

Ancient DNA and human history

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We review studies of genomic data obtained by sequencing hominin fossils with particular emphasis on the unique information that ancient DNA (aDNA) can provide about the demographic history of humans and our closest relatives. We concentrate on nuclear genomic sequences that have been published in the past few years. In many cases, particularly in the Arctic, the Americas, and Europe, aDNA has revealed historical demographic patterns in a way that could not be resolved by analyzing present-day genomes alone. Ancient DNA from archaic hominins has revealed a rich history of admixture between early modern humans, Neanderthals, and Denisovans, and has allowed us to disentangle complex selective processes. Information from aDNA studies is nowhere near saturation, and we believe that future aDNA sequences will continue to change our understanding of hominin history.

human history | Neanderthal | Denisovan | ancient DNA | demography

The genomics revolution is well under way. At the time that the first human genomic sequences were obtained (1, 2), it was almost inconceivable that within 15 y thousands of genomes from people around the world would be sequenced, many to a high depth of coverage (3). It was probably even less conceivable that partial or complete genomic sequences would be obtained from hundreds of modern human fossils (4–6), several Neanderthal fossils (7, 8), and even fossils of a previously unknown sister group of Neanderthals, called Denisovans (9, 10) (Fig. 1). Some of these ancient genomes have been sequenced to such high depth that their error rates rival those of high-coverage sequences from present-day humans.

The wealth of present-day and ancient genomic data has greatly increased what is demanded of population geneticists. When relatively few loci could be studied using marker loci—chiefly blood groups, allozymes, and microsatellites—gross descriptive statistics, such as heterozygosity, Wright's F_{ST} , and various genetic distances were sufficient to characterize broad patterns of population differentiation. Application of these classic methods was pioneered by Luca Cavalli-Sforza and his many collaborators. As early as 1964, Cavalli-Sforza et al. (11) published a phylogenetic tree of 15 human populations based on a total of 20 alleles at 5 loci, mostly blood groups, for which adequate published data were available. The authors superimposed the tree on a world map to suggest

past dispersal routes. Their map is surprisingly consistent with more recent studies based on vastly more data. Only the connection of Maori to Native Americans disagrees with currently accepted theory, that the Maori descended from Polynesians (12).

At present, not only can geneticists elucidate broad patterns of relationship among populations, but they can also provide detailed answers to historical questions of relevance to archeology and paleoanthropology. When, where, and from what source did particular human populations arise? Who admixed with whom and when did the admixture take place? Are obvious changes in the archaeological record the result of population replacement or cultural innovation? Did past cultures leave any genetic descendants? As we will discuss, analysis of ancient DNA (aDNA) has been successful in answering several of these questions, but has also raised new questions in the process. Importantly, aDNA provides a temporal dimension to genetic studies that would be inaccessible with present-day genomes alone, and only now is the full significance of aDNA being explored.

Contamination

One of the major problems that prevented the widespread sequencing of hominin aDNA for several years was contamination. Genetic material extracted and sequenced from a tissue sample of a living individual

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Ancient Admixture In Human History Genetics

**Niko Balkenhol, Samuel
Cushman, Andrew Storfer, Lisette Waits**

Ancient Admixture In Human History Genetics:

