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Cover; Title Page; Copyright; Contents; Preface to the second edition; Preface to the first edition; Chapter 1 Introduction; 1.1 Weight-of-evidence theory; 1.2 About the book; 1.3 DNA profiling technology; 1.4 What you need to know already; 1.5 Other resources; Chapter 2 Crime on an island; 2.1 Warm-up examples; 2.1.1 People v. Collins (California, 1968); 2.1.2 Disease testing: positive predictive value (PPV); 2.1.3 Coloured taxis; 2.2 Rare trait identification evidence; 2.2.1 The 'island' problem; 2.2.2 A first lesson from the island problem; 2.3 Making the island problem more realistic; 2.3.1 The effect of uncertainty about p ; 2.3.2 Uncertainty about N ; 2.3.3 The effect of possible typing errors; 2.3.4 The effect of searches; 2.3.5 The effect of other evidence; 2.3.6 The effects of relatives and population subdivision; 2.4 Weight-of-evidence exercises; Chapter 3 Assessing evidence using likelihoods; 3.1 Likelihoods and their ratios; 3.2 The weight-of-evidence formula; 3.2.1 The population P ; 3.2.2 Grouping the RX ; 3.2.3 Application to the island problem; 3.3 General application of the formula; 3.3.1 Several items of evidence; 3.3.2 The role of the expert witness; 3.4 Consequences for DNA evidence; 3.4.1 Many possible culprits; 3.4.2 Incorporating the non-DNA evidence; 3.4.3 Relatives; 3.4.4 Laboratory and handling errors; 3.4.5 Database searches; 3.5 Derivation of the weight-of-evidence formula; 3.5.1 Bayes' theorem; 3.5.2 Uncertainty about p and N ; 3.5.3 Grouping the alternative possible culprits; 3.5.4 Typing errors; 3.6 Further weight-of-evidence exercises; Chapter 4 Profiling technologies; 4.1 STR typing; 4.1.1 Anomalies; 4.1.2 Contamination; 4.1.3 Low-template DNA (LTDNA) profiling; 4.2 mtDNA typing; 4.3 Y-chromosome markers; 4.4 X-chromosome markers; 4.5 SNP profiles; 4.6 Sequencing; 4.7 Methylation; 4.8 RNA; 4.9 Fingerprints; Chapter 5 Some population genetics for DNA evidence; 5.1 A brief overview; 5.1.1 Drift; 5.1.2 Mutation; 5.1.3 Migration; 5.1.4 Selection; 5.2 F_{ST} or F_{IS} ; 5.2.1 Population genotype probabilities; 5.3 A statistical model and sampling formula; 5.3.1 Diallelic loci; 5.3.2 Multi-allelic loci; 5.4 Hardy-Weinberg equilibrium; 5.4.1 Testing for deviations from HWE; 5.4.2 Interpretation of test results; 5.5 Linkage equilibrium; 5.6 Coancestry; 5.6.1 One allele; 5.6.2 Two alleles; 5.6.3 Three alleles; 5.6.4 General proof via recursion; 5.7 Likelihood-based estimation of F_{ST} ; 5.8 Population genetics exercises; Chapter 6 Inferences of identity; 6.1 Choosing the hypotheses; 6.1.1 Post-data equivalence of hypotheses; 6.2 Calculating LR's; 6.2.1 The match probability; 6.2.2 Single locus; 6.2.3 Multiple loci: the 'product rule'; 6.2.4 Relatives of Q ; 6.2.5 Confidence limits; 6.2.6 Other profiled individuals; 6.3 Application to STR profiles; 6.3.1 Values for the p_j ; 6.3.2 The value of F_{ST} ; 6.3.3 Choice of population; 6.3.4 Errors; 6.4 Application to haploid profiles; 6.4.1 mtDNA profiles

DNA evidence is widely used in the modern justice system. Statistical methodology plays a key role in ensuring that this evidence is collected, interpreted, analysed and presented correctly. This book is a guide to assessing DNA evidence and presenting that evidence in a courtroom setting. It offers practical guidance to forensic scientists with little dependence on mathematical ability, and provides the scientist with the understanding they require to apply the methods in their work. Since the publication of the first edition of this book in 2005 there have been many incremental changes