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Titolo	Evolutionary Genomics [[electronic resource]] : Statistical and Computational Methods / / edited by Maria Anisimova
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Descrizione fisica	1 online resource (XVII, 780 p. 189 illus., 110 illus. in color.)
Collana	Methods in Molecular Biology, , 1064-3745 ; ; 1910
Disciplina	570.285
Soggetti	Bioinformatics Genetics Evolution (Biology) Genetics and Genomics Evolutionary Biology Genètica evolutiva Genòmica Models matemàtics Bioinformàtica Llibres electrònics
Lingua di pubblicazione	Inglese
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Livello bibliografico	Monografia
Nota di contenuto	Introduction to Genome Biology and Diversity -- Probability, Statistics, and Computational Science -- A Not-So-Long Introduction to Computational Molecular Evolution -- Whole-Genome Alignment -- Inferring Orthology and Paralogy -- Transposable Elements and Their Identification -- Modern Phylogenomics: Building Phylogenetic Trees Using the Multispecies Coalescent Model -- Genome-Wide Comparative Analysis of Phylogenetic Trees: The Prokaryotic Forest of Life -- The Methodology Behind Network-Thinking: Graphs to Analyze Microbial Complexity and Evolution -- Bayesian Molecular Clock Dating Using Genome-Scale Datasets -- Genome Evolution in Outcrossing vs. Selfing vs. Asexual Species -- Selection Acting on Genomes -- Looking for Darwin in Genomic Sequences: Validity and Success Depends on the

	Relationship between Model and Data -- Evolution of Viral Genomes: Interplay between Selection, Recombination, and Other Forces -- Evolution of Protein Domain Architectures -- New Insights on the Evolution of Genome Content: Population Dynamics of Transposable Elements in Flies and Humans -- Association Mapping and Disease: Evolutionary Perspectives -- Ancestral Population Genomics -- Introduction to the Analysis of Environmental Sequences: Metagenomics with MEGAN -- Multiple Data Analyses and Statistical Approaches for Analyzing Data from Metagenomic Studies and Clinical Trials -- Systems Genetics for Evolutionary Studies -- Analyzing Epigenome Data in Context of Genome Evolution and Human Diseases -- Semantic Integration and Enrichment of Heterogeneous Biological Databases -- High-Performance Computing in Bayesian Phylogenetics and Phylodynamics Using BEAGLE -- Scalable Workflows and Reproducible Data Analysis for Genomics -- Sharing Programming Resources between Bio* Projects.
Sommario/riassunto	This open access book addresses the challenge of analyzing and understanding the evolutionary dynamics of complex biological systems at the genomic level, and elaborates on some promising strategies that would bring us closer to uncovering of the vital relationships between genotype and phenotype. After a few educational primers, the book continues with sections on sequence homology and alignment, phylogenetic methods to study genome evolution, methodologies for evaluating selective pressures on genomic sequences as well as genomic evolution in light of protein domain architecture and transposable elements, population genomics and other omics, and discussions of current bottlenecks in handling and analyzing genomic data. Written for the highly successful Methods in Molecular Biology series, chapters include the kind of detail and expert implementation advice that lead to the best results. Authoritative and comprehensive, Evolutionary Genomics: Statistical and Computational Methods, Second Edition aims to serve both novices in biology with strong statistics and computational skills, and molecular biologists with a good grasp of standard mathematical concepts, in moving this important field of study forward.