| | | |
|---|---|---|
| 1. | Record Nr. | UNINA9910787845903321 |
| | Titolo | Bayesian phylogenetics : methods, algorithms, and applications / / edited by Ming-Hui Chen, Lynn Kuo, and Paul O. Lewis, University of Connecticut Storrs, USA |
| | Pubbl/distr/stampa | Boca Raton : , : CRC Press, , [2014] ©2014 |
| | ISBN | 0-429-18426-3 1-4665-0079-4 |
| | Descrizione fisica | 1 online resource (391 p.) |
| | Collana | Chapman and Hall/CRC Mathematical and Computational Biology Series |
| | Disciplina | 576.8/8 |
| | Soggetti | Phylogeny Biometry Molecular genetics Bayesian statistical decision theory |
| | Lingua di pubblicazione | Inglese |
| | Formato | Materiale a stampa |
| | Livello bibliografico | Monografia |
| | Note generali | Description based upon print version of record. |
| | Nota di bibliografia | Includes bibliographical references. |
| | 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 analysisChapter 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-