A Primer Of Population Genetics

A new and completely revised edition of a classic book on the tropical rain forest.

This accessible primer has been completely revised and updated to provide a concise but comprehensive introduction to the basic concepts of population genetics and genomics.

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: ahref="http://www.wiley.com/go/allendorf/populations"www.wiley.com/go/allendorf/populations/a.

This book covers basic concepts in population and quantitative genetics, including measuring selection on phenotypic traits. The emphasis is on material applicable to field studies of evolution focusing on ecologically important traits. Topics addressed are critical for training students in ecology, evolution, conservation biology, agriculture, forestry, and wildlife management. Many texts in this field are too complex and mathematical to allow the average beginning student to readily grasp the key concepts. A Primer of Ecological Genetics, in contrast, employs mathematics and statistics-fully explained, but at a less advanced level-as tools to improve understanding of biological principles. The main goal is to enable students to understand the concepts well enough that they can gain entry into the primary literature. Integration of the different chapters of the book shows students how diverse concepts relate to each other.

Primer of Genetic Analysis

Human Genetics: The Basics

Coalescent Theory

Molecular Population Genetics

A Primer of Ecological Genetics

This collection of specially commissioned articles looks at fragmented habitats, bringing together recent theoretical advances and empirical studies applying the metapopulation approach. Several chapters closely integrate ecology with genetics and evolutionary biology, and others illustrate how metapopulation concepts and models can be applied to answer questions about conservation, epidemiology, and speciation. The extensive coverage of theory from highly regarded scientists and the many substantive applications in this one-of-a-kind work make it invaluable to graduate students and researchers in a wide range of disciplines. * Provides a comprehensive and authoritative account of all aspects of metapopulation biology, integrating ecology, genetics, and evolution * Developed by recognized experts, including Hanski who won the Balzan Prize for Ecological Sciences * Covers novel applications of the metapopulation approach to conservation

Wide-ranging and inclusive, this text provides an invaluable review of an expansive selection of topics in human evolution, variation and adaptability for professionals and students in biological anthropology, evolutionary biology, medical sciences and psychology. The chapters are organized around four broad themes, with sections devoted to phenotypic and genetic variation within and between human populations, reproductive physiology and behavior, growth and development, and human health from evolutionary and ecological perspectives. An introductory section provides readers with the historical, theoretical and methodological foundations needed to understand the more complex ideas presented later. Two hundred discussion questions provide starting points for class debate and assignments to test student understanding.

What are genes? What do genes do? These seemingly simple questions are in fact challenging to answer accurately. As a result, there are widespread misunderstandings and over-simplistic answers, which lead to common conceptions widely portrayed in the media, such as the existence of a gene 'for' a particular characteristic or disease. In reality, the DNA we inherit interacts continuously with the environment and functions differently as we age. What our parents hand down to us is just the beginning of our life story. This comprehensive book analyses and explains the gene concept, combining philosophical, historical, psychological and educational perspectives with current research in genetics and genomics. It summarises what we currently know and do not know about genes and the potential impact of genetics on all our lives. Making Sense of Genes is an accessible but rigorous introduction to contemporary genetics concepts for non-experts, undergraduate students, teachers and healthcare professionals.

This book aims to make population genetics approachable, logical and easily understood. To achieve these goals, the book's design emphasizes well explained introductions to key principles and predictions. These are augmented with case studies as well as illustrations along with introductions to classical hypotheses and debates. Pedagogical features in the text include: Interact boxes that guide readers step-by-step through computer simulations using public domain software. Math boxes that fully explain mathematical derivations. Methods boxes that give insight into the use of actual genetic data. Numerous Problem boxes are integrated into the text to reinforce concepts as they are encountered. Dedicated website at www.wiley.com/go/hamiltongenetics This text also offers a highly accessible introduction to coalescent theory, the major conceptual advance in population genetics of the last two decades.

A Primer

Primer to Analysis of Genomic Data Using R

Evolutionary Genetics

Introduction to Conservation Genetics

An Introduction to Genetic Epidemiology

"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. 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."--back cover.

Phylogenomics: A Primer, Second Edition is for advanced undergraduate and graduate biology students studying molecular biology, comparative biology, evolution, genomics, and biodiversity. This book explains the essential concepts underlying the storage and manipulation of genomics level data, construction of phylogenetic trees, population genetics, natural selection, the tree of life, DNA barcoding, and metagenomics. The inclusion of problem-solving exercises in each chapter provides students with a solid grasp of the important molecular and evolutionary questions facing modern biologists as well as the tools needed to answer them.

