

"Want to construct a phylogeny, add in calibrated time points or work out the past history of an epidemic? The open source package BEAST has established itself as the industry standard for all this and more. This definitive book, explaining what is under the hood, how the user can customise extensions and most critically, a simple 'how to' users guide, is necessary reading for beginners and specialists alike."

Laurence D. Hurst, *University of Bath, UK*

"...Bayesian inference has revolutionized population genetics, phylogenetics, and divergence time estimation ... This book is an accessible and thorough introduction to these Bayesian procedures ... includes clear guides on how to use the BEAST 2 software for performing Bayesian analyses and how to visualize the results ... timely and is written by two of the leaders of the field. I highly recommend it."

Jeff Thorne, *North Carolina State University, USA*

What are the models used in phylogenetic analysis and what exactly is involved in Bayesian evolutionary analysis using Markov chain Monte Carlo (MCMC) methods? How can you choose and apply these models, which parameterisations and priors make sense, and how can you diagnose Bayesian MCMC when things go wrong?

These are just a few of the questions answered in this comprehensive overview of Bayesian approaches to phylogenetics. From addressing theoretical aspects of the field to providing pragmatic advice on how to prepare and perform phylogenetic analysis, this practical guide also includes coverage of the interpretation of analyses and visualisation of phylogenies. The software architecture is described and a guide to developing BEAST 2.2 extensions is provided to allow these models to be extended further.

With an accompanying website (<http://beast2.org/>) providing example files and tutorials, this one-stop reference to applying the latest phylogenetic models in BEAST 2 will provide essential guidance for all users – from those using phylogenetic tools, to computational biologists and Bayesian statisticians.

Alexei J. Drummond is Professor of Computational Biology and Principal Investigator at the Allan Wilson Centre of Molecular Ecology and Evolution. He is the lead author of the BEAST software package and has gained a reputation in the field as one of the most knowledgeable experts for Bayesian evolutionary analyses.

Remco R. Bouckaert is a computer scientist with a strong background in Bayesian methods. He is the main architect of version 2 of BEAST and has been working on extensions to the BEAST software and other phylogenetics projects in Alexei Drummond's group at the University of Auckland.

Cover illustration: three phylogenetic trees from the posterior sample of a Bayesian evolutionary analysis of Dengue virus samples. © Alexei J. Drummond.

CAMBRIDGE
UNIVERSITY PRESS
www.cambridge.org

ISBN 978-1-107-01965-2



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