Book review

DNA Microarrays: Gene Expression Applications

Edited by B Jordan
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The heady euphoria of the late nineties, promising that DNA microarrays would be ubiquitous tools for analysing gene expression and routinely used in every molecular biology laboratory, has been replaced by the sobering realisation that the methodologies are technically difficult to implement. Unfortunately, a bountiful supply of DNA microarrays in the commercial arena has yet to materialise, because of these technical difficulties as well as a variety of intellectual property squabbles, and most researchers are faced with the realisation that they have to make their own arrays if they want access to these 'bleeding edge' methods. A flurry of manuals and technical monographs have appeared over the past few years to try and guide the novice investigator through the pitfalls of implementing microarray production in their laboratories and, more importantly, through the statistical minefield that accompanies the analysis of gene expression data. This book does fairly well with the former but sadly disappoints with the latter.

The book is organised into a set of four chapters dealing with a variety of different microarray platforms as well as a chapter on aspects of data analysis, each prepared by active practitioners in the field and collected together by an editor, Bertrand Jordan, with considerable experience in array and hybridisation technologies. This approach is to be commended because it informs the uninitiated that there is life outside the glass-slide and oligonucleotide array world and that frequently alternative methods are, in many cases, quicker, cheaper and easier to implement. The methods covered include glass slide spotted cDNA arrays, Affymetrix GeneChips, micro and macro arrays spotted on nylon membranes and interrogated with radiolabeled samples and a chapter on the beautiful microarrays detected by colorimetric methods. Each method is basically presented as a recipe, describing in detail what each of the authors do in their own laboratory, from the preparation of probes for spotting through to the acquisition of the microarray image. While this is a reasonable approach, and gives novices a starting point with a coherent collection of protocols, it can on occasions fail to provide a more critical overview of the pitfalls of each approach with authors lapsing into proselytism at times. The chapter on data analysis deals with the statistical approaches used to organise, interrogate and visualize gene expression data and includes pointers to many publicly available analysis resources. Here is where I see a major omission in the book, and one that is perhaps most critical in the field today; there is barely any discussion or description of the statistical approaches or methods that are needed for rigorous experimental design and for normalization of microarray data to allow comparisons between multiple experiments. This is a pity since it is perhaps in this area that biologists need most help and guidance.

The methods chapters are sandwiched between a historical perspective and speculations on future developments in the arena, provided by the editor; a couple of interesting chapters that remind readers of the fact that these approaches have been around for some time (I myself have somewhat grim memories of manually constructing arrays with lambda phage while a graduate student in the late eighties) and that the technologies are both fluid and constantly evolving.

On the whole the book is a useful laboratory manual covering most of the practicalities that need to be considered when contemplating a DNA microarray approach in ones own lab. However, if you are thinking about dipping your toe in the microarray world, make sure you talk to a statistician for advice on the important areas not covered here.

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