
Editor's Preface to the Third Edition

In the four years that have elapsed since the highly successful second edition of the *Handbook of Statistical Genetics*, the field has moved on, in some areas dramatically. This is reflected in the present thorough revision and comprehensive updating: 17 chapters are entirely new, 6 providing a fresh approach to topics that had been covered in the second edition, while 11 new chapters cover areas of recent growth, or important topics not previously addressed. These new topics include microarray data analysis (two new chapters to complement the existing one), eQTL analyses and metabonomics. There are also new chapters on graphical models and on pedigrees and genealogies, admixture mapping and genome-wide association studies, cancer genetics, epigenetics, and genetical aspects of insurance. Of the 26 chapters carried over from the second edition, 21 have been revised, among which 5 very substantial revisions are close to being new chapters.

It will be clear from the topics listed above that we continue to define statistical genetics very broadly. Statistics for us goes beyond mathematical models and techniques, and includes the management and presentation of data, as well as its analysis and interpretation. Genetics includes the search for and study of genes implicated in human health and the economic value of plants and animals, the evolution of genes within natural populations, the evolution of genomes and of species, and the analysis of DNA, RNA, gene expression, protein sequence and structure, and now metabonomics. The latter topics probably fall outside even a liberal definition of 'genetics', but we believe they will be of interest to our readers because of their relevance to studies of gene function and because of the statistical methods being used.

We regard more recent terms, such as 'genomics' and 'transcriptomics' as designating new avenues within genetics, rather than as entirely new fields, and we include their statistical aspects as part of statistical genetics. Similarly, we include much of 'bioinformatics', but we do not systematically survey the available genetic databases or computer software, nor methods and protocols for archiving and annotating genetic data. Some pointers to computer software and other Internet resources are given at the end of relevant chapters.

The 43 chapters are intended to be largely independent, so that to benefit from the handbook it is not necessary to read every chapter, nor read chapters sequentially. This structure necessitates some duplication of material, which we have tried to minimise but could not always eliminate. Alternative approaches to the same topic by different authors can convey benefits. The extensive subject and author indexes allow easy reference to topics covered in different chapters.

For those with minimal genetics background, the glossary of genetic terms (newly updated) should be of assistance, while Wiley's *Biostatistical Genetics and Genetic Epidemiology*, edited by Elston, Olson, and Palmer (2002) provides a more substantial

resource of definitions and explanations of key terms from both genetics and statistics. For those seeking a more substantial introduction to the foundations of modern statistical methods applied in genetics, we suggest *Likelihood, Bayesian, and MCMC methods in Quantitative Genetics* by Sorenson and Gianola (2003).

We thank the many commentators of the first two editions who were generous in their praise. We have tried to take on board many of the constructive criticisms and suggestions. No doubt many more improvements will be possible for future editions and we welcome comments e-mailed to any of the editors. We are grateful to all of our outstanding set of authors for taking the time to write and update their chapters with care, and for meeting their deadlines (and sometimes ours as well). Finally, we would like to express our appreciation to the staff of John Wiley & Sons for initially proposing the project to us, and for their friendly professionalism in the preparation of both editions. In particular, we thank Martine Bernardes-Silva, Layla Harden, and Kathryn Sharples.

DAVID BALDING
MARTIN BISHOP
CHRIS CANNINGS
August 2007