Ancient Admixture In Human History Genetics

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 tended to focus on such specialized topics as the coalescent, molecular evolution, human population genetics, or genomics. This primer bucks that trend by encouraging a broader familiarity with, and understanding of, population genetics and genomics as a whole. The overview ranges from mating systems through the causes of evolution, molecular population genetics, and the genomics of complex traits. Interwoven are discussions of ancient DNA, gene drive, landscape genetics, identifying risk factors for complex diseases, the genomics of adaptation and speciation, and other active areas of current research. The principles are illuminated by numerous examples from a wide variety of animals, plants, microbes, and human populations. The approach also emphasizes learning by doing, which in this case means solving numerical or conceptual problems. The rationale behind this is that the use of concepts in problem-solving lead to deeper understanding and longer knowledge retention. This accessible, introductory textbook is aimed principally at students of various levels and abilities (from senior undergraduate to postgraduate) as well as practising scientists in the fields of population genetics, ecology, evolutionary biology, computational biology, bioinformatics, biostatistics, physics, and mathematics.
Discover best practices for data analysis and software development in R and start on the path to becoming a fully-fledged data scientist. This book teaches you techniques for both data manipulation and visualization and shows you the best way for developing new software

packages for R. Beginning Data Science in R details how data science is a combination of statistics, computational science, and machine learning. You'll see how to efficiently structure and mine data to extract useful patterns and build mathematical models. This requires computational methods and programming, and R is an ideal programming language for this. This book is based on a number of lecture notes for classes the author has taught on data science and statistical programming using the R programming language. Modern data analysis requires computational skills and usually a minimum of programming. What You Will Learn Perform data science and analytics using statistics and the R programming language Visualize and explore data, including working with large data sets found in big data Build an R package Test and check your code Practice version control Profile and optimize your code Who This Book Is For Those with some data science or analytics background, but not necessarily experience with the R programming language.

This volume reports on the ways in which humans engaged in their material and biotic environments at Çatalhöyük, using a wide range of archaeological evidence. This volume also summarizes work on the skeletal remains recovered from the site, as well as analytical research on isotopes and aDNA.

Comprehensive, advanced treatment of nature and source of inherited characteristics, with treatment of mathematical techniques. Mendelian populations, mutations, polymorphisms, genetic demography, much more. Emphasizes interpretation of data in relation to theoretical models.

A Research Strategy to Examine the Taxonomy of the Red Wolf provides independent guidance about taxonomic research on the red wolf, Canis rufus. Building from the 2019 report

Evaluating the Taxonomic Status of the Mexican Gray Wolf and the Red Wolf, this report reviews and ranks research applications to determine the taxonomy of wild canid populations in southern Louisiana and other relevant locations. The report then develops a research strategy to examine the evolutionary relationships between ancient red wolves, the extant managed red wolf populations, and the unidentified canid populations.

On Human Nature: Biology, Psychology, Ethics, Politics, and Religion covers the present state of knowledge on human diversity and its adaptative significance through a broad and eclectic selection of representative chapters. This transdisciplinary work brings together specialists from various fields who rarely interact, including geneticists, evolutionists, physicians, ethologists, psychoanalysts, anthropologists, sociologists, theologians, historians, linguists, and philosophers. Genomic diversity is covered in several chapters dealing with biology, including the differences in men and apes and the genetic diversity of mankind. Top specialists, known for their open mind and broad knowledge have been carefully selected to cover each topic. The book is therefore at the crossroads between biology and human sciences, going beyond classical science in the Popperian sense. The book is accessible not only to specialists, but also to students, professors, and the educated public. Glossaries of specialized terms and general public references help nonspecialists understand complex notions, with contributions avoiding technical jargon. Provides greater understanding of diversity and population structure and history, with crucial foundational knowledge needed to conduct research in a variety of fields, such as genetics and disease Includes three robust sections on biological, psychological, and ethical aspects, with cross-fertilization and reciprocal references between the three sections Contains contributions by leading experts in their

respective fields working under the guidance of internationally recognized and highly respected editors

