

An Introduction To Molecular Ecology

The basic principle of all molecular genetic methods is to employ inherited, discrete and stable markers to identify genotypes that characterize individuals, populations or species. Such genetic data can provide information on the levels and distribution of genetic variability in relation to mating patterns, life history, population size, migration and environment. Although molecular tools have long been employed to address various questions in fisheries biology and management, their contributions to the field are sometimes unclear, and often controversial. Much of the initial impetus for the deployment of molecular markers arose from the desire to assess fish stock structure based on various interpretations of the stock concept. Although such studies have met with varying success, they continue to provide an impetus for the development of increasingly sensitive population discriminators, yielding information that can be valuable for both sustainable exploitation and the conservation of fish populations. In the last major synthesis of the subject, Ryman and Utter (1987) summarized progress and applications, though this was prior to the wide-scale adoption of DNA methodology. New sources of genetic markers and protocols are now available, in particular those that exploit the widely distributed and highly variable repeat

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sequences of DNA, and the amplification technique of the polymerase chain reaction.

This book focuses on the use of molecular tools to study small populations of rare and endangered mammals, and presents case studies that apply an evolutionary framework to address innovative questions in the emerging field of mammalian conservation genomics using a highly diverse set of novel molecular tools. Novel and more precise molecular technologies now allow experts in the field of mammology to interpret data in a more contextual and empirical fashion and to better describe the evolutionary and ecological processes that are responsible for the patterns they observe. The book also demonstrates how recent advances in genetic/genomic technologies have been applied to assess the impact of environmental/anthropogenic changes on the health of small populations of mammals. It examines a range of issues in the field of mammalian conservation genomics, such as the role that the genetic diversity of the immune system plays in disease protection and local adaptation; the use of noninvasive techniques and genomic banks as a resource for monitoring and restoring populations; the structuring of population by physical barriers; and genetic diversity. Further, by integrating research from a variety of areas – including population genetics, molecular ecology, systematics, and evolutionary and

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conservation biology – it enables readers to gain a deeper understanding of the conservation biology of mammals that are at increasing risk of extinction at local, regional and global scales. As such, it offers a unique resource for a broad readership interested in the conservation biology of mammals and conservation management strategies to better preserve biodiversity.

Shortlisted for the 2018 TWS Wildlife Publication Awards in the edited book category Decomposition and recycling of vertebrate remains have been understudied, hampered largely due to these processes being aesthetically challenging (e.g., smell and sight). Technological innovations have provided the means to explore new and historically understood natural systems to give us a plethora of new information. Carrion Ecology, Evolution, and Their Applications covers a broad spectrum of topics including the molecular mechanistic foundations that provide the basis for intra- and interspecific interactions related to population biology, community ecology, and how this manifests into habitat- and ecosystem-level importance. The book connects the science of carrion decomposition from genes to ecosystems in multidisciplinary synthesis of the science. This book brings together a team of global experts involved with measuring and understanding the process and effects of carrion ecology in nature, with special application in such applied fields as forensic entomology,

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habitat management, animal production (e.g., livestock and aquaculture), and human and environmental health. It fills a large literature gap in ecology, providing a synthesis and future directions important for studies of carrion decomposition that improve the general understanding of decomposition in ecosystems. The book fuses multiple disciplines into a single message explaining the importance of vertebrate carrion ecology in nature. Illustrates Carrion Decomposition in a 16-Page Color Insert with 40 Photos The authors illustrate how the study of carrion transcends the globe and expands systems of inquiry, broadening awareness of this important ecosystem process. Whether you are a student, academic, or professional, you will find this book insightful for the fields of molecular ecology, microbiology, entomology, forensics, population biology, community and ecosystem ecology, and human and environmental health. Computational biology is a rapidly expanding field, and the number and variety of computational methods used for DNA and protein sequence analysis is growing every day. These algorithms are extremely valuable to biotechnology companies and to researchers and teachers in universities. This book explains the latest computer technology for analyzing DNA, RNA, and protein sequences. Clear and easy to follow, designed specifically for the non-computer scientist, it will help biologists make better choices on which algorithm to use. New techniques and

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demonstrations are elucidated, as are state-of-the-art problems, and more advanced material on the latest algorithms. The primary audience for this volume are molecular biologists working either in biotechnology companies or academic research environments, individual researchers and the institutions they work for, and students. Any biologist who relies on computers should want this book. A secondary audience will be computer scientists developing techniques with applications in biology. An excellent reference for leading techniques, it will also help introduce computer scientists to the biology problems. This is an outstanding work which will be ideal for the increasing number of scientists moving into computational biology.

