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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 Carsten Wiuf are both at the ...

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Gene Genealogies, Variation and Evolution A Primer in Coalescent Theory Jotun Hein, Mikkel H. Schierup, and Carsten Wiuf Coalescent theory tells us what gene genealogies are expected to look like if populations have different demographic histories - i.e, population size, structure, etc.

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Authored by leading experts, and rich in examples and illustrations, Gene Genealogies, Variation and Evolution is highly suitable for a graduate course in statistics; population, molecular and medical genetics; and for bioscience and medicine and students studying the evolution of human population and disease.

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Gene Genealogies, Variation and Evolution: A primer in ...
Coalescent theory tells us what gene genealogies are expected to look like if populations have different demographic histories - i.e, population size, structure, 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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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

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 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.

Annotation In 1950, Stebbins (d. 2000) published Variation and Evolution in Plants, which extended the synthetic theory of evolution or "the modern synthesis" to plants. These 17 papers are drawn from a National Academy of Sciences colloquium held in January 2000 on the 50th anniversary of the publication of Stebbins' classic. Following a Stebbins appreciation talk (originally slotted for his own words), papers branch into sections on: early evolution and the origin of cells, virus and bacterial models, protoctist models (having to do with RNA editing), population variation, and trends and patterns in plant evolution. Annotation c. Book News, Inc., Portland, OR (booknews.com).

"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 anyalyzed.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.

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.

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.

Molecular understanding of cancer and cancer progression is at the forefront of many research programs today. High-throughput array technologies and other modern molecular techniques produce a wealth of molecular data about the structure, and function of cells, tissues, and organisms. Correctly analyzed and interpreted these data hold the promise of bringing new markers for prognostic and diagnostic use, for new treatment schemes, and of gaining new biological insight into the evolution of cancer and its molecular, pathological, and clinical consequences. Aimed at graduates and researchers, this book discusses novel advances in informatics and statistics in molecular cancer research. Through eight chapters from carefully chosen experts it brings the reader up to date with specific topics in cancer research, how the topics give rise to development of new informatics and statistics tools, and how the tools can be applied. The focus of the book is to give the reader an understanding of key concepts and tools, rather than focusing on technical issues. A main theme is the extensive use of array technologies in modern cancer research - gene expression and exon arrays, SNP and copy number arrays, and methylation arrays - to derive quantitative and qualitative statements about cancer, its progression and aetiology, and to understand how these technologies on one hand allow us learn about cancer tissue as a complex system and on the other hand allow us to pinpoint key genes and events as crucial for the development of the disease.

"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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