Genetic History of Human Populations Along the Ancient Silk Road Shaoqing Wen, Horolma Pamjav, Maxat Zhabagin, 2024-04-05 The Silk Road a historical network of interlinking trade routes across the Afro Eurasian landmass was of great importance to the transport of peoples goods and ideas between the East and the West Although its main use was for importing silk from China traders moving in the opposite direction carried to Central China jewellery glassware and other exotic goods from the Mediterranean jade from Khotan and horses and furs from the nomads of the Steppe The Silk Road brought together the achievements of the different peoples of Eurasia to advance the Old World as a whole **Die große Odyssee** Lluís Quintana-Murci, 2024-03-14 Der international renommierte Biologe Lluís Quintana-Murci zeichnet in dieser so bahnbrechenden wie meisterhaften Darstellung die außergewöhnliche Geschichte der menschlichen Besiedlung auf der ganzen Welt nach Er belegt die Existenz ausgestorbener Menschenarten und enthält wie sich die menschlichen Populationen ständig untereinander aber auch mit archaischen Menschen wie dem Neandertaler oder dem Denisova-Menschen vermischt Ohne Vielfalt gibt es keine Evolution und keinen Fortschritt in irgendeinem Sinne des Wortes Vor etwa sechzigtausend Jahren haben unsere Vorfahren Afrika verlassen um sich über den gesamten Planeten zu verbreiten Dies ist die erste große Migration in der Geschichte der Menschheit gewesen Alle Menschen nicht afrikanischer Herkunft sind Nachkommen dieser ersten Migranten Es war der Beginn einer langen Geschichte von Wanderungen in deren Verlauf Europa Asien und Australien vor etwa fünfzigtausend Jahren Amerika vor weniger als dreißigtausend Jahren und schließlich die Inseln des fernen Ozeaniens wurden Die moderne Populationsgenetik ermöglicht uns Wanderungsereignisse und andere demografische Prozesse zu datieren Heute wissen wir dass Vermischung ein kontinuierlicher Prozess im Laufe der Menschheitsgeschichte war und ist Wir alle sind in unterschiedlichem Maße multiethnisch da unsere Genome aus einer Vielzahl von DNA Segmenten unterschiedlichster Herkunft bestehen ein historischer und geografischer Flickenteppich in dem sich Völker und Generationen vermischen Die Reise unserer Gene Johannes Krause, Thomas Trappe, 2019-02-22 Migration und Wanderungsbewegungen sind keine Phänomene der Neuzeit Seit der Mensch den aufrechten Gang beherrschte trieb es ihn aus seiner Heimat Afrika in die ganze Welt auch nach Europa Bis vor Kurzem lag diese Urgeschichte noch im Dunkeln doch mit den neuen Methoden der Genetik hat sich das grundlegend geändert Johannes Krause einer der führenden Experten auf dem Gebiet erzählt gemeinsam mit Thomas Trappe was uns die Gene über unsere Herkunft verraten Gibt es Urvölker Wann verloren die frühen Europäer ihre dunkle Haut Welche Rolle spielte die Balkanroute in den vergangenen 40 000 Jahren Eine große Erzählung die zeigt Ohne die Einwanderer die über Jahrtausende aus allen Richtungen nach Europa kamen und immer wieder Innovationen mitbrachten wäre unser Kontinent gar nicht denkbar Johannes Krause und Thomas Trappe geben einen spannenden Überblick über das was uns die Revolution der Archäogenetik über die europäische Bevölkerungsgeschichte lehrt Ihr Buch fängt die Begeisterung ein die diese junge Wissenschaft auslöst Wall Street Journal

Bioinformatics Andreas D. Baxevanis, Gary D. Bader, David S. Wishart, 2020-05-12 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 Foundations of Population Genetics Daniel M. Weinreich, 2023-08-29 An accessible but rigorous treatment of the theoretical foundations of population genetics Population genetics the branch of evolutionary biology concerned with understanding how and why populations genetic compositions change over time rests on a well developed theoretical foundation that draws on genetics mathematics and computer science This textbook provides an approachable but rigorous treatment for advanced undergraduate and graduate students interested in building a quantitative understanding of the genetics of evolution Existing texts either assume very mathematically advanced readers or avoid much of the underlying theory instead focusing on current methods of data analysis In contrast The Foundations of Population Genetics develops the theory from first principles Requiring only confidence in algebra this self contained student friendly book illustrates the conceptual framework terminology and methods of mathematical modeling It progressively introduces concepts from genetics as needed while emphasizing

biological implications throughout As a result readers come away with a deep understanding of the structure of population genetics without needing to master its mathematics Connects theory with the most recent genetic data better than existing texts Features engaging real world examples and extensive original figures Provides dozens of carefully scaffolded questions that deepen the reader's understanding of key concepts Ideal as a succinct reference for established scientists in biology medicine and computer science Instructor resources available

A Companion to Anthropological Genetics Dennis H. O'Rourke, 2019-03-11 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

Handbook of Statistical Genomics David J. Balding, Ida Moltke, John Marioni, 2019-07-09 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

Population Genomics with R Emmanuel Paradis, 2020-05-05 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>

Genomics and Society Dhavendra Kumar, Ruth Chadwick, 2015-10-29 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 *An Archaeology of the Bantu Expansion* Peter R. Coutros, Jessamy H. Doman, Igor Matonda Sakala, Koen Bostoen, 2025-07-22 The Bantu Expansion is one of the most intriguing issues in African history Based on extensive fieldwork in the Democratic Republic of the Congo and laboratory analysis this book provides the most comprehensive up to date and multi proxy account of the first Bantu speakers south of the Congo rainforest This volume begins with state of the art reviews of the archaeological palaeoenvironmental genetic linguistic and oral historical contexts of the Bantu Expansion and includes evidence from over 150 previously unknown archaeological sites with extensive analyses of pottery lithics soil stable isotopes phytoliths charcoal and human remains Seven appendices contain the full metadata radiometric and geographical data for each site and comparative language data The volume concludes with a sweeping interdisciplinary reconstruction of the first Bantu speaking settlers in the Kwilu Kasai region and rethinks how farming climate change and contact with Central African hunter gatherers and Ubangi speakers impacted their lifeworld This book is indispensable for scholars and students of Africa from a wide variety of fields such as archaeology palaeoecology linguistics population genetics history and anthropology and of considerable interest to scientists active in other parts of the world All who think African history matters will find it a valuable source

