

*Statistics for Biology and Health*

**Rasmus Nielsen**  
Editor

**Statistical  
Methods in  
Molecular  
Evolution**

 Springer

# Statistical Methods In Molecular Evolution

**Kenneth Lange**



## **Statistical Methods In Molecular Evolution:**

Statistical Methods in Molecular Evolution Rasmus Nielsen, 2006-05-06 In the field of molecular evolution inferences about past evolutionary events are made using molecular data from currently living species. With the availability of genomic data from multiple related species, molecular evolution has become one of the most active and fastest growing fields of study in genomics and bioinformatics. Most studies in molecular evolution rely heavily on statistical procedures based on stochastic process modelling and advanced computational methods including high dimensional numerical optimization and Markov Chain Monte Carlo. This book provides an overview of the statistical theory and methods used in studies of molecular evolution. It includes an introductory section suitable for readers that are new to the field, a section discussing practical methods for data analysis, and more specialized sections discussing specific models and addressing statistical issues relating to estimation and model choice. The chapters are written by the leaders of the field and they will take the reader from basic introductory material to the state of the art statistical methods. This book is suitable for statisticians seeking to learn more about applications in molecular evolution and molecular evolutionary biologists with an interest in learning more about the theory behind the statistical methods applied in the field. The chapters of the book assume no advanced mathematical skills beyond basic calculus, although familiarity with basic probability theory will help the reader. Most relevant statistical concepts are introduced in the book in the context of their application in molecular evolution, and the book should be accessible for most biology graduate students with an interest in quantitative methods and theory. Rasmus Nielsen received his Ph.D. from the University of California at Berkeley in 1998 and after a postdoc at Harvard University he assumed a faculty position in Statistical Genomics at Cornell University. He is currently an Ole R. Merz Fellow at the University of Copenhagen and holds a Sloan Research Fellowship. He is an associate editor of the *Journal of Molecular Evolution* and has published more than fifty original papers in peer-reviewed journals on the topic of this book. From the reviews: Overall, this is a very useful book in an area of increasing importance. *Journal of the Royal Statistical Society*: I find *Statistical Methods in Molecular Evolution* very interesting and useful. It delves into problems that were considered very difficult just several years ago; the book is likely to stimulate the interest of statisticians that are unaware of this exciting field of applications. It is my hope that it will also help the wet lab molecular evolutionist to better understand mathematical and statistical methods. *Marek Kimmel for the Journal of the American Statistical Association*, September 2006: 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. *Dan Graur and Dror Berel for Biometrics*, September 2006: Coalescence theory facilitates the merger of population genetics theory with phylogenetic approaches, but still there are mostly two camps: phylogeneticists and population geneticists. Only a few people are moving freely between them. Rasmus Nielsen is certainly one of these researchers, and his work so far has merged many population genetic and phylogenetic aspects of biological research under

the umbrella of molecular evolution Although Nielsen did not contribute a chapter to his book his work permeates all its chapters This book gives an overview of his interests and current achievements in molecular evolution In short this book should be on your bookshelf Peter Beerli for Evolution 60 2 2006 *Molecular Evolution* Ziheng Yang,2014 Studies of evolution at the molecular level have experienced phenomenal growth in the last few decades due to rapid accumulation of genetic sequence data improved computer hardware and software and the development of sophisticated analytical methods The flood of genomic data has generated an acute need for powerful statistical methods and efficient computational algorithms to enable their effective analysis and interpretation Molecular Evolution a statistical approach presents and explains modern statistical methods and computational algorithms for the comparative analysis of genetic sequence data in the fields of molecular evolution molecular phylogenetics statistical phylogeography and comparative genomics Written by an expert in the field the book emphasizes conceptual understanding rather than mathematical proofs The text is enlivened with numerous examples of real data analysis and numerical calculations to illustrate the theory in addition to the working problems at the end of each chapter The coverage of maximum likelihood and Bayesian methods are in particular up to date comprehensive and authoritative This advanced textbook is aimed at graduate level students and professional researchers both empiricists and theoreticians in the fields of bioinformatics and computational biology statistical genomics evolutionary biology molecular systematics and population genetics It will also be of relevance and use to a wider audience of applied statisticians mathematicians and computer scientists working in computational biology *Evolutionary Genomics* Maria Anisimova,2012-03-13 Together with early theoretical work in population genetics the debate on sources of genetic makeup initiated by proponents of the neutral theory made a solid contribution to the spectacular growth in statistical methodologies for molecular evolution Evolutionary Genomics Statistical and Computational Methods is intended to bring together the more recent developments in the statistical methodology and the challenges that followed as a result of rapidly improving sequencing technologies Presented by top scientists from a variety of disciplines the collection includes a wide spectrum of articles encompassing theoretical works and hands on tutorials as well as many reviews with key biological insight Volume 1 includes a helpful introductory section of bioinformatician primers followed by detailed chapters detailing genomic data assembly alignment and homology inference as well as insights into genome evolution from statistical analyses Written in the highly successful Methods in Molecular Biology™ series format this work provides the kind of advice on methodology and implementation that is crucial for getting ahead in genomic data analyses Comprehensive and cutting edge Evolutionary Genomics Statistical and Computational Methods is a treasure chest of state of the art methods to study genomic and omics data certain to inspire both young and experienced readers to join the interdisciplinary field of evolutionary genomics