Technological advances in generated molecular and cell biological data are transforming biomedical research. Sequencing, multi-omics and imaging technologies are likely to have deep impact on the future of medical practice. In parallel to technological developments, methodologies to gather, integrate, visualize and analyze heterogeneous and large-scale data sets are needed to develop new approaches for diagnosis, prognosis and therapy. Systems Medicine: Integrative, Qualitative and Computational Approaches is an innovative, interdisciplinary and integrative approach that extends the concept of systems biology and the unprecedented insights that computational methods and mathematical modeling offer of the interactions and network behavior of complex biological systems, to novel clinically relevant applications for the design of more successful prognostic, diagnostic and therapeutic approaches. This 3 volume work features 132 entries from renowned experts in the fields and covers the tools, methods, algorithms and data analysis workflows used for integrating and analyzing multi-dimensional data routinely generated in clinical settings with the aim of providing medical practitioners with robust clinical decision support systems. Importantly the work delves into the applications of systems medicine in areas such as tumor systems biology, metabolic and cardiovascular diseases as well as immunology and infectious diseases amongst others. This is a fundamental resource for biomedical students and researchers as well as medical practitioners who need to need to adopt advances in computational tools and methods into the clinical practice. Encyclopedic coverage: 'one-stop' resource for access to information written by world-leading scholars in the field of Systems Biology and Systems

Medicine, with easy cross-referencing of related articles to promote understanding and further research Authoritative: the whole work is authored and edited by recognized experts in the field, with a range of different expertise, ensuring a high quality standard Digitally innovative: Hyperlinked references and further readings, cross-references and diagrams/images will allow readers to easily navigate a wealth of information

This textbook provides a concise introduction and useful overview of the field of human population genomics, making the highly technical and contemporary aspects more accessible to students and researchers from various fields. Over the past decade, there has been a deluge of genetic variation data from the entire genome of individuals from many populations. These data have allowed an unprecedented look at human history and how natural selection has impacted humans during this journey. Simultaneously, there have been increased efforts to determine how genetic variation affects complex traits in humans. Due to technological and methodological advances, progress has been made at determining the architecture of complex traits. Split in three parts, the book starts with the basics, followed by more advanced and current research. The first part provides an introduction to essential concepts in population genetics, which are relevant for any organism. The second part covers the genetics of complex traits in humans. The third part focuses on applying these techniques and concepts to genetic variation data to learn about demographic history and natural selection in humans. This new textbook aims to serve as a gateway to modern human population genetics research for those new to the field. It provides an indispensable resource for students, researchers and practitioners from disparate areas of expertise.

"Thrilling . . . a bracing summary of what we have learned [from] 'archaeogenetics'—the study

of ancient DNA . . . Krause and Trappe capture the excitement of this young field."—Kyle Harper, The Wall Street Journal Johannes Krause is the director of the Max Planck Institute for Evolutionary Anthropology and a brilliant pioneer in the field of archaeogenetics—archaeology augmented by DNA sequencing technology—which has allowed scientists to reconstruct human history reaching back hundreds of thousands of years before recorded time. In this surprising account, Krause and journalist Thomas Trappe rewrite a fascinating chapter of this history, the peopling of Europe, that takes us from the Neanderthals and Denisovans to the present. We know now that a wave of farmers from Anatolia migrated into Europe 8,000 years ago, essentially displacing the dark-skinned, blue-eyed hunter-gatherers who preceded them. This Anatolian farmer DNA is one of the core genetic components of people with contemporary European ancestry. Archaeogenetics has also revealed that indigenous North and South Americans, though long thought to have been East Asian, also share DNA with contemporary Europeans. Krause and Trappe vividly introduce us to the prehistoric cultures of the ancient Europeans: the Aurignacians, innovative artisans who carved flutes and animal and human forms from bird bones more than 40,000 years ago; the Varna, who buried their loved ones with gold long before the Pharaohs of Egypt; and the Gravettians, big-game hunters who were Europe's most successful early settlers until they perished in the ice age. Genetics has earned a reputation for smuggling racist ideologies into science, but cutting-edge science makes nonsense of eugenics and "pure" bloodlines. Immigration and genetic exchanges have always defined our species; who we are is a question of culture, not biological inheritance. This revelatory book offers us an entirely new way to understand ourselves, both past and present. Genomics and Society; Ethical, Legal-Cultural, and Socioeconomic Implications is the first

