

Introduction To Conservation Genetics

Presented in an easy-to-follow format, this clear and comprehensive textbook provides an accessible introduction to the emerging discipline of genetic studies in conservation. Includes chapter summaries, text boxes, worked examples, problems and solutions as aids to revision.

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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 mammalogy 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 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.

Biodiversity studied by researching island species recovery and management.

Genome sequencing enables scientists to study genes over time and to test the genetic variability of any form of life, from bacteria to mammals. Thanks to advances in molecular genetics, scientists can now determine an animal's degree of inbreeding or compare genetic variation of a captive species to wild or natural populations. Mapping an organism's genetic makeup recasts such terms as biodiversity and species and enables the conservation of rare or threatened species, populations, and genes. By introducing a new paradigm for studying and preserving life at a variety of levels, genomics offers solutions to previously intractable problems in understanding the biology of complex organisms and creates new tools for preserving the patterns and processes of life on this planet. Featuring a number of high-profile researchers, this volume introduces the use of molecular genetics in conservation biology and provides a historical perspective on the opportunities and challenges presented by new technologies. It discusses zoo-, museum-, and herbarium-based biological collections, which have expanded over the past decade, and covers the promises and problems of genomic and reproductive technology. The collection concludes with the philosophical and legal issues of conservation genetics and their potential effects on public policy.

?????: The neutral theory of molecular evolution/Kimura Motoo. -- 1983. -- ??: 1. ????; 2. ????; 3. ????

Fred Van Dyke's new textbook, *Conservation Biology: Foundations, Concepts, Applications*, 2nd Edition, represents a major new text for anyone interested in conservation. Drawing on his vast experience, Van Dyke's organizational clarity and readable style make this book an invaluable resource for students in conservation around the globe. Presenting key information and well-selected examples, this student-friendly volume carefully integrates the science of conservation biology with its implications for ethics, law, policy and economics.

Molecular Ecology, 2nd Edition provides an accessible introduction to the many diverse aspects of this subject. The book takes a logical and progressive approach to uniting examples from a wide range of taxonomic groups. The straightforward writing style offers in depth analysis whilst making often challenging subjects such as population genetics and phylogenetics highly comprehensible to the reader. The first part of the book introduces the essential underpinnings of molecular ecology and gives a review of genetics and discussion of the molecular markers that are most frequently used in ecological research, and a chapter devoted to the newly emerging field of ecological genomics. The second half of the book covers specific applications of molecular ecology, covering phylogeography, behavioural ecology and conservation genetics. The new edition provides a thoroughly up-to-date introduction to the field, emphasising new types of analyses and including current examples and techniques whilst also retaining the information-rich, highly readable style which set the first edition apart. Incorporates both theoretical and applied perspectives Highly accessible, user-friendly approach and presentation Includes self-assessment activities with hypothetical cases based on actual species and realistic data sets Uses case studies to place the theory in context Provides coverage of population genetics, genomics, phylogeography, behavioural ecology and conservation genetics.

Delta smelt are small, planktivorous, pelagic fish endemic to the upper San Francisco Estuary (SFE), California, USA. The SFE is a highly urbanized ecosystem that is affected by the introduction of nonnative species, water diversions, contaminants, and the creation of an extensive levee system, which are all considered threats to delta smelt. A captive breeding program for delta smelt has been established at the UC Davis Fish Conservation & Culture Laboratory to preserve this species in the event of extinction in the wild. The overall goal of this dissertation is to inform conservation efforts for delta smelt by 1. developing a genetic management and monitoring plan for the captive delta smelt population, and 2. exploring the genetic diversity of this species in its native range. In Chapter 1, I describe 24 microsatellite loci developed for delta smelt to assess wild delta smelt population genetics and to genetically manage the captive population. In Chapter 2, I describe the development and implementation of a genetic management plan for the delta smelt captive population. The goals of the genetic management plan are to equalize founder representation and maximize the captive effective population size. In Chapter 3, I assess the genetic diversity within the captive delta smelt population and compare it to the wild delta smelt population to determine the utility of the genetic management plan. I found that the genetic diversity was sufficiently retained in the genetically managed captive population. In Chapter 4, I conducted a population genetic study on delta smelt collected from 2003 to 2009. I found reduced effective population size and a significant genetic bottleneck in all sampling years and determined that delta smelt exist in the SFE as a single, panmictic population. The results of this study demonstrate the utility of population genetics in prioritizing conservation management of this imperiled species. Collectively, the significance of this body of work includes the application of novel hatchery genetic management techniques and an increased understanding of delta smelt in its native range to inform conservation management of this species. A new and completely revised edition of a classic book on the tropical rain forest.