While it is true that members of most sexually reproducing species can be defined as either male or female, those who belong to the rest of the biological world are not so simply understood. Hermaphroditic creatures reproduce both as male and as female individuals, providing a fascinating glimpse into alternative sexual practices in nature and their ecological and evolutionary successes and failures. Eloquently written by an award-winning biologist and pioneer in molecular ecology, this primer on hermaphroditism traces the phenomenon throughout Earth's myriad species, accounting for the adaptive significance of alternative sexual systems. Accessible and richly illustrated, the text maps the

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evolutionary origins of hermaphroditism, as well as its historical instances and fictional representations, underscoring the relevance of dual sexuality to our biological, intellectual, and cultural making. John C. Avise describes the genetics, ecology, phylogeny, and natural history of hermaphroditic plants, fish, and invertebrate animals and details organisms that either reproduce simultaneously as male and female or switch routinely between one sex and the other. Filled with surprising creatures and compelling revelations, this textbook stands alone in its clear yet comprehensive treatment of hermaphroditism and its unique challenge to the supremacy of separate sexes.

Evolutionary Behavioral Ecology presents a comprehensive treatment of the evolutionary and ecological processes shaping behavior across a wide array of organisms and a diverse set of behaviors and is suitable as a graduate-level text and as a sourcebook for professional scientists.

Ecological Genetics addresses the fundamental problems of which of the many molecular markers should be used and how the resulting data should be analysed in clear, accessible language, suitable for upper-level undergraduates through to research-level professionals. A very accessible straightforward text to deal with this difficult topic - applying modern molecular techniques to ecological processes. Written by active researchers and teachers within the field. There will

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be an accompanying web site managed by the authors, comprising of worked examples, test data sets and hyperlinks to relevant web pages.

Aquatic Photosynthesis is a comprehensive guide to understanding the evolution and ecology of photosynthesis in aquatic environments. This second edition, thoroughly revised to bring it up to date, describes how one of the most fundamental metabolic processes evolved and transformed the surface chemistry of the Earth. The book focuses on recent biochemical and biophysical advances and the molecular biological techniques that have made them possible. In ten chapters that are self-contained but that build upon information presented earlier, the book starts with a reductionist, biophysical description of the photosynthetic reactions. It then moves through biochemical and molecular biological patterns in aquatic photoautotrophs, physiological and ecological principles, and global biogeochemical cycles. The book considers applications to ecology, and refers to historical developments. It can be used as a primary text in a lecture course, or as a supplemental text in a survey course such as biological oceanography, limnology, or biogeochemistry.

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

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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

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of molecular and analytical methods that have only recently become available. Insects represent the most abundant and diverse animal group on Earth. The number of described species is more than one million and up to ten million are estimated. Insects have one of the widest distributions in the world because they have adapted to extreme ranges of environments. Molecular ecology studies ecological processes based on the analysis

This established textbook continues to provide a comprehensive and stimulating introduction to marine ecological concepts and processes. Based on a wealth of international teaching expertise, *An Introduction to Marine Ecology* is written to be the basis for an entire undergraduate course in marine biology or ecology. It covers the trophic, environmental and competitive interactions of marine organisms, and the effects of these on the productivity, dynamics and structure of marine systems. The strength of the book lies in its discussion of core topics which remains at the heart of the majority of courses in the subject, despite an increasing emphasis on more applied aspects. The authors maintain the tradition of clarity and conciseness set by previous editions, and the text is extensively illustrated with colour plates, photographs and diagrams. Examples are drawn from all over the world. In this edition, the scientific content of the text has been fully revised and updated. An emphasis has been placed on human impacts, and

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completely new chapters have been added on fisheries, marine ecosystems, and human interference and conservation. Completely revised and updated with a twofold increase in the number of illustrations. Adopts a more applied approach in keeping with current teaching. New chapters on fisheries, the marine ecosystem, conservation and pollution. Based on a proven and successful course structure.

