of how scientific materialism can be reconciled with what is arguably a religious tradition represent one group and academics trying to understand the relationship that science shares with traditions of religion represent another. However, academics are likely to be unsatisfied by the book since it is, as Barash himself notes, a personal manifesto. The volume itself is part of a growing body of literature on Buddhism from the perspective of individual scientists. In the case of the current book we are introduced to a kind of existentially informed Buddhist biology.

As a text approaching the forging of a meaningful life by those scientific materialists open to Buddhism, as Barash is, *Buddhist Biology* lends insight and clarity into how a person of such materialist convictions could understand important points of conceptual convergence between the sciences and Buddhism. The author is writing to an audience of the educated with overlapping interests in science, Buddhism, and personal fulfillment. He clarifies some aspects of evolutionary biology and neuroscience and demonstrates how those interested in Buddhism might be able to reconcile the science with various aspects of the tradition. He takes time to discuss concepts of basic importance to those interested in Buddhism such as *anatman, dukkha, anitya,* and *pratitya-samutpada* from the perspective of one who is learning to incorporate these concepts into a worldview very different from the one in which they appeared.

This book is less helpful for anyone looking for an academic treatment of the subject. This is mainly because, from the very beginning, Barash makes it clear that he considers some aspects of Buddhism more legitimate than others, mainly on the basis of what he perceives as its rationality. As tongue-in-cheek philosophy humor, the author entertains in passages such as these but he fails to draw in readers who prefer less polarization and more clarity. On many occasions he alludes to a view that does not see Buddhism as a religion but then does not clarify what it is he takes religion to entail with the exception of using what he calls the Abrahamic traditions as a foil. He freely admits to suspicion of institutionalized religion and makes it clear that he intends, in his presentation, to clean up aspects of Buddhist thought and history that are unscientific and superstitious.

Throughout the book, Barash reinterprets both the meaning and history of Buddhist ideas in ways that support his contentions. When he encounters resistance from historical facts, he simply dismisses them as being part of that pool of undesirable and thus fully ignorable aspects of Buddhism. He frequently emphasizes that Buddhism is, like any tradition that is practiced, a living, changing thing

that has no one "correct" incarnation or understanding. It is a bit confusing then that the author openly claims that certain aspects of Buddhist history, literature, and beliefs are regrettable and undesirable. In his attempts to paint a Buddhism that is a broad representation of the best (as he sees it) of its myriad incarnations, Barash ends up committing the error of many early Western scholars of Buddhism, in that his "Buddhism" is only that of the elite, philosophically educated intellectuals who end up presenting Buddhism to wider audiences. Because he relies entirely on what intellectuals have said about Buddhism, rather than also exploring what larger numbers of practitioners believed or did, he is able to easily rewrite Buddhist history as a struggle over ideals and choose to emphasize those he finds most appealing. Unfortunately, these do not necessarily or exclusively represent the larger history of practitioners of the tradition.

In short, Barash's volume is a fascinating personal manifesto, full of humor and intellectual historical references that mark an exploration of Buddhism from the perspective of a trained scientist embedded in Western culture. Taken this way, it offers readers an opportunity to see how one could be a scientific materialist as well as a practicing Buddhist and how one pursuit can inform the other. However, as a text presenting an investigation of the concepts and ideas shared between biology and Buddhism, it ignores important aspects of Buddhism that would more fully inform a strictly academic exploration of the topic. Regardless, given Barash's own claims regarding the project, this is what he intended.

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GENERAL BIOLOGY

Case Studies in Bayesian Statistical Modelling and Analysis. *Wiley Series in Probability and Statistics.*
   Edited by Clair L. Alston, Kerrie L. Mengersen, and Anthony N. Pettitt. Hoboken (New Jersey): Wiley. $105.00. xxi + 464 p.; ill.; index. ISBN: 978-1-1199-4182-8. 2013.