Forensic Investigative Genetic Genealogy and Fine-Scale Structure of Human Populations Guanglin He, Mengge Wang, Ryan Lan-Hai Wei, 2023-02-03 An Introduction to Molecular Anthropology Mark Stoneking, 2016-10-17 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 **The Archaeology Coursebook** Jim Grant, Sam Gorin, Neil Fleming, 2015-03-27 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 *Frontiers in Developmental Biology* Robert A. Meyers, 2019-04-02 Dieser aktuelle Band aus der renommierten enzyklopädischen Reihe ist der erste in vielen Jahren der alle wichtigen Aspekte der Entwicklungsbiologie vereint von der Morphogenese und Organogenese über die epigenetische Regulation der Genexpression bis hin zur evolutionären Entwicklungsbiologie Der Herausgeber hat ein herausragendes Team zusammengestellt das diese Themen beleuchtet und damit ein wegweisendes Werk für die kommenden Jahre geschaffen Das Ergebnis ist ein einzigartiges herausragendes Referenzwerk der Entwicklungsbiologie für Forscher Studenten und Fachexperten

Molecular Genetics and Genomics Tools in Biodiversity Conservation Ashwani Kumar, Baharul Choudhury, Selvadurai Dayanandan, Mohammed Latif Khan, 2022-02-01 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

The Indo-European Controversy Asya Pereltsvaig, Martin W. Lewis, 2015-04-30 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

Phenotypic Characterization, Genetics and Genomics of Livestock in Low Input Systems Mohammed Ali Al Abri, Olivier Hubert Hanotte, Younes Miar, 2022-10-19

Landscape Genetics Niko Balkenhol, Samuel Cushman, Andrew Storfer, Lisette Waits, 2015-11-09

LANDSCAPE GENETICS CONCEPTS METHODS APPLICATIONS LANDSCAPE GENETICS CONCEPTS METHODS APPLICATIONS Edited by Niko Balkenhol Samuel A Cushman Andrew T Storfer Lisette P Waits Landscape genetics is an exciting and rapidly growing field melding methods and theory from landscape ecology and population genetics to address some of the most challenging and urgent ecological and evolutionary topics of our time Landscape genetic approaches now enable researchers to study in detail how environmental complexity in space and time affect gene flow genetic drift and local adaptation However learning about the concepts and methods underlying the field remains challenging due to the highly interdisciplinary nature of the field which relies on topics that have traditionally been treated separately in classes and textbooks In this edited volume some of the leading experts in landscape genetics provide the first comprehensive introduction to underlying concepts commonly used methods and current and future applications of landscape genetics Consistent with the interdisciplinary nature of the field the book includes textbook like 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 Aimed at beginning landscape geneticists and experienced researchers alike this book will be helpful for all scientists and practitioners interested in learning teaching and applying landscape genetics

A Research Strategy to Examine the Taxonomy of the Red Wolf National Academies of Sciences, Engineering, and Medicine, Division on Earth and Life Studies, Board on Agriculture and Natural Resources, Board on Life Sciences, Committee on Assistance to the U.S. Fish and Wildlife Service on Taxonomic Studies of the Red Wolf: A Review of Applications to Carry Out Research and Development of a Research Strategy, 2020-12-29 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

Species Tree Inference Laura Kubatko, L. Lacey Knowles, 2023-03-14 Inferring evolutionary relationships among a collection of organisms that is their relationship to each other on the tree of life remains a central focus of much of evolutionary biology as these relationships provide the background for key hypotheses For example support for different hypotheses about early animal evolution are contingent

upon the phylogenetic relationships among the earliest animal lineages Within the last 20 years the field of phylogenetics has grown rapidly both in the quantity of data available for inference and in the number of methods available for phylogenetic estimation The authors first book *Estimating Species Trees Practical and Theoretical Aspects* published in 2010 gave an overview of the state of phylogenetic practice for analyzing data at the time but much has changed since then The goal of this book is to serve as an updated reference on current methods within the field The book is organized in three sections the first of which provides an overview of the analytical and methodological developments of species tree inference Section two focuses on empirical inference Section three explores various applications of species trees in evolutionary biology The combination of theoretical and empirical approaches is meant to provide readers with a level of knowledge of both the advances and limitations of species tree inference that can help researchers in applying the methods while also inspiring future advances among those researchers with an interest in methodological development

Ancient Admixture In Human History Genetics Book Review: Unveiling the Magic of Language

In an electronic era where connections and knowledge reign supreme, the enchanting power of language has become much more apparent than ever. Its capability to stir emotions, provoke thought, and instigate transformation is actually remarkable. This extraordinary book, aptly titled "**Ancient Admixture In Human History Genetics**," compiled by a very acclaimed author, immerses readers in a captivating exploration of the significance of language and its profound effect on our existence. Throughout this critique, we shall delve into the book's central themes, evaluate its unique writing style, and assess its overall influence on its readership.

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