Ecology and Evolution of Cancer is a timely work outlining ideas that not only represent a substantial and original contribution to the fields of evolution, ecology, and cancer, but also goes beyond by connecting the interfaces of these disciplines. This work engages the expertise of a multidisciplinary research team to collate and review the latest knowledge and developments in this exciting research field. The evolutionary perspective of cancer has gained significant international recognition and interest, which is fully understandable given that somatic cellular selection and evolution are elegant explanations for carcinogenesis. Cancer is now generally accepted to be an evolutionary and ecological process with complex interactions between tumor cells and their environment sharing many similarities with organismal evolution. As a critical contribution to this field of research the book is important and relevant for the applications of evolutionary biology to understand the origin of cancers, to control

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neoplastic progression, and to prevent therapeutic failures. Covers all aspects of the evolution of cancer, appealing to researchers seeking to understand its origins and effects of treatments on its progression, as well as to lecturers in evolutionary medicine Functions as both an introduction to cancer and evolution and a review of the current research on this burgeoning, exciting field, presented by an international group of leading editors and contributors Improves understanding of the origin and the evolution of cancer, aiding efforts to determine how this disease interferes with biotic interactions that govern ecosystems Highlights research that intends to apply evolutionary principles to help predict emergence and metastatic progression with the aim of improving therapies

This book provides a comprehensive review of the ecology of freshwater bivalves and gastropods worldwide. It deals with the ecology of these species in its broadest sense, including diet, habitat and reproductive biology, emphasising in particular the tremendous diversity of these freshwater invertebrates. Following on from these introductory themes, the author develops a life history model that unifies them, and serves as a basis for reviews of their population and community ecology, including treatments of competition, predation, parasitism and biogeography. Extensively referenced and providing a synthesis of work from the

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nineteenth century onwards, this book includes original analyses that seek to unify previous work into a coherent whole. It will appeal primarily to professional ecologists and evolutionary biologists, as well as to parasitologists. Although all living beings modify their environment, human beings have acquired the ability to do so on a superlative space-time scale. As a result of industrialization and the use of new technologies, the anthropogenic impact has been increasing in the last centuries, causing reductions in the sizes or the extinction of numerous wild populations. In this sense, from the field of conservation genetics, various efforts have been made in recent decades to provide new knowledge that contributes to the conservation of populations, species, and habitats. In this book, we summarize the concrete contributions of researchers to the conservation of the Neotropical mammals using Molecular Ecology techniques. The book is divided into three major sections. The first section provides an up-to-date review of the conservation status of Neotropical mammals, the applications of the molecular markers in its conservation, and the use of non-invasive and forensic genetic techniques. The second and third sections present, respectively, a series of case studies in various species or taxonomic groups of Neotropical mammals. A fully updated guide to the increasingly prevalent use of molecular data in

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ecological studies Molecular ecology is concerned with how molecular biology and population genetics may help us to better understand aspects of ecology and evolution including local adaptation, dispersal across landscapes, phylogeography, behavioral ecology, and conservation biology. As the technology driving genetic science has advanced, so too has this fast-moving and innovative discipline, providing important insights into virtually all taxonomic groups. This third edition of *Molecular Ecology* takes account of the breakthroughs achieved in recent years to give readers a thorough and up-to-date account of the field as it is today. New topics covered in this book include next-generation sequencing, metabarcoding, environmental DNA (eDNA) assays, and epigenetics. As one of molecular ecology's leading figures, author Joanna Freeland also provides those new to the area with a full grounding in its fundamental concepts and principles. This important text: Is presented in an accessible, user-friendly manner Offers a comprehensive introduction to molecular ecology Has been revised to reflect the field's most recent studies and research developments Includes new chapters covering topics such as landscape genetics, metabarcoding, and community genetics Rich in insights that will benefit anyone interested in the ecology and evolution of natural populations, *Molecular Ecology* is an ideal guide for all students and professionals who wish

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to learn more about this exciting field.

