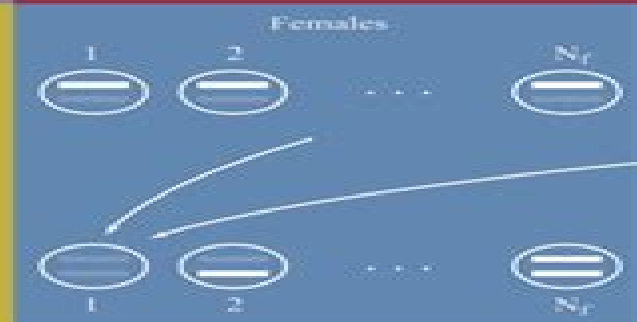
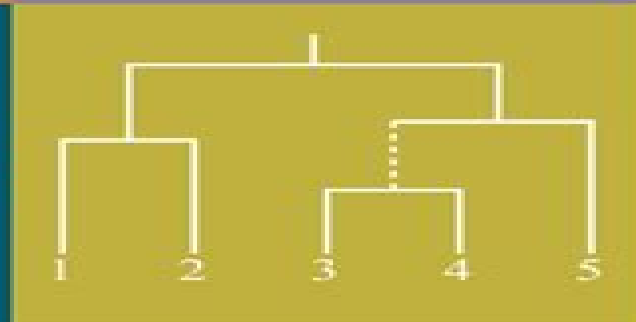
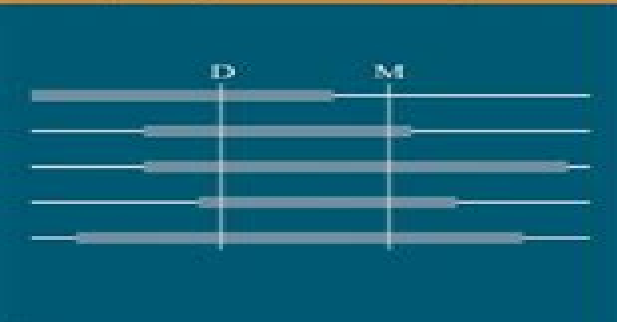
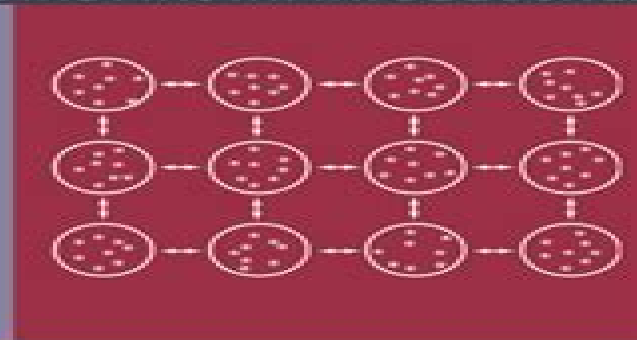
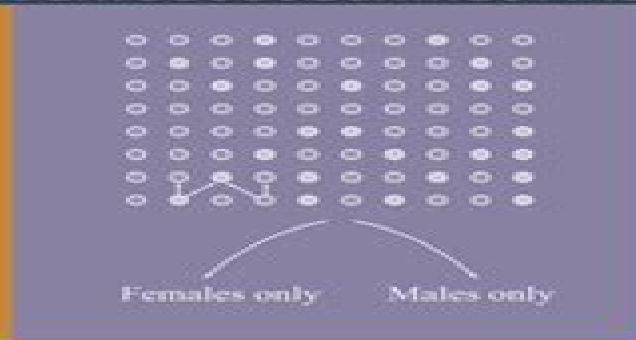
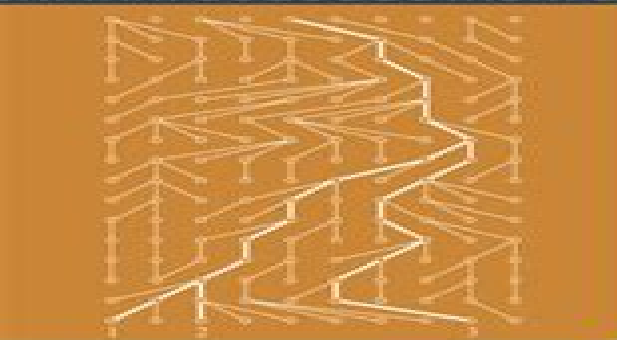