book to address the vast and thorny web of ELSI topics identified as core priorities of the NHGRI in 2011. The work addresses fundamental issues of biosociety and bioeconomy as the revolution in biology moves from research lab to healthcare system. Of particular interest to healthcare practitioners, bioethicists, and health economists, and of tangential interest to the gamut of applied social scientists investigating the societal impact of new medical paradigms, the work describes a myriad of issues around consent, confidentiality, rights, patenting, regulation, and legality in the new era of genomic medicine. Addresses the vast and thorny web of ELSI topics identified as core priorities of the NHGRI in 2011 Presents the core fundamental issues of biosociety and bioeconomy as the revolution in biology moves from research lab to healthcare system Describes a myriad of issues around consent, including confidentiality, rights, patenting, regulation, and more

This authoritative textbook/reference presents a comprehensive introduction to the field of evolutionary genomics. The opening chapters describe the fundamental concepts in molecular biology and genome evolution for readers without any prior background in this area. This is followed by a detailed examination of genome evolution in various different groups of organisms. The text then concludes with a review of practical methods essential to researchers in the field. This updated and revised new edition also features historical perspectives on contributions to evolutionary genomics from related fields such as molecular evolution, genetics, and numerical taxonomy. Topics and features: introduces the basics of molecular biology, covering protein structure and diversity, as well as DNA replication, transcription, and translation; examines the phylogenetic relationships of DNA sequences, and the processes of mutation, neutral evolution, and natural selection; presents a brief evolutionary history of life,

surveying the key features of the genomes of prokaryotes, eukaryotes, viruses and phages, vertebrates, and humans; reviews the various biological "omic" databases, and discusses the analysis of homologous nucleotide and amino acid sequences; provides an overview of the experimental sequencing of genomes and transcriptomes, and the construction of phylogenetic trees; describes methods for estimating of evolutionary distances, and performing studies of population genetics; supplies additional supporting material at an associated website. Serving as an indispensable textbook for graduate and advanced undergraduate courses on evolutionary genomics, this accessible overview will also prove invaluable to researchers from both computer science and the biological sciences seeking a primer on the field.

This fully updated and revised edition of the best-selling title The Archaeology Coursebook is a guide for students studying archaeology for the first time. Including new methods and key studies in this fourth edition, it provides pre-university students and teachers, as well as undergraduates and enthusiasts, with the skills and technical concepts necessary to grasp the subject. The Archaeology Coursebook: introduces the most commonly examined archaeological methods, concepts and themes, and provides the necessary skills to understand them explains how to interpret the material students may meet in examinations supports study with key studies, key sites, key terms, tasks and skills development illustrates concepts and commentary with over 400 photos and drawings of excavation sites, methodology and processes, tools and equipment provides an overview of human evolution and social development with a particular focus upon European prehistory. Reflecting changes in archaeological practice and with new key studies, methods, examples, boxes, photographs and diagrams, this is definitely a book no archaeology student should be without.

Human Population Genetics and Genomics provides researchers/students with knowledge on population genetics and relevant statistical approaches to help them become more effective users of modern genetic, genomic and statistical tools. In-depth chapters offer thorough discussions of systems of mating, genetic drift, gene flow and subdivided populations, human population history, genotype and phenotype, detecting selection, units and targets of natural selection, adaptation to temporally and spatially variable environments, selection in age-structured populations, and genomics and society. As human genetics and genomics research often employs tools and approaches derived from population genetics, this book helps users understand the basic principles of these tools. In addition, studies often employ statistical approaches and analysis, so an understanding of basic statistical theory is also needed. Comprehensively explains the use of population genetics and genomics in medical applications and research Discusses the relevance of population genetics and genomics to major social issues, including race and the dangers of modern eugenics proposals Provides an overview of how population genetics and genomics helps us understand where we came from as a species and how we evolved into who we are now

A New York Times Notable Book of 2014 We are doomed to repeat history if we fail to learn from it, but how are we affected by the forces that are invisible to us? What role does Neanderthal DNA play in our genetic makeup? How did the theory of eugenics embraced by Nazi Germany first develop? How is trust passed down in Africa, and silence inherited in Tasmania? How are private companies like Ancestry.com uncovering, preserving and potentially editing the past? In The Invisible History of the Human Race, Christine Kenneally reveals that, remarkably, it is not only our biological history that is coded in our DNA, but also

our social history. She breaks down myths of determinism and draws on cutting - edge research to explore how both historical artefacts and our DNA tell us where we have come from and where we may be going.