The premiere two-volume reference on revelations from studying complex microbial communities in many distinct habitats Metagenomics is an emerging field that has changed the way microbiologists study microorganisms. It involves the genomic analysis of microorganisms by extraction and cloning of DNA from a group of microorganisms, or the direct use of the purified DNA or RNA for sequencing, which allows scientists to bypass the usual protocol of isolating and culturing individual microbial species. This method is now used in laboratories across the globe to study microorganism diversity and for isolating novel medical and industrial compounds. Handbook of Molecular Microbial Ecology is the first comprehensive two-volume reference to cover unculturable microorganisms in a large variety of habitats, which could not previously have been analyzed without metagenomic methodology. It features review articles as well as a large number of case studies, based largely on original publications and written by international experts. This first volume, Metagenomics and Complementary Approaches, covers such topics as: Background information on DNA reassociation and use of 16 rRNA and other DNA fingerprinting approaches Species designation in microbiology Metagenomics: Introduction to the basic tools with examples Consortia and databases Bioinformatics Computer-assisted analysis

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Complementary approaches—microarrays, metatranscriptomics, metaproteomics, metabolomics, and single cell analysis A special feature of this volume is the highlighting of the databases and computer programs used in each study; they are listed along with their sites in order to facilitate the computer-assisted analysis of the vast amount of data generated by metagenomic studies.

Handbook of Molecular Microbial Ecology I is an invaluable reference for researchers in metagenomics, microbiology, and environmental microbiology; those working on the Human Microbiome Project; microbial geneticists; molecular microbial ecologists; and professionals in molecular microbiology and bioinformatics.

Never HIGHLIGHT a Book Again! Virtually all of the testable terms, concepts, persons, places, and events from the textbook are included. Cram101 Just the FACTS101 studyguides give all of the outlines, highlights, notes, and quizzes for your textbook with optional online comprehensive practice tests. Only Cram101 is Textbook Specific. Accompanys: 9780199292059 .

Molecular approaches have opened new windows on a host of ecological and evolutionary disciplines, ranging from population genetics and behavioral ecology to conservation biology and systematics. Molecular Markers, Natural History and Evolution summarizes the multi-faceted discoveries about organisms in nature

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that have stemmed from analyses of genetic markers provided by polymorphic proteins and DNAs. The first part of the book introduces rationales for the use of molecular markers, provides a history of molecular phylogenetics, and describes a wide variety of laboratory methods and interpretative tools in the field. The second and major portion of the book provides a cornucopia of biological applications for molecular markers, organized along a scale from micro-evolutionary topics (such as forensics, parentage, kinship, population structure, and intra-specific phylogeny) to macro-evolutionary themes (including species relationships and the deeper phylogenetic structure in the tree of life). Unlike most prior books in molecular evolution, the focus is on organismal natural history and evolution, with the macromolecules being the means rather than the ends of scientific inquiry. Written as an intellectual stimulus for the advanced undergraduate, graduate student, or the practicing biologist desiring a wellspring of research ideas at the interface of molecular and organismal biology, this book presents material in a manner that is both technically straightforward, yet rich with concepts and with empirical examples from the world of nature.

Introduction to Population Ecology, 2nd Edition is a comprehensive textbook covering all aspects of population ecology. It uses a wide variety of field and laboratory examples, botanical to zoological, from the tropics to the tundra, to

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illustrate the fundamental laws of population ecology. Controversies in population ecology are brought fully up to date in this edition, with many brand new and revised examples and data. Each chapter provides an overview of how population theory has developed, followed by descriptions of laboratory and field studies that have been inspired by the theory. Topics explored include single-species population growth and self-limitation, life histories, metapopulations and a wide range of interspecific interactions including competition, mutualism, parasite-host, predator-prey and plant-herbivore. An additional final chapter, new for the second edition, considers multi-trophic and other complex interactions among species. Throughout the book, the mathematics involved is explained with a step-by-step approach, and graphs and other visual aids are used to present a clear illustration of how the models work. Such features make this an accessible introduction to population ecology; essential reading for undergraduate and graduate students taking courses in population ecology, applied ecology, conservation ecology, and conservation biology, including those with little mathematical experience.

