Hierarchical Modelling for the Environmental Sciences

Statistical Methods and Applications

James S. Clark and **Alan E. Gelfand**, both at Duke University, USA

'...if you are already quite well acqainted with Bayesian concepts and terminology then this book should provide an excellent guide to the application of these advanced statistical techniques within ecology.'

Justin Travis, Bulletin of the British Ecological Society 2007 38:1

New statistical tools are changing the way in which scientists analyze and interpret data and models. Hierarchical Bayes and Markov Chain Monte Carlo methods for analysis provide a consistent framework for inference and prediction where information is heterogeneous and uncertain, processes are complicated, and responses depend on scale. Nowhere are these methods more promising than in the environmental sciences.

2006 | 216 pages

978-0-19-856967-1, PAPERBACK £34.95/$59.50
978-0-19-856966-4, HARDBACK £65.00/$156.00

Theories of Molecular Reaction Dynamics

The Microscopic Foundation of Chemical Kinetics

Niels E. Henriksen and **Flemming Y. Hansen**, both at the Technical University of Denmark, Lyngby

This book deals with a central topic at the interface of chemistry and physics—the understanding of how the transformation of matter takes place at the atomic level. Building on the laws of physics, the book focuses on the theoretical framework for predicting the outcome of chemical reactions.

Oxford Graduate Texts

December 2007 | 368 pages

978-0-19-920386-4, HARDBACK £45.00/$90.00

Ancestral Sequence Reconstruction

Edited by **David A Liberles**, University of Wyoming, USA

Ancestral sequence reconstruction is an interdisciplinary field of growing importance for understanding the evolution of molecular function. The technique is poised to become a mainstream component of molecular biology and functional genomics. This book represents the first synthesis of theories, methodologies and applications.

May 2007 | 272 pages

978-0-19-929918-8, HARDBACK £49.95/$100.00

BIOGRAPHY

Olivier Gascuel

Olivier Gascuel first studied mathematics although his PhD was in computer science, and he started working in bioinformatics in the 80's, at the very beginning of the genomic era and of the rapid development of interactions between mathematicians, computer scientists and molecular biologists. His first interests were in sequence analysis and protein structure prediction, using machine learning approaches. Since the mid-90's, Olivier Gascuel has concentrated on evolution and phylogenetics, with particular focus on the mathematical and computational tools and concepts. He now leads a research group at the Centre National de la Recherche Scientifique, Montpellier (France). He is an associate editor of *Systematic Biology* (leading journal in the field of Evolution) and belongs to the editorial board of *BMC Bioinformatics*, *BMC Evolutionary Biology*, and *BMC Algorithms for Molecular Biology*. He has published 110 papers and book chapters, and authored several widely used computer programs in phylogenetics and bioinformatics.

He has recently started a new adventure fighting pathogens, especially in Africa and endemic countries.

Reconstructing Evolution

New Mathematical and Computational Advances

Edited by **Olivier Gascuel**, Laboratoire d'Informatique, de Robotique et de Micro-électronique de Montpellier, and **Mike Steel**, University of Canterbury, New Zealand

Evolution is a complex process, acting at multiple scales, from DNA sequences and proteins to populations of species. This collection of 10 chapters—based around five themes—provides a detailed overview of the key topics, from the underlying concepts to the latest results.

June 2007 | 348 pages

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NEW IN PAPERBACK

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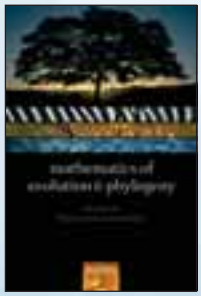

Edited by **Olivier Gascuel**, Centre National de La Recherche Scientifique

'In-depth discussions make *Mathematics of Evolution and Phylogeny* a key reference for those with mathematical or computational perspectives on evolution.'

Systematic Biology 2006

'...an important contribution because it highlights the analysis of evolutiomary problems as potential research avenues in applied mathematics.'

Systematic Biology, Vol 55

'*Mathematics of Evolution and Phylogeny* is a valuable research tool for postgraduate students and researchers wanting an in-depth, overall introduction of the topics that it covers.'

Charles Semple, TRENDS in Ecology and Evolution, Vol 20 No 9

This book of contributed chapters is authored by renowned scientists and covers recent results in the highly topical area of mathematics in evolution and phylogeny. Each chapter is a detailed overview of a specific topic, from the underlying concepts to the latest results.

August 2007 | 440 pages

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978-0-19-856610-6, HARDBACK £60.00/$79.50

Computational Text Analysis

For Functional Genomics and Bioinformatics

Soumya Raychaudhuri, Stanford University, USA

This book brings together the two disparate worlds of computational text analysis and biology and presents some of the latest methods and applications to proteomics, sequence analysis, and gene expression data. Including background chapters on the necessary biology, statistics, and genomics it is ideal for students and researchers in computational biology, bioinformatics, genomics, statistics and computer science.

2006 | 312 pages

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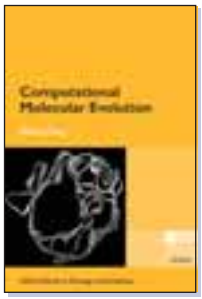
Computational Molecular Evolution



Ziheng Yang, University College London, UK

This book describes the models, methods and algorithms that are most useful for analysing the ever-increasing supply of molecular sequence data, with a view to furthering our understanding of the evolution of genes and genomes.

