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KEY=GENETICS - REED LANE

Who We Are and How We Got Here Ancient DNA and the New Science of the Human Past Oxford University Press *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.* **Exploring the Effects of Migration and Admixture on Human Populations Through Time, Using Ancient DNA** *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.* **Empires and Barbarians The Fall of Rome and the Birth of Europe Oxford University Press** "*At the start of the first millennium AD, southern and western Europe formed part of the Mediterranean-based Roman Empire, the largest state western Eurasia has ever known, and was set firmly on a trajectory*

towards towns, writing, mosaics, and central heating. Central, northern and eastern Europe was home to subsistence farmers, living in wooden houses with mud floors, whose largest political units weighed in at no more than a few thousand people. By the year 1000, Mediterranean domination of the European landscape had been destroyed. Instead of one huge Empire facing loosely organized subsistence farmers, Europe - from the Atlantic almost to the Urals - was home to an interacting commonwealth of Christian states, many of which are still with us today. This book tells the story of the transformations which changed western Eurasia forever: of the birth of Europe itself"--Provided by publisher. **Human Population Genetics and Genomics Academic Press** *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* **The Genetics of Human Populations Courier Corporation** *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.* **Reflections of Our Past How Human History Is Revealed in Our Genes Routledge** *The rise of the multi-billion dollar ancestry testing industry points to one immutable truth about us as human beings: we want to know where we come from and who our ancestors were. John H. Relethford and Deborah A. Bolnick explore this topic and many more in this second edition of Reflections of Our Past. Where did modern humans come from and how important are the biological differences among us? Are we descended from Neandertals? How should we understand the connections between genetic ancestry, race, and identity? Were Native Americans the first to inhabit the Americas? Can we see evidence of the Viking invasions of Ireland a millennium ago even in the Irish of today? Through engaging examination of issues such as these, and using non-technical language, Reflections of Our Past shows how anthropologists use genetic information to suggest answers to fundamental questions about human history. By looking at genetic variation in the world today and in the past, we can reconstruct the recent and remote events and processes that have created the variation we see, providing a fascinating reflection of our genetic past.* **A Genetic Perspective on Asian Populations Frontiers**

Media SA Current and Emerging Trends in Human Identification and Molecular Anthropology Frontiers Media SA Handbook of Statistical Genomics John Wiley & Sons *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.* **Human Population Genomics Introduction to Essential Concepts and Applications Springer Nature** *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. **Archaeological Science An Introduction Cambridge University Press** *An accessible and wide-ranging introduction to the exciting and expanding field of archaeological science, for students, professionals and academics.* **A Companion to Anthropological Genetics Wiley-Blackwell** *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.* **Introduction to Evolutionary Genomics Springer** *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. **A Primer of Population Genetics and Genomics Oxford University Press, USA** *This accessible primer has been completely revised and updated to provide a concise but comprehensive introduction to the basic concepts of population genetics and genomics.* **Genome-Wide Association Studies From Polymorphism to Personalized Medicine Developmental Biology Wiley-Blackwell** *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.* **Evolution of the Human Genome II Human Evolution Viewed from Genomes Springer Nature** *This two-volume set provides a general overview of the evolution of the human genome; The first volume overviews the human genome with descriptions of important gene groups. This second volume provides up-to-date, concise yet ample knowledge on the genome evolution of modern humans. It comprises twelve chapters divided into two parts discussing "Non-neutral Evolution on Human Genes" (Part I) and "Evolution of Modern Human Populations" (Part II.) The most significant feature of this book is the continent-wise discussion of modern human dispersal using human genomic data in Part II. Recent results such as introgression of paleogenomes to modern humans, new methods such as computer simulation of global human dispersals, and new information on genes for humanness will be of particular interest to the readers. Since the euchromatin regions of the human genome was sequenced in 2003, a huge number of research papers were published on modern human evolution for a variety of populations. It is now time to summarize these achievements. This book stands out as the most comprehensive book on the modern human evolution, focusing on genomic points of view with a broad scope. Primary target audiences are researchers and graduate students in evolutionary biology.* **Research in Computational Molecular Biology 22nd Annual International Conference, RECOMB 2018, Paris, France, April 21-24, 2018, Proceedings Springer** *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.* **Paleogenomics Genome-Scale Analysis of Ancient DNA Springer** *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. **Human Migration Biocultural Perspectives Oxford University Press** *This book combines the most recent research in population development, human genetics, archaeology, anthropology, biology, linguistics, and more to create a comprehensive picture of human migratory patterns.* **Bioinformatics John Wiley & Sons** *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. **The Oxford Handbook of Evolution, Biology, and Society Oxford University Press** *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.* **The Archaeology Coursebook An Introduction to Themes, Sites, Methods and Skills Routledge** *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.* **THE SECOND REPORT ON THE STATE OF THE WORLD's ANIMAL GENETIC RESOURCES FOR FOOD AND AGRICULTURE FAO**

COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE. ASSESSMENTS • 2015 Food & Agriculture Org. *Animal genetic resource diversity underpins the supply livestock products and services across a wide range of production environments. It promotes resilience and serves as a basis for adapting livestock management to changing conditions. It is vital to livelihoods of many of the world's poor people. It can contribute to the delivery of ecosystem services such as landscape management and the maintenance of wildlife habitats. However, it is often undervalued, underused and under threat. This report updates the global assessment provided in the first report on The State of the World's Animal Genetic Resources for Food and Agriculture, published in 2007. It focuses particularly on changes that have occurred during the period since the first report was published. It serves as a basis for a review, and potential update, of the Global Plan of Action for Animal Genetic Resources, which since 2007 has provided an agreed international framework for the management of livestock biodiversity. Drawing on 129 country reports, it presents an analysis of the state of livestock diversity, the influence of livestock-sector trends on the management of animal genetic resources, the state of capacity to manage animal genetic resources, including legal and policy frameworks, and the state of the art in tools and methods for characterization, valuation, use, development and conservation.* **A Primer of Molecular Population Genetics Oxford University Press, USA** *What are the genomic signatures of adaptations in DNA? How often does natural selection dictate changes to DNA? How does the ebb and flow in the abundance of individuals over time get marked onto chromosomes to record genetic history? Molecular population genetics seeks to answer such questions by explaining genetic variation and molecular evolution from micro-evolutionary principles. It provides a way to learn about how evolution works and how it shapes species by incorporating molecular details of DNA as the heritable material. It enables us to understand the logic of how mutations originate, change in abundance in populations, and become fixed as DNA sequence divergence between species. With the revolutionary advances in genomic data acquisition, understanding molecular population genetics is now a fundamental requirement for today's life scientists. These concepts apply in analysis of personal genomics, genome-wide association studies, landscape and conservation genetics, forensics, molecular anthropology, and selection scans. This book introduces, in an accessible way, the bare essentials of the theory and practice of molecular population genetics.* **Evolutionary Patterns and Processes Academic Press** *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 **Landscape Genetics Concepts, Methods, Applications John Wiley & Sons** *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 applications of landscape genetics for a variety of environments and species. Consistent with the interdisciplinary nature of landscape genetics, the book combines an introductory, textbook like section with additional sections on advanced topics and applications that are more typical of edited volumes. The chapter topics and the expertise of the authors and the editorial team make the book a standard reference for anyone interested in landscape genetics. The book includes contributions from many of the leading researchers in landscape genetics. The group of scientists we have assembled has worked on several collaborative projects over the last years, including a large number of peer reviewed papers, several landscape genetics workshops at international conferences, and a distributed graduate seminar on landscape genetics. Based on the experiences gained during these collaborative teaching and research activities, the book includes chapters that synthesize fundamental concepts and methods underlying landscape genetics (Part 1), chapters on advanced topics that deserve a more in depth treatment (Part 2), and chapters illustrating the use of concepts and methods in empirical applications (Part 3). This structure ensures a high usefulness of the book for beginning landscape geneticists and experienced researchers alike, so that it has a broad target audience. At least one of the four co editors is involved in almost every chapter of the book, thereby ensuring a high consistency and coherency among chapters.* **Molecular Genetics and Genomics Tools in Biodiversity Conservation Springer Nature** *This book provides insight into the use of molecular and genomic techniques to the study of populations of critically important species at various geographical scales. It delves into a wide range of issues relevant to biodiversity conservation, such as population differentiation, landscape genomics, ecological interactions, phylogenetics, phylogeography, metagenomics, molecular methods, and data processing. The current rate of biodiversity loss is unprecedented and valuable genetic resources are being lost at an alarmingly rate. Effective strategies to conserve these genetic resources are essential to maintain healthy ecosystems with inter-dependent species. The book is an invaluable resource for training undergraduate and graduate students,*