Practical Conservation Biology covers the complete array of topics that are central to conservation biology and natural resource management, thus providing the essential framework for under-graduate and post-graduate courses in these subject areas. Written by two of the world's leading environment experts, it is a "must have" reference for environment professionals in government, non-government and industry sectors. The book reflects the latest thinking on key topics such as extinction risks, losses of genetic variability, threatening processes, fire effects, landscape fragmentation, habitat loss and vegetation clearing, reserve design, sustainable harvesting of natural populations, population viability analysis, risk assessment, conservation biology policy, human population growth and its impacts on biodiversity. Practical Conservation Biology deals primarily with the Australian context but also includes many overseas case studies. The book is the most comprehensive assessment of conservation topics in Australia and one of the most comprehensive worldwide.

In the face of ever-declining biodiversity, zoos have a major role to play in species conservation. Written by professionals involved in in situ conservation and restoration projects internationally, this is a critical assessment of the contribution of zoos to species conservation through evidence amassed from a wide range of sources. The first part outlines the biodiversity context within which zoos should operate, introducing the origins and global spread of zoos and exploring animal collection composition. The second part focuses on the basic elements of keeping viable captive animal populations. It considers the consequences of captivity on animals, the genetics of captive populations and the performance of zoos in captive breeding. The final part examines ways in which zoos can make a significant difference to conservation now and in the future. Bridging the gap between pure science and applied conservation, this is an ideal resource for both conservation biologists and zoo professionals.

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

The Kern River rainbow trout (*Oncorhynchus mykiss gilberti*, "KRRT"), like many freshwater fish, has been heavily impacted by the introduction of non-native species into its native range. Angling interest in the region beginning over a century ago led to rampant translocation of several different types of trout into lakes and streams throughout KRRT's range, the upper Kern River basin in southern California. These introductions resulted in hybridization and introgression with KRRT, and a dwindling number of purely native fish. In the following chapters I use genetic tools to examine the impact of this history of introductions, to measure current genetic characteristics of wild populations, and to provide guidance for the development of KRRT hatchery broodstock with the hope of helping to preserve one of California's native fish. In Chapter 1, I used SNP (single nucleotide polymorphism) and microsatellite markers to determine if a consistent genetic signature of KRRT within the upper Kern River basin still exists. I then measured introgression between KRRT and non-native trout, including coastal rainbow trout (*O. mykiss*), Little Kern golden trout (*O. m. whitei*), and California golden trout (*O. m. aguabonita*). We found that there is indeed still a genetic signature distinct from the non-native trout that have been introduced, but that introgression with those fish is widespread. Nonetheless, we did find several populations with very little introgression, and discovered that a number of populations in the upper Kern River basin still largely represent the native genotype, despite the lengthy history of stocking. In Chapter 2, I used microsatellites to examine gene flow and genetic diversity, particularly as they related to introgression. I found that those populations that have escaped introgression seem to have done so by being reproductively isolated from other populations. This isolation, however, coincides with reduced genetic diversity and genetic signs of population bottlenecks. In this way, avoidance of the primary threat to KRRT has exposed isolated populations to the threats of small population size and reduced genetic diversity. In Chapter 3, I present a Hatchery Genetic Management Plan for KRRT. This plan details recommendations for the collection of wild KRRT, and the development and maintenance of a hatchery broodstock to be planted back into the Kern River in areas currently planted with non-native trout. I describe the genetic factors germane to maximizing genetic diversity, limiting inbreeding, and limiting adaptation to captivity. I also provide guidelines for planting the resulting fish, and for monitoring both existing wild populations as well as hatchery-origin fish. This plan is an important part of helping to restore KRRT to its native range, while ensuring proper management of KRRT populations that still exist. Although this research focuses on KRRT, the issues addressed are relevant to a broader array of taxa threatened by the introduction of non-native species. In particular, the retention of a KRRT genetic signal despite a long history of introductions indicates some degree of resistance on the part of native taxa, and has implications for invasion biology. In addition, the balance between the competing threats of introgression and low genetic diversity provides an example of the many challenges involved in the attempt to preserve biodiversity in a changing world.

Conservation genetics focuses on understanding the role of genetic variation for population persistence. This book is about the methods used to study genetic variation in endangered species and whether genetic variation matters in the extinction of species. Antelopes constitute a fundamental part of ecosystems throughout Africa and Asia where they act as habitat architects, dispersers of seeds, and prey for large carnivores. The fascination they hold in the human mind is evident from prehistoric rock paintings and ancient Egyptian art to today's wildlife documentaries and popularity in zoos. In recent years, however, the spectacular herds of the past have been decimated or extirpated over wide areas in the wilds, and urgent conservation action is needed to preserve this world heritage for generations to come. As the first book dedicated to antelope conservation, this volume sets out to diagnose the causes of the drastic declines in antelope biodiversity and on this basis identify the most effective points of action. In doing so, the book covers central issues in the current conservation debate, especially related to the management of overexploitation, habitat fragmentation, disease transmission, climate change, populations genetics, and reintroductions. The contributions are authored by world-leading experts in the field, and the book is a useful resource to conservation scientists and practitioners, researchers, and students in related disciplines as well as interested lay people.

