

## BOOK REVIEW

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### Review of Genetic Data Analysis II. Method for Discrete Population Genetic Data, (Bruce Weir) (Second Edition)

**REFERENCE:** Weir B, Genetic data analysis II. Methods for discrete population genetic data, 2nd ed. Sinauer Associates Inc., Sunderland MA. 1996; 376 pp.

The second, expanded edition of this single-authored treatise was written to serve geneticists who have limited statistical training and for statisticians who have been asked to apply quantitative methods to the rapid advances in fields such as molecular, population and evolutionary genetics, genomic mapping, sequencing and linkage analyses and forensic sciences. The paperback book is also a shelf reference and serves as a simple and useful review of concepts and applications. The book appears to be well-edited and without errors of notation, logic or typography because the republished material was already extensively reviewed by experts, and the author's students.

Material consists of brief narratives that are easily read, followed by supplemental tabulated data, appendices containing statistical tables and abundant references. References include referred articles, textbooks on specific subjects and computer programmatic and posted descriptive information. There are ten chapters (with exercises for readers) that logically progress from the definitional and statistical to the genetic and then to the applied.

The first chapter, "Nature of Discrete Genetic Data," describes the collection of data from analyses of bloodgroups, allozymes, protein sequences, nucleic acid restriction fragments, DNA repeat sequences and coding sequences. The author explains two kinds of variation, statistical (sampling methods and sample sizes) and genetic (random intergenerational increase or decrease in allele frequencies), for which any mathematical treatments and comparisons must account. There is a lengthy example of recent analyses using Mendel's "too perfect" pea plant segregation frequencies.

Ways of estimating frequencies are described briefly in the second chapter. The author explains why specific statistical tests apply to genetic data, assuming that the reader knows the fundamentals of both classical statistics and population genetics. Exam-

ples clarify the methods, if not the principles of the classical methods. Explanations and limitations of Bayesian reasoning prepare the reader for applications in later chapters. A summary offers a path through the preceding mathematical notation.

The following chapters, titled "Disequilibrium, Diversity, Population Structure, Individual Identification, Linkage, Outcrossing and Selection, Sequence Data, and Phylogeny Reconstruction" deal with practical issues of most interest to students of evolution, population genetics, agriculture and husbandry. There is some scattered subject matter, however, that has relevance to forensic geneticists who use genetic markers to establish identity or relationship. Examples include treatments of departure from Hardy-Weinberg equilibrium, linkage disequilibrium, heterozygosity, and population substructure.

Of most interest to *JFS* subscribers is Chapter 6, "Individual Identification," whose text contains a variety of applications of genetic data analysis. Bayes theorem is reviewed in the context of questionable paternity testing and personal identity. The text logically introduces the concept of inheritance by descent and its importance in inbreeding as a result of either genetic drift or consanguineous mating. The probability of paternity exclusion is briefly discussed using codominant (e.g., single DNA loci) and dominant (e.g., ABO blood group) allelic markers. Subsequently, there is mathematical consideration of prior, conditional, joint, and posterior probabilities, the relative odds of paternity and the odds of paternity for accused relatives of the biologic father.

The rest of Chapter 6 is devoted to forensic tests and includes estimates of genetic (DNA) profile frequency, likelihood ratios for members of the same population or the same family, and how to deal with forensic samples that are mixtures of alleles from more than one person. Examples are given of calculations for mixed samples, dealing with alternative hypotheses, and determining error rates. Text references are indexed by the single bibliography at the end of the book includes publications that are not mentioned in the text. This suggests that there are omissions, a suspicion borne out by absence of a critical review of multilocus DNA fingerprinting methods, no explicit description of human racial groups, and exclusion of methods for matching nondiscrete alleles.

The forensic biologist who uses genetic markers will find this reference book creditable, concise and current, but not complete.

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