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Nota di contenuto	Cover; title; Copyright; Dedication; Preface; Acknowledgments; 1: Molecular Genetics; 1.1 WHAT IS THE NATURE OF GENETIC INFORMATION?; 1.2 HOW IS GENETIC INFORMATION TRANSMITTED FROM GENERATION TO GENERATION?; 1.3 WHAT IS INDIVIDUAL VARIATION IN GENETIC INFORMATION?; 1.4 PROBLEMS; URLs; 2: Formal Genetics; 2.1 WHAT ARE MENDEL'S LAWS?; 2.2 HOW ARE PHENOTYPES TRANSMITTED IN FAMILIES?; 2.3 WHICH COMPLICATIONS TO THE GENERAL INHERITANCE PATTERNS EXIST?; 2.4 WHAT IS THE LAW DETECTED BY HARDY AND WEINBERG?; 2.5 PROBLEMS; URLs; 3: Genetic Markers; 3.1 WHAT IS A GENETIC MARKER? 3.2 WHAT TYPES OF GENETIC MARKERS ARE THERE? 3.3 WHAT ARE GENOTYPING METHODS FOR SINGLE NUCLEOTIDE POLYMORPHISMS?; 3.4 PROBLEMS; URLs; 4: Data Quality; 4.1 HOW CAN PEDIGREE ERRORS BE DETECTED?; 4.2 HOW CAN GENOTYPING ERRORS BE DETECTED IN FAMILY-BASED STUDIES?; 4.3 HOW SHOULD GENOTYPING ERRORS BE

CHECKED IN POPULATION-BASED STUDIES USING THE HARDY-WEINBERG EQUILIBRIUM?; Algorithm 4.1.; Algorithm 4.2.; Algorithm 4.3.; 4.4 HOW CAN GENOTYPING ERRORS BE DETECTED IN HIGH-THROUGHPUT GENOTYPING STUDIES?

4.5 HOW SHOULD CLUSTER PLOTS AND HOW CAN THE QUALITY OF CLUSTERS BE INVESTIGATED IN HIGH-THROUGHPUT GENOTYPING STUDIES? 4.6 PROBLEMS; URLs; 5: Genetic Map Distances; 5.1 WHAT IS PHYSICAL DISTANCE?; 5.2 WHAT IS MAP DISTANCE?; 5.3 WHAT ARE LINKAGE DISEQUILIBRIUM UNITS?; 5.4 PROBLEMS; URLs; 6: Familiality, Heritability, and Segregation Analysis; 6.1 WHAT IS THE DIFFERENCE BETWEEN THE FAMILY HISTORY METHOD AND THE FAMILY STUDY METHOD?; 6.2 HAS THE PHENOTYPE OF INTEREST A FAMILIAL COMPONENT? WHAT ARE RECURRENCE RISK RATIOS?; 6.3 WHAT IS THE CONCEPT OF HERITABILITY?

6.4 WHAT ARE TWIN STUDIES? WHAT ARE ADOPTION STUDIES? 6.5 WHAT ARE CRITICAL ASPECTS WHEN INVESTIGATING FAMILIAL RESEMBLANCE?; 6.6 HOW CAN EVIDENCE FOR A MAJOR GENE EFFECT BE ESTABLISHED? HOW CAN A SEGREGATION PATTERN FOLLOWING MENDELIAN INHERITANCE BE DETERMINED?; 6.7 PROBLEMS; URLs; 7: Model-Based Linkage Analysis; 7.1 HOW CAN THE RECOMBINATION FRACTION BE ESTIMATED BETWEEN TWO GENETIC MARKERS?; 7.2 HOW CAN THE RECOMBINATION FRACTION BE ESTIMATED BETWEEN A GENETIC MARKER AND A DISEASE?; 7.3 WHAT IS SIGNIFICANT EVIDENCE OF LINKAGE?; 7.4 PROBLEMS; URLs
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8.8 HOW CAN THE AFFECTED SIB-PAIR METHOD BE EXTENDED TO ARBITRARY UNILINEAL RELATIONSHIPS?

Sommario/riassunto

This is the second edition of the successful textbook written by the prize-winning scientist Andreas Ziegler, former President of the German Chapter of the International Biometric Society, and Inke Konig, who has been teaching the subject over many years. The book gives a comprehensive introduction into the relevant statistical methods in genetic epidemiology. The second edition is thoroughly revised, partly rewritten and includes now chapters on segregation analysis, twin studies and estimation of heritability. The book is ideally suited for advanced students in epidemiology, genet