Oxford Series in Ecology and Evolution

2006 | 376 pages

978-0-19-856702-8, PAPERBACK £27.50/$52.50
978-0-19-856699-1, HARDBACK £60.00/$115.00

NEW IN PAPERBACK

Advanced Distance Sampling

Estimating Abundance of Biological Populations

Edited by **S.T. Buckland**, University of St Andrews, **D.R Anderson**, Colorado Cooperative Fish and Wildlife Research Unit, **K.P. Burnham**, Colorado Cooperative Fish and Wildlife Research Unit, **J.L. Laake**, National Marine Mammal Laboratory, **D.L. Borchers**, University of St Andrews, and **L. Thomas**, University of St Andrews

In this text, a general theoretical basis is established for methods of estimating animal abundance from sightings surveys, and a wide range of approaches to analysis of sightings data is explored. These approaches include: modelling animal detectability as a function of covariates, where the effects of habitat, observer, weather, etc. on detectability can be assessed; estimating animal density as a function of location, allowing for example animal density to be related to habitat and other locational covariates; estimating change over time in populations, a necessary aspect of any monitoring programme; estimation when detection of animals on the line or at the point is uncertain, as often occurs for marine populations, or when the survey region has dense cover; survey design and automated design algorithms, allowing rapid generation of sound survey designs using geographic information systems; adaptive distance sampling methods, which concentrate survey effort in areas of high animal density; passive distance sampling methods, which extend the application of distance sampling to species that cannot be readily detected in sightings surveys, but can be trapped; and testing of methods by simulation, so that performance of the approach in varying circumstances can be assessed.

September 2007 | 434 pages

978-0-19-922587-3, PAPERBACK £24.95/$49.95
978-0-19-850783-3, HARDBACK £56.00/$119.50

Computational Complexity and Statistical Physics

Edited by **Allon Percus**, Institute for Pure & Applied Mathematics, UCLA, **Gabriel Istrate**, Los Alamos National Laboratory, and **Cristopher Moore**, University of New Mexico

Computer science and physics have been closely linked since the birth of modern computing. In recent years, an interdisciplinary area has blossomed at the junction of these fields, connecting insights from statistical physics with basic computational challenges. Researchers have successfully applied techniques from the study of phase transitions to analyze NP-complete problems such as satisfiability and graph coloring. This is leading to a new understanding of the structure of these problems, and of how algorithms perform on them. *Computational Complexity and Statistical Physics* will serve as a standard reference and pedagogical aid to statistical physics methods in computer science, with a particular focus on phase transitions in combinatorial problems. Addressed to a broad range of readers, the book includes substantial background material along with current research by leading computer scientists, mathematicians, and physicists. It will prepare students and researchers from all of these fields to contribute to this exciting area.

Santa Fe Institute Studies on the Sciences of Complexity

2006 | 382 pages

978-0-19-517738-1, PAPERBACK £26.99/$44.50

Statistical Mechanics

Entropy, Order Parameters and Complexity

James Sethna, Cornell University, USA

'The author's style, although quite concentrated, is simple to understand, and has many lovely visual examples to accompany formal ideas and concepts, which makes the exposition live and intuitvely appealing.'

Olga K. Dudko, Journal of Statistical Physics, Vol 126

Sethna's book distills the core ideas of statistical mechanics to make room for new advances important to information theory, complexity, and modern biology. Aimed at advanced undergraduates and early graduate students, Sethna's text explores everything from chaos through information theory to life at the end of the universe.

Oxford Master Series in Physics No. 14

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Journal of Biological Education, Autumn 2006

'This is an excellent book for learning how to approach the design of experimental and, indeed, observational work. It avoids the usual inclusion of statistical detail that turns many students off while retaining all the key issues that are necessary for planning studies that produce good science. I commend this book to all those who struggle to get students to think seriously about designing good scientific studies.'

Higher Education Academy, Bioscience e-Journal, June 2006.

Experimental Design for the Life Sciences explains how to organise experiments and collect data to make analysis easier, and conclusions more robust. An approachable and articulate style conveys even the most challenging concepts in clear and practical terms, showing how experimental design is about clear thinking and biological understanding, not mathematical or statistical complexity.

2006 | 184 pages

978-0-19-928511-2, PAPERBACK £17.99/$20.95

Systems Biology

Edited by **Isidore Rigoutsos**, Lecturer, MIT, and **Gregory Stephanopoulos**, Professor of Chemical Engineering and Biotechnology, MIT

Systems Biology I: Genomics and Systems Biology II: Networks, Models, and Applications offer a much-needed study of genomic principles and their associated networks and models. Written for a wide audience, each volume presents a timely compendium of essential information that is necessary for a comprehensive study of the subject. The chapters in the two volumes reflect the hierarchical nature of systems biology. Chapter authors-world-recognized experts in their fields-provide authoritative discussions on a wide range of topics along this hierarchy. Volume I explores issues pertaining to genomics that range from prebiotic chemistry to noncoding RNAs. Volume II covers an equally wide spectrum, from mass spectrometry to embryonic stem cells. The two volumes are meant to provide a reliable reference for students and researchers alike.

Volume 1: Genomics

Series in Systems Biology

2006 | 360 pages | OUP USA

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Volume II: Networks, Models, and Applications

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