

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-art Bayesian statistics to the phylogenetics community. The book emphasizes model selection, reflecting recent interest in accurately estimating marginal likelihoods. It also discusses new approaches to improve mixing in Bayesian phylogenetic analyses in which the tree topology varies. In addition, the book covers divergence time estimation, biologically realistic models, and the burgeoning interface between phylogenetics and population genetics.

Features

- Represents one of the first books on statistical/computational aspects of phylogenetics to focus exclusively on Bayesian methods
- Explores current research in Bayesian phylogenetics of interest to both the statistical and biology communities
- Covers model selection, sampling efficiency, priors, recombination, phylodynamics, evolutionary dependence, and divergence time estimation
- Stimulates collaborations among phylogenetic, population genetic, and statistical researchers to solve theoretical and computational challenges

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