Gene Genealogies, Variation and Evolution

A PRIMER IN COALESCENT THEORY

Jotun Hein
Mikkel H. Schierup
Carsten Wiuf



Gene Genealogies Variation And Evolution A Primer In Coalescent Theory

Jotun Hein, Mikkel Schierup, Carsten Wiuf



Gene Genealogies Variation And Evolution A Primer In Coalescent Theory:

Gene Genealogies, Variation and Evolution: A primer in coalescent theory Jotun Hein, Mikkel Schierup, Carsten Wiuf, 2004-12-09 Authored by leading experts this seminal text presents a straightforward and elementary account of coalescent theory which is a central concept in the study of genetic sequence variation observed in a population Rich in examples and illustrations it is ideal for a graduate course in statistics population molecular and medical genetics bioscience and medicine and for students studying the evolution of human population and disease It is also an invaluable reference for bioscientists and statisticians in the pharmaceutical industry and academia Coalescent theory is a central concept in the study of genetic sequence variation that probabilistically describes the genealogy relating the sampled sequences In this text besides fulfilling the glaring need for such a book the authors present this theory in a straightforward and elementary manner and describe the statistical and computational methods used in modelling and analyzing genetic sequence variation Rich in examples and illustrations the book covers basic concepts complications arising from geographical structure and recombination before considering aspects of statistical inference based on these models The book ends with chapters on Gene Mapping which combines sequence variation data with phenotypic data such as disease to define areas of the genome where genes are responsible for the trait and Human Evolution a research area that is experiencing a renaissance due to the enormous amounts of data produced in molecular studies Authored by leading experts this seminal text presents a straightforward and elementary account of coalescent theory which is a central concept in the study of genetic sequence variation observed in a population It is highly suitable for a graduate course in statistics population molecular and medical genetics bioscience and medicine and students studying the evolution of human population and disease and will be an invaluable reference for bioscientists and statisticians in the pharmaceutical industry and academia an excellent and timely book that should appeal to a variety of people in genetics and applied mathematics Professor Montgomery Slatkin Berkeley the authors are outstanding experts in the field and the book is topical and timely Professor David Balding Imperial College Hein Schierup and Wiuf have written the first general book on the coalescent It is an engaging combination of clear mathematical derivation and real data examples Professor Joe Felsenstein University of Washington

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Bioinformatics Research and Applications Ion Mandoiu, Giri Narasimhan, Yanqing Zhang, 2009-04-29 This book constitutes the refereed proceedings of the 5th International Symposium on Bioinformatics Research and Applications ISBRA 2009 held in Fort Lauderdale FL USA in May 2009 The 26 revised full papers presented together four invited papers were carefully reviewed and selected from a total of 55 submissions The papers cover a wide range of topics including clustering and classification gene expression analysis gene networks genome analysis motif finding pathways protein structure prediction protein domain interactions phylogenetics and software tools

Computational Molecular Evolution Ziheng Yang, 2006-10-05 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

Application and Theory of Petri Nets Serge Haddad, Lucia Pomello, 2012-06-06 This book constitutes the refereed proceedings of the 33rd International Conference on Applications and Theory of Petri Nets and Concurrency PETRI NETS 2012 held in Hamburg Germany in June 2012 The 18 regular papers and 3 tool papers presented were carefully reviewed and selected from 55 submissions The book also contains 2 invited talks All current issues on research and development in the area of Petri nets and related models of concurrent systems are addressed