postdoctoral fellows, and for young researchers. This book is particularly useful for the policy makers and academics who want to learn about important concepts in population and conservation genetics and genomics. **Population Genomics Concepts, Approaches and Applications Springer** *Population genomics has revolutionized various disciplines of biology including population, evolutionary, ecological and conservation genetics, plant and animal breeding, human health, medicine and pharmacology by allowing to address novel and long-standing questions with unprecedented power and accuracy. It employs large-scale or genome-wide genetic information and bioinformatics to address various fundamental and applied aspects in biology and related disciplines, and provides a comprehensive genome-wide perspective and new insights that were not possible before. These advances have become possible due to the development of new and low-cost sequencing and genotyping technologies and novel statistical approaches and software, bioinformatics tools, and models. Population genomics is tremendously advancing our understanding the roles of evolutionary processes, such as mutation, genetic drift, gene flow, and natural selection, in shaping up genetic variation at individual loci and across the genome and populations; improving the assessment of population genetic parameters or processes such as adaptive evolution, effective population size, gene flow, admixture, inbreeding and outbreeding depression, demography, and biogeography; resolving evolutionary histories and phylogenetic relationships of extant, ancient and extinct species; understanding the genomic basis of fitness, adaptation, speciation, complex ecological and economically important traits, and disease and insect resistance; facilitating forensics, genetic medicine and pharmacology; delineating conservation genetic units; and understanding the genetic effects of resource management practices, and assisting conservation and sustainable management of genetic resources. This Population Genomics book discusses the concepts, approaches, applications and promises of population genomics in addressing most of the above fundamental and applied crucial aspects in a variety of organisms from microorganisms to humans. The book provides insights into a range of emerging population genomics topics including population epigenomics, landscape genomics, seascape genomics, paleogenomics, ecological and evolutionary genomics, biogeography, demography, speciation, admixture, colonization and invasion, genomic selection, and plant and animal domestication. This book fills a vacuum in the field and is expected to become a primary reference in Population Genomics world-wide.* **Population Genetics of Ancient and Modern DNA** *In this work, I develop computational tools focused around the utilization of DNA sequence data to address questions relative to forensic science, medical genetics, human evolution and ancient DNA. First, I compute the theoretical probability that two individual profiles match by chance at two loci in a subdivided population. This question is of particular interest in forensic science, where DNA evidence has become a widespread tool of investigation and criminal conviction. I find that the effect of ignoring population subdivision can be unfavorable to the defendant, but that the two loci can essentially be treated as unlinked. Second, I develop a method to identify genes that are interacting, or in epistasis, to produce a particular phenotype. Determining interacting genes is indeed of particular relevance in medical genetics to help map disease genes. I*