Archaeogenetics is the research field of studying the genetic information contained in ancient DNA (aDNA) to gain insight into the past. Analysis of human aDNA from archaeological material has allowed archaeogeneticists to observe changes in the genetic composition of populations in an area through time. By using aDNA in this manner, a higher degree of resolution can be gained into the timing of past genetic transitions, compared to the resolution that is available when inferring the past from modern genomic data alone. In this thesis, I focus on the movement of genes, via migration of people and/or admixture, and the information that this movement can provide about human history. I introduce the differences between the inheritance mechanisms of uniparental (mitochondrial DNA and the Y-chromosome) and autosomal markers; the forces of evolution in population genetics; some methods commonly used in the analysis of human aDNA in the manuscripts included in this thesis; prior (archaeo-)genetics research regarding the population history of West Eurasia and the Americas -as context for my own research in these geographic areas-, and discuss the information gained by my own work about the population history of the areas

studied, the limitations of archaeogenetic inferences, and the importance of combining archaeogenetic results with those from other disciplines when studying human history.

Over the past decade, a group of prolific and innovative evolutionary biologists has sought to reinvent historical linguistics through the use of phylogenetic and phylogeographical analysis, treating cognates like genes and conceptualizing the spread of languages in terms of the diffusion of viruses. Using these techniques, researchers claim to have located the origin of the Indo-European language family in Neolithic Anatolia, challenging the near-consensus view that it emerged in the grasslands north of the Black Sea thousands of years later. But despite its widespread celebration in the global media, this new approach fails to withstand scrutiny. As languages do not evolve like biological species and do not spread like viruses, the model produces incoherent results, contradicted by the empirical record at every turn. This book asserts that the origin and spread of languages must be examined primarily through the time-tested techniques of linguistic analysis, rather than those of evolutionary biology.

David Reich describes how the revolution in the ability to sequence ancient DNA has changed our understanding of the deep human past. This book tells the emerging story of our often surprising ancestry - the extraordinary ancient

migrations and mixtures of populations that have made us who we are.
Praise for the third edition of Bioinformatics "This book is a gem to read and use
in practice." —Briefings in Bioinformatics "This volume has a distinctive, special
value as it offers an unrivalled level of details and unique expert insights from the
leading computational biologists, including the very creators of popular
bioinformatics tools." —ChemBioChem "A valuable survey of this fascinating field.
. . I found it to be the most useful book on bioinformatics that I have seen and
recommend it very highly." —American Society for Microbiology News "This
should be on the bookshelf of every molecular biologist." —The Quarterly Review
of Biology The field of bioinformatics is advancing at a remarkable rate. With the
development of new analytical techniques that make use of the latest advances
in machine learning and data science, today's biologists are gaining fantastic
new insights into the natural world's most complex systems. These rapidly
progressing innovations can, however, be difficult to keep pace with. The
expanded fourth edition of the best-selling Bioinformatics aims to remedy this by
providing students and professionals alike with a comprehensive survey of the
current field. Revised to reflect recent advances in computational biology, it offers
practical instruction on the gathering, analysis, and interpretation of data, as well
as explanations of the most powerful algorithms presently used for biological

discovery. Bioinformatics, Fourth Edition offers the most readable, up-to-date, and thorough introduction to the field for biologists at all levels, covering both key concepts that have stood the test of time and the new and important developments driving this fast-moving discipline forwards. This new edition features: New chapters on metabolomics, population genetics, metagenomics and microbial community analysis, and translational bioinformatics A thorough treatment of statistical methods as applied to biological data Special topic boxes and appendices highlighting experimental strategies and advanced concepts Annotated reference lists, comprehensive lists of relevant web resources, and an extensive glossary of commonly used terms in bioinformatics, genomics, and proteomics Bioinformatics is an indispensable companion for researchers, instructors, and students of all levels in molecular biology and computational biology, as well as investigators involved in genomics, clinical research, proteomics, and related fields.