**Computational Molecular Evolution** Ziheng Yang,2006-10-05 The field of molecular evolution has experienced explosive growth in recent years due to the rapid accumulation of genetic sequence data continuous improvements to

computer hardware and software and the development of sophisticated analytical methods The increasing availability of large genomic data sets requires powerful statistical methods to analyse and interpret them generating both computational and conceptual challenges for the field Computational Molecular Evolution provides an up to date and comprehensive coverage of modern statistical and computational methods used in molecular evolutionary analysis such as maximum likelihood and Bayesian statistics Yang 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 The book emphasizes essential concepts rather than mathematical proofs It includes detailed derivations and implementation details as well as numerous illustrations worked examples and exercises It will be of relevance and use to students and professional researchers both empiricists and theoreticians in the fields of molecular phylogenetics evolutionary biology population genetics mathematics statistics and computer science Biologists who have used phylogenetic software programs to analyze their own data will find the book particularly rewarding although it should appeal to anyone seeking an authoritative overview of this exciting area of computational biology

*Molecular Evolution and Phylogenetics* Masatoshi Nei, Sudhir Kumar, 2000-07-27 During the last ten years remarkable progress has occurred in the study of molecular evolution Among the most important factors that are responsible for this progress are the development of new statistical methods and advances in computational technology In particular phylogenetic analysis of DNA or protein sequences has become a powerful tool for studying molecular evolution Along with this developing technology the application of the new statistical and computational methods has become more complicated and there is no comprehensive volume that treats these methods in depth *Molecular Evolution and Phylogenetics* fills this gap and present various statistical methods that are easily accessible to general biologists as well as biochemists bioinformaticists and graduate students The text covers measurement of sequence divergence construction of phylogenetic trees statistical tests for detection of positive Darwinian selection inference of ancestral amino acid sequences construction of linearized trees and analysis of allele frequency data Emphasis is given to practical methods of data analysis and methods can be learned by working through numerical examples using the computer program MEGA2 that is provided

Statistical Techniques in Molecular Evolution Eli Levy Karin, 2017

**Evolutionary Genomics** Maria Anisimova, 2012-03-08 Together with early theoretical work in population genetics the debate on sources of genetic makeup initiated by proponents of the neutral theory made a solid contribution to the spectacular growth in statistical methodologies for molecular evolution *Evolutionary Genomics Statistical and Computational Methods* is intended to bring together the more recent developments in the statistical methodology and the challenges that followed as a result of rapidly improving sequencing technologies Presented by top scientists from a variety of disciplines the collection includes a wide spectrum of articles encompassing theoretical works and hands on tutorials as well as many reviews with key biological insight Volume 2 begins with phylogenomics and continues with in depth coverage of natural

selection recombination and genomic innovation The remaining chapters treat topics of more recent interest including population genomics omics studies and computational issues related to the handling of large scale genomic data Written in the highly successful Methods in Molecular Biology™ series format this work provides the kind of advice on methodology and implementation that is crucial for getting ahead in genomic data analyses Comprehensive and cutting edge Evolutionary Genomics Statistical and Computational Methods is a treasure chest of state of the art methods to study genomic and omics data certain to inspire both young and experienced readers to join the interdisciplinary field of evolutionary genomics

