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Nota di contenuto	Contents; PART I: MODELLING MOLECULAR EVOLUTION; 1 Models of nucleotide substitution; 2 Models of amino acid and codon substitution; PART II: PHYLOGENY RECONSTRUCTION; 3 Phylogeny reconstruction: overview; 4 Maximum likelihood methods; 5 Bayesian methods; 6 Comparison of methods and tests on trees; PART III: ADVANCED TOPICS; 7 Molecular clock and estimation of species divergence times; 8 Neutral and adaptive protein evolution; 9 Simulating molecular evolution; 10 Perspectives; Appendices; A: Functions of random variables; B: The delta technique; C: Phylogenetics software; References; Index; A BC; D; E; F; G; H; I; J; K; L; M; N; O; P; Q; R; S; T; U; W; Y
Sommario/riassunto	This book describes the models, methods and algorithms that are most useful for analysing the ever-increasing supply of molecular sequence

data, with a view to furthering our understanding of the evolution of genes and genomes. - ;The field of molecular evolution has experienced explosive growth in recent years due to the rapid accumulation of genetic sequence data, continuous improvements to computer hardware and software, and the development of sophisticated analytical methods. The increasing availability of large genomic data sets requires powerful statistical methods to analyse and interpr
