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BOOK REVIEWS

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BUCKLAND, S. T., ANDERSON, D. R., BURNHAM, K. P., LAAKE, J. L., BORCHERS, D. L., and THOMAS, L. (eds). **Advanced Distance Sampling: Estimating Abundance of Biological Populations**. Oxford University Press, Oxford, 2004. xvii + 416 pp. US$119.50/£50.00, ISBN 0-19-850783-6.

This book is edited by recognized leading experts in the field. Distance sampling methodology has been rapidly evolving since 1993 when the first four editors (STB, DRA, KPB, and JLL) published the book *Distance Sampling. Estimating Abundance of Biological Populations.* An updated version was published in 2001, entitled *Introduction to Distance Sampling. Estimating Abundance of Biological Populations*, also co-authored by the other two editors of the present volume (DLB and LT).

This volume mainly reflects trends and new developments in distance sampling that these experts have been advocating according to their views of what is needed by the users' community. In the Preface, the editors state "the book does not provide a snapshot of distance sampling research around the world; rather, it reflects our own priorities for making new methods available in the distance software." It is a compilation of articles written by the editors and their previous and current Ph.D. students. In fact, some of these recent developments have already been published in the form of journal articles, although the book also refers to work that is actually in preparation or unpublished. This may not be proper in the view of some readers, as that work may not be readily available. I did a search on the Internet but could not find some of those references in the published literature yet. However, I would expect that this promising work is coming out soon. Also, only relatively few articles of new developments written by other authors and dated after 2001 appear in the list of references. My impression is that the last few years as modern life sciences and on recent methodological developments relevant in these applications.

At least for readers with interest in modern biomathematics, biostatistics, and life sciences, such a selection of topics would have been more attractive.

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NEILSEN, R. (ed). **Statistical Methods in Molecular Evolution**. Springer, New York, 2005. xii + 508 pp. US$89.95/€85.55, ISBN 0-387-22333-9.

The *Statistics for Biology and Health* series that is published by Springer Science+Business Media is an amazing collection of edited compilations that are becoming quite indispensable for scientists interested in the proper analysis of biological data. *Statistical Methods in Molecular Evolution* is similar in structure, content, and aims to two previous tomes in this series: *Mathematical and Statistical Methods for Genetic Analysis* (Lange, 1997) and *Statistical Methods in Bioinformatics* (Ewens and Grant, 2001). In this book, the study of molecular evolution is correctly presented as a series of inferences about past history that are based on incomplete data. It is, therefore, a truism that the field of molecular evolution relies heavily on statistical theory and analysis. Rasmus Nielsen's book presupposes a great deal of mathematical and statistical knowledge, and as such, may only be useful to a small subset of active professionals in the field of molecular evolution. There is very little softening or sweetening of the mathematical bitter rigor; however, we believe that all graduate students in the field of molecular evolution should study this book very carefully and very methodologically, at least if their aim in life is to become something bigger and better than high-end users of black boxes and prepackaged computer programs. We note that several subjects covered by the book, such as MCMC methods and statistical alignment, may also be useful for scientists other than molecular evolutionists.

Rasmus Nielsen's compilation uses a step-by-step approach to introducing statistical models and statistical tools that fit biology reality. He leads the reader through tough mathematical exactitudes until achieving results that best describe the biological subjects under study. The combination of biological accuracy and strong mathematical precision yields a winning approach for studying the statistical underpinnings of molecular evolution.

The book is divided into 4 sections and 17 chapters, and as expected from such a book there is a degree of heterogeneity in quality and coverage that is sometimes disconcerting but rarely disheartening. In the first section of the book, one is introduced to Markov models for describing sequence evolution and phylogenetic analyses, likelihood functions, Monte Carlo approaches and simulations, and population genetics. All four chapters in this section are heavy on theory and light on practical examples, and as such require a degree of immersion and concentration that is uncommon among biologists. The second part of the book is probably the most useful as it deals with questions that are frequently encountered by molecular evolutionists in their daily lives. Here we have the nitty-gritty of detecting adaptive evolution at the protein level, testing of phylogenetic hypotheses, and estimation of divergence times. This part of the book deals exhaustively with computer packages, such as HyPhy and MrBayes, and the reader is provided with intelligent decipherments of two popular black boxes that are sometimes used indiscriminately by practitioners of molecular evolution. All of these chapters include examples and case studies, as well as screenshots from the software packages that were used. The chapter on Bayesian analysis is curiously located in the second section of the volume; it should have been part of the first section of the book because it is largely devoted to methodology. The separation between likelihood and Bayesian methodology seems artificial.

The third part deals with models of molecular evolution. The chapters deal with sequence evolution, evolution of repeated sequences, genomic rearrangements, and phylogenetic testing. We confess that we are not very clear why these chapters were clustered together, although we admire the quality of writing of each chapter. The last part of the book deals with inferences in molecular evolution. Again, we found each chapter useful and enlightening, but we have no clue as to why these chapters were deemed to have a certain theme in common. One of the most interesting chapters in this section deals with recent progress and new applications in the field of sequence alignment.

Who should read this book? We suggest that anyone who deals with molecular data (who does not?) and anyone who asks evolutionary questions (who should not?) ought to consult the relevant chapters in this book. So although *Statistical Methods in Molecular Evolution* is not exactly a *Guide to the Perplexed*, it may help to reduce perplexity considerably. Readers with biological backgrounds are advised not to be intimidated by jargon and obscure mathematical notations; the professional reward of reading this book is too great to be defeated by the compound posterior probability of a Gamma discretization function.

References

Ewens, W. J. and Grant, G. (2001). *Statistical Methods in Bioinformatics: An Introduction.* New York: Springer Verlag.

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WEISS, R. **Modeling Longitudinal Data**. Springer, New York, 2005. xxii + 432 pp. US$84.95/€71.64 (hardback), ISBN 0-387-40271-3.

Longitudinal data are routinely collected in many substantive areas. Statistical methods for the analysis of longitudinal data