*Introduction to Evolutionary Genomics* Naruya Saitou, 2018-10-25 This authoritative textbook reference presents a comprehensive introduction to the field of evolutionary genomics The opening chapters describe the fundamental concepts in molecular biology and genome evolution for readers without any prior background in this area This is followed by a detailed examination of genome evolution in various different groups of organisms The text then concludes with a review of practical methods essential to researchers in the field This updated and revised new edition also features historical perspectives on contributions to evolutionary genomics from related fields such as molecular evolution genetics and numerical taxonomy Topics and features introduces the basics of molecular biology covering protein structure and diversity as well as DNA replication transcription and translation examines the phylogenetic relationships of DNA sequences and the processes of mutation neutral evolution and natural selection presents a brief evolutionary history of life surveying the key features of the genomes of prokaryotes eukaryotes viruses and phages vertebrates and humans reviews the various biological omic databases and discusses the analysis of homologous nucleotide and amino acid sequences provides an overview of the experimental sequencing of genomes and transcriptomes and the construction of phylogenetic trees describes methods for estimating of evolutionary distances and performing studies of population genetics supplies additional supporting material at an associated website Serving as an indispensable textbook for graduate and advanced undergraduate courses on evolutionary genomics this accessible overview will also prove invaluable to researchers from both computer science and the biological sciences seeking a primer on the field

*Algebraic Biology* Katsuhisa Horimoto, Georg Regensburger, Markus Rosenkranz, Hiroshi Yoshida, 2008-07-30 This volume contains the proceedings of the Third International Conference on Algebraic Biology AB 2008 Jointly organized by the National Institute of Advanced Industrial Science and Technology AIST Tokyo and the Research Institute for Symbolic Computation RISC Hagenberg Austria it was held from July 31 to August 2 2008 in the Castle of Hagenberg Algebraic biology is an interdisciplinary forum for research on all aspects of applying symbolic computation in biology The first conference on algebraic biology AB 2005 was held November 28 30 2005 in Tokyo the second during July 2 4 2007 in Hagenberg The AB conference series is intended as a bridge between life sciences and symbolic computation On the one hand new insights in biology are found by powerful symbolic methods on the other hand biological problems suggest new algebraic structures and algorithms While this profile has been established in the previous

proceedings the papers in the present volume demonstrate the continuous growth of algebraic biology We received 27 submissions from 14 countries Australia Austria Canada China Colombia France Germany Italy Japan Norway Russia Switzerland UK USA and 14 papers were accepted for publication Each submission was assigned to at least three ProgramCommittee members who carefully reviewed the papers in many cases with the help of external referees The reviews were discussed by the ProgramCommittee for oneweek via the EasyChair conference management system

Encyclopedia of Evolutionary Biology, 2016-04-14 Encyclopedia of Evolutionary Biology Four Volume Set is the definitive go to reference in the field of evolutionary biology It provides a fully comprehensive review of the field in an easy to search structure Under the collective leadership of fifteen distinguished section editors it is comprised of articles written by leading experts in the field providing a full review of the current status of each topic The articles are up to date and fully illustrated with in text references that allow readers to easily access primary literature While all entries are authoritative and valuable to those with advanced understanding of evolutionary biology they are also intended to be accessible to both advanced undergraduate and graduate students Broad topics include the history of evolutionary biology population genetics quantitative genetics speciation life history evolution evolution of sex and mating systems evolutionary biogeography evolutionary developmental biology molecular and genome evolution coevolution phylogenetic methods microbial evolution diversification of plants and fungi diversification of animals and applied evolution Presents fully comprehensive content allowing easy access to fundamental information and links to primary research Contains concise articles by leading experts in the field that ensures current coverage of each topic Provides ancillary learning tools like tables illustrations and multimedia features to assist with the comprehension process

