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10 **Mysterious Extinct Human Species** **Map Shows How Humans Migrated Across The Globe** **Human Population Through Time** **The Remains Of The Oldest Human Ancestor Ever Found | First Human | Timeline** What Happened Before History? Human Origins ~~How to Argue With a Racist~~ ~~Adam Rutherford~~ *How Evolution Works, Part 2* **Blood Exhibition: Dr Adam Rutherford on Jewish Genetics** **Adam Rutherford: The genetics of skin colour** Genes, variation, and evolution **Seven Million Years of Human Evolution Everything you know about genetics is wrong (Adam Rutherford)** 9+ ~~Inbreeding and genetic variation in evolution and conservation~~ Biblical Family Tree 1 - Adam & Eve to King David *'The evolution of vicarious liability': 2017 Allen Overy Lecture*

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Genetics, Genealogy, and You Meeting July 19, 2020 *Gene Genealogies Variation And Evolution*

*Gene Genealogies, Variation and Evolution* fills this important gap this book should be mandatory reading for any graduate student working on population-level molecular data."-Evolution. About the Author. Jotun Hein is a Professor of Bioinformatics Department of Statistics, University of Oxford. Mikkel Schierup and

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Carsten Wiuf are both at the ...

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Gene Genealogies, Variation and Evolution: A primer in coalescent theory. Jotun Hein, Mikkel Schierup, Carsten Wiuf. Oxford University Press, USA, Dec 9, 2004 - 296 pages. 1 Review.

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Coalescent theory tells us what gene genealogies are expected to look like if populations have different demographic histories - i.e, population size, structure,

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etc. The aim of this book is to provide an accessible introduction to Coalescent Theory with a view towards data analysis. Coalescent...

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Coalescent theory is a central concept in the study of genetic sequence variation that probabilistically describes the genealogy relating the sampled sequences. In this text, besides fulfilling the glaring need for such a book, the authors present this theory in a straightforward and elementary manner and describe the statistical and computational methods used in modelling and analyzing genetic sequence variation.

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Gene genealogies have lead to several important insights into plant evolution and have the potential for far greater contributions. Many of the processes that affect the evolution of plant populations, such as selection, isolation, size fluctuations, and gene flow, are amenable to genealogical analysis.

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Coalescent theory is a model of how gene variants sampled from a population may have originated from a common ancestor. In the simplest case, coalescent theory assumes no recombination, no natural selection, and no gene flow or population structure, meaning that each variant is equally likely to have been passed from one generation to the next. The model looks backward in time, merging alleles into a single ancestral copy according to a random process in coalescence events. Under this model, the

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Authored by leading experts, this seminal text presents a straightforward and elementary account of coalescent theory, which is a central concept in the study of genetic sequence variation observed in a population. Rich in examples and illustrations it is ideal for a graduate course in statistics, population, molecular and medical genetics, bioscience and medicine, and for students studying the evolution of human population and disease. It is also an invaluable reference for bioscientists and statisticians in the pharmaceutical industry and academia - ;Coalescent theory is a central concept in the study of genetic sequence variation that probabilistically describes the genealogy relating the sampled sequences. In this text, besides fulfilling the glaring need for such a book, the authors present this theory in a straightforward and elementary manner and describe the statistical and computational methods used in modelling and analyzing genetic sequence variation. Rich in examples and illustrations the book covers basic concepts, complications arising from geographical structure and recombination before considering aspects of statistical inference based on these models. The book ends with chapters on Gene Mapping, which combines sequence variation data with phenotypic data (such as disease) to define areas of the genome where genes are responsible for the trait, and Human Evolution, a research area that is experiencing a renaissance due to the enormous amounts of data produced in molecular

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studies. Authored by leading experts, this seminal text presents a straightforward and elementary account of coalescent theory, which is a central concept in the study of genetic sequence variation observed in a population. It is highly suitable for a graduate course in statistics, population, molecular and medical genetics, bioscience and medicine and students studying the evolution of human population and disease, and will be an invaluable reference for bioscientists and statisticians in the pharmaceutical industry and academia - ;an excellent and timely book that should appeal to a variety of people in genetics and applied mathematics. - Professor Montgomery Slatkin (Berkeley);the authors are outstanding experts in the field, and the book is topical and timely. - Professor David Balding (Imperial College);Hein, Schierup and Wiuf have written the first general book on the coalescent. It is an engaging combination of clear mathematical derivation and real data examples. - Professor Joe Felsenstein (University of Washington)

"An introduction to coalescent theory, which provides the foundation for molecular population genetics and genomics. Coalescent theory is the conceptual framework for studies of DNA sequence variation within species, and is the source of essential tools for making inferences about mutation, recombination, population structure and natural selection from DNA sequence data"--Provided by publisher.