Bayesian data analysis is increasingly popular in the biological sciences and provides a framework to address challenging research problems for which inference through classical approaches would be difficult. There are a number of textbooks available to learn Bayesian theory and basic applica-

tions but less tackling complicated model structures and the associated research that necessitates such models. This edited volume aims to fill that gap by introducing Bayesian statistics through a series of case studies ranging from simple (e.g., linear regression) to complicated (e.g., spatial conditional autoregressive, multivariate state space, and directed graphical models). Each chapter presents a particular model and highlights a research project(s) that uses the model, including descriptions of the problem and data, a proposed analysis framework, and interpretation of results. The model code for each of the case studies is available online at the publisher's website. However, the usefulness of the code varies by chapter. Most (but not all) of the examples are taken from fields in biology, primarily focused on epidemiology and human health, but also on ecology and the environment.

This volume is suited for those with prior knowledge of Bayesian statistics and experience coding. The introductory chapters on Markov chain Monte Carlo (MCMC), prior selection, and regression models (Chapters 2–6) and early sections on hierarchical and mixed models and advanced regression models (Chapters 7–12) are too advanced for beginners but provide interesting insights for experienced modelers. The discussions on prior choice (Chapter 3) and ordering of levels in hierarchical models (Chapter 9) contain valuable summaries on important practical considerations and offer suggestions for model construction.

The next sections of the book (Chapters 13–20) focus on presenting more complicated models whose structures naturally lend themselves to Bayesian analysis. These chapters highlight the many advantages of Bayesian statistics, such as the ability to handle complex data structures and the ease with which latent or unobserved states can be incorporated into models (Chapters 15–18). There are a number of useful examples in these sections illustrating the wide range of problems that can be addressed using Bayesian statistics and the software platforms that can be used for analysis (e.g., WinBUGS, MATLAB).

The book concludes with discussions on alternative computational approaches, including sequential Monte Carlo (Chapter 21), approximate Bayesian computation (Chapter 22), variational Bayes (Chapter 23), and hybrid MCMC algorithms (Chapter 24). Although a number of software programs are used throughout the book, the final chapter (Chapter 25) provides a detailed introduction to PyMCMC, a Python module for construction of MCMC samplers.

The case studies in this volume are independent and can thus be read out of order or consulted when one is interested in learning about a particular model. As such, this book can serve as a handy reference for proficient statisticians and programmers. The volume also contains a number of relevant citations (and see Chapter 1 for lists of textbooks on additional topics in Bayesian statistics). Although this publication is not geared toward a general audience, there are certainly a number of researchers who will find it helpful.

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Hidden Markov Processes: Theory and Applications to Biology. *Princeton Series in Applied Mathematics.*

By M. Vidyasagar. Princeton (New Jersey): Princeton University Press. $59.50. xiv + 287 p.; ill.; index. ISBN: 978-0-691-13315-7. 2014.

Hidden Markov Models (HMMs) are arguably one of the most widely used models in biological sequence analysis, such as sequence alignment and gene prediction. Considering the popularity of HMMs and their successful application to various problems in biology, it is rather surprising to realize that there are very few volumes devoted to HMMs in biological applications. This is not to say that there is not any useful reference for HMMs in bioinformatics and computational biology. In fact, there are a number of introductory and advanced bioinformatics books that include detailed discussions on HMMs—at least to a certain extent—with introduction to a wide array of applications in bioinformatics. However, seldom do they delve deeper into technical aspects of HMMs that are of theoretical importance. Instead, the focus is often on providing a quick introduction to HMMs, mostly from a practical point of view, that may be just enough to understand how they are applied to address problems in computational biology. Such an introduction is typically followed by practical applications of HMMs in biology and possibly some discussion on variations of the model.

The present volume takes a completely different approach from most other books that discuss HMMs in the context of bioinformatics. Instead of attempting to present an encyclopedic overview of diverse models and algorithms used in bioinformatics, this work solely focuses on the theory of Hidden Markov Processes (HMPs) or HMMs. The author intentionally restricts the discussion on processes in a finite setting (i.e., HMPs with finite state spaces that generate symbol sequences over a finite alphabet), thereby keeping the technicality of the book at a level that is sufficient to cover most (if not all) bioinformatics applications, while making it accessible for engineers and biologists who are not experts in stochastic processes. Based on this focus, the present volume provides a self-contained and