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searching; Multiple relatives; 3.3 Blind Search; 3.3.1 Kinship Matching; 3.3.2 Direct Matching; 3.4 Familial Searching; 3.4.1 Implementation; 3.4.2 *Relatives and Mixtures; 3.4.3 Select Subsets; Top k; LR threshold; Profile centered; Conditional; 3.5 Exercises; Chapter 4: Dependent markers; 4.1 Linkage; 4.1.1 Recombination; 4.1.2 Introduction to Calculations 4.1.3 Generalization and the Lander-Green Algorithm 4.1.4 Extensions; X-chromosomal markers; Mutations; Subpopulation correction; Dropouts and silent alleles; 4.2 Linkage Disequilibrium; 4.2.1 Introduction to Calculations; 4.2.2 *Generalization; Cluster approach; Exact calculations; 4.3 Haplotype Frequency Estimation; 4.4 Programs for Linked Markers; 4.4.1 FamLink; 4.4.2 FamLinkX; 4.5 Exercises; 4.5.1 Autosomal Markers and FamLink; 4.5.2 X-Chromosomal Markers and FamLinkX; Chapter 5: Relationship inference with R; 5.1 Using R; 5.1.1 R Packages for Relationship Inference 5.1.2 The Familias Package 5.2 Exercises; Chapter 6: Models for pedigree inference; 6.1 Population-Level Models; 6.1.1 *Frequency Uncertainty; 6.1.2 *Taking Frequency Uncertainty into Account; 6.1.3 *Population Structure and Subpopulations; 6.1.4 *Haplotype Models; 6.1.5 Population Models for Nonautosomal Markers; 6.2 Pedigree-Level Models; 6.2.1 Mutation Models; The ""Equal"" model; The ""Stepwise"" model; *Stationary mutation models; *Model based on frequencies; *Stabilizing existing mutation models; 6.3 Observational-Level Models; 6.4 Computations; 6.4.1 Identical by Descent Assuming independent markers, two tested persons, and no inbreeding

Sommario/riassunto

Relationship Inference in Familias and R discusses the use of Familias and R software to understand genetic kinship of two or more DNA samples. This software is commonly used for forensic cases to establish paternity, identify victims or analyze genetic evidence at crime scenes when kinship is involved. The book explores utilizing Familias software and R packages for difficult situations including inbred families, mutations and missing data from degraded DNA. The book additionally addresses identification following mass disasters, familial searching, non-autosomal marker analysis and relationship inference using linked markers. The second part of the book focuses on more statistical issues such as estimation and uncertainty of model parameters. Although written for use with human DNA, the principles can be applied to non-human genetics for animal pedigrees and/or analysis of plants for agriculture purposes. The book contains necessary tools to evaluate any type of forensic case where kinship is an issue.--