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"What underlying forces are responsible for the observed patterns of variability, given a collection of DNA sequences?" In approaching this question a number of probability models are introduced and analyzed. Throughout the book, the theory is developed in close connection with data from more than 60 experimental studies that illustrate the use of these results.

"The present book is intended as a progress report on [the] synthetic approach to evolution as it applies to the plant kingdom." With this simple statement, G. Ledyard Stebbins formulated the objectives of *Variation and Evolution in Plants*, published in 1950, setting forth for plants what became known as the "synthetic theory of evolution" or "the modern synthesis." The pervading conceit of the book was the molding of Darwin's evolution by natural selection within the framework of rapidly advancing genetic knowledge. At the time, *Variation and Evolution in Plants* significantly extended the scope of the science of plants. Plants, with their unique genetic, physiological, and evolutionary features, had all but been left completely out of the synthesis until that point. Fifty years later, the National Academy of Sciences convened a colloquium to update the advances made by Stebbins. This collection of 17 papers marks the 50th anniversary of the publication of Stebbins' classic. Organized into five sections, the book covers: early evolution and the origin of cells, virus and bacterial models, protoctist models, population variation, and trends and patterns in plant evolution.

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Wide-ranging and inclusive, this text provides an invaluable review of an expansive selection of topics in human evolution, variation and adaptability for professionals and students in biological anthropology, evolutionary biology, medical sciences and psychology. The chapters are organized around four broad themes, with sections devoted to phenotypic and genetic variation within and between human populations, reproductive physiology and behavior, growth and development, and human health from evolutionary and ecological perspectives. An introductory section provides readers with the historical, theoretical and methodological foundations needed to understand the more complex ideas presented later. Two hundred discussion questions provide starting points for class debate and assignments to test student understanding.

Phylogeography is a discipline concerned with various relationships between gene genealogies--phylogenetics--and geography. This book captures the conceptual and empirical richness of the field, and also the sense of genuine innovation that phylogeographic perspectives have brought to evolutionary studies.

Charles Fox and Jason Wolf have brought together leading researchers to produce a cutting-edge primer introducing readers to the major concepts in modern evolutionary genetics. This book spans the continuum of scale, from studies of DNA

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sequence evolution through proteins and development to multivariate phenotypic evolution, and the continuum of time, from ancient events that lead to current species diversity to the rapid evolution seen over relatively short time scales in experimental evolution studies. Chapters are accessible to an audience lacking extensive background in evolutionary genetics but also current and in-depth enough to be of value to established researchers in evolution biology.

'Phylogenetics' is the reconstruction and analysis of phylogenetic (evolutionary) trees and networks based on inherited characteristics. It is a flourishing area of interreaction between mathematics, statistics, computer science and biology. The main role of phylogenetic techniques lies in evolutionary biology, where it is used to infer historical relationships between species. However, the methods are also relevant to a diverse range of fields including epidemiology, ecology, medicine, as well as linguistics and cognitive psychology. This graduate-level book, based on the authors lectures at The University of Canterbury, New Zealand, focuses on the mathematical aspects of phylogenetics. It brings together the central results of the field (providing proofs of the main theorem), outlines their biological significance, and indicates how algorithms may be derived. The presentation is self-contained and relies on discrete mathematics with some probability theory. A set of exercises and at least one specialist topic ends each chapter. This book is intended for biologists interested in the mathematical theory behind phylogenetic methods, and for mathematicians, statisticians, and computer scientists eager to

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learn about this emerging area of discrete mathematics.'Phylogenetics' in the 24th volume in the Oxford Lecture Series in Mathematics and its Applications. This series contains short books suitable for graduate students and researchers who want a well-written account of mathematics that is fundamental to current to research. The series emphasises future directions of research and focuses on genuine applications of mathematics to finance, engineering and the physical and biological sciences.

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