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Population Genetics of Multiple Loci

F. B. Christiansen

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Population Genetics Of Multiple Loci

**Tyler J. Carrier, Adam M.
Reitzel, Andreas Heyland**



Population Genetics Of Multiple Loci:

Population Genetics of Multiple Loci Freddy B. Christiansen, 2000-01-10 Population Genetics of Multiple Loci F B Christiansen University of Aarhus Denmark This is a very beautiful and powerful study of an area that Christiansen has dominated for many years Marcus Feldman Stanford University USA Population genetics thrives on the constant interaction between theoretical and empirical knowledge In the first instance population genetics was developed using one locus two allele models for genetic variation The simplicity of these models opened up theoretical developments in population and evolutionary genetics to biologists without specialist training in mathematics Population genetics of multi allelic loci is more complex and requires more mathematical insight and its study is predominantly undertaken by mathematical biologists Traditional formulations of multi locus theory do not simplify by assuming two alleles per locus In this elegant presentation the author provides a formulation of multi locus population genetics that retains the simplicity of two allele models Provides an accessible and natural extension of classical population genetics to multiple loci Exposes the population genetic aspects of sexual reproduction Describes the complexity of evolutionary interactions among genes Provides the background for insight into the functioning of genetic algorithms applied in computer science Written by a world leader in the field The book is divided into two main sections Part I Recombination and Segregation includes coverage of random mating inbreeding migration and mixing Part II Selection covers numerous phenomena involving natural selection including viability fertility mutation and migration The author has successfully presented the theory in a way that is intelligible to anyone with a reasonably good background in basic mathematics and is devoted to learning multiple loci population genetics The text is primarily aimed at advanced undergraduate and postgraduate students and researchers interested in genetics and population biology It is also essential reading for those working or researching in biomathematics and adaptive computing

Population Genetics Matthew B. Hamilton, 2021-02-09 Now updated for its second edition Population Genetics is the classic accessible introduction to the concepts of population genetics Combining traditional conceptual approaches with classical hypotheses and debates the book equips students to understand a wide array of empirical studies that are based on the first principles of population genetics Featuring a highly accessible introduction to coalescent theory as well as covering the major conceptual advances in population genetics of the last two decades the second edition now also includes end of chapter problem sets and revised coverage of recombination in the coalescent model metapopulation extinction and recolonization and the fixation index

Population Genetics and Microevolutionary Theory Alan R. Templeton, 2021-05-04 Population Genetics and Microevolutionary Theory Explore the fundamentals of the biological implications of population genetic theory In the newly revised Second Edition of Population Genetics and Microevolutionary Theory accomplished researcher and author Alan R Templeton delivers a fulsome discussion of population genetics with coverage of exciting new developments in the field including new discoveries in epigenetics and genome wide studies The book prepares students to

successfully apply population genetics analytical tools by providing a solid foundation in microevolutionary theory. The book emphasizes that population structure forms the underlying template upon which quantitative genetics and natural selection operate and is a must read for future population and evolutionary geneticists and those who wish to work in genetic epidemiology or conservation biology. You will learn about a wide array of topics including quantitative genetics, the interactions of natural selection with other evolutionary forces and selection in heterogeneous environments and age structured populations. Appendices that cover genetic survey techniques and probability and statistics conclude the book. Readers will also benefit from the inclusion of a thorough introduction to population genetics including the scope of the subject, its premises and the Hardy Weinberg Model of Microevolution. An exploration of systems of mating including a treatment of the use of runs of homozygosity to show pedigree inbreeding in distant ancestors. A practical discussion of genetic drift including the use of effective sizes in conservation biology with a discussion of African rhinos as an example. A concise examination of coalescence including a treatment of the infinite sites model. Perfect for graduate students in genetics and evolutionary biology programs and advanced undergraduate biology majors. *Population Genetics and Microevolutionary Theory* will also earn a place in the libraries of students taking courses in conservation biology, human genetics, bioinformatics and genomics.

