are relevant to medical statistics. It describes the statistical theory behind each technique, provides the SAS code that is needed to perform it, shows the SAS output and describes how to interpret it. As a trial statistician, for me the one thing that is missing is much detail of clinical trials—the index has no entries for randomization or crossover trials. However, other books on analysing clinical trials in SAS are available, so maybe I should just buy one of those.

This is primarily a book for someone who is fairly new to SAS. It would be an ideal book for students on undergraduate or post-graduate medical statistics courses that involve SAS and would also be a very useful addition to the libraries of statistical teams in pharmaceuticals companies, to give to new members of staff. But, even for experienced readers, there are new hints or tips to pick up. It is a great book to have on your shelf to dip into and to remind yourself about things that you have forgotten, or for a straightforward guide to techniques that you have not previously used.

This book inspired me finally to get to grips with the output delivery system, which is something that I have been meaning to do for years but have never quite got round to. Having a friendly step-by-step guide in front of me, rather than a technical SAS bulletin that is full of far too many options, made all the difference.

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Bayesian Inference for Gene Expression and Proteomics
K.-A. Do, P. Müller and M. Vannucci (eds), 2006
New York, Cambridge University Press
xviii + 438 pp., £45.00
ISBN 978-0-521-86092-5

Although quite a few books have been published on microarray data analysis in recent years, this volume is a collection of 22 high quality chapters, authored by several distinguished groups of academic researchers, which capture recent advances on using Bayesian statistical methods for statistical inference in the areas of microarray data analysis, proteomics and gene regulatory networks. To give some samples, Chapter 1 by Baggerly and co-workers is a clear introduction to many measurement issues in high throughput biological measurements, including several platforms of microarrays (Affymetrix and SAGE), mass spectrometry and related databases. Chapter 2 by Newton and co-workers reviews the Bayesian approach to differential gene expression. Chapter 3 by Hein and co-workers provides an especially impressive and ambitious approach to Affymetrix data analysis, by proposing a hierarchical Bayesian model approach combining Bayesian analysis at the probe level data (using so-called BGX software written by the authors) with differential gene expression inference, which appears to be the most promising way of combining uncertainty at different levels of preprocessing, normalization and gene differential inference. Chapter 4 presents a similar Bayesian approach to two-channel complementary DNA microarray experiments. There are many well-written chapters on various other topics on gene expression data analysis, such as biomarker identification, cell cycle studies, quantitative trait loci mapping and SAGE data analysis. There are at least three chapters on mass spectrometry and proteomics data analysis, including one on peak identification by Clyde and co-workers using Gaussian mixture (kernel) models. I am also impressed with several well-written reviews on Bayesian inference for sequence motif discovery (Chapter 16 by Gupta and Liu), inferring transcriptional regulatory networks by Sun and Zhao, and others. The last chapter is by Müller and co-workers on sample size determination for multiple testing using the Bayesian decision framework.

Although I agree with the authors that Bayesian model-based inference represents the ultimate approach to uncertainty analysis and propagation of errors from multiple layers of sources, I would like to caution inexperienced users early on that, for high throughput and high dimensional measurement platforms such as microarray or proteomics, much work remains to be done with respect to the needs for improvements in both technological and experimental means, as well as the needs to address pressing issues in improving data quality and establishment of standards to improve data reproducibility and interoperability. I have commented in reviewing another microarray data analysis book how statisticians have contributed greatly in the area of exploratory and graphical data analysis to microarray data, such as in normalization procedures. Much recent improvements in understanding Affymetrix data can be attributed to contributions by statisticians in probe level modelling using nonparametric statistical methods including robust and log-scale linear models. I expect many more developments in these cutting edge scientific areas in the future. I am sure that researchers and students will appreciate an authoritative volume like the present one, which presents the state of the art statistical techniques that are starting to make an impact at the forefronts of modern scientific discovery.

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