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BOOK REVIEW

What? Where? Which? WWW Resources for Geneticists

Bioinformatics for geneticists: a bioinformatics primer for the analysis of genetic data

Michael R Barnes, John Wiley & Sons, NY, USA, 2007. £45.00.
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Peter AC 't Hoen

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A number of changes have taken place in the world of geneticists since the publication of the first edition of *Bioinformatics for Geneticists* in 2003. The availability of 100K to 1M SNP chips and massive parallel sequencing technology has radically changed the set-up of genetic linkage and association studies. With the increased throughput in these studies, new algorithms and software for high-throughput data analysis became available. Therefore, a new edition of *Bioinformatics for Geneticists* seems to be adequately timed.

Given the rapid developments in the field, such a book is per definition outdated. Yet, the book is reasonably up-to-date, which was only possible by including contributions from authors who are at the front-end of science. It is also noted that the development of new data analysis routines will never be able to keep up with the requirements from the newest technologies. For the analysis of massive parallel sequencing data, analysis tools are hardly available, partly explaining why there is, also in the current edition, hardly any attention paid to this type of analysis. To program yourself is the best option, and is also advocated by the editor. In Chapter 2, a short appetizer for programming with Perl is provided, although probably still too far-fetched for a person with a biological or medical background. A more likely option in current-day genetic research is a tight collaboration between geneticists and informaticians. For both groups, the book provides useful material. Given the amount of background in classical and current methods in genetics, the editor might as well have chosen *Genetics for Bioinformaticians* as a subtitle. This book may really help to get geneticists and bioinformaticians on 'speaking-terms'.

The book gives the geneticist a valuable survey of the enormously rich data resources and numerous analysis tools available. It focuses on human genetics, and covers gene annotation, comparative genomics, disease gene mapping, prediction of the effects of mutations, non-coding RNAs, microarrays, and the use of gene expression data as quantitative traits. Some chapters merely contain lists of available tools and regrettably refrain from a discussion of their advantages and limitations and fail to give insight into which tool to be used in which situation. Given the expected frequent changes in web addresses and the availability of these tools, a web page with the updated links to the resources listed would be extremely helpful, but is currently not available. On the positive side, the book provides a considerable amount of case studies that nicely illustrate the reasoning and research path one can follow in current-day genetics. A point of criticism would be that some cross-references between chapters are lacking and that there is some redundancy here and there (eg, programs for finding exon-splice enhancer sites are dealt with in chapters 11 and 12).

What is clear after reading the book is that there are many possibilities to improve the design and the interpretation of wet-lab experiments by *in silico* tools. This is not only true for expensive high-throughput experiments but also for more targeted and everyday experiments. Therefore, this book contains some essential reading for almost any person working in the field of molecular genetics■

Dr Peter AC 't Hoen is at Center for Human and Clinical Genetics, Leiden University Medical Center, Postzone S-04-P, P.O. Box 9600, 2300 RC Leiden, Netherlands.
Tel: +31 71 5269421;
Fax +31 71 5268285;
E-mail: p.a.c.hoen@lumc.nl