This book brings together papers presented at the 2nd Sudan Studies Research Conference, held at the McDonald Institute for Archaeological Research, University of Cambridge, 2018. The papers collected here focus on early administrative and mortuary material culture in the Nile valley and adjacent areas.

It is well established that all humans today, wherever they live, belong to one single species. Yet even many people who claim to abhor racism take for granted that human "races" have a biological reality. In Troublesome Science, Rob DeSalle and Ian Tattersall provide a lucid and forceful critique of how scientific tools have been misused to uphold misguided racial categorizations. DeSalle and Tattersall argue that taxonomy, the scientific classification of organisms, provides an antidote to the myth of race's biological basis. They explain how taxonomists do their science—how to identify a species and to understand the relationships among different species and the variants within them. DeSalle and Tattersall also detail the use of genetic data to trace human origins and look at how scientists have attempted to recognize discrete populations within Homo sapiens. Troublesome Science demonstrates conclusively that modern genetic tools, when applied correctly to the study of human variety, fail to find genuine differences. While the diversity that exists within our species is a real phenomenon, it nevertheless defeats any systematic attempt to recognize discrete units within it. The stark lines that humans insist on drawing between their own groups and others are nothing but a mixture of imagination and ideology. Troublesome Science is an important call for researchers, journalists, and citizens to cast aside the belief that race has a biological meaning, for the

sake of social justice and sound science alike.

Molecular anthropology uses molecular genetic methods to address questions and issues of anthropological interest. More specifically, molecular anthropology is concerned with genetic evidence concerning human origins, migrations, and population relationships, including related topics such as the role of recent natural selection in human population differentiation, or the impact of particular social systems on patterns of human genetic variation. Organized into three major sections, An Introduction to Molecular Anthropology first covers the basics of genetics – what genes are, what they do, and how they do it – as well as how genes behave in populations and how evolution influences them. The following section provides an overview of the different kinds of genetic variation in humans, and how this variation is analyzed and used to make evolutionary inferences. The third section concludes with a presentation of the current state of genetic evidence for human origins, the spread of humans around the world, the role of selection and adaptation in human evolution, and the impact of culture on human genetic variation. A final, concluding chapter discusses various aspects of molecular anthropology in the genomics era, including personal ancestry testing and personal genomics. An Introduction to Molecular Anthropology is an invaluable resource for students studying human evolution, biological

anthropology, or molecular anthropology, as well as a reference for anthropologists and anyone else interested in the genetic history of humans. Advances in genome-scale DNA sequencing technologies have revolutionized genetic research on ancient organisms, extinct species, and past environments. When it is recoverable after hundreds or thousands of years of unintended preservation, "ancient DNA" (or aDNA) is often highly degraded, necessitating specialized handling and analytical approaches. Paleogenomics defines the field of reconstructing and analyzing the genomes of historic or long-dead organisms, most often through comparison with modern representatives of the same or similar species. The opportunity to isolate and study paleogenomes has radically transformed many fields, spanning biology, anthropology, agriculture, and medicine. Examples include understanding evolutionary relationships of extinct species known only from fossils, the domestication of plants and animals, and the evolution and geographical spread of certain pathogens. This pioneering book presents a snapshot view of the history, current status, and future prospects of paleogenomics, taking a broad viewpoint that covers a range of topics and organisms to provide an up-to-date status of the applications, challenges, and promise of the field. This book is intended for a variety of readerships, including upper-level undergraduate and graduate students, professionals and experts in the field, as well as anyone excited by the extraordinary insights that paleogenomics offers. Studying human migratory patterns can help us make sense of evolution, biology,

linguistics, and so much more. Human Migration takes readers through population development and their respective origins to create a comprehensive picture of human migratory patterns. This book explores human migration as a major contributor to globalization that facilitates gene flow and the exchange of cultures and languages. It also traces evolutionary success of a hybrid population, the Black Caribs, after their forced relocation from St. Vincent Island to the Bay Islands and Central America. The volume is split into four sections: Theoretical Overview; Ancient DNA and Migration; Regional Migration; Culture and Migration: and Disease and Migration. This division allows for a seamless transition between a broad range of topics, including molecular genetics, linguistics, cultural anthropology, history, archaeology, demography, and genetic epidemiology. Assembled by volume editors and migration specialists María de Lourdes Muñoz-Moreno and Michael H. Crawford, Human Migration creates an opportunity for researchers, professionals, and students from different fields to review and discuss the most recent trends and challenges surrounding migration, genetics, and anthropology.

