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Nota di contenuto	Front Cover; Contents; List of Figures; List of Tables; Preface; Editors; Contributors; Chapter 1: Bayesian phylogenetics: methods, computational algorithms, and applications; Chapter 2: Priors in Bayesian phylogenetics; Chapter 3: Inated density ratio (IDR) method for estimating marginal likelihoods in Bayesian phylogenetics; Chapter 4: Bayesian model selection in phylogenetics and genealogy-based population genetics; Chapter 5: Variable tree topology stepping-stone marginal likelihood estimation; Chapter 6: Consistency of marginal likelihood estimation when topology varies Chapter 7: Bayesian phylogeny analysis Chapter 8: SMC (sequential Monte Carlo) for Bayesian phylogenetics; Chapter 9: Population model comparison using multi-locus datasets; Chapter 10: Bayesian methods in the presence of recombination; Chapter 11: Bayesian nonparametric phylodynamics; Chapter 12: Sampling and summary statistics of endpoint-conditioned paths in DNA sequence evolution; Chapter 13: Bayesian inference of species divergence times; Bibliography; Back

Cover

Sommario/riassunto

Offering a rich diversity of models, Bayesian phylogenetics allows evolutionary biologists, systematists, ecologists, and epidemiologists to obtain answers to very detailed phylogenetic questions. Suitable for graduate-level researchers in statistics and biology, *Bayesian Phylogenetics: Methods, Algorithms, and Applications* presents a snapshot of current trends in Bayesian phylogenetic research. Encouraging interdisciplinary research, this book introduces state-of-the-art phylogenetics to the Bayesian statistical community and, likewise, presents state-of-the-