of bioinformatics they could be involved in IT-infrastructure, including data management and storage, or involved in data processing and analysis using any combination of the myriad of software tools available in each field of genetics. It is essential, therefore, to restrict the scope of any book that deals with bioinformatics. "*Bioinformatics for Geneticists*" does that by focusing on human disease genetics and limits the bioinformatics aspect to associated software tools and techniques. Given this (relatively) specialised viewpoint a layperson may question the need for a new edition of this book as the last was published under three years ago. However the fundamental changes to our understanding of some areas such as non-coding RNAs and the rapid expansion of key resources such as single nucleotide polymorphism data produced from the HAPMAP project, have left a void in the knowledge base covered by textbooks. To this book's credit, these topics, in conjunction with more mature areas, are covered in a way that is both understandable and interesting.

The book is split into 19 chapters with five main sections: An introduction to bioinformatics for the geneticist, Mastering genes, genomes and genetic variation data, Bioinformatics for genetic study design and analysis, Moving from associated genes to disease alleles, and Analysis at the genetic and genomic data interface. Each chapter is written by different authors but assembled such that they describe a different and often research-focused area. As the book's subtitle "*a bioinformatics primer for the analysis of genetic data*" suggests, the chapters are often useful for directing the reader to further information resources. However, the level of detail differs considerably between chapters. The HAPMAP project for example is covered at great length, and as arguably one of newer and faster growing datasets this attention is easily justifiable. Microarray analysis on the other hand is described at a more fundamental level and mentions alternative applications such as chIP-chip, going into much detail on their analysis.

A benefit of research focused chapters is that the reader gains a basis in a variety of bioinformatics tools and techniques aplicable to each subject area. One of my favourite chapters in this aspect is Chapter 9 "*Integrating genetics, genomics and epigenomics to identify disease genes*". Here a range of software tools and techniques are taught together while focusing on a particular case study. Despite this, the opportunity to summarise the relevant resources and repositories is not missed. Perhaps the main drawback to this integrated approach is that knowledge from many of the data repositories and software packages common to multiple fields (such as those at ensEMBL, SwissProt and NCBI) is learned in a piecemeal fashion to the detriment of understanding the ethos and connectivity behind these key data sources.

Other aspects of a bioinformatician's job are data management and programming. Chapter 2 "*Managing and manipulating genetic data*" alludes to covering these topics but the focus of the chapter is extremely basic. Although essential reading for complete novices, some of the Perl code examples are quite confusing to the target audience. Moreover, it does not emphasise the use of the pre-existing libraries available in BioPerl. In my opinion the premise of showing and teaching limited code examples (especially just one programming language), to a target audience of non-programmers is flawed. A more useful approach may have been to suggest the best languages to learn, based on their ease of use and the availability of existing code repositories for specific tasks, and to emphasise the best books and resources for self-learning. On the whole the absence of any mention or review of the repositories of reusable code is rather disappointing as although the R-language, Perl and BioPerl are briefly mentioned, ensEMBL Perl API, BioConductor [R-language], BioPython [Python], BioRuby [Ruby] and BioPostgres [Postgres database] are not. Lastly, as both academic and corporate labs are now generating a mountain of data, a review of specific database storage solutions would have been advantageous. Only the microarray chapter (15.5) addresses this, providing an excellent (albeit already slightly outdated) review of microarray data storage.

Although I have highlighted some drawbacks in the style and scope of the book I wish to emphasise that the content in the chapters is mostly of the highest quality. *Bioinformatics for Geneticists* is an excellent resource not just for the geneticist wishing to learn bioinformatics tools available in their field, but also for bioinformaticians wanting to learn background genetics in new or parallel areas of research. Moreover this book should ensure that any researcher's skill base is maintained, and that they are exploiting the growing and maturing bioinformatics resources freely available to the scientific community.

ALASTAIR KERR
Wellcome Trust Centre for Cell Biology
School of Biological Sciences
The University of Edinburgh

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Epigenetics. Eds. C. D. Allis, T. Jenuwein, D. Reinberg & M.-L. Caparros. Cold Spring Harbor Laboratory Press. 2007. 502 pages. ISBN 0 87969 724 5. Price $150. (hardback)

"Epigenetics" – the New Testament of chromatin biology

In the past fifteen years several books have attempted to provide a coherent overview of the rapid and

exciting advances in chromatin biology. Of these "Chromatin structure and function" by Alan Wolffe (Academic Press, 1995) is perhaps the far most popular and widely read book. Our current understanding of chromatin organization and the impact of various chromatin-related phenomena on gene expression, chromosome structure, development, cell differentiation and human disease has expanded into a much wider field of research currently known as "epigenetics". Although the debates on the precise definition of this term and what it should or should not include are still ongoing[1], it is clear that what we call epigenetics nowadays is quite different from what this term meant when used by C. H. Waddington to describe how genotypes give rise to phenotypes during development[2].

The recent advanced textbook "Epigenetics" edited by C. David Allis, Thomas Jenuwein and Danny Reinberg and published by Cold Spring Harbor Press is a monumental 500-page effort to collate, describe and explain the most essential concepts in modern chromatin biology and to bring these up to date. The book also provides a detailed account of specific molecular mechanisms underlying epigenetic phenomena in different organisms from bacteria to mammals.

"Epigenetics" contains 24 chapters, written by an international team of 47 experts. The book opens with an interesting historical perspective which follows the emergence of epigenetics from a collection of seemingly random observations into an exciting field of research that affects many areas of modern biology and "is founded upon trying to explain the unexpected – perhaps more than any other field of biological research". The general layout of the book roughly follows the phylogenetic tree of eukaryotic model organisms, starting with budding yeast *Saccharomyces cerevisiae*, *Drosophila melanogaster* and plants, research on which has shaped the framework and the most basic perceptions of chromatin research in the past decades. It is not a surprise that these species still dominate the scientific landscape as the most commonly used models for high-throughput epigenetic studies. The chapters dedicated to individual model organisms are punctuated by others that focus in more detail on specific mechanisms that regulate chromatin structure and gene expression or participate in the formation of specialized chromosomal domains. These chapters describe the role of RNA interference in the assembly of heterochromatin, transcriptional gene regulation by Polycomb and Trithorax group proteins, the role of chromatin modifications and chromatin variants in the organization and function of genomes as well as more complex phenomena related to dosage compensation of gene expression in *Drosophila* and mammals. The last 8 chapters of the book are fully dedicated to mammalian epigenetics, with specific focus on DNA methylation, genomic imprinting and the involvement of chromatin in specification of the pluripotent state of germ and stem cells and the control of cellular differentiation. Last but not least, the final two chapters of the book summarize the current knowledge of changes in post-synthetic modifications of DNA and histone proteins that lead to complex human disease states such as ICF Syndrome, Rett Syndrome and cancer. Beautifully illustrated, this book is a rich resource of information for a diverse pool of readers, ranging from graduate students making their first steps in a new field of knowledge to more experienced scientists whose research has led them to unfamiliar grounds.

One may argue that in a rapidly developing field such as epigenetics any textbook written today is bound to be out of date the very day it is published. However, what makes "Epigenetics" a truly remarkable and, I believe, a long-lasting achievement is the clear and accessible overview of the major concepts and mechanisms that lay in the foundation of contemporary chromatin research. New details of how specific enzymes and proteins shape chromatin structure and composition may emerge, but the general principles that define how chromatin impacts on many cellular processes are likely to hold true.

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IRINA STANCHEVA
The Wellcome Trust Centre for Cell Biology
School of Biological Sciences
The University of Edinburgh

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