Genet. Res., Camb. (2006), **87**, *pp.* 217–220.
Printed in the United Kingdom

Book Reviews

doi:10.1017/S0016672306218251

Lab Dynamics: Management Skills for Scientists. C. M. Cohen & S. L. Cohen. Cold Spring Harbor Laboratory Press. 2005. 176 pages. ISBN 0 87969 741 5. Price £30. (hardback)

A rough guide to management for scientists

How to manage successfully a productive scientific lab? It seems important and obvious that scientists ought to acquire some basic management skills before taking the critical step to leadership. And yet, postgraduate students and postdoctoral researchers learn very little about the caveats of lab management during their decade-long training in scientific institutions. Ironically, scientific departments, whose institutional success and funding are dependent on the achievements of individual principal investigators and their labs, are often of little or no help to ensure that the newly established group leaders are aware of what it takes to run a productive team of scientists. Thus, invariably, it is up to the principal investigators to find their way around in dealing with colleagues and various problems. It often happens that they learn ''the hard way'' that the success of a scientific project may be hampered by trivial personal conflicts within their labs. I am not a big fan of self-help books but, having not so long ago gone through the stressful experience of starting my own lab, I recognize that guidance of some form or another can be very helpful.

Lab Dynamics by Carl and Suzanne Cohen is a book that explores the specifics of professional and personal interactions between individuals working in a scientific environment. It is a useful practical management guide not only for those who are considering scientific leadership as the next step of their career, but also for postdocs and postgraduate students, who need to interact productively with their peers and scientific advisors. What makes *Lab dynamics* an unusual book is that it is largely based on personal experience and is written from the perspective of social and behavioural psychology. The authors, one is a successful scientist and President of Science Management Associations, the other is a Licensed Psychologist and Clinical instructor in Psychology at Harvard Medical School, use real-life examples to illustrate how simple and seemingly unessential conflicts may have serous implications if systematically ignored. Detailed analysis of critical situations is accompanied by valuable exercises and practical advice ranging from how to resolve delicate situations to how to deal with obnoxious behaviour of inconsiderate individuals. For those unfamiliar with research in the industry, the book also illustrates the basic differences between academia and biotech companies in the management of scientific projects and teams.

Carl and Susanne Cohen make a point at the beginning of the book that what distinguishes scientists as a group of professionals is their highly individualistic behaviour as well as an inclination to argue their point of view. I fully agree with the authors that scientists are not only less likely to be aware of the dynamics of interpersonal relationships, but also less likely to recognize and manage their own emotions and reactions. Thus self-awareness is an important starting point in resolving any difficult situation, no matter whether it is an argument over the authorship of a paper, a negotiation over allocation of space or dealing with a disruptive person in the lab.

Another essential point, which recurs throughout the book, is the importance of recognizing the interests of all parties involved either in a negotiation or in a specific personal conflict. Therefore the successful outcome of any dispute may not necessarily be the one in which your own wishes are fulfilled but the one achieving reasonable compromise of all underlying interests. Being able to see the problems in some perspective is an important prerequisite for their successful solution.

Lab dynamics is a very enjoyable read and one of the most valuable contributions to the slowly growing collection of books on laboratory management. My only, minor, criticism is that while the book is directed to the general scientific community and deals with universal issues, I felt that it is (not surprisingly) strongly biased towards the American audience. That is, the authors assume that most postdoctoral

scientists are ambitious, independent and opinionated. This, however, is not always the case in the European scientific environment, where independent positions are not easily obtainable. It is also not a common practise for the junior researchers to compete for the attention of their scientific mentor. European laboratories, on average, tend to be smaller than the American ones, and every researcher is likely to get sufficient attention and recognition. Thus geographical and cultural factors to some extent affect the way in which scientists behave and run their laboratories.

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

doi:10.1017/S0016672306228258

Computational Genome Analysis: An Introduction. R. C. Deonier, S. Tavaré & M. S. Waterman. Springer. 2005. 515 pages. ISBN 0 387 98785 1. Price $79.95. (hardback)

