

Bioinformatics for Geneticists. Michael R. Barnes and Ian C. Gray (ed). Chichester, West Sussex, United Kingdom: John Wiley & Sons Ltd, 2003, 422 pp., \$65 Softcover. ISBN 0-470-84394-2.

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This book addresses a curious need for greater interaction between Genetics and Bioinformatics. One would expect the two disciplines to interact profusely, given, as the authors put it, their “strong common grounding in statistical methodology, dependence on efficient computational algorithms, rapidly growing biological data, and shared principles of molecular biology”. However, until recently, most of the research in bioinformatics has focused on sequencing genomes. That research goal, in particular, is quite “foreign to the core genetics principles of variability and individual differences”, since it aims at discovering representative (consensus) sequences in a given species’ genome.

But clearly both disciplines can profit from, and indeed need, a deeper integration. The book aims, and succeeds, in describing bioinformatics tools and research to primarily an audience with expertise in molecular and medical genetics. Specifically, the book is organized around methods and tools for disease gene search, identification, and characterization. This leaves out the exploration of a natural affinity between bioinformatics and statistical and population genetics, which often focus on common mathematical and computational biology models and tools. The decision to target the more specific audience working on molecular and medical genetics, pays off in both technical coherence and thoroughness.

Another welcomed feature of the book, emphasizing one of the most esteemed aspects of the bioinformatics collaborative culture, is the focus on public databases, and not on “off the shelf” or custom-built laboratory information management systems. Thus, the authors focus on web-based methods and databases that try to integrate different information sources. They clearly highlight the functionality limits of existing databases for geneticists, from an understanding that most resources have been developed for genome annotation. The authors attempt, and mostly succeed in giving practical advice on how to use the available functionality best.

Several resources for geneticists are introduced in detail, but we found the discussion of at least two very important and highly used resources insufficient and disappointing: the *Gene Ontology* (GO) and the *SwissProt* database. Indeed, the book does not always succeed in its goal of providing many examples and case studies. The topics that are best presented with good examples are the Genetic Studies from Genomic Sequence (chapter 9) and Gene Expression Informatics and Analysis (chapter 15).

Furthermore, the discussion of gene expression informatics and analysis, currently a large chunk of research in bioinformatics, though very interesting and providing specific examples, is a bit too narrow. It is based on specific technology, namely using the Human Transcriptome Map (HTM) with Serial Analysis of Gene Expression (SAGE).

Additionally, while the authors emphasize the importance of microarray technology, they offer only a very short introduction to this technology. In contrast, the discussion of

proteomic informatics is a very broad overview of protein expression measurement techniques, with less specific results to report.

In summary, while some important tools and methods are not fully presented, and some of the discussion is already somewhat dated, this book is nonetheless a very valuable and important resource for bringing bioinformatics into the work practice of geneticists. We expect the book to entice more geneticists to seek existing bioinformatics technology and collaborate with bioinformatics practitioners. Developing a more intense collaboration between the two communities will naturally lead existing bioinformatics technology to evolve towards more appropriate functionality for molecular and medical genetics. We strongly recommend this book for geneticists who want to understand what is currently available and what the future of bioinformatics could bring to their research.

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