"Handbook of Molecular Microbial Ecology I: Metagenomics and Complementary Approaches is the first comprehensive reference covering the various metagenomics in a large variety of habitats, which could not previously have

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been analysed without metagenomic methodology. This Volume includes topics such as species designations in microbiology, metagenomics, consortia and databases, bioinformatics, microarrays, and other metagenomics applications. This reference is ideal for researchers in metagenomics, microbiology, environmental microbiology, those working on the Human Microbiome Project, microbial geneticists, molecular microbiology, and bioinformatics"--

This title describes the driving forces behind the evolutionary process at the molecular and genome levels, the effects of the various molecular mechanisms on the structure of genes, proteins, and genomes.

Revised edition of: Introduction to molecular ecology / Trevor J. C. Beebee, Graham Rowe. 2008. 2nd ed.

Population Genomics With R presents a multidisciplinary approach to the analysis of population genomics. The methods treated cover a large number of topics from traditional population genetics to large-scale genomics with high-throughput sequencing data. Several dozen R packages are examined and integrated to provide a coherent software environment with a wide range of computational, statistical, and graphical tools. Small examples are used to illustrate the basics and published data are used as case studies. Readers are expected to have a basic knowledge of biology, genetics, and statistical inference

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methods. Graduate students and post-doctorate researchers will find resources to analyze their population genetic and genomic data as well as help them design new studies. The first four chapters review the basics of population genomics, data acquisition, and the use of R to store and manipulate genomic data. Chapter 5 treats the exploration of genomic data, an important issue when analysing large data sets. The other five chapters cover linkage disequilibrium, population genomic structure, geographical structure, past demographic events, and natural selection. These chapters include supervised and unsupervised methods, admixture analysis, an in-depth treatment of multivariate methods, and advice on how to handle GIS data. The analysis of natural selection, a traditional issue in evolutionary biology, has known a revival with modern population genomic data. All chapters include exercises. Supplemental materials are available on-line (<http://ape-package.ird.fr/PGR.html>).

Environmental DNA (eDNA) refers to DNA that can be extracted from environmental samples (such as soil, water, feces, or air) without the prior isolation of any target organism. The analysis of environmental DNA has the potential of providing high-throughput information on taxa and functional genes in a given environment, and is easily amenable to the study of both aquatic and terrestrial ecosystems. It can provide an understanding of past or present

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biological communities as well as their trophic relationships, and can thus offer useful insights into ecosystem functioning. There is now a rapidly-growing interest amongst biologists in applying analysis of environmental DNA to their own research. However, good practices and protocols dealing with environmental DNA are currently widely dispersed across numerous papers, with many of them presenting only preliminary results and using a diversity of methods. In this context, the principal objective of this practical handbook is to provide biologists (both students and researchers) with the scientific background necessary to assist with the understanding and implementation of best practices and analyses based on environmental DNA.

Molecular Ecology provides a comprehensive introduction to the many diverse aspects of this subject. The book unites theory with examples from a wide range of taxa in a logical and progressive manner, and its accessible writing style makes subjects such as population genetics and phylogenetics highly comprehensible to its readers. The first part of the book introduces the essential underpinnings of molecular ecology, starting with a review of genetics and a discussion of the molecular markers that are most frequently used in ecological research. This leads into an overview of population genetics in ecology. The second half of the book then moves on to specific applications of molecular ecology, covering phylogeography, behavioural ecology and conservation genetics. The final chapter looks at molecular ecology in a wider context by using a number of case studies that are relevant to various economic and

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social concerns, including wildlife forensics, agriculture, and overfishing * comprehensive overview of the different aspects of molecular ecology * attention to both theoretical and applied concerns * accessible writing style and logical structure * numerous up-to-date examples and references This will be an invaluable reference for those studying molecular ecology, population genetics, evolutionary biology, conservation genetics and behavioural ecology, as well as researchers working in these fields.