validate the method with simulations and demonstrate an improved performance over existing approaches. I also apply the method to recently available genomic data from domesticated dogs, identifying genes in epistastis for the hair length phenotype - thus representing candidate genes for functional validation. Third, I use a summary statistic of DNA sequences, the site frequency spectrum, to estimate parameters of recent human history, and to characterize the potential event of admixture between Neanderthals and humans. I find evidence for recent gene flow between Neanderthals and Europeans, and to a lesser extent between Neanderthals and Africans. Finally, I develop a likelihood method to jointly estimate the age and selection coefficient of an identified mutation, along with the population size, by using time serial samples. Such datasets are widespread in the fields of ancient DNA as well as experimental and viral evolution. I validate the method through simulations. I re-analyze a recent dataset for a locus coding for the distribution of black pigmentation in horses - and estimate that the allele far predates domestication, arising between 20,000 and 13,000 years ago. **Biotechnology: Concepts, Methodologies, Tools, and Applications Concepts, Methodologies, Tools, and Applications IGI Global** *Biotechnology can be defined as the manipulation of biological process, systems, and organisms in the production of various products. With applications in a number of fields such as biomedical, chemical, mechanical, and civil engineering, research on the development of biologically inspired materials is essential to further advancement. Biotechnology: Concepts, Methodologies, Tools, and Applications is a vital reference source for the latest research findings on the application of biotechnology in medicine, engineering, agriculture, food production, and other areas. It also examines the economic impacts of biotechnology use. Highlighting a range of topics such as pharmacogenomics, biomedical engineering, and bioinformatics, this multi-volume book is ideally designed for engineers, pharmacists, medical professionals, practitioners, academicians, and researchers interested in the applications of biotechnology.* **Research and Applications in Global Supercomputing IGI Global** *Rapidly generating and processing large amounts of data, supercomputers are currently at the leading edge of computing technologies. Supercomputers are employed in many different fields, establishing them as an integral part of the computational sciences. Research and Applications in Global Supercomputing investigates current and emerging research in the field, as well as the application of this technology to a variety of areas. Highlighting a broad range of concepts, this publication is a comprehensive reference source for professionals, researchers, students, and practitioners interested in the various topics pertaining to supercomputing and how this technology can be applied to solve problems in a multitude of disciplines.* **An Introduction to Molecular Anthropology John Wiley & Sons** *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. **Peopling the Landscape of Çatalhöyük Reports from the 2009-2017 Seasons British Institute of Archaeology at Ankara** *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.* **Ethnolinguistic Prehistory The Peopling of the World from the Perspective of Language, Genes and Material Culture BRILL** *This volume provides the most up-to-date and holistic but compact account of the peopling of the world from the perspective of language, genes and material culture. The book provides detailed answers to the question of where we all came from.* **The Indo-European Controversy Cambridge University Press** *This book challenges media-celebrated evolutionary studies linking Indo-European languages to Neolithic Anatolia, instead defending traditional practices in historical linguistics.* **The Formation of Latin American Nations From Late Antiquity to Early Modernity University of Oklahoma Press** *This pioneering work brings the pre-Columbian and colonial history of Latin America home: rather than starting out in Spain and following Columbus and the conquistadores as they "discover" New World peoples, The Formation of Latin American Nations begins with the Mesoamerican and South American nations as they were before the advent of European colonialism—and only then moves on to the sixteenth-century Spanish arrival and its impact. To form a clearer picture of precolonial Latin America, Thomas Ward reads between the lines in the "Chronicles of the Indies," filling in the blanks with information derived from archaeology, anthropology, genetics, and common-sense logic. Although he finds fascinating points of comparison among the K'iche' Maya in Central America, the polities (señoríos) of Colombia, and the Chimú of the northern Peruvian coast, Ward focuses on two of the best-known peoples: the Nahua (Aztec) of Central Mexico and the Inka of the Andes. His study privileges indigenous-identified authors such as Diego Muñoz Camargo, Fernando de Alva Ixtlilxóchitl, Inca Garcilaso de la Vega, and Felipe Guaman Poma de Ayala while it also consults Spanish chroniclers like Hernán Cortés, Bernal Diaz del Castillo, Pedro Cieza de León, and Bartolomé de las Casas. The nation-forming processes that Ward theorizes feature two forms of cultural appropriation: the horizontal, in which nations appropriate people and customs from adjacent cultures, and the vertical, in which nations dig into their own past to fortify*

their concept of exceptionality. In defining these processes, Ward eschews the most common measure, race, instead opting for the Nahua altepetl, the Inka panaka, and the K'iche' amaq'. His work thus approaches the nation both as the indigenous people conceptualized it and with terminology that would have been familiar to them before and after contact with the Spanish. The result is a truly decolonial account of the formation and organization of Latin American nations, one that puts the indigenous perspective at its center. **Something Out of the Ordinary? Interpreting Diversity in the Early Neolithic Linearbandkeramik and Beyond Interpreting Diversity in the Early Neolithic Linearbandkeramik and Beyond Cambridge Scholars Publishing** *More than 7000 years ago, groups of early farmers (the Linearbandkeramik, or LBK) spread over vast areas of Europe. Their cultural characteristics comprised common choices and styles of execution, with a central meaning and functionality attached to 'doing things a certain way', over an enormous geographical area. However, recent evidence suggests that the reality was much more varied and diverse. The central question of this book is the extent to which notions of 'uniformity' and 'diversity' have caused a wider shift in archaeological perspective. Using the LBK case study as a starting point, the volume brings together contributions by international specialists tackling the notion of cultural diversity and its explanatory power in archaeological analysis more generally. Through discussions of the domestic architecture, stone tool inventory, pottery traditions, landscape use and burial traditions of the LBK, this book provides a crucial reappraisal of the culture's potential for adaptability and change. Papers in the second part of the volume are devoted to archaeological case studies from around the globe in which the tension between diversity and uniformity has also proved controversial, including the Near Eastern Halaf culture, the North American Mississippian, the Pacific expansion of the Lapita culture, and the European Bell Beaker phenomenon. All provide exciting theoretical and methodological contributions on how the appreciation of cultural diversity as a whole can be moved forward. These papers expose diversity and uniformity as cultural strategies, and as such provide essential reading for scholars in archaeology and anthropology, and for anyone interested in the interplay between material culture and human social change.* **Human Evolutionary Genetics Origins, Peoples & Disease Garland Pub** *'Human Evolutionary Genetics' describes the molecular basis of human genetic variation and the mechanisms which give rise to it. It introduces principles behind the use of molecular genetic data to understand human evolution and population histories.* **Beginning Data Science in R Data Analysis, Visualization, and Modelling for the Data Scientist Apress** *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.