A fully updated guide to the increasingly prevalent use of molecular data in 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 to learn more about this exciting field.

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This book is particularly interesting for both horse breeders and molecular geneticists. Equids (horses and asses) have a particular place in the human culture and history. There are strong arguments for conservation of rare, endangered horse breeds and populations, however the maintenance of native breeds does not result in profitable business. Some populations and namely rare horse breeds need to be re-evaluated yet, others need to be saved from extinction very urgently. Enlisting the aid of modern science gives us many tools for reaching decisions to realize the preservation of different rare populations and not to use solely pedigrees, conformation and historical data. The molecular genetic approach and the phenotypic estimation of the values of different breeds is more and more useful. Hence, it was the right time for Horse Commission of EAAP together with Rare Breeds International (RBI) to perform a session devoted to the topic of progress in molecular genetics of horses. This book summarizes the papers on molecular genetic description of horse breeds and some aspects of evolution of horse species.

Wolves are controversial figures worldwide and much effort has focused on how to conserve them while addressing public concerns. With its solitary habits and fruit-eating diet, the endangered maned wolf roams the South American grasslands and swamps, playing a vital part in maintaining biodiversity hotspots. Compared to the grey wolf, little is known about its relationship with local people and the environment and the reasons for its decline, making research about this unique species an urgent concern. *Ecology and Conservation of the Maned Wolf: Multidisciplinary Perspectives* gathers the work of leading researchers from diverse disciplines and countries, covering up-to-date research on the biology, ecology, and conservation of the maned wolf. It presents innovative insights that can benefit conservation strategies and offers perspectives for the future of the species. The book is divided into three parts. Part I explains the general issues concerning the maned wolf: population viability, the relationship between maned wolves and people, and the management of captive maned wolves. It also reviews current aspects of species biology, including conservation genetics, feeding ecology, social structure and reproduction, and conservation medicine. Part II contains case studies that present knowledge gathered from conservation programs and field research in all countries where the species is currently found—Brazil, Uruguay, Argentina, Bolivia, and Paraguay. Part III offers perspectives from diverse fields of research, exploring the challenges and opportunities connecting maned wolf conservation efforts with those of its habitat and of other endangered species. This includes education and communication tools, the application of human dimensions research to maned wolf conservation, ethnoconservation perspectives, and the ecological and socioeconomic challenges to the conservation of the cerrado habitat.

Forest management must be sustainable not only in ecological, economic and social, but also genetic terms. Many forest managers are advocating and developing management strategies that give priority to conserving genetic diversity within production systems, or that recognise the importance of genetic considerations in achieving sustainable management. *Forest Conservation Genetics* draws together much previously uncollected information relevant to managing and conserving forests. The content emphasises the importance of conserving genetic diversity in achieving sustainable management. Each chapter is written by a leading expert and has been peer reviewed. Readers without a background in genetics will find the logical sequence of topics allows easy understanding of the principles involved and how those principles may impact on day-to-day forest planning and management decisions. The book is primarily aimed at undergraduate students of biology, ecology, forestry, and graduate students of forest genetics, resource management policy and/or conservation biology. It will prove useful for those teaching courses in these fields and as such help to increase the awareness of genetic factors in conservation and sustainable management, in both temperate and tropical regions.

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

The main goal of this book is to encourage and formalize the infusion of evolutionary thinking into mainstream conservation biology. It reviews the evolutionary foundations of conservation issues, and unifies conceptual and empirical advances in evolutionary conservation biology. The book can be used either as a primary textbook or as a supplementary reading in an advanced undergraduate or graduate level course - likely to be called Conservation Biology or in some cases Evolutionary Ecology. The focus of chapters is on current concepts in evolution as they pertain to conservation, and the empirical study of these concepts. The balanced treatment avoids exhaustive reviews and overlapping duplication among the chapters. Little background in genetics is assumed of the reader.

Despite the substantial interest in landscape genetics from the scientific community, learning about the concepts and methods underlying the field remains very challenging. The reason for this is the highly interdisciplinary nature of the field, which combines population genetics, landscape ecology, and spatial statistics. These fields have traditionally been treated separately in classes and textbooks, and very few scientists have received the interdisciplinary training necessary to efficiently teach or apply the diversity of techniques encompassed by landscape genetics. To address the current knowledge gap, this book provides the first in depth treatment of landscape genetics in a single volume. Specifically, this book delivers fundamental concepts and methods underlying the field, covering particularly important analytical methods in detail, and presenting empirical and theoretical

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

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 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.

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