DNA can be extracted and sequenced from a diverse range of biological samples, providing a vast amount of information about evolution and ecology. The analysis of DNA sequences contributes to evolutionary biology at all levels, from dating the origin of the biological kingdoms to untangling family relationships. An Introduction to Molecular Evolution and Phylogenetics presents the fundamental concepts and intellectual tools you need to understand how the genome records information about evolutionary past and processes, how that information can be "read", and what kinds of questions we can use that information to answer. Starting with evolutionary principles, and illustrated throughout with biological examples, it is the perfect starting point on the journey to an understanding of the way molecular data is used in modern biology. Online Resource Centre The Online Resource Centre features: For registered adopters of the book: - Class plans for one-hour hands-on sessions associated with each chapter - Figures from the textbook to view and download An Introduction to Molecular Ecology Oxford University Press

In the field of molecular evolution, inferences about past evolutionary events are made using molecular data from currently living species. With the availability of genomic data from multiple related species, molecular evolution has become one of the most active and fastest growing

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fields of study in genomics and bioinformatics. Most studies in molecular evolution rely heavily on statistical procedures based on stochastic process modelling and advanced computational methods including high-dimensional numerical optimization and Markov Chain Monte Carlo. This book provides an overview of the statistical theory and methods used in studies of molecular evolution. It includes an introductory section suitable for readers that are new to the field, a section discussing practical methods for data analysis, and more specialized sections discussing specific models and addressing statistical issues relating to estimation and model choice. The chapters are written by the leaders of field and they will take the reader from basic introductory material to the state-of-the-art statistical methods. This book is suitable for statisticians seeking to learn more about applications in molecular evolution and molecular evolutionary biologists with an interest in learning more about the theory behind the statistical methods applied in the field. The chapters of the book assume no advanced mathematical skills beyond basic calculus, although familiarity with basic probability theory will help the reader. Most relevant statistical concepts are introduced in the book in the context of their application in molecular evolution, and the book should be accessible for most biology graduate students with an interest in quantitative methods and theory. Rasmus Nielsen received his Ph.D. from the University of California at Berkeley in 1998 and after a postdoc at Harvard University, he assumed a faculty position in Statistical Genomics at Cornell University. He is currently an Ole Rømer Fellow at the University of Copenhagen and holds a Sloan Research Fellowship. His is an associate editor of the Journal of Molecular Evolution and has published more than fifty original papers in peer-reviewed journals on the topic of this book. From the reviews: "...Overall this is a very useful book in an area of increasing importance."

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Journal of the Royal Statistical Society "I find Statistical Methods in Molecular Evolution very interesting and useful. It delves into problems that were considered very difficult just several years ago...the book is likely to stimulate the interest of statisticians that are unaware of this exciting field of applications. It is my hope that it will also help the 'wet lab' molecular evolutionist to better understand mathematical and statistical methods." Marek Kimmel for the Journal of the American Statistical Association, September 2006 "Who should read this book? We suggest that anyone who deals with molecular data (who does not?) and anyone who asks evolutionary questions (who should not?) ought to consult the relevant chapters in this book." Dan Graur and Dror Berel for Biometrics, September 2006 "Coalescence theory facilitates the merger of population genetics theory with phylogenetic approaches, but still, there are mostly two camps: phylogeneticists and population geneticists. Only a few people are moving freely between them. Rasmus Nielsen is certainly one of these researchers, and his work so far has merged many population genetic and phylogenetic aspects of biological research under the umbrella of molecular evolution. Although Nielsen did not contribute a chapter to his book, his work permeates all its chapters. This book gives an overview of his interests and current achievements in molecular evolution. In short, this book should be on your bookshelf." Peter Beerli for Evolution, 60(2), 2006

The authors also provide a comparative survey of the properties of genomes (genome size, gene families, synteny, and polymorphism) for prokaryotes as well as the main eukaryotic models.

Microorganisms are distributed across every ecosystem, and microbial transformations are fundamental to the operation of the biosphere. Microbial ecology is the study of this interaction

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between microorganisms and their environment, and arguably represents one of the most important areas of biological research. Yet for many years our study of microbial flora was severely limited: the primary method of culturing microorganisms on media allowed us to study only between 0.1 and 10% of the total microbial flora in any given environment. *Molecular Microbial Ecology* gives a comprehensive guide to the recent revolution in the study of microorganisms in the environment. Details are given on molecular methods for isolating some of the previously uncultured and numerically dominant microbial groups. PCR-based approaches to studying prokaryotic systematics are described, including ribosomal RNA analysis and stable isotope probing. Later chapters cover DNA hybridisation techniques (including fluorescent in situ hybridisation), as well as genomic and metagenomic approaches to microbial ecology. Gathering together some of the world's leading experts, this book provides an invaluable introduction to the modern theory and molecular methods used in studying microbial ecology.

