

## Book Review

doi:10.1017/S0016672307009123

*Statistical Genetics of Quantitative Traits: Linkage, Maps and QTL*. R. Wu, C.-X. Ma & G. Casella. Springer. 2007. 354 pages. ISBN 978 0 387 20334 8. Price \$84.95. (hardback).

The hardcover version of this book weighs just 653 g, it has 365 pages and can cost you between \$74 and \$85 buying it either at Amazon.com or Springer.com. It has been published by Springer in the Series: Statistics for Biology and Health and delivers exactly “what it says on the tin”. It has been written by some well known statistical geneticists for undergraduates, graduates and researchers in the fields of genetics, statistical genomics, experimental biology, animal and plant science, human genetics and forestry. In short, it is for everybody who is interested in methods and understanding of the genetic basis of quantitative traits, in unravelling the secrets of genetic variation, in identification and mapping of quantitative trait loci or genes underlying quantitative traits. In writing the book the authors used the experience gathered both in their research programmes and also during delivery of numerous lectures to even more numerous classes of students, whose enthusiasm impressed the authors and stimulated them to finally write this book.

Writing such a book in this special field of science, which might be considered a centrepiece of the ongoing biological revolution and is characterised by rapid development and change, is certainly a challenge since new publications appear with such speed and number. So you have to decide or better balance between textbooks like this one and a vast number of publications dispersed over a wide variety of journals, with the latter often assuming you know ‘how they did it’. Although this book assumes some previous knowledge in statistics and genetics by the reader, and is certainly not written for people suffering from *formulae phobia*, it is a big help and guidance in the field of statistical developments for genetic mapping, synthesised all in one volume helping to build a bridge between Genetics and Statistics.

Before you go and buy this book you can read more about it at:

<http://www.springer.com/west/home/life+sci/zoology?SGWID=4-10039-22-52090809-detailsPage=ppmmedia/aboutThisBook>

where you also find the full table of contents, the preface and chapter 2 as sample pages.

The book is split into 14 chapters with three main parts: Part 1 provides an introduction to genetics and statistics; Part 2 (chapters 3–7) covers linkage analysis with molecular genetic markers. It presents models and methods for linkage analysis and map construction for different experimental designs (e.g. backcross and F2 designs, outbred crosses, recombinant inbred lines and structured pedigrees, and for special markers (distorted, misclassified and dominant markers). Part 3 looks at various statistical models and algorithms of QTL mapping, including simple marker-phenotype association studies, statistical structure of interval mapping, regression and maximum likelihood-based analysis of interval mapping, threshold and confidence interval determination, composite interval mapping using multiple markers as cofactors, and interval mapping for outbred mapping populations. In the Appendices (A, B, C) the authors provide general statistical theories directly related to the genetic mapping approaches (A), the code for various R programs for some of the used examples (B) and 12 pages with selected references (C).

The authors also created a specific webpage for their book:

<http://www.acsu.buffalo.edu/~cxma/book/>  
which has a table of contents and provides a complete list of programs and algorithms written in R or MatLab for all the examples used in the book.

As I included the reference to this book into my Reference Manager database I inserted as keywords: linkage analysis, molecular markers, QTL, QTL mapping, review, teaching and ‘must read’!

LUTZ BUNGER  
Scottish Agricultural College  
Edinburgh