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## Preface

The genetic analysis of quantitative traits in humans began in earnest in the early part of the 20th century, after the rediscovery of Mendel's work, and it was R. A. Fisher's seminal 1918 paper that clarified the main concepts of biometrical genetics. At the start of the 21st century, statistical methods for quantitative trait locus (QTL) analysis are being refined and added to at an astonishing rate. Methods based on the analysis of quantitative traits tend to be more powerful than the equivalent binary trait methods, and, in conjunction with whole-genome screening technologies, are yielding exciting results in agriculture, experimental organisms, and the study of human disease.

*Quantitative Trait Loci: Methods and Protocols* aims to review the current methodologies available in three main areas: human traits (investigation of QTLs underlying human disease), experimental organisms (as models for human disease), and agriculture (crop and livestock improvement). The aim of each chapter is to provide a practical guide to the topic under discussion, including an overview of the technique in a style that is accessible to the non-mathematician. Thus, investigators will be able to use the book from the study design stage of a project onwards. Each chapter includes a detailed description of how to proceed with a specific analysis, including the use of and where to find appropriate computer software, a guide to the interpretation of the results, and worked examples. The chapters also include citations for the original papers and variations on methods where appropriate. In addition to being a reference for investigators and a text for students starting in the field, this book will prove useful for anyone interested in gaining an overview of the current state-of-the-art in QTL analysis.

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