Population Genetics W.J. Ewens, 2013-03-12. Population genetics is the mathematical investigation of the changes in the genetic structure of populations brought about by selection, mutation, inbreeding, migration and other phenomena together with those random changes deriving from chance events. These changes are the basic components of evolutionary progress and an understanding of their effect is therefore necessary for an informed discussion of the reasons for and nature of evolution. It would however be wrong to pretend that a mathematical theory depending as it must on a large number of simplifying assumptions should be accepted unreservedly and that its conclusions should be accepted uncritically. No one would pretend that in the event of disagreement between observation and mathematical prediction the discrepancy is due to anything other than the inadequacy of the mathematical treatment. The biological world is of course far too complex for the study of population genetics to be simply a branch of applied mathematics so that while we are concerned here with the mathematical theory I have tried to indicate which of our results should continue to apply in a context wider than that in which they are formally derived. The difficulties involved in the joint discussions of mathematical and genetical problems are obvious enough. I have tried to aim this book rather more at the mathematician than at the geneticist and for this reason a brief glossary of common genetical terms is included. One-Locus and Multi-Locus Theory and Recombination Igor M. Rouzine, 2020-11-23. The book will benefit a reader with a background in physical sciences and applied mathematics interested in the mathematical models of genetic evolution. In the first chapter we analyze several thought experiments based on a basic model of stochastic evolution of a single genomic site in the presence of the factors of random mutation, directional natural selection and random genetic drift. In the second chapter we present a more advanced theory for a large number of

linked loci In the third chapter we include the effect of genetic recombination into account and find out the advantage of sexual reproduction for adaptation These models are useful for the evolution of a broad range of asexual and sexual populations including virus evolution in a host and a host population *Conservation and the Genetics of Populations* Fred W. Allendorf, Gordon H. Luikart, Sally N. Aitken, 2012-12-17 Loss of biodiversity is among the greatest problems facing the world today Conservation and the Genetics of Populations gives a comprehensive overview of the essential background concepts and tools needed to understand how genetic information can be used to conserve species threatened with extinction and to manage species of ecological or commercial importance New molecular techniques statistical methods and computer programs genetic principles and methods are becoming increasingly useful in the conservation of biological diversity Using a balance of data and theory coupled with basic and applied research examples this book examines genetic and phenotypic variation in natural populations the principles and mechanisms of evolutionary change the interpretation of genetic data from natural populations and how these can be applied to conservation The book includes examples from plants animals and microbes in wild and captive populations This second edition contains new chapters on Climate Change and Exploited Populations as well as new sections on genomics genetic monitoring emerging diseases metagenomics and more One third of the references in this edition were published after the first edition Each of the 22 chapters and the statistical appendix have a Guest Box written by an expert in that particular topic including James Crow Louis Bernatchez Loren Rieseberg Rick Shine and Lisette Waits This book is essential for advanced undergraduate and graduate students of conservation genetics natural resource management and conservation biology as well as professional conservation biologists working for wildlife and habitat management agencies Additional resources for this book can be found at www.wiley.com/go/allendorf/populations

Bacterial Population Genetics in Infectious Disease D. Ashley Robinson, Edward J Feil, Daniel Falush, 2010-03-16 This book is a unique synthesis of the major concepts and methods in bacterial population genetics in infectious disease a field that is now about 35 yrs old Emphasis is given to explaining population level processes that shape genetic variation in bacterial populations and statistical methods of analysis of bacterial genetic data A how to of bacterial population genetics which covers an extremely large range of organisms Expanding area of science due to high throughput genome sequencing of bacterial pathogens Covers both fundamental approaches to analyzing bacterial population structures with conceptual background in bacterial population biology Detailed treatment of statistical methods **Population Genetics for Animal Conservation** Giorgio Bertorelle, 2009-05-28 Illustrates the power and utility of the synergy between population genetics and conservation biology in animal conservation *Molecular Evolution and Population Genetics for Marine Biologists* Yuri Kartavtsev, 2015-08-24 Research in modern experimental and theoretical population genetics has been strengthened by advances in molecular techniques for the analysis of genetic variability The evolutionary relationships of organisms may be investigated by comparing DNA sequences This book covers chapters on population genetics DNA polymorphism genetic

homeostasis and Population Genetics of Bacteria Society for General Microbiology. Symposium, S. Baumberg, 1995-02-02 A authoritative summary of the current knowledge of the genetic organisation of bacterial populations