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,...

Brown Trout: Biology, Ecology and Management A comprehensive guide to the most current research, history, genetics and ecology of the brown trout including challenging environmental problems The brown trout is an iconic species across its natural European distribution and has

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been introduced throughout the World. Brown Trout offers a comprehensive review of the scientific information and current research on this major fish species. While the brown trout is the most sought species by anglers, its introduction to various waters around the world is causing serious environmental problems. At the same time, introduction of exogenous brown trout lineages threatens conservation of native gene pools of populations in many regions. The authors summarize the important aspects of the brown trout's life history and ecology and focus on the impact caused by the species. The text explores potential management strategies in order to maintain numerous damaged populations within its natural distributional range and to ameliorate its impacts in exotic environments. The authors include information on a wide-range of topics such as recent updates in population genetics, evolutionary history, reproductive traits and early ontogeny, life history plasticity in anadromous brown trout and life history of the adfluvial brown trout and much more. This vital resource: Contains the latest research on the biology and ecology of brown trout Includes information on phylogeography, genetics, population dynamics and stock management Spotlights the brown trout's introduction to regions around the world and the serious environmental impacts Offers a comprehensive review of conservation and management techniques Written for salmonid scientists and researchers, fishery and environmental managers, and students of population genetics, ecology and population dynamics, Brown Trout explores the most recent findings on the history, ecology and sustainability of this much-researched species.

The Tropics are home to the greatest biodiversity in the world, but tropical species are at risk due to anthropogenic activities, mainly land use change,

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habitat loss, invasive species, and pathogens. Over the past 20 years, the avian malaria and related parasites (Order: Haemosporida) systems have received increased attention in the tropical regions from a diverse array of research perspectives. However, to date no attempts have been made to synthesize the available information and to propose new lines of research. This book provides such a synthesis by not only focusing on the antagonistic interactions, but also by providing conceptual chapters on topics going from avian haemosporidians life cycles and study techniques, to chapters addressing current concepts on ecology and evolution. For example, a chapter synthesizing basic biogeography and ecological niche model concepts is presented, followed by one on the island biogeography of avian haemosporidians. Accordingly, researchers and professionals interested in these antagonistic interaction systems will find both an overview of the field with special emphasis on the tropics, and access to the necessary conceptual framework for various topics in ecology, evolution and systematics. Given its conceptual perspective, the book will appeal not only to readers interested in avian haemosporidians, but also to those more generally interested in the ecology, evolution and systematics of host-parasite interactions. Students often find it difficult to grasp fundamental ecological and evolutionary concepts because of their inherently mathematical nature. Likewise, the

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application of ecological and evolutionary theory often requires a high degree of mathematical competence. This book is a first step to addressing these difficulties, providing a broad introduction to the key methods and underlying concepts of mathematical models in ecology and evolution. The book is intended to serve the needs of undergraduate and postgraduate ecology and evolution students who need to access the mathematical and statistical modelling literature essential to their subjects. The book assumes minimal mathematics and statistics knowledge whilst covering a wide variety of methods, many of which are at the fore-front of ecological and evolutionary research. The book also highlights the applications of modelling to practical problems such as sustainable harvesting and biological control. Key features: Written clearly and succinctly, requiring minimal in-depth knowledge of mathematics Introduces students to the use of computer models in both fields of ecology and evolutionary biology Market - senior undergraduate students and beginning postgraduates in ecology and evolutionary biology

The third edition of this bestselling text has been rigorously updated to reflect major new discoveries and concepts since 2011, especially progress due to extensive application of high-throughput sequencing, single cell genomics and analysis of large datasets. Significant advances in understanding the diversity

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and evolution of bacteria, archaea, fungi, protists, and viruses are discussed and their importance in marine processes is explored in detail. Now in full colour throughout, all chapters have been significantly expanded, with many new diagrams, illustrations and boxes to aid students' interest and understanding. Novel pedagogy is designed to encourage students to explore current high-profile research topics. Examples include the impacts of rising CO₂ levels on microbial community structure and ocean processes, interactions of microbes with plastic pollution, symbiotic interactions, and emerging diseases of marine life. This is the only textbook addressing such a broad range of topics in the specific area of marine microbiology, now a core topic within broader Marine Science degrees. A Companion Website provides additional online resources for instructors and students, including a summary of key concepts and terminology for each chapter, links to further resources, and flashcards to aid self-assessment.