Through this book, researchers and students will learn to use R for analysis of large-scale genomic data and how to create routines to automate analytical steps. The philosophy behind the book is to start with real world raw datasets and perform all the analytical steps needed to reach final results. Though theory plays an important role, this is a practical book for graduate and undergraduate courses in bioinformatics and genomic analysis or for use in lab sessions. How to handle and manage high-throughput genomic data, create automated workflows and speed up analyses in R is also taught. A wide range of R packages useful for working with genomic data are illustrated with practical examples. The key topics covered are association studies, genomic prediction, estimation of population genetic parameters and diversity, gene expression analysis, functional annotation of results using publically available databases and how to work efficiently in R with large genomic datasets. Important principles are demonstrated and illustrated through engaging examples which invite the reader to work with the provided datasets. Some methods that are discussed in this volume include: signatures of selection, population parameters (LD, FST, FIS, etc); use of a genomic relationship matrix for population diversity studies; use of SNP data for parentage testing; snpBLUP and gBLUP for genomic prediction. Step-by-step, all the R code required for a genome-wide association study is shown: starting from raw SNP data, how to build databases to handle and manage the data, quality control and filtering measures, association testing and evaluation of results, through to identification and functional annotation of candidate genes. Similarly, gene expression analyses are shown using microarray and RNAseq data. At a time when genomic data is decidedly big, the skills from this book are critical. In recent years R has become the de facto tool for analysis of gene expression data, in addition to its prominent role in analysis of genomic data. Benefits to using R include the integrated development environment for analysis, flexibility and control of the analytic workflow. Included topics are core components of advanced undergraduate and graduate classes in bioinformatics, genomics and statistical genetics. This book is also designed to be used by students in computer science and statistics who want to learn the practical aspects of genomic analysis without delving into algorithmic details. The datasets used throughout the book may be downloaded from the publisher's website.

Conservation and the Genetics of Populations gives acomprehensive overview of the essential background, concepts, andtools needed to understand how genetic information can be used todevelop conservation plans for species threatened withextinction. Provides a thorough understanding of the genetic basis ofbiological problems in conservation. Uses a balance of data and theory, and basic and appliedresearch, with examples taken from both the animal and plantkingdoms. An associated website contains example data sets and softwareprograms to illustrate population genetic processes and methods ofdata analysis. Discussion questions and problems are included at the end ofeach chapter to aid understanding. Features Guest Boxes written by leading people in the fieldincluding James F. Crow, Nancy FitzSimmons, Robert C. Lacy, MichaelW. Nachman, Michael E. Soule, Andrea Taylor, Loren H. Rieseberg,R.C. Vrijenhoek, Lisette Waits, Robin S. Waples and AndrewYoung. Supplementary information designed to support Conservationand the Genetics of Populations including: Downloadable sample chapter Answers to questions and problems Data sets illustrating problems from the book Data analysis software programs Website links An Instructor manual CD-ROM for this title is available. Pleasecontact our Higher Education team at ahref="mailto:HigherEducation@wiley.com"HigherEducation@wiley.com/afor more information.

Genetic Management of Fragmented Animal and Plant Populations
A Problems Approach
Gene Genealogies, Variation and Evolution: A primer in coalescent theory
Conservation and the Genetics of Populations
Population Genetics with R

This concise introduction addresses the theories behind population genetics and relevant empirical evidence, genetic drift, natural selection, nonrandom mating, quantitative genetics, and the evolutionary advantage of sex.

Genes, genetic codes, and mutation. Dynamics of genes in populations. Evolutionary change in nucleotide sequences. Rates and patterns of nucleotide substitution. Molecular phylogenetics. Gene duplication, exon shuffling, and concerted evolution. Evolution by transposition. Genome evolution. Spatial and temporal frameworks of the evolutionary process. Basics of probability.

Population genetics is the basis of evolutionary studies, and has been widely used in several researches. This recent field of science has important applications for the management of populations (natural and domesticated), as well as for evolutionary studies of the various factors that affect gene frequencies over time and spatial distribution.In this work, presented in three sections (Population and Quantitative Genetics, Genetic Diversity in Crop Management, Population Genetics for Conservation Studies), the reader will find cutting-edge information in carefully selected and revised works.This book is intended for all researchers, academics, and students who are interested in the intriguing area of population genetics.