Richard C. Deonier, Simon Tavare and Michael S. Waterman provide us with a "roll up your sleeves and get dirty" (as the authors phrase it in their preface) introduction to the field of computational genome analysis. Their text is aimed at a late undergraduate or early postgraduate level audience. Laying out an introductory text on this topic is a difficult task as students (or readers in general) interested in this field are coming from quite different scientific backgrounds. Based on the authors' extensive experience from computational biology courses, the book caters for this in two ways. For the reader who is not familiar with statistical applications and computing via command line and terminal windows it provides a concise, though sometimes a bit short, introduction to the freely available statistics language "R" in Appendix A. The examples given are described in a clear fashion and easy enough to get a "newbie" started without requiring much background in statistics and computation. The knowledge acquired here is then built upon in the practical examples and exercises which are accompanying the main chapters of the book. For the reader coming from a computer science background the basic terms and concepts required for the formulation of the biological problems to be dealt with in later chapters are outlined in Chapter 1. Both, the appendix on "R" and the biological background chapter might be too condensed for readers who are completely new to the respective topic, but they are written in a way to encourage further reading. Also helpful, in particular for the uninitiated reader, is the 20 pages glossary covering terms and acronyms, since the huge number of acronyms used in the field sometimes makes understanding more difficult than it need be.

The biological background chapter is followed by two chapters centred around main statistical concepts, but discussed in a biological context. The following chapters cover most of the topics one expects to find in a book about computational genome analysis: physical mapping of DNA, genome rearrangements, sequence alignments and alignment methods, sequence assembly, signals in DNA, clustering, microarrays, phylogenetic trees, genetic variation in populations and comparative genomics. I particularly liked the way in which these chapters are structured. Each starts with a clear statement describing the biological problem to be addressed. The importance of this can not be over emphasised as it is all to easy to hide the biological problem behind computational details. Computational examples throughout the text illustrate the ground covered. As an additional bonus come short descriptions of the experimental procedures behind the data generation – lack of knowledge here is a common source of misunderstandings between the "computation" and "biology" communities. At the end of each chapter the reader finds a selection of references for further details and additional reading, as well as computational examples exercises to get the "hands on" experience.

To some extent it is always a personal choice as to what to include and what to omit in the limited space of a textbook. For example, I miss "muscle", the multiple sequence alignment program, which revolutionised the field in 2004 in the respective chapter. While this is a matter of choice, space or timing, another omission is harder to understand. It seems to be a bit strange covering "bioinformatics resources for molecules and structures" without mentioning the core resource: the protein data base "PDB". As one might expect for a text book on "Computational Genome Analysis" there is an accompanying webpage: "http://www.cmb.usc.edu", although it seems that this web resource has not fully taken off yet and is awaiting more content. Also, the links that should point to data on the "Data for Exercises" page are not going anywhere yet.

Overall, I can recommend "Computational Genome Analysis" – I intend to use parts of it for my own teaching. The book is carefully written and carefully edited, this means fewer typos and errors (one example: "cnideria" should read "cnidaria") than usually found in text books. As it mostly focuses on principles and understanding it will stay useful for some time. Of course, the user has to be aware that some details such as "at the time of writing 2 million non-redundant sequences …" may be out of date already at the time of print. When writing this review the respective number is "3·5 million sequences" and

surely at the time you are reading this it will be even more.

RALF SCHMID
Department of Biochemistry
University of Leicester

doi:10.1017/S0016672306238254

Imaginal Discs, the Genetic and Cellular Logic of Pattern Formation. Lewis I Held, Jr. Cambridge University Press. 2005. 461 pages. ISBN 0 521 01835 8. Price £38. (paperback). (ISBN 0521 58445 0. Price £120. (hardback) published 2002)

We first picked up this book when our very different research programs turned toward the genetic controls of development in the imaginal discs of Drosophila. How wonderful to have such a complete guide and extensive review of imaginal disc development. The comprehensive nature of this book makes it an essential reference, and though this was our initial reason for obtaining the book, it is more valuable than a simple reference. *Imaginal Discs* provides a wealth of information for anyone studying Drosophila biology, and the models, history and scientific thought provide a wonderful teaching resource. Following the logic of how the models have changed with new discoveries provides important lessons for young and experienced scientists, alike.

Held takes a somewhat historic approach with the models, but also provides individual chapters covering development, genetics of specification and growth of the major discs (leg, wing and eye). There are also chapters on related topics, bristles and homeosis, providing further insights into these aspects. This historic record is quite interesting to follow, and will provide an educational experience for all who should read the book. Unfortunately, this approach to examining the models of pattern formation sometimes makes it difficult to see how they all properly relate to one another. However, it is clear that the more specific developmental details are an essential guide for researchers in the field. The extensive references to the primary literature (4900) will be an aid to anyone working on Drosophila pattern formation. Furthermore, there are many detailed diagrams depicting, for instance, genetic cascades of development, that are helpful. These are not merely supplements to the text, as many molecular details are presented only in the figures (and in the figure legends in extremely minute fonts). Though the diagrams are very helpful, there are no actual images of imaginal discs, and this is a downside. Furthermore, the diagrams, though well done, do not always convey the variations in expression/phenotype that actual images can. And in a few instances, multiple shadings (all images are black and white drawings) can get confusing. Color would be a welcome addition.

