Editors' Preface to the Fourth Edition

After a break of more than 10 years since the third edition, we are pleased to present the fourth edition of the *Handbook of Statistical Genomics*. Genomics has moved on enormously during this period, and so has the *Handbook*: almost everything is new or much revised, with only a small amount of material carried forward from previous editions. Two new editors have joined, Ida Moltke from Copenhagen and John Marioni from Cambridge. With sadness we note the death of founding editor Professor Chris Cannings during 2018. He first saw the need and had the vision for the *Handbook*, one of his many contributions to mathematical and statistical genetics. We also acknowledge the fundamental contribution of the other founding editor, Professor Martin Bishop.

While the content has changed, the mission has not: the *Handbook* is intended as an introduction suitable for advanced graduate students and early-career researchers who have achieved at least a good first-year undergraduate level in both statistics and genetics, and preferably more in at least one of those fields. The chapters are not thorough literature reviews, but focus on explaining the key ideas, methods and algorithms, citing key recent and historic literature for further details and references.

The change of title (from *Genetics* to *Genomics*) is not intended to indicate a substantial change of focus, but reflects both changes in the field, with increased emphasis on transcriptomics and epigenetics for example, and changes in usage. We interpret 'genomics' broadly, to include studies of whole genomes and epigenomes, near-genome processes such as transcription and metabolomics, as well as genomic mechanisms underlying whole-organism outcomes related to selection, adaptation and disease. We also interpret 'statistics' broadly, to include for example relevant aspects of data science and bioinformatics.

The 36 chapters are intended to be largely independent, so that to benefit from the *Handbook* it is not necessary to read every chapter, or to read chapters in order. This structure necessitates some duplication of material, which we have tried to minimize but not always eliminate. Alternative approaches to the same topic by different authors can be beneficial. The extensive subject and author indexes allow easy reference to topics arising in different chapters.

For those with minimal genetics background the glossary has been newly updated. Thanks to Keren Carss for contributing many new terms, in particular those relevant to genomic medicine. Gerry Tonkin-Hill and John Lees also contributed some advanced statistical terminology, but the glossary is predominantly of genetic terms. For those with limited background in statistical modeling and inference we have added an initial chapter that covers these topics, ranging from basic concepts to state-of-art models and methods.

We thank the many commentators on previous editions who were generous in their praise and helpful feedback. 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 authors for taking the time to write and update their chapters with care, and we would like to express our appreciation to all the professional staff working with and for Wiley who helped us to bring this project to fruition.