to consider further the impact of these potential complexities on the conclusions reached.

Several of the papers deal with another of Bill Hill's long term interests – that of animal breeding. This area is of some considerable economic, social and environmental interest, sitting as it does at the top of a production pyramid that encompasses a major part of world agriculture. Work in Edinburgh over the last 50 years has made a substantial contribution to the development of this technology. Bill Hill, working alongside others such as the late Alan Robertson has had a significant input. Animal breeding often imposes high selection intensity in relatively small populations and so imposes a severe challenge for quantitative genetic theory. Nonetheless, Brotherstone and Goddard (2005) in their review on selection in dairy cattle echo the point made by Johnson and Barton in pointing out that intense selection with rapid genetic progress is not accompanied by an observable decline in the heritability and noting that work is required to fully reconcile these observations.

The last contribution in the volume from Frank Nicholas (2005) also focuses on animal breeding, this time in relation to disease. Nicholas reviews evidence on single gene and multifactorial susceptibility to both infectious and inherited disorders, information he has been involved in painstakingly cataloguing online (http://www.angis.org.au/omia). Nicholas points out that Bill Hill's first publication was also the first to identify a single gene disorder in Japanese quail and that he has since made contributions to the debate on the relationship between breeding, inbreeding and the occurrence of inherited disorders in livestock. Nicholas puts in a plea for Bill Hill to write the definitive paper on the occurrence and control of single-locus disorders in animal breeding programmes. Whether Bill chooses to take up this challenge in a retirement in which he remains as sharp and as active as ever remains to be seen. In the meantime we have this volume to remind us that the fields of quantitative and population genetics are as relevant and as full of new challenges as they have been at any time during the last fifty years.

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Proteomics for Biological Discovery. T. D. Veenstra & J. R. Yates III. Wiley-Liss. 2006. 307 pages. ISBN 0 471 16005 9. Price £41.50. (paperback)

The rise of the proteome

In days gone by the analysis of proteins was very much the provenance of Biochemistry Departments with the focus on isolating and characterising individual polypeptides. In the post-genome era, where we have the genetic blueprints of hundreds of organisms readily available, the focus has changed to a

more global analysis of biological molecules with the aim of characterising all of the genes, and their products, encoded in an organisms genome. Now everyone wants to get in on the protein analysis act. The overall aim is to understand how biological systems are wired together, how the genome is dynamically regulated and, more importantly, how the hundreds of thousands of protein isoforms present in a cell (the proteome) interact to generate biological function – a daunting task. We now have available increasingly reliable high-throughput techniques for the global analysis of gene expression and transcription factor-DNA interactions, generally utilising microarray-based technologies. Such methods are facilitated by the relative chemical simplicity of nucleic acid molecules and the range of enzymatic techniques available for amplifying minute quantities of DNA or RNA from virtually any biological sample. Proteins, however, are an entirely different kettle of fish, not only are they chemically extremely heterogeneous but we currently have no way of amplifying even the simplest polypeptide purified from an *in vivo* source. Therefore, protein analysis relies on being able to handle, purify and identify sometimes tiny amounts of protein from complex mixtures. The rise in large-scale and comprehensive proteomics has been almost entirely driven by technologies that facilitate these goals, principally the developments in mass-spectrometry that allow accurate and sensitive protein analysis.

With the increasing interest in dealing with the proteome, many biologist now look to the biochemist to help collect and interpret high-throughput protein data, but what is possible? How can quantitative measures of protein abundance be obtained? How can the components of protein complexes be identified? Can I look at single cell resolution and if so what can I measure? For the biochemically naïve or those whose brushes with proteomics are limited to the geneticists approach – the 2-hybrid screen – advice is needed. This edited volume attempts to introduce the novice to the range of techniques available in the proteomics field as well as provide reviews of a range of technologies for those more expert in aspects of proteomics. Put together by two renowned experts in the proteomics arena who have made significant contributions to the development of modern proteomics methods, the book collects together a series of reviews by leaders in various areas. It is divided into three sections: the basic methodologies or foundations of proteomics, which covers protein fractionation methods and the mass spectrometric techniques used to identify proteins or measure their abundance. A section on functional proteomics, covering protein complex identification, *in vivo* localisation methods in cell biology and the use of NMR techniques for assessing protein structures. A final set of chapters deals with more novel proteomics approaches such as protein microarrays, microfluidics-based techniques, single cell methods, automation and, somewhat bizarrely, a final chapter on bioinformatics tools – one would think that the informatics section should be close to the start, they are, after all, absolutely fundamental for dealing with any aspect of modern proteomics!

Clearly the idea behind this book is laudable and all of the chapters are informative. Some of the contributions are excellent; I found the fractionation chapter by Rabilloud and the cell imaging chapter by Muller and Davis particularly enlightening, though most provide well-described real-world examples of the principals they are trying to illustrate. However, I was a little disappointed with a couple of aspects. First, the proteomics arena is a rapidly developing field with improvements and new methods becoming available on an seemingly daily basis. Obviously this presents difficulties in book production since chapters have to be finalised at some point and inevitably it is impossible to accommodate the very latest research. Having said that, the book was published in June 2006 and yet there are only a handful of references later than 2003. This suggests a difficult birth! For example, the lack of any discussion of the recent development of improved strategies for isotopic labelling and quantitative proteomics, such as Applied Biosystems iTRAQ method, is a clear oversight. The exciting development of "robot scientist" techniques for improving the efficiency and cost effectiveness of high-throughput methods would, I think, be worth a mention somewhere. Other omissions are odd, there is virtually no discussion of the Difference Gel Electrophoresis (DiGE); a short paragraph for, in my view, a powerful differential proteomics technique that has been around for almost 10 years is a bit remiss for a comprehensive review. As I alluded to above, the computational methods are essential for handling and interpreting proteomics data – here I feel much more could have been done, for example a chapter on interaction mapping and visualisation software would not have been out of place as well as some discussion of the reliability of high-throughput data and the increased confidence that comes from combining different noisy datasets. Another gripe is the repetitive nature of some material: 2D gels and the basics of mass-spectrometry are described in several chapters, giving basically the same information. Finally, some of the figures are inadequately described, clearly experts have no difficulty in interpreting mass spectrometry spectra, but the novice need some guidance with the aid of well annotated figures.

While the book is clearly a useful source of information for the novice (i.e. what might be possible to address my biological problem) and the expert

(i.e. what's the best buffer for solubilising membrane proteins). Ultimately I was a little disappointed in the volume, this is not to say that the individual chapters are poor or uninformative, far from it – the authors know what they are talking about and any chapter would make a pretty good stand alone review. Rather it is the whole that fails to satisfy: I expected more from such a distinguished collection of contributors.

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