Genomic characterization of animal genetic resources Food and Agriculture Organization of the United Nations, Ajmone-Marsan, P, Boettcher, P. J., Ginja, C., Kantanen J., Lenstra, J.A, 2023-01-12 Molecular biotechnologies have developed rapidly and substantially since the release of these previous guidelines The livestock sector has been an active participant in the so called genomic revolution Advancements in the sequencing of genomes and related genotyping methods have created opportunities for gathering much more information on the molecular level than ever possible at a faster rate and for exponentially decreased costs Scientists and other livestock stakeholders in countries with highly developed economies have been among the main beneficiaries of this revolution However the greatly decreased costs of genomic applications have also created opportunities in countries with developing and transitional economies In many instances the lack of awareness of these opportunities and in the technical capacity for the full application of genomic tools may represent a greater obstacle to their utilization than the expenses involved The development of these guidelines and the subsequent application of the information contained herein may help to bridge this gap bringing new opportunities to light and transferring knowledge that can be used to increase the genetic characterization of AnGR and subsequently improve the sustainable use and conservation of

livestock genetic diversity **Problem Solving Handbook in Computational Biology and Bioinformatics** Lenwood S. Heath, Naren Ramakrishnan, 2010-10-20 Bioinformatics is growing by leaps and bounds theories algorithms statistical techniques are constantly evolving Nevertheless a core body of algorithmic ideas have emerged and researchers are beginning to adopt a problem solving approach to bioinformatics wherein they use solutions to well abstracted problems as building blocks to solve larger scope problems Problem Solving Handbook for Computational Biology and Bioinformatics is an edited volume contributed by world renowned leaders in this field This comprehensive handbook with problem solving emphasis covers all relevant areas of computational biology and bioinformatics Web resources and related themes are highlighted at every opportunity in this central easy to read reference Designed for advanced level students researchers and professors in computer science and bioengineering as a reference or secondary text this handbook is also suitable for professionals working in this industry *Reconstructing Evolution* Olivier Gascuel, Mike Steel, 2007-06-28 Evolution is a complex process acting at multiple scales from DNA sequences and proteins to populations of species Understanding and reconstructing evolution is of major importance in numerous subfields of biology For example phylogenetics and sequence evolution is central to comparative genomics attempts to decipher genomes and molecular epidemiology Phylogenetics is also the focal point of large scale international biodiversity assessment initiatives such as the Tree of Life project which aims to build the evolutionary tree for all extant species Since the pioneering work in phylogenetics in the 1960s models have become increasingly sophisticated to account for the inherent complexity of evolution They rely heavily on mathematics and aim at modelling and analyzing biological phenomena such as horizontal gene transfer heterogeneity of mutation and speciation and extinction processes This book presents these recent models their biological relevance their mathematical basis their properties and the algorithms to infer them from data A number of subfields from mathematics and computer science are involved combinatorics graph theory stringology probabilistic and Markov models information theory statistical inference Monte Carlo methods continuous and discrete algorithmics This book arises from the Mathematics of Evolution Phylogenetics meeting at the Mathematical Institute Henri Poincaré Paris in June 2005 and is based on the outstanding state of the art reports presented by the conference speakers Ten chapters based around five themes provide a detailed overview of key topics from the underlying concepts to the latest results some of which are at the forefront of current research

Probability and Mathematical Genetics N. H. Bingham, C. M. Goldie, 2010-07-15 Focussing on the work of Sir John Kingman one of the world's leading researchers in probability and mathematical genetics this book touches on the important areas of these subjects in the last 50 years Leading authorities give a unique insight into a wide range of currently topical problems Papers in probability concentrate on combinatorial and structural aspects in particular exchangeability and regeneration The Kingman coalescent links probability with mathematical genetics and is fundamental to the study of the latter This has implications across the whole of genomic modelling including the Human Genome Project Other papers in

mathematical population genetics range from statistical aspects including heterogeneous clustering to the assessment of molecular variability in cancer genomes Further papers in statistics are concerned with empirical deconvolution perfect simulation and wavelets This book will be warmly received by established experts as well as their students and others interested in the content **Biodiversity and Evolution** Philippe Grandcolas,Marie-Christine Maurel,2018-04-17