Ancestral DNA, Human Origins, and Migrations describes the genesis of humans in Africa and the subsequent story of how our species migrated to every corner of the globe. Different phases of this journey are presented in an integrative format with information from a number of disciplines, including population genetics, evolution, anthropology, archaeology, climatology, linguistics, art, music, folklore and history. This

unique approach weaves a story that has synergistic impact in the clarity and level of understanding that will appeal to those researching, studying, and interested in population genetics, evolutionary biology, human migrations, and the beginnings of our species. Integrates research and information from the fields of genetics, evolution, anthropology, archaeology, climatology, linguistics, art, music, folklore and history, among others Presents the content in an entertaining and synergistic style to facilitate a deep understanding of human population genetics Informs on the origins and recent evolution of our species in an approachable manner

This book constitutes the proceedings of the 22nd Annual Conference on Research in Computational Molecular Biology, RECOMB 2018, held in Paris, France, in April 2018. The 16 extended and 22 short abstracts presented were carefully reviewed and selected from 193 submissions. The short abstracts are included in the back matter of the volume. They report on original research in all areas of computational molecular biology and bioinformatics.

Explanations and accounts of our own origins have become one of the most popular of all the areas in science that are now regularly brought into the public arena via television, lavishly illustrated books, and even cartoons.

Evolution, biology, and society is a catch-all phrase encompassing any scholarly work that utilizes evolutionary theory and/or biological or behavioral genetic methods in the study of the human social group, and The Oxford Handbook of Evolution, Biology, and

Society contains an much needed overview of research in the area by sociologists and other social scientists. The examined topics cover a wide variety of issues, including the origins of social solidarity; religious beliefs; sex differences; gender inequality; determinants of human happiness; the nature of social stratification and inequality and its effects; identity, status, and other group processes; race, ethnicity, and race discrimination; fertility and family processes; crime and deviance; and cultural and social change. The scholars whose work is presented in this volume come from a variety of disciplines in addition to sociology, including psychology, political science, and criminology. Yet, as the essays in this volume demonstrate, the potential of theory and methods from biology for illuminating social phenomena is clear, and sociologists stand to gain from learning more about them and using them in their own work. The theory focuses on evolution by natural selection, the primary paradigm of the biological sciences, while the methods include the statistical analyses sociologists are familiar with, as well as other methods that they may not be familiar with, such as behavioral genetic methods, methods for including genetic factors in statistical analyses, gene-wide association studies, candidate gene studies, and methods for testing levels of hormones and other biochemicals in blood and saliva and including these factors in analyses. This work will be of interest to any sociologist with an interest in exploring the interaction of biological and sociological processes. As an introduction to the field it is useful for teaching upper-level or graduate students in sociology or a related social

science.
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 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).

Evolution is the central theme of all biology. Researcarcch in the many branches of evolutionary study continues to flourish. This book, based on a symposium of the Linnean Society, discusses the diversity in currentevolutionary research. It approaches the subject ambitiously and from several angles, bringing ttogether eminent authors from a variety of disciplines paleontologists traditionally with a macroevolutionary bias, neontologists concentrating on microevolutionary processes, and those studying the very essence ofsses and those studying the very essence of evolution the process of speciation in living organisms. Evolutionary Patterns and Processes will appeal to a broad spectrum of professional biologistsworking in such fields as paleontology, population biology, and evolutionary genetics. Biologists will enjoy chapters by Stephen J. Gould, discovering in the much earlier work of Hugo de Vries parallels with his ideas on punctuational evolution; Guy Bush,considering why there are so many small animals; Peter Sheldon, examining detailed fossil trilobite sequences for evidence of microevolutionary processes and considering models of speciation; as well as others dealing with cytological, ecological, and behavioral processes leading to the evolution of new species. None

This topical volume in the respected Encyclopedia series is the first in many years to bring together all important aspects of developmental biology in one source, from morphogenesis and organogenesis, via epigenetic regulation of gene expression to evolutionary developmental biology. The editor-in-chief has assembled an outstanding team of contributors to review these topics, creating an authoritative work for many years to come. The result is a unique, top-level reference in developmental biology for researchers, students and

professionals alike.