If there is a downside to this book it is that, given the density of the material covered, it can be difficult to see the forest from the trees. While this tome provides an effective synthesis of the literature, it is sometimes hard to assimilate generalities resulting from the inclusion of all the data. In addition, the focus is clearly on the molecular genetic aspects of pattern formation of the disc, and the relevant cellular components (for instance cellular memory, tissue growth as well as orientation and rate of cell division) are only given minor consideration.

We highly recommend this book to all researchers studying Drosophila pattern formation in particular, and to developmental biologists and geneticists in general. The historical accounts of how a field of science changes and matures, especially one that has contributed to our understanding of development, gene regulation, cancer makes this book suitable as a teaching tool. However, as it is currently written, it is accessible only for those with prior knowledge of the techniques used in Drosophila molecular-genetic research. If there is a second addition, adding an introduction to these techniques to facilitate the use of this by non-Drosophila researchers would be recommended. Then this book would be very suitable for an advanced course in development. However, we suspect it will end up mainly as a reference book for those in the pattern formation field. But read and enjoy the history behind the models!

JAMES W. MAHAFFEY and IAN DWORKIN
Department of Genetics
North Carolina State University

doi:10.1017/S0016672306248250

The Dog and its Genome. Edited by E. A. Ostrander, U. Giger & K. Lindblad-Toh. Cold Spring Harbor Laboratory Press. 2006. 584 pages. ISBN 0-87969-742-3. Price £80. (hardback)

The dog was the first animal to be domesticated by man. From its origins in the grey wolf, it has evolved under our influence over 15 000 or so years into the species with by far the greatest range of physical and behavioural diversity. The variously selected breeds of dogs provide companionship, assist with hunting as pointers, retrievers, trackers, work as herders, guides and assist the blind and deaf, are sniffers, trackers, or guards for the police, and race for the gamblers. Through its association with man, it is also highly successful: the dog is by far the most numerous carnivore species in the world. The breed diversity in phenotype implies it is of importance to us genetically as a model species for studying many genetic diseases

and possible treatments for them, and as a model for study of, notably, behaviour.

Its importance in genetics has been recognised as it is only the third mammal for which the genome has been sequenced. Further, breed diversity has been determined using molecular markers: what is striking about this is that most breeds do not diverge enormously, and have a star like phylogeny, indicating a radiation with rather small population size. Even so, breeds show characteristic size, conformation, behaviour and often disease susceptibility. Among many examples, relatively high incidences are found of leukocyte adhesion deficiency and progressive retinal degeneration in Irish setters, of dilated cardiomyopathy and of osteosarcoma in many larger breeds, and of lymphoma in golden retrievers; Labradors have a high incidence and Greyhounds a low incidence of hip dysplasia.

The dog provides startling evidence of the strength of selection, as Darwin noted in the first chapter of The Origin of Species. It appears that domestication was a rather quick process, judging by the relatively brief period between when the dog first appears in archaeological remains and becoming widespread, and from the evidence that it has a rather narrow mitochondrial base. Further, the classic experiment by Belyaev and colleagues in Novosibirsk, reviewed in this volume, in which domestication in the silver fox was effected in under 40 generations, when animals were tamed to the extent of being eager to have human contact, shows how little fundamental change is needed, The ability to produce the great diversity of size, for example, from the wolf base, illustrates how man can utilise both original and de novo variation to effect large changes.

This volume is a comprehensive collection of papers from those working on various aspects of canine genetics and breeding. It covers some of the breed history and registration procedures, its genomics, and, extensively, the genetics of diseases in the dog. With the information on the genome and chromosomal synteny, the homologous causes of disease in man and dog receive particular attention. The coverage is a little uneven in scientific depth, but basically informative. Much of the material is very recent, e.g. on the genome, and some of the chapters are little more than précis of one or two recent papers, but it is useful to have them in one place. There is a comprehensive review of the state of gene therapy in dogs.

Overall, the book will be of most use to the veterinary researchers in canine disease where genetic origins or associations are suspected, and to those likewise in human genetics who are considering a dog, model. It is rather technical for most dog breeders and, I suspect, for many practicing veterinarians. For the general animal geneticist and particularly canine geneticist it provides a most useful reference.

WILLIAM G. HILL
Institute of Evolutionary Biology
School of Biological Sciences
University of Edinburgh