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Nota di contenuto	1. Genomes -- 01.1 Prokaryotes vs. Eukaryotes -- 01.2 Genome Structure -- 01.3 Genome Sizes -- 01.4 Human Genome and Ancient DNA (Neandertaler, Denisova) -- 2. Genomes of Organelles -- 02.1 Mitochondria -- 02.2 Plastids -- 02.3 Outlook Obligate Endosymbionts -- 3. Transcriptomes -- 03.1 mRNA -- 03.2 Transcripts -- 03.3 Expression Level -- 03.4 Alternative Splicing -- 4. Sequencing Techniques -- 04.1 Sanger -- 04.2 Illumina -- 04.3 454 -- 04.4 PacBio -- 04.5 Outlook Nanopore Sequencing -- 5. Genome Sequencing Strategies -- 05.1 Whole Genome Shotgun -- 05.2 RADseq -- 05.3 Target Enrichment -- 05.4 RNAseq -- 6. Assembly and Mapping -- 06.1 Assembling Strategies (kmer vs OLC) -- 06.2 Data Quality and Filtering -- 06.3 Re-Sequencing and Mapping -- 06.4 De novo Assembly Genome -- 06.5 De novo Assembly Transcriptome --

7. Locating Genes -- 07.1 Orthology vs. Paralogy -- 07.2 BLAST and Successors -- 07.3 Hidden Markov Profile -- 07.4 Ortholog Conjecture -- 8. Alignment -- 08.1 Alignment Strategies -- 08.2 Alignment Masking -- 9. Phylogenetic Analysis -- 09.1 Distance Measurements -- 09.2 Maximum Parsimony -- 09.3 Maximum Likelihood -- 09.4 Bayesian Inference -- 09.5 Supermatrix vs. Single Gene Analysis (Gene Trees vs. Species Trees) -- 10. Systematic Errors in phylogenetic Analysis -- 10.1 Prediction: Evolutionary Models -- 10.2 Heterogeneity Nucleotide/Amino Acid-Composition -- 10.3 Variation of substitution rate between the lines -- 10.4 Variation of substitution rate over time -- 10.5 New Approaches to Correct systematic Errors -- 11. Genome-wide Characteristics -- 11.1 Gene Order -- 11.2 Mobile Elements -- 11.3 microRNAs -- 11.4 Differences in the genetic code -- 12. Index -- 13. References.

Sommario/riassunto

This unique textbook provides a clear and concise overview of the key principles of the complex field of phylogenomics, with a particular focus on sequencing technologies that are crucial to studying and understanding interrelations in evolutionary genomics. It includes chapters dedicated to the analysis of nucleotide sequences using assembling and alignment methods and also discusses the main strategies for phylogenetic studies, systematic errors and their correction. This highly readable textbook is intended for graduate students and young researchers with an interest in phylogenetics and evolutionary developmental biology.
