taught at the well-respected Ecole Polytechnique in Palaiseau. This edition has been fully revised and updated by the authors. After a brief introduction to gene structure and sequence determination, it describes the techniques used to identify genes, their protein-coding sequences and regulatory regions. The book discusses the methodology of comparative genomics, using informati

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Autore	Engels Friedrich
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Nota di contenuto	I. LES STADES PREHISTORIQUEES DE LA CIVILISATION -- 1. L'Etat sauvage -- 2. La barbarie -- II. LA FAMILLE -- 1. La famille consanguine -- 2. La famille punaluenne -- 3. La famille appariee -- 4. La famille monogamique -- III. LA GENS IROQUOISE -- IV. LA GENS GRECQUE -- V. GENESE DE L'ETAT ATHENIEN -- VI. LA GENS ET L'ETAT A ROME -- VII. LA GENS CHEZ LES CELTES ET LES GERMAINS -- VIII. LA FORMATION DE L'ETAT CHEZ LES GERMAINS -- IX. BARBARIE ET CIVILISAT10N -- Index des noms -- Personnages mythologiques et litteraires -- Index des noms ethnographiques.