Transmission and Population Genetics Benjamin A. Pierce, 2006-01-09 This new brief version of Benjamin Pierce's *Genetics: A Conceptual Approach* Second Edition responds to a growing trend of focusing the introductory course on transmission and population genetics and covering molecular genetics separately The book is comprised of following chapters and case studies from Pierce's complete text 1 Introduction to Genetics 2 Chromosomes and Cellular Reproduction 3 Basic Principles of Heredity 4 Sex Determination and Sex Linked Characteristics 5 Extensions and Modifications of Basic Principles 6 Pedigree Analysis and Applications INTEGRATIVE CASE STUDY Phenylketonuria Part I 7 Linkage Recombination and Eukaryotic Gene Mapping 8 Bacterial and Viral Genetic Systems 9 Chromosome Variation INTEGRATIVE CASE STUDY Phenylketonuria Part II 22 Quantitative Genetics 23 Population Genetics and Molecular Evolution INTEGRATIVE CASE STUDY Phenylketonuria Part III

Population Genetics of Forest Trees W.T. Adams, Steven H. Strauss, Donald L. Copes, A.R. Griffin, 2012-12-06 Tropical climates which occur between 23° 30' N and S latitude Jacob 1988 encompass a wide variety of plant communities Hartshorn 1983 1988 many of which are diverse in their woody floras Within this geographic region temperature and the amount and seasonality of rainfall define habitat types UNESCO 1978 The FAO has estimated that there are about 19 million km² of potentially forested area in the global tropics of which 58% were estimated to still be in closed forest in the mid 1970s Sommers 1976 UNESCO 1978 Of this potentially forested region 42% is categorized as dry forest lifezone 33% is tropical moist forest and 25% is wet or rain forest Lugo 1988 The species diversity of these tropical habitats is very high Raven 1976 in Mooney 1988 estimated that 65% of the 250 000 or more plant species of the earth are found in tropical regions Of this floristic assemblage a large fraction are woody species In the well collected tropical moist forest of Barro Colorado Island Panama 39 7% 481 of 1212 species of the native phanerogams are woody arborescent species Croat 1978 Another 21 9% are woody vines and lianas Southeast Asian Dipterocarp forests may contain 120 200 species of trees per hectare Whitmore 1984 and recent surveys in upper Amazonia recorded from 89 to 283 woody species 10 cm dbh per hectare Gentry 1988 Tropical communities thus represent a global woody flora of significant scope

Theories of Population Variation in Genes and Genomes Freddy B. Christiansen, 2008 This textbook provides an authoritative introduction to both classical and coalescent approaches to population genetics Written for graduate students and advanced undergraduates by one of the world's leading authorities in the field the book focuses on the theoretical background of population genetics while emphasizing the close interplay between theory and empiricism Traditional topics such as genetic and phenotypic variation mutation migration and linkage are covered and advanced by contemporary coalescent theory which describes the genealogy of genes in a population ultimately connecting them to a single common ancestor Effects of selection particularly genomic effects are discussed with reference to molecular genetic variation The book is designed for students of population genetics bioinformatics evolutionary

biology molecular evolution and theoretical biology as well as biologists molecular biologists breeders biomathematicians and biostatisticians Contains up to date treatment of key areas in classical and modern theoretical population genetics Provides in depth coverage of coalescent theory Discusses genomic effects of selection Gives examples from empirical population genetics Incorporates figures diagrams and boxed features throughout Includes end of chapter exercises Speaks to a wide range of students in biology bioinformatics and biostatistics

