

BOOK REVIEW

Microarray basics

Microarray gene expression data analysis: a beginner's guide

HC Causton, J Quackenbush and A Brazma
Blackwell Science Ltd, Oxford; 2003. 160 pp.
£34.99, paperback. ISBN 1405106824

Heredity (2004) 92, 475. doi:10.1038/sj.hdy.6800417

Reviewed by DC Jamison

Every decade or so, it seems, a new laboratory technique comes along which promises to revolutionize the way we study biology. In the 70s it was molecular cloning; in the 80s it was PCR; and in the 90s it was four-color sequencing. At the moment, one of the hot methodologies that is making a bid for technology of the decade is microarray gene expression. Since the first major paper exploring the use of microarrays to study gene expression in 1995, there have been over 4500 papers using this technology introduced into the biomedical literature (as represented in PubMed), and uncounted others published in meeting proceedings, IEEE Transactions, and other sources. Despite this apparent wealth of literature, the basic fundamentals of gene expression technology are still relatively unfamiliar to many researchers. Numerous introductory papers and dozens of books fail to give an adequate theoretical underpinning to the microarray experimental and analytical design for novices.

Into the gap steps this modest tome by Causton, Quackenbush, and Brazma. The authors, all three experts in microarray experimentation and analysis, present a primer guide to microarray gene expression analysis. The intended target is 'graduates and researchers in bioinformatics,' but anyone wishing to gain a basic understanding of microarray gene expression studies will come away enriched. The book truly does live up to its subtitle, presenting the material in a straightforward, nonthreatening manner, which should be quite accessible to anyone. Laid out for self-study, this book is not particularly suitable for the classroom, except as perhaps a supplemental book. Divided into four chapters, the book gives a brief overview of microarray technology and then covers the basics of experimental design of microarray experiments, data collection and normalization, and data analysis techniques. In each section, a clear and concise explanation of the technology, data treatment, or algorithm is presented.

By far, the strongest section is Chapter two, which covers the intricacies of experimental design. This chapter should be required reading for all researchers

designing their first microarray experiment. The different considerations for each of the experimental approaches are laid out in good detail, and the reader is left with a very clear view of which designs to use to collect which sort of data.

Unfortunately, that clarity did not extend into the data processing or data analysis chapters. Each of the normalization and analysis techniques are presented as summaries, and, while they do an excellent job of explaining the complex algorithms, little evaluation of the techniques or guidance on when to use them are presented. All normalization techniques do not perform equally, nor do all analysis techniques work equally well, but the reader is not told about any of the limitations of the techniques. While it is clear that the authors are attempting to be unbiased in presenting the methods to avoid letting their prejudices creep in, the reader is left wishing the authors had been a little more critical and helpful in judging which methods work better. In part, the lack of evaluation is due to the organization of the book. Dividing the material into three sections, while quite logical, does impose an artificial separation between analysis and experimental design, and the authors fail to provide a clear linkage back. The reader is not told which algorithms are appropriate for which design, nor how to design an experiment to fit a particular analysis. Like a mystery novel, a final summing up to bring the information back together into a comprehensive whole is needed to avoid leaving the reader hanging without a conclusion. Instead, we are presented with an appendix containing a nonjudgmental compendium of the available software, with descriptions so brief that it is impossible to determine exactly what they do, much less whether it is worth the effort to type the URL into our browser.

The deceptive simplicity of microarray technology and the existence of push-button analysis software mask the need for integrated experimental and analysis design. The authors have made a valiant attempt to pull away that mask and to expose us to the thought processes needed to design good microarray experiments with meaningful data analysis. Even if they have fallen a bit short, they have provided a good and accessible entry point for any biologist who is interested in getting an overview about how to perform microarray gene expression studies.

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