Book Review

Likelihood, Bayesian, and MCMC Methods in Quantitative Genetics. DANIEL SORENSEN AND DANIEL GIANOLA. Springer-Verlag. 2002. 740 pages. ISBN 0 387 95440 6. Price €89.95. (hardback).

The genetic analysis of quantitative traits raises fundamental problems of models, techniques, and inference in statistics. The scientific discipline of quantitative genetics is therefore based on and has been a major stimulus to the development of statistical methods, most notably Fisher's invention of the analysis of variance and Wright's of path coefficients. Subsequently Henderson stimulated much fundamental thinking on inferences about random effects, specifically breeding values, using BLUP, and the associated problems of analysis of unbalanced genetic data contributed much to the development of REML. Most recently, the availability of molecular genetic information that could be used to draw inferences about linked genes or QTL affecting quantitative traits has generated enormous development of ideas and methods, further stimulated by the awareness of human geneticists that traits had complex inheritance. Alongside, the development of computer intensive techniques enabled Bayesian methods to be applied, and progress in this area had been greatly stimulated by potential applications to genetics, both at the solely quantitative and at the molecular/quantitative interface. There are many other examples of how the statistical and quantitative genetic disciplines have coevolved and continue to do so.

Even so, this book covers much more ground than its title would suggest, for specific genetic applications occupy only the final quarter or so. This last section includes chapters on models for quantitative genetic data analysis, on analyses of categorical (threshold) and longitudinal data, and on segregation and QTL analysis. It primarily focuses on Bayesian methods, and is weighted more heavily towards the analysis of data obtained solely on quantitative traits rather than their joint analysis with data on molecular genetic markers. In earlier parts there is a substantial covering of basic probability, multivariate statistics and inference. There are more specialised sections on methods in likelihood analysis, such as the EM algorithm, and in Bayesian analysis, in particular Markov chain Monte Carlo (MCMC) methods which are reviewed in considerable detail. Hence the book would be more appropriately titled: Likelihood, Bayesian and MCMC methods, and their application to quantitative genetics. It is not written, however, for the statistically illiterate, or for the student with an aversion to mathematics. A foundation is needed, and the text builds on it towards the ultimate applications. The presentation is clear and detailed rather than intuitive, following formally and rigorously through derivations; there is a great deal there if the student is prepared to put in the effort.

Both authors, 'Dan and Dan', have made significant contributions to development of statistical methods in quantitative genetics and in particular have been at the forefront of the adoption of MCMC methods for Bayesian analysis, which can be applied to an enormous range of problems involving complex models and data structures. They have, furthermore, taught the subject widely. It is both a text book and, as it leads up to and focuses on their own important work, a duograph.

Genetics is one of the (few?) areas in which Bayesian methods can be used where the prior probabilities are actually known (e.g. in progeny testing the son of a mating between known heterozygotes to determine if he is a carrier of a deleterious recessive gene). Beyond such applications its use is controversial, as prior probabilities are chosen not just as some indicator of belief but also to have nice mathematical properties. The authors, committed Bayesians, mostly just duck the philosophical issues and refer us elsewhere for these, regrettably I think in such an extensive text. Even so, although it is clear where their allegiance lies, their coverage of likelihood methods is both extensive and fair.

I would have liked to see rather more on the applications in QTL and pedigree analysis using marker genetic data, where the MCMC methods are developing rapidly and where alternatives are not a practical option. Overall, however, this is a valuable book, in that it presents so much background essential for subsequent application and merits a much broader market than it is likely to get.

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