The Applications of New Multi-Locus GWAS Methodologies in the Genetic Dissection of Complex Traits Yuan-Ming Zhang,Zhenyu Jia,Jim M Dunwell,2019-06-19 Genome Wide Association Studies GWAS are widely used in the genetic dissection of complex traits Most existing methods are based on single marker association in genome wide scans with population structure and polygenic background controls To control the false positive rate the Bonferroni correction for multiple tests is frequently adopted This stringent correction results in the exclusion of important loci especially for GWAS in crop genetics To address this issue multi locus GWAS methodologies have been recommended i e FASTmrEMMA ISIS EM BLASSO mrMLM FASTmrMLM pLARmEB pKWmEB and FarmCPU In this Research Topic our purpose is to clarify some important issues in the application of multi locus GWAS methods Here we discuss the following subjects First we discuss the advantages of new multi locus GWAS methods over the widely used single locus GWAS methods in the genetic dissection of complex traits metabolites and gene expression levels Secondly large experiment error in the field measurement of phenotypic values for complex traits in crop genetics results in relatively large P values in GWAS indicating the existence of small number of significantly associated SNPs To solve this issue a less stringent P value critical value is often adopted i e 0.001 0.0001 and $1/m$ m is the number of markers Although lowering the stringency with which an association is made could identify more hits confidence in these hits would significantly drop In this Research Topic we propose a new threshold of significant QTN LOD 3.0 or P value 2.0×10^{-4} in multi locus GWAS to balance high power and low false positive rate Thirdly heritability missing in GWAS is a common phenomenon and a series of scientists have explained the reasons why the heritability is missing In this Research Topic we also add one additional reason and propose the joint use of several GWAS methodologies to capture more QTNs Thus overall estimated heritability would be increased Finally we discuss how to select and use these multi locus GWAS methods

Solanaceae VII: Biology, Genetics, and Evolution Peter Poczai,Nunzio D'Agostino,Rocio Deanna,Ezio Portis,2023-02-10

Phylogeography and Population Genetics in Crustacea Christoph Held,Stefan Koenemann,Christoph D. Schubart,2016-04-19 Recently technological progress and the rise of DNA barcoding efforts have led to a significant increase in the availability of molecular datasets on intraspecific variability Carcinologists and other organismal biologists who want to use molecular tools to investigate patterns on the scale of populations face a bewildering variety of genetic m

Evolutionary Ecology of Marine Invertebrate Larvae Tyler J. Carrier,Adam M. Reitzel,Andreas Heyland,2018 Marine invertebrate larvae are an integral part of pelagic diversity and have stimulated the curiosity of researchers for centuries This book integrates the latest research in

order to provide a modern synthesis of this interdisciplinary field *Population Genetics* Laurence Cook, 2012-12-06

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 **Introduction to Theoretical Population Genetics** Thomas

Nagylaki, 2013-03-12 This book covers those areas of theoretical population genetics that can be investigated rigorously by elementary mathematical methods I have tried to formulate the various models fairly generally and to state the biological assumptions quite explicitly I hope the choice and treatment of topics will enable the reader to understand and evaluate detailed analyses of many specific models and applications in the literature Models in population genetics are highly idealized often even over idealized and their connection with observation is frequently remote Further more it is not practicable to measure the parameters and variables in these models with high accuracy These regrettable circumstances amply justify the use of appropriate lucid and rigorous approximations in the analysis of our models and such approximations are often illuminating even when exact solutions are available However our empirical and theoretical limitations justify neither opaque incomplete formulations nor unconvincing inadequate analyses for these may produce uninterpretable misleading or erroneous results Intuition is a principal source of ideas for the construction and investigation of models but it can replace neither clear formulation nor careful analysis Fisher 1930 1958 pp x 23 24 38 not only espoused similar ideas but he recognized also that our concepts of intuition and rigor must evolve in time The book is neither a review of the literature nor a compendium of results The material is almost entirely self contained The first eight chapters are a thoroughly revised and greatly extended version of my published lecture notes Nagylaki 1977a

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