

Statistics for Biology and Health

Rasmus Nielsen
Editor

**Statistical
Methods in
Molecular
Evolution**

 Springer

Statistical Methods In Molecular Evolution

Ziheng Yang



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, 2016-05-01 This book examines developments in statistical methodology and the challenges that followed rapidly improving sequencing technologies Includes articles encompassing theoretical works and hands on tutorials as well as many reviews with key biological insight

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 *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 *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 presents 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.

Plant Molecular Evolution J.J. Doyle, Brandon S. Gaut, 2012-12-06

Plant molecular biology has produced an ever increasing flood of data about genes and genomes. Evolutionary biology and systematics provides the context for synthesizing this information. This book brings together contributions from evolutionary biologists, systematists, developmental geneticists, biochemists, and others working on diverse aspects of plant biology whose work touches to varying degrees on plant molecular evolution. The book is organized in three parts, the first of which introduces broad topics in evolutionary biology and summarizes advances in plant molecular phylogenetics with emphasis on model plant systems. The second segment presents a series of case studies of gene family evolution, while the third gives overviews of the evolution of important plant processes such as disease resistance, nodulation, hybridization, transposable elements, and genome evolution and polyploidy.

Phylogenetic Trees and Molecular Evolution David R. Bickel, 2022-09-29

This book serves as a brief introduction to phylogenetic trees and molecular evolution for biologists and biology students. It does so by presenting the main concepts in a variety of ways: first visually, then in a history, next in a dice game, and finally in simple equations. The content is primarily designed to introduce upper level undergraduate and graduate students of biology to phylogenetic tree reconstruction and the underlying models of molecular evolution. A unique feature, also of interest to experienced researchers, is the emphasis on simple ways to quantify the uncertainty in the results more fully than is possible with standard methods.

Molecular Evolution Vadim A. Ratner, Andrey A. Zharkikh, Nikolay Kolchanov, Sergey N. Rodin, Viktor V. Solovyov, Andrey S. Antonov, 2013-03-09

In 1970 Manfred Eigen initiated the study of the origin of self-reproducing systems of macromolecules and their evolution. Large scale nucleotide sequencing with computer methods was introduced from 1977. The authors of this book, the first edition of which appeared in Russian in 1985, have been engaged in the research of the evolution of molecular genetic regulatory systems ever since those pioneering years. The book considers many fundamental problems of molecular biology: evolution, molecular genetic organization, the structure and function of macromolecules, always with the underlying motive of developing a unified theory. It describes many original theoretical results as well as computational methods.

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