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# Population Genetics of Multiple Loci

E. B. Christiansen

 WILEY

# Population Genetics Of Multiple Loci

**Mark Nelson Grote**



## **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 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 ll 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** Matthew B. Hamilton, 2021-01-26 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

**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

**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 pLARM EB 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 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  $2.0 \times 10^{-4}$  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 **Population Genetics in Animal**

**Breeding** Franz Pirchner, 1983-04 Genetic structure of population Changes in gene frequency Inbreeding Quantitative genetics Repeatability Heritability Aids to selection Empirical tests of selection theory Crossbreeding Breeding plans

*Population Genetics and Molecular Evolution* Tomoko Ohta, Kenichi Aoki, 1986 **Population Genetics and Genetic Conservation of Forest Trees** Ph Baradat, W. T. Adams, Gerhard Müller-Starck, 1995 **Genetic Variation in European Populations of Forest Trees** Gerhard Müller-Starck, Martin Ziehe, 1991 *Genetics of Cellular, Individual, Family, and Population Variability* Charles F. Sing, Craig L. Hanis, 1993 The objective of this book is to review the impact of genetic variation on risk of human disease at the different major levels of organization cells individuals families and populations The volume begins with a discussion of sources and rates of mutation which ultimately give rise to the vast amount of extant genetic variation This is followed by presentations of current understanding of how genetic variation is maintained within

and among populations The volume ends with discussions of the implications of such variation for understanding the evolution of our species This collection gives an unusually broad treatment of the subject with chapters from some of the leading workers in the field James Neel s chapter on human consanguinity effects and M Otake s on the genetic effects of radiation associated with the dropping of the Hiroshima and Nagasaki atomic bombs should be singled out for special emphasis As an up to date overview of ongoing research this work will be of interest to a wide range of workers in the fields of human population genetics evolution and epidemiology

**Linkage Analysis and Gene Mapping** Jiankang WANG,Huihui LI,Luyan ZHANG,2023-07-07T00:00:00+02:00 One major task of genetic studies is to construct the genetic map through linkage analysis and then locate the genetic loci of important traits on the constructed linkage maps identify favorable alleles which are of values to human beings and investigate their biochemical pathways from genotype to phenotype This book presents the linkage analysis and gene mapping methodologies which are applicable to self pollinated cross pollinated and asexual propagated species and genetic populations derived from two homozygous parents two heterozygous parents and multiple homozygous parents Chapter 1 in this book begins with genetic mating designs and various types of genetic populations followed by the structure of commonly used populations and analysis methods of phenotypic data In chapters 2 and 3 estimation of recombination frequency and construction of linkage map are introduced for twenty bi parental populations Chapter 4 deals with two classical gene mapping methods where no background control is considered while chapters 5 and 6 describe the inclusive composite interval mapping ICIM with background control Chapter 7 is focused on populations derived from two heterozygous parents which can be two individuals in a random mating population two clonal cultivars or two single crosses from four homozygous inbred lines Chapter 8 provides knowledge on the pure line progeny populations derived from four to eight homozygous parents The last two chapters covers populations methods and commonly asked questions in genetic mapping which cannot be included previously This book is intended for readers working on plant and animal genetics population and quantitative genetics and plant and animal breeding

*Computer Intensive Statistical Methods for Population Genetic Models* Sing Kai Lo,1987 **Population Genetic and Ecological Approaches for Improving Biological Control of Mealy Plum Aphid, *Hyalopterus Pruni*, in California** Jeffrey Lozier,2007 Population Genetic Structure of the California Sea Mussel, *Mytilus Californianus* Jonna D. Engel,2004

Population Genetics and Evolution Lawrence E. Mettler,Thomas G. Gregg,Henry E. Schaffer,1988 Self contained and reader friendly this volume provides a balanced blend of evolutionary theory population genetics and systematics with an emphasis on the experimental approach **Population Genetics** ,1955 Models of Genetic Selection and the Human Leukocyte Antigen Loci Mark Nelson Grote,1996 Genome Research ,2009 **Population Genetic Analysis of Complex Human Traits** Edward John Louis,1986

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