This book aims to be a comprehensive review of the literature on the conservation genetics of the New World crocodylians, from the biological and demographical aspects of the living species to the application of molecular techniques for conservation purposes. It covers the current status of the molecular genetics applied to phylogenetics, phylogeography, diversity, kinship and mating system, and hybridization, as well its implications for decision making

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with regards to the conservation of these species at academic and governmental levels. This book can be used as a guide for graduate and undergraduate students to understand how conservation genetics techniques are carried out and how they can help preserve not only crocodylians but also other living species. An innovative introduction to ecology and evolution This unique textbook introduces undergraduate students to quantitative models and methods in ecology, behavioral ecology, evolutionary biology, and conservation. It explores the core concepts shared by these related fields using tools and practical skills such as experimental design, generating phylogenies, basic statistical inference, and persuasive grant writing. And contributors use examples from their own cutting-edge research, providing diverse views to engage students and broaden their understanding. This is the only textbook on the subject featuring a collaborative "active learning" approach that emphasizes hands-on learning. Every chapter has exercises that enable students to work directly with the material at their own pace and in small groups. Each problem includes data presented in a rich array of formats, which students use to answer questions that illustrate patterns, principles, and methods. Topics range from Hardy-Weinberg equilibrium and population effective size to optimal foraging and indices of biodiversity. The book also includes a comprehensive glossary. In addition to the

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editors, the contributors are James Beck, Cawas Behram Engineer, John Gaskin, Luke Harmon, Jon Hess, Jason Kolbe, Kenneth H. Kozak, Robert J. Robertson, Emily Silverman, Beth Sparks-Jackson, and Anton Weisstein. Provides experience with hypothesis testing, experimental design, and scientific reasoning Covers core quantitative models and methods in ecology, behavioral ecology, evolutionary biology, and conservation Turns "discussion sections" into "thinking labs" Professors: A supplementary Instructor's Manual is available for this book. It is restricted to teachers using the text in courses. For information on how to obtain a copy, refer to: http://press.princeton.edu/class_use/solutions.html

Inland fisheries are vital for the livelihoods and food resources of humans worldwide but their importance is underestimated, probably because large numbers of small, local operators are involved. Freshwater Fisheries Ecology defines what we have globally, what we are going to lose and mitigate for, and what, given the right tools, we can save. To estimate potential production, the dynamics of freshwater ecosystems (rivers, lakes and estuaries) need to be understood. These dynamics are diverse, as are the earth's freshwater fisheries resources (from boreal to tropical regions), and these influence how fisheries are both utilized and abused. Three main types of fisheries are illustrated within the book: artisanal, commercial and recreational, and the tools which have evolved

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for fisheries governance and management, including assessment methods, are described. The book also covers in detail fisheries development, providing information on improving fisheries through environmental and habitat evaluation, enhancement and rehabilitation, aquaculture, genetically modified fishes and sustainability. The book thoroughly reviews the negative impacts on fisheries including excessive harvesting, climate change, toxicology, impoundments, barriers and abstractions, non-native species and eutrophication. Finally, key areas of future research are outlined. Freshwater Fisheries Ecology is truly a landmark publication, containing contributions from over 100 leading experts and supported by the Fisheries Society of the British Isles. The global approach makes this book essential reading for fish biologists, fisheries scientists and ecologists and upper level students in these disciplines. Libraries in all universities and research establishments where biological and fisheries sciences are studied and taught should have multiple copies of this hugely valuable resource. About the Editor John Craig is Editor-in-Chief of the Journal of Fish Biology and has an enormous range of expertise and a wealth of knowledge of freshwater fishes and their ecology, having studied them around the globe, including in Asia, North America, Africa, the Middle East and Europe. His particular interests have been in population dynamics and life history strategies.

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He is a Fellow of the Linnean Society of London and the Royal Society of Biology.

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, an

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