Explore the latest research in anthropological genetics and understand the genome's role in cultural and social development A Companion to Anthropological Genetics illustrates the role of genetic analysis in advancing the modern study of human origins, populations, evolution, and diversity. Broad in scope, this essential reference work establishes and explores the relationship between genetic research and the major questions of anthropological study. Through contributions by leading researchers, this collection explores molecular genetics and evolutionary mechanisms in the context of macro- and microevolution, paleontology, phylogeny, diet, and disease, with detailed explanations of quantitative methods, including coalescent and approximate Bayesian computation. With an emphasis on contextualizing new and developing genetic research within anthropological frameworks, this text offers critical perspective on the conditions of molecular evolution that accompany cultural and social transformation, while also addressing critical disciplinary questions, such as the ethical issues surrounding ancestry testing and community-based genetic research. Acts as an essential reference on the contributions of genetic science to the field of anthropology Features new work by leading researchers of the field Explores the evolution of immunity, including the genetics and epigenetics of pathogens, chronic illness, and disease resistance Provides in-depth examination of mutation and dietary adaptation, including AMY1, lactase persistence, and sensory polymorphisms Explains essential quantitative and phylogenetic methods for aligning genomic analysis with evolution and migration time scales Offering thorough coverage on leading questions and developing research, A Companion to Anthropological Genetics is a comprehensive resource for students and scholars.

This book is devoted to the collection, interpretation and analysis of population genetic data. Among the topics included here are studies on human evolutionary history, molecular techniques for generating data, statistical and computational techniques for the interpretation of such data, and stochastic models for genealogy and population structure. The chapters reflect the close interaction between experimental molecular biologists and theoreticians. The book will be useful for specialists in the area, as well as mathematicians, statisticians, computer scientists and biologists wanting a brief overview of current problems in the field. An accessible examination of what the genes of people living today can tell us about the history of the human race demonstrates how anthropologists use genetic information to answer fundamental questions, from the links between humans and neanderthals to the way historical events have shaped us genetically. 20,000 first printing. A timely update of a highly popular handbook on statistical genomics This new, two-volume edition of a classic text provides a thorough introduction to statistical genomics, a vital resource for advanced graduate students, early-career researchers and new entrants to the field. It introduces new and updated information on developments that have occurred since the 3rd edition. Widely regarded as the reference work in the field, it features new chapters focusing on statistical aspects of data generated by new sequencing technologies, including sequence-based functional assays. It expands on previous coverage of the many processes between genotype and phenotype, including gene expression and epigenetics, as well as metabolomics. It also examines population genetics and evolutionary models and inference, with new chapters on the multi-species coalescent, admixture and ancient DNA, as well as genetic association studies including causal analyses and variant interpretation. The Handbook

of Statistical Genomics focuses on explaining the main ideas, analysis methods and algorithms, citing key recent and historic literature for further details and references. It also includes a glossary of terms, acronyms and abbreviations, and features extensive cross-referencing between chapters, tying the different areas together. With heavy use of up-to-date examples and references to web-based resources, this continues to be a must-have reference in a vital area of research. Provides much-needed, timely coverage of new developments in this expanding area of study Numerous, brand new chapters, for example covering bacterial genomics, microbiome and metagenomics Detailed coverage of application areas, with chapters on plant breeding, conservation and forensic genetics Extensive coverage of human genetic epidemiology, including ethical aspects Edited by one of the leading experts in the field along with rising stars as his co-editors Chapter authors are world-renowned experts in the field, and newly emerging leaders. The Handbook of Statistical Genomics is an excellent introductory text for advanced graduate students and early-career researchers involved in statistical genetics.

An accessible and wide-ranging introduction to the exciting and expanding field of archaeological science, for students, professionals and academics.

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