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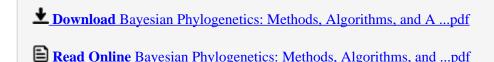
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Offering a rich diversity of models, Bayesian phylogenetics allows evolutionary biologists, systematists, ecologists, and epidemiologists to obtain answers to very detailed phylogenetic questions. Suitable for graduate-level researchers in statistics 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.

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Editorial Review

Review

"… a great resource to get up to speed with the current state and future directions of many areas of research in Bayesian phylogenetics. I expect **Bayesian Phylogenetics** will be an important resource as Bayesian approaches to phylogenetics continue to advance and diversify. It introduces many novel methods and proofs that will be of broad interest to statisticians, and includes thorough reviews of several exciting areas of statistical phylogenetics. As a result, many of the book's chapters will be important (and likely highly cited) references."
?*Systematic Biology,* August *2015*

"… the first book devoted solely to Bayesian methods in this field … . The affiliations of the editors of the volume reflect the strong interdisciplinary flavor of the book … . The diversity of contributing authors further reinforces this focus, with authors spanning the range from statisticians to phylogeneticists. … the volume does achieve the editors' primary goal of bringing state-of-the-art developments at the intersection of Bayesian methodology and phylogenetic inference to the forefront in a manner in which they can be appreciated by researchers in both fields."
?*Journal of the American Statistical Association*, June 2015

"**Bayesian Phylogenetics** has the distinction of being the first published text devoted solely to the Bayesian approach to phylogenetics. … a useful resource for many researchers in the field and for statisticians interested in joining the game."
?*International Statistical Review*, 2015

"This book provides an extensive and concrete account of modern Bayesian phylogenetics … a good starting point for entering each subarea of Bayesian phylogenetics. … this book can serve as a road map for both starters and those who are already in this field. … The book is concise, and the examples accompanying each topic are clear and supported by relevant illustrations. … useful to researchers and graduate students."
?*Biometrics*, March 2015

About the Author

Ming-Hui Chen is a professor of statistics and director of the Statistical Consulting Services at the University of Connecticut. He was the recipient of the 2013 American Association of the University Professors Research Excellence Award, the 2013 College of Liberal Arts and Sciences Excellence in Research Award in the Physical Sciences Division at the University of Connecticut, and the 2011 International Chinese Statisticians Association (ICSA) Outstanding Service Award. An elected fellow of the ASA and the IMS, Dr. Chen has served on numerous professional committees, including the 2013 president of the ICSA, the 2011-2013 board of directors of the International Society for Bayesian Analysis, the 2007-2010 executive director of the ICSA, and the 2004-2006 board of directors of the ICSA. He has also served on editorial boards of *Bayesian Analysis*, *Journal of the American Statistical Association*, *Journal of Computational and Graphical Statistics*, *Lifetime Data Analysis*, *Sankhya*, and *Statistics and Its Interface*. His research interests include Bayesian statistical methodology, Bayesian computation, Bayesian phylogenetics, categorical data analysis, design of Bayesian clinical trials, DNA microarray data analysis, meta-analysis, missing data analysis, Monte Carlo methodology, prior elicitation, statistical methodology and

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Lynn Kuo is a professor of statistics at the University of Connecticut. An elected fellow of the ASA, she was previously a research fellow in the Statistical Survey Institute at the USDA and at the Statistical and Applied Mathematical Sciences Institute (SAMSI). Dr. Kuo received an outstanding service award from ICSA in 2013 and was the secretary and treasurer of the Section of Bayesian Statistics of the ASA in 1998-1999. She has been an associate editor of the *Journal of American Statistical Association* and *Naval Research Logistics* and has served on many review panels for the CDC, NIH, and NSF. She has published more than 80 papers in numerous journals, including *Systematic Biology, Molecular Biology and Evolution, Nature Genetics,* and *Statistics in Biosciences*. Her research areas include nonparametric Bayesian statistics, survey sampling, survival analysis, longitudinal data analysis, Bayesian phylogenetics, and "omics" data analysis.

Paul O. Lewis is an associate professor of ecology and evolutionary biology and co-director of the Bioinformatics Facility in the Biotechnology/Bioservices Center at the University of Connecticut. His postdoctoral training was under Bruce S. Weir in the Department of Statistics at North Carolina State University and under David L. Swofford at the Smithsonian Institution Laboratory of Molecular Systematics. Dr. Lewis has been an associate editor of *Systematic Biology* and is the elected president of the Society of Systematic Biologists for 2015. His research interests include maximum likelihood and Bayesian methods in phylogenetics and the systematic evolution of green plants from green algae to angiosperms.

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