"A text for a one-semester course in population genetics. It introduces students to classical population genetics (in terms of allele and haplotype frequencies) and modern population genetics (in terms of coalescent theory). It presents numerous applications of population genetic methods to practical problems, including testing for natural selection, detecting genetic hitchhiking and inferring the history of populations"--Provided by publisher.

A Statistical Approach
An Introduction
The Tropical Rain Forest
Theory and Applications
Fundamentals of Molecular Evolution

The use of molecular methods to study genetic polymorphisms has made a familiarity with population genetics essential for any biologist whose work is at the population level. A Primer of Population Genetics, Third Edition provides a concise but comprehensive introduction to population genetics. The four chapters of the book address genetic variation, the causes of evolution, molecular population genetics, and the genetic architecture of complex traits. Chapter-end problems reinforce ideas and, while there are some equations, the emphasis is on explanation rather than derivation.

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)

In response to many requests, the Third Edition of A Primer of Population Genetics has been dramatically shortened and streamlined for greater accessibility. Designed primarily for undergraduates, it will also serve for graduate students and professionals in biology and other sciences who desire a concise but comprehensive overview of the field with a primary focus on the integration of experimental results with theory. The abundance of experimental data generated by the use of molecular methods to study genetic polymorphisms sparked a transformation in the field of population genetics. Present in virtually all organisms, molecular polymorphisms allow populations to be studied without regard to species or habitat, and without the need for controlled crosses, mutant genes, or for any prior genetic studies. Thus a familiarity with population genetics has become essential for any biologist whose work is at the population level. These fields include evolution, ecology, systematics, plant breeding, animal breeding, conservation and wildlife management, human genetics, and anthropology. Population genetics seeks to understand the causes of genetic differences within and among species, and molecular biology provides a rich repertoire of techniques for identifying these differences.

An up-to-date, accessible guide to the main concepts and applications of quantitative genetics.

Integrated View of Population Genetics
Human Evolutionary Biology
Genetics of Populations
Population Genetics and Microevolutionary Theory
A Primer of Population Genetics and Genomics

Population genetics is an inherently quantitative discipline, yet often focuses upon abstract concepts which can b conceptualize and appropriately visualize at first glance. This book focuses on applying the hugely popular R softw specifically to the field, offering an accessible, step-by-step guide to tackling the challenges of achieving effective interpretation and summary. The authors adopt an engaging "learning by doing" approach that will enable readers develop an intuitive understanding of key population genetics concepts through the use of R. Beginning with the g of installing and using R (including CRAN and the RStudio IDE), the book works through the use of basic command data manipulation. An introduction to basic terminology in population genetics follows, clearly explaining how thes fundamental assumptions can provide insights and form basic inferences for real populations. The focus then move statistical tests including writing and running algorithms as functions. Subsequent chapters examine genetic varia adaptation, and natural selection as well as different approaches to population differences. Importantly, the accom set of practical exercises demonstrate that implementing all of these concepts via programming can actually help understanding them, even if they may at first seem insurmountably complex. Finally, this accessible textbook point forwards to other key concepts that are important to understanding modern day population genetics research (in coalescent theory) and offers the reader useful launching points for further learning. Population Genetics with R i students ranging from undergraduate to postgraduate level in the fields of population genetics, ecology, evolution conservation genetics, computational biology, and biostatistics.

The advances made possible by the development of molecular techniques have in recent years revolutionized quant genetics and its relevance for population genetics. Population Genetics and Microevolutionary Theory takes a mod approach to population genetics, incorporating modern molecular biology, species-level evolutionary biology, and a acknowledgment of quantitative genetics as the theoretical basis for population genetics. Logically organized into sections on population structure and history, genotype-phenotype interactions, and selection/adaptation Extensive examples to illustrate concepts Written in a clear and accessible manner and devoid of complex mathematical equ

Includes the author's introduction to background material as well as a conclusion for a handy overview of the field modern applications Each chapter ends with a set of review questions and answers Offers helpful general referen Internet links

