1. Record Nr. UNINA9910815015203321

Autore	Peng Bo <1974->
Titolo	Forward-time population genetics simulations : methods, implementation, and applications / / Bo Peng, Marek Kimmel, Christopher I. Amos
Pubbl/distr/stampa	Hoboken, N.J., : Wiley Blackwell, c2012
ISBN	1-283-45393-2 9786613453938 1-118-18034-8 1-118-18035-6 1-118-18032-1
Edizione	[1st ed.]
Descrizione fisica	1 online resource (258 p.)
Altri autori (Persone)	KimmelMarek <1959-> AmosChristopher I
Disciplina	576.5/8
Soggetti	Population genetics Evolution (Biology) - Computer simulation
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	FORWARD-TIME POPULATION GENETICS SIMULATIONS: Methods, Implementation, and Applications; CONTENTS; PREFACE; ACKNOWLEDGMENTS; LIST OF EXAMPLES; 1 BASIC CONCEPTS AND MODELS; 1.1 Biological and Genetic Concepts; 1.1.1 Genome and Chromosomes; 1.1.2 Genes, Markers, Loci, and Alleles; 1.1.3 Recombination and Linkage; 1.1.4 Sex Chromosomes; 1.1.5 Mutation and Mutation Models; 1.2 Population and Evolutionary Genetics; 1.2.1 Population Variation and Mutation; 1.2.2 The Wright-Fisher Model and Random Mating; 1.2.3 The Hardy-Weinberg Equilibrium; 1.2.4 Genetic Drift and Effective Population Size 1.2.5 Natural Selection1.2.6 Linkage Equilibrium; 1.2.7 Population Structure and Migration; 1.2.8 Demographic History of Human Populations; 1.2.9 Coalescent and Backward-Time Simulations; 1.2.10 Forward-Time Simulations; 1.3 Statistical Genetics and Genetic Epidemiology; 1.3.1 Penetrance Models; 1.3.2 Simple and Complex Genetic Diseases; 1.3.3 Phenotypic, Allelic, and Locus Heterogeneity;

1.3.4 Study Designs of Gene Mapping; References; 2 SIMULATION OF POPULATION GENETICS MODELS; 2.1 Random Genetic Drift; 2.1.1 Dynamics of Allele Frequency and Heterozygosity; 2.1.2 Persistence Time
2.2 Demographic Models2.2.1 The Bottleneck Effect; 2.3 Mutation; 2.3.1 A Diallelic Mutation Model; 2.3.2 Multiallelic Mutation Models; 2.4 Migration; 2.4.1 An Island Model of Migration; 2.5 Recombination and Linkage Disequilibrium; 2.6 Natural Selection; 2.6.1 Single-Locus Diallelic Selection Models; 2.6.2 Multilocus Selection Models; 2.7 Genealogy of Forward-Time Simulations; 2.7.1 Genealogy of Haploid Simulations; 2.7.2 Genealogy of Diploid Simulations; References; 3 ASCERTAINMENT BIAS IN POPULATION GENETICS; 3.1 Introduction; 3.2 Methods; 3.2.1 Evolution of a DNA Repeat Locus
3.2.2 Conditional Distributions and Ascertainment Bias of Allele Sizes3. 2.3 Simulation Method; 3.3 Results; 3.3.1 Summary of Modeling Results; 3.3.2 Comparisons of Empirical Statistics Derived from Human and Chimpanzee Microsatellite Data; 3.4 Discussion and Conclusions; References; 4 OBSERVING PROPERTIES OF EVOLVING POPULATIONS; 4.1 Introduction; 4.1.1 Allelic Spectra of Complex Human Diseases; 4.1.2 An Evolutionary Model of Effective Number of Disease Alleles; 4.1.3 Simulation of the Evolution of ne; 4.2 Simulation of the Evolution of Allele Spectra; 4.2.1 Demographic Models
4.2.2 Output Statistics4.2.3 Mutation Models; 4.2.4 Multilocus Selection Models; 4.2.5 Evolve!; 4.2.6 Validation of Theoretical Results; 4.3 Extensions to the Basic Model; 4.3.1 Impact of Demographic Models; 4.3.2 Impact of the Mutation Model; 4.3.3 Impact of Subpopulation Structure; 4.3.4 Impact of Migration; 4.3.5 Distribution of Equilibrium Disease Allele Frequency; 4.3.6 Varying Selection and Mutation Coefficients; 4.3.7 Evolution of Disease Predisposing Loci Under Weak Selection; 4.3.8 Discussion; References; 5 SIMULATING POPULATIONS WITH COMPLEX HUMAN DISEASES; 5.1 Introduction
5.2 Controlling Disease Allele Frequencies at the Present Generation

Sommario/riassunto

The only book available in the area of forward-time population genetics simulations-applicable to both biomedical and evolutionary studies The rapid increase of the power of personal computers has led to the use of serious forward-time simulation programs in genetic studies. Forward-Time Population Genetics Simulations presents both new and commonly used methods, and introduces simuPOP, a powerful and flexible new program that can be used to simulate arbitrary evolutionary processes with unique features like customized chromosome types, arbitrary nonrandom mating schemes, virtual subp