

1. Record Nr.	UNINA9910146066803321
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Titolo	Handbook of comparative genomics [[electronic resource]] : principles and methodology // Cecilia Saccone, Graziano Pesole
Pubbl/distr/stampa	New York, : Wiley-Liss, c2003
ISBN	1-280-25276-6 9786610252763 0-470-35602-2 0-471-32641-0 0-471-72272-3
Descrizione fisica	1 online resource (444 p.)
Altri autori (Persone)	PesoleGraziano
Disciplina	572.8 572.86
Soggetti	Genomics Evolutionary genetics Electronic books.
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 (p. 377-422) and index.
Nota di contenuto	HANDBOOK OF COMPARATIVE GENOMICS Principles and Methodology; CONTENTS; PREFACE; I GENOME FEATURES; 1 PROKARYOTES; 1.1 Introduction; 1.2 Morphology and Classification; 1.3 Genome Shape and Size; 1.4 Gene Content and Organization; 1.5 Base Composition; 1.6 Codon Use; 1.7 Replication and Expression; 2 EUKARYOTES; 2.1 Introduction; 2.2 Classification and Time Scale; 2.3 Genome Shape and Size; 2.4 Base Composition; 2.5 Replication, Repair, and Recombination; 2.6 Gene Expression; 2.6.1 Transcription and Posttranscriptional Regulation; 2.6.2 Genetic Code and Codon Use 2.6.3 Translation and Posttranslation Modifications2.7 Completely Sequenced Eukaryotic Genomes; 2.7.1 Saccharomyces cerevisiae Genome; 2.7.2 Schizosaccharomyces pombe Genome; 2.7.3 Caenorhabditis elegans Genome; 2.7.4 Drosophila melanogaster Genome; 2.7.5 Arabidopsis thaliana Genome; 2.7.6 Oryza sativa Genome; 2.7.7 Homo sapiens Genome; 3 ORGANELLES; 3.1 Mitochondria; 3.1.1 General Structure and Function; 3.1.2 DNA and

Genetic System; 3.1.3 Genome Features; 3.2 Chloroplasts and Other Plastids; II METHODOLOGIES; 4 MOLECULAR BIOLOGY TECHNIQUES FOR GENOMICS; 4.1 Genome DNA Sequencing
4.1.1 DNA-Sequencing Techniques 4.1.2 The Human Genome Project;
4.2 Analysis of the Transcriptome; 4.2.1 Analysis of Gene Expression;
4.2.2 Expressed Sequence Tags; 4.2.3 Serial Analysis of Gene Expression; 4.2.4 Differential Display; 4.2.5 Representational Difference Analysis; 4.2.6 DNA Microarrays; 4.3 Analysis of the Proteome; 4.3.1 Two-Dimensional Gel Electrophoresis; 4.3.2 Protein Identification; 4.3.3 Study of Protein-DNA and Protein-Protein Interactions; 4.3.4 Proteome Analysis Using Biochips; 5 BIOLOGICAL DATABASES IN THE GENOME ERA; 5.1 Introduction
5.2 Primary and Specialized Databases 5.3 Database Structures; 5.4 Linked Databases and Database Interoperability; 5.5 Database Annotation; 5.6 Retrieval Systems; 5.6.1 SRS; 5.6.2 Entrez; 5.6.3 Other Retrieval Systems; 5.7 Nucleotide Databases; 5.8 Protein Databases; 5.9 Other Protein Databases; 5.10 Genomic Databases and Resources; 5.11 Gene Databases and Resources; 5.12 Transcriptome Databases; 5.13 Metabolism Databases; 5.14 Mutation Databases; 5.15 Mitochondrial Databases and Resources; 6 COMPUTATIONAL METHODS FOR THE ANALYSIS OF GENOME SEQUENCE DATA; 6.1 Introduction; 6.2 Dot-Plot Matrix
6.3 Sequence Pairwise Alignment 6.3.1 Needleman-Wunsch Global Alignment Algorithm; 6.3.2 Smith-Waterman Algorithm for the Identification of Common Molecular Subsequences; 6.3.3 Alignment of cDNA and Genomic DNA Sequences; 6.3.4 Genome Alignment; 6.3.5 Cleanup of Sequence Databases from Redundancy; 6.3.6 Measure of the Similarity Degree between Homologous Sequences; 6.4 Database Searching; 6.4.1 FASTA; 6.4.2 BLAST; 6.4.3 BLAST and FASTA Family of Programs; 6.4.4 Filtering Matches to Unwanted Sequences; 6.4.5 Filtering Matches to Repetitive Sequences
6.4.6 Statistical Significance of Alignment Scores

Sommario/riassunto

This comprehensive reference covers the comparative methodology involved in studying molecular evolution. Providing a practical introduction to the role of bioinformatics in comparative genomics, this publication further discusses the basic technology used in genome sequencing projects and provides an overview of genome storage databases currently in use. This timely and cutting-edge text also:
Reviews the basic principles of genomics and gene expression analysis
Discusses analytic methods in proteomics and transcriptomics
Includes a comprehensive list of Web resource