A Primer of Population Genetics and Genomics has been completely revised and updated to provide a concise but comprehensive introduction to the basic concepts of population genetics and genomics. Recent textbooks have te on such specialized topics as the coalescent, molecular evolution, human population genetics, or genomics. This pr that trend by encouraging a broader familiarity with, and understanding of, population genetics and genomics as a The overview ranges from mating systems through the causes of evolution, molecular population genetics, and the of complex traits. Interwoven are discussions of ancient DNA, gene drive, landscape genetics, identifying risk facto complex diseases, the genomics of adaptation and speciation, and other active areas of current research. The prin illuminated by numerous examples from a wide variety of animals, plants, microbes, and human populations. The ap also emphasizes learning by doing, which in this case means solving numerical or conceptual problems. The rationa this is that the use of concepts in problem-solving lead to deeper understanding and longer knowledge retention. accessible, introductory textbook is aimed principally at students of various levels and abilities (from senior underg postgraduate) as well as practising scientists in the fields of population genetics, ecology, evolutionary biology, co biology, bioinformatics, biostatistics, physics, and mathematics.

One of the greatest unmet challenges in conservation biology is the genetic management of fragmented populatio threatened animal and plant species. More than a million small, isolated, population fragments of threatened speci likely suffering inbreeding depression and loss of evolutionary potential, resulting in elevated extinction risks. Altho effects can often be reversed by re-establishing gene flow between population fragments, managers very rarely d contrary, genetic methods are used mainly to document genetic differentiation among populations, with most stu concluding that genetically differentiated populations should be managed separately, thereby isolating them yet fu dooming many to eventual extinction! Many small population fragments are going extinct principally for genetic re Although the rapidly advancing field of molecular genetics is continually providing new tools to measure the exten population fragmentation and its genetic consequences, adequate guidance on how to use these data for effectiv is still lacking. This accessible, authoritative text is aimed at senior undergraduate and graduate students intereste conservation biology, conservation genetics, and wildlife management. It will also be of particular relevance to con practitioners and natural resource managers, as well as a broader academic audience of conservation biologists an evolutionary ecologists.

Primer Of Population Biology

Molecular Evolution

Population Genetics

A Primer of Molecular Population Genetics

Population and Evolutionary Genetics

The Fourth Edition of Genetics of Populations is the most current, comprehensive, and accessible introduction to the field for advanced undergraduate and graduate students, and researchers in genetics, evolution, conservation, and related fields. In the past several years, interest in the application of population genetics principles to new molecular data has increased greatly, and Dr. Hedrick's new edition exemplifies his commitment to keeping pace with this dynamic area of study. Reorganized to allow students to focus more sharply on key material, the Fourth Edition integrates coverage of theoretical issues with a clear presentation of experimental population genetics and empirical data. Drawing examples from both recent and classic studies, and using a variety of organisms to illustrate the vast developments of population genetics, this text provides students and researchers with the most comprehensive resource in the field.

This edition provides a balanced presentation of theory and observation. It introduces the principles of genetics and statistics that are relevant to population studies, and examines the forces affecting genetic variation from the molecular to the organismic level.

Genetic epidemiology is a field that has acquired a central role in modern biomedical science. This book provides an introduction to genetic epidemiology that begins with a primer in human molecular genetics and then examines the standard methods in population genetics and genetic epidemiology

Human genetics has blossomed from an obscure branch of biological science and occasional explanation for exceedingly rare disorders to a field all of its own that affects everyone. Human Genetics: The Basics introduces the key questions and issues in this emerging field, including: The common ancestry of all humanity The role of genes in sickness and health Debates over the use of genetic technology Written in an engaging, narrative manner, this concise introduction is an ideal starting point for anyone who wants to know more about genes, DNA, and the genetic ties that bind us all.

Concepts, Analysis, and Practice

An Ecological Study

Phylogenomics

A Concise Guide

Calculating the Secrets of Life

As researchers have pursued biology's secrets to the molecular level, mathematical and computer sciences have played an increasingly important role--in genome mapping, population genetics, and even the controversial search for "Eve," hypothetical mother of the human race. In this first-ever survey of the partnership between the two fields, leading experts look at how mathematical research and methods have made possible important discoveries in biology. The volume explores how differential geometry, topology, and differential mechanics have allowed researchers to "wind" and "unwind" DNA's double helix to understand the phenomenon of supercoiling. It explains how mathematical tools are

revealing the workings of enzymes and proteins. And it describes how mathematicians are detecting echoes from the origin of life by applying stochastic and statistical theory to the study of DNA sequences. This informative and motivational book will be of interest to researchers, research administrators, and educators and students in mathematics, computer sciences, and biology.