Biodiversity and Evolution includes chapters devoted to the evolution and biodiversity of organisms at the molecular level based on the study of natural collections from the Museum of Natural History The book starts with an epistemological and historical introduction and ends with a critical overview of the Anthropocene epoch Explores the study of natural collections of the Museum of Natural History Examines evolution and biodiversity at the molecular level Features an introduction focusing on epistemology and history Provides a critical overview Estimating Species Trees L. Lacey Knowles,Laura S. Kubatko,2011-05-09 Recent computational and modeling advances have produced methods for estimating species trees directly avoiding the problems and limitations of the traditional phylogenetic paradigm where an estimated gene tree is equated with the history of species divergence The overarching goal of the volume is to increase the visibility and use of these new methods by the entire phylogenetic community by specifically addressing several challenges i firm understanding of the theoretical underpinnings of the methodology ii empirical examples demonstrating the utility of the methodology as well as its limitations and iii attention to technical aspects involved in the actual software implementation of the methodology As such this volume will not only be poised to become the quintessential guide to training the next generation of researchers but it will also be instrumental in ushering in a new phylogenetic paradigm for the 21st century **Theory and Practice of**

Natural Computing Carlos Martín-Vide,Geoffrey Pond,Miguel A. Vega-Rodríguez,2019-11-22 This book constitutes the refereed proceedings of the 8th International Conference on Theory and Practice of Natural Computing TPNC 2019 held in Kingston ON Canada in December 2019 The 15 full papers presented in this book together with two invited talk were carefully reviewed and selected from 38 submissions The papers are organized in topical sections named Applications of Natural Computing Evolutionary Computation Genetic Algorithms Swarm Intelligence and Heuristics Quantum Computing and Information **Research in Computational Molecular Biology** Alberto Apostolico,Concettina Guerra,Sorin

Istrail,Pavel Pevzner,Michael Waterman,2006-03-22 This book constitutes the refereed proceedings of the 10th Annual International Conference on Research in Computational Molecular Biology RECOMB 2006 held in Venice Italy in April 2006 The 40 revised full papers presented together with abstracts of 7 keynote talks were carefully reviewed and selected from 212 submissions As the top conference in computational molecular biology RECOMB addresses all current issues in algorithmic theoretical and experimental bioinformatics **The Philosophy of Evolutionary Theory** Elliott

Sober,2024-02-08 Natural selection mutation and adaptation are well known and central topics in Darwin s theory of evolution and in the 20th and 21st century theories which grew out of it but many other important topics are used in

evolutionary biology that raise interesting philosophical questions In this book Elliott Sober analyses a much larger range of topics including fitness altruism common ancestry chance taxonomy phylogenetic inference operationalism reductionism conventionalism null hypotheses and default reasoning instrumentalism versus realism hypothetico deductivism essentialism falsifiability the principle of parsimony the principle of the common cause causality determinism versus indeterminism sensitivity to initial conditions and the knowability of the past Sober's clear philosophical analyses of these key concepts arguments and methods of inference will be valuable for all readers who want to understand evolutionary biology in both its Darwinian and its contemporary forms

Comparative Genomics Giltai Song, 2025-08-31 This book constitutes the proceedings of the 22nd International Conference on Comparative Genomics RECOMB CG 2025 which was held in Seoul South Korea during April 24-25, 2025. The 21 full papers presented in this book were carefully reviewed and selected from 27 submissions. The papers are divided into the following topical sections: Cancer Genomics, Homology and Reconciliation, Phylogenetics, Sequence Analysis, Epidemiology and Genome Evolution.