Mathematical and Statistical Methods for Genetic Analysis Kenneth Lange, 2012-12-06 During the past decade geneticists have cloned scores of Mendelian disease genes and constructed a rough draft of the entire human genome The unprecedented insights into human disease and evolution offered by mapping cloning and sequencing will transform medicine and agriculture This revolution depends vitally on the contributions of applied mathematicians statisticians and computer scientists Mathematical and Statistical Methods for Genetic Analysis is written to equip students in the mathematical sciences to understand and model the epidemiological and experimental data encountered in genetics research Mathematical statistical and computational principles relevant to this task are developed hand in hand with applications to population genetics gene mapping risk prediction testing of epidemiological hypotheses molecular evolution and DNA sequence analysis Many specialized topics are covered that are currently accessible only in journal articles This second edition expands the original edition by over 100 pages and includes new material on DNA sequence analysis diffusion processes binding domain identification Bayesian estimation of haplotype frequencies case control association studies the gamete competition model QTL mapping and factor analysis the Lander Green Kruglyak algorithm of pedigree analysis and codon and rate variation models in molecular phylogeny Sprinkled throughout the chapters are many new problems

**Statistical Methods in Molecular Biology** Heejung Bang, Xi Kathy Zhou, Heather L. van Epps, Madhu

Mazumdar, 2016-08-23 This progressive book presents the basic principles of proper statistical analyses. It progresses to more advanced statistical methods in response to rapidly developing technologies and methodologies in the field of molecular biology.

Problems and Solutions in Biological Sequence Analysis Mark Borodovsky, Svetlana Ekisheva, 2006-09-04 This book is the first of its kind to provide a large collection of bioinformatics problems with accompanying solutions. Notably, the problem set includes all of the problems offered in *Biological Sequence Analysis* by Durbin et al. (Cambridge, 1998), widely adopted as a required text for bioinformatics courses at leading universities worldwide. Although many of the problems included in *Biological Sequence Analysis* as exercises for its readers have been repeatedly used for homework and tests, no detailed solutions for the problems were available. Bioinformatics instructors had therefore frequently expressed a need for fully worked solutions and a larger set of problems for use on courses. This book provides just that, following the same structure as *Biological Sequence Analysis* and significantly extending the set of workable problems; it will facilitate a better understanding of the contents of the chapters in BSA and will help its readers develop problem-solving skills that are vitally important for conducting successful research in the growing field of bioinformatics. All of the material has been class-tested by the authors at Georgia Tech, where the first ever MSc degree program in Bioinformatics was held.

*American Book Publishing Record*, 2003

Population Genetics and Molecular Evolution Tomoko Ohta, Kenichi Aoki, 1986

**Techniques in Molecular Systematics and Evolution** Rob DeSalle, Gonzalo Giribet, Ward Wheeler, 2013-12-01 The amount of information that can be obtained by using molecular techniques in evolution, systematics, and ecology has increased exponentially over the last ten years. The need for more rapid and efficient methods of data acquisition and analysis is growing accordingly. This manual presents some of the most important techniques for data acquisition developed over the last years. The choice and justification of data analysis techniques is also an important and critical aspect of modern phylogenetic and evolutionary analysis, and so a considerable part of this volume addresses this important subject. The book is mainly written for students and researchers from evolutionary biology in search for methods to acquire data, but also from molecular biologists who might be looking for information on how data are analyzed in an evolutionary context. To aid the user, information on web-located sites is included wherever possible. Approaches that will push the amount of information which systematics will gather in the

Biostatistical Genetics and Genetic Epidemiology Robert C. Elston, Jane M. Olson, Lyle Palmer, 2002-04-22 Human Genetics concerns the study of genetic forces in man. By studying our genetic make-up, we are able to understand more about our heritage and evolution. Some of the original and most significant research in genetics centred around the study of the genetics of complex diseases, genetic epidemiology. This is the third in a highly successful series of books based on articles from the *Encyclopedia of Biostatistics*. This volume will be a timely and comprehensive reference for a subject that has seen a recent explosion of interest following the completion of the first draft of the Human

Genome Mapping Project The editors have updated the articles from the Human Genetics section of the EoB have adapted other articles to give them a genetic feel and have included a number of newly commissioned articles to ensure the work is comprehensive and provides a self contained reference

*Molecular Evolution of Physiological Processes* Society of General Physiologists. Symposium,1994     **Folia Zoologica** ,2008     *Mathematical Reviews* ,2006

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