What are the genomic signatures of adaptations in DNA? How often does natural selection dictate changes to DNA? How does the ebb and flow in the abundance of individuals over time get marked onto chromosomes to record genetic history? Molecular population genetics seeks to answer such questions by explaining genetic variation and molecular evolution from micro-evolutionary principles. It provides a way to learn about how evolution works and how it shapes species by incorporating molecular details of DNA as the heritable material. It enables us to understand the logic of how mutations originate, change in abundance in populations, and become fixed as DNA sequence divergence between species. With the revolutionary advances in genomic data acquisition, understanding molecular population genetics is now a fundamental requirement for today's life scientists. These concepts apply in analysis of personal genomics, genome-wide association studies, landscape and conservation genetics, forensics, molecular anthropology, and selection scans. This book introduces, in an accessible way, the bare essentials of the theory and practice of molecular population genetics.

Published by Sinauer Associates, an imprint of Oxford University Press. Provides descriptions of the methods and tools used in molecular population genetics, which has combined advances in molecular biology and genomics with mathematical and empirical findings to uncover the history of natural selection and demographic shifts in many organisms.

How to learn population biology. Population genetics. Ecology. Biogeography: species equilibrium theory.

An Introduction for Life Scientists

Making Sense of Genes

An Introduction to Population Genetics

Quantitative Genetics

Principles of Population Genetics

Evolutionary genetics is the study of how genetic variation leads to evolutionary change. With the recent explosion in the availability of whole genome sequence data, vast quantities of genetic data are being generated at an ever-increasing pace with the result that programming has become an essential tool for researchers. Most importantly, a thorough understanding of evolutionary principles is essential for making sense of this genetic data. This up-to-date textbook covers all the major components of modern evolutionary genetics, carefully explaining fundamental processes such as mutation, natural selection, genetic drift, and speciation, together with their consequences. The book also draws on a rich literature of exciting and inspiring examples to demonstrate the diversity of evolutionary research, including an emphasis on how evolution and selection has shaped our own species. Furthermore, at the end of each chapter, study questions are provided to motivate the reader to think and reflect on the concepts introduced. Practical experience is essential when it comes to developing an understanding of how to use genetic and genomic data to analyze and address interesting questions in the life sciences and how to interpret results in meaningful ways. In addition to the main text, a series of online tutorials using the R language serves as an introduction to programming, statistics, and the analysis of evolutionary genetic data. The R environment stands out as an ideal all-purpose, open source platform to handle and analyze such data. The book and its online materials take full advantage of the authors' own experience in working in a post-genomic revolution world, and introduce readers to the plethora of molecular and analytical methods that have only recently become available.

Darwinian evolution in mendelian populations. Random genetic drift. Mutation and the neutral theory. Natural selection. Inbreeding and other forms of nonrandom mating. Population subdivision and migration. Molecular population genetics. Evolutionary genetics of quantitative characters. Ecological genetics and speciation.

An invaluable student-tested study aid, this primer, first published in 2007, provides guided instruction for the analysis and interpretation of genetic principles and practice in problem solving. Each section is introduced with a summary of useful hints for problem solving and an overview of the topic with key terms. A series of problems, generally progressing from simple to more complex, then allows students to test their understanding of the material. Each question and answer is accompanied by detailed explanation. This third edition includes additional problems in basic areas that often challenge students, extended coverage in molecular biology and development, an expanded glossary of terms, and updated historical landmarks. Students at all levels, from beginning biologists and premedical students to graduates seeking a review of basic genetics, will find this book a valuable aid. It will complement the formal presentation in any genetics textbook or stand alone as a self-paced review manual.

"An introduction to coalescent theory, which provides the foundation for molecular population genetics and genomics. Coalescent theory is the conceptual framework for studies of DNA sequence variation within species, and is the source of essential tools for making inferences about mutation, recombination, population structure and natural selection from DNA sequence data"--Provided by publisher.

Contributions of the Mathematical Sciences to Molecular Biology

A Primer of Population Genetics

Ecology, Genetics and Evolution of Metapopulations

This impressive author team brings the wealth of advances in conservation genetics into the new edition of this introductory text, including new chapters on population genomics and genetic issues in introduced and invasive species. They continue the strong learning features for students - main points in the margin, chapter summaries, vital support with the mathematics, and further reading - and now guide the reader to software and databases. Many new references reflect the expansion of this field. With examples from mammals, birds,...