The Evolutionary Biology of Species Timothy G. Barraclough, 2019 Species are central to understanding the origin and dynamics of biological diversity explaining why lineages split into multiple distinct species is one of the main goals of evolutionary biology. However, the existence of species is often taken for granted and precisely what is meant by species and whether they really exist as a pattern of nature has rarely been modelled or critically tested. This novel book presents a synthetic overview of the evolutionary biology of species describing what species are, how they form, the consequences of species boundaries and diversity for evolution and patterns of species accumulation over time. The central thesis is that species represent more than just a unit of taxonomy; they are a model of how diversity is structured as well as how groups of related organisms evolve. The author adopts an intentionally broad approach, stepping back from the details to consider what species constitute both theoretically and empirically and how we detect them, drawing on a wealth of examples from microbes to multicellular organisms.

Statistical Modelling in Biostatistics and Bioinformatics Gilbert MacKenzie, Defen Peng, 2014-05-08 This book presents selected papers on statistical model development related mainly to the fields of Biostatistics and Bioinformatics. The coverage of the material falls squarely into the following categories: a) Survival analysis and multivariate survival analysis, b) Time series and longitudinal data analysis, c) Statistical model development, and d) Applied statistical modelling. Innovations in statistical modelling are presented throughout each of the four areas with some intriguing new ideas on hierarchical generalized non-linear models and on frailty models with structural dispersion, just to mention two examples. The contributors include distinguished international statisticians such as Philip Hougaard, John Hinde, Il Do Ha, Roger Payne, and Alessandra Durio, among others, as well as promising newcomers. Some of the contributions have come from researchers working in the BIO-SI research programme on Biostatistics and Bioinformatics centred on the Universities of Limerick and Galway in Ireland and funded by the Science Foundation Ireland under its Mathematics Initiative.

Algebraic and Discrete Mathematical Methods for Modern

Biology Raina Robeva, 2015-05-09 Written by experts in both mathematics and biology Algebraic and Discrete Mathematical Methods for Modern Biology offers a bridge between math and biology providing a framework for simulating analyzing predicting and modulating the behavior of complex biological systems Each chapter begins with a question from modern biology followed by the description of certain mathematical methods and theory appropriate in the search of answers Every topic provides a fast track pathway through the problem by presenting the biological foundation covering the relevant mathematical theory and highlighting connections between them Many of the projects and exercises embedded in each chapter utilize specialized software providing students with much needed familiarity and experience with computing applications critical components of the modern biology skill set This book is appropriate for mathematics courses such as finite mathematics discrete structures linear algebra abstract modern algebra graph theory probability bioinformatics statistics biostatistics and modeling as well as for biology courses such as genetics cell and molecular biology biochemistry ecology and evolution Examines significant questions in modern biology and their mathematical treatments Presents important mathematical concepts and tools in the context of essential biology Features material of interest to students in both mathematics and biology Presents chapters in modular format so coverage need not follow the Table of Contents Introduces projects appropriate for undergraduate research Utilizes freely accessible software for visualization simulation and analysis in modern biology Requires no calculus as a prerequisite Provides a complete Solutions Manual Features a companion website with supplementary resources Bioinformatics for Biologists Pavel Pevzner, Ron Shamir, 2011-09-15 The computational education of biologists is changing to prepare students for facing the complex datasets of today's life science research In this concise textbook the authors fresh pedagogical approaches lead biology students from first principles towards computational thinking A team of renowned bioinformaticians take innovative routes to introduce computational ideas in the context of real biological problems Intuitive explanations promote deep understanding using little mathematical formalism Self contained chapters show how computational procedures are developed and applied to central topics in bioinformatics and genomics such as the genetic basis of disease genome evolution or the tree of life concept Using bioinformatic resources requires a basic understanding of what bioinformatics is and what it can do Rather than just presenting tools the authors each a leading scientist engage the students problem solving skills preparing them to meet the computational challenges of their life science careers Molecular Evolution Ziheng Yang, 2014-05-16 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

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