
Book Reviews

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Drosophila Neurobiology. A Laboratory Manual. Eds. B. Zhang, M. R. Freeman & S. Waddell. Cold Spring Harbor Laboratory Press. 2010. 534 pages. ISBN 9780879699055. Price \$250 (hardback), \$150 (paperback).

Drosophila neurobiology is one of the most exciting areas of biology because of the quite extraordinary fly toolkit that is available for doing almost anything you want. As Jim Truman said to me a decade ago while waiting for a train somewhere in central Europe, ‘the only thing that is limiting in fly biology is your imagination’. He was right, in that my imagination is extremely limiting, but, thankfully that of others is not. One only has to inspect the titles of the top-tier journals to see how much fly neurobiology punches above its weight. The subject cuts across several disciplines, but has genetics at its core, with two major approaches historically dominating the panorama – development and behaviour. A third area, imaging, that cuts across both, has more recently emerged in its own right. Finally, physiological recording in *Drosophila* has also upgraded itself in recent years to make light of the old adage that in terms of practicality ‘physiology \times genetics = constant’ for each organism. This basic division of labour is represented in *Drosophila Neurobiology. A Laboratory Manual.*, edited by Zhang, Freeman and Waddell, with the section on imaging and electrophysiology sandwiched between the other two more traditional areas.

The text grew out of the Cold Spring Harbor *Drosophila Neurobiology* course that has been held on Long Island every summer for more than a quarter of a century, and to which I contributed a day’s worth of behavioural genetics about 20 years ago. It is/was an intense course that lasted for three weeks, was lots of fun (perhaps too much fun in those days!), and attracts a highly motivated group of about a dozen students who are on their way to becoming the stars of the future. Zhang *et al.* have now distilled the key elements of this well-trying and tested learning environment into a vibrant 500 page laboratory manual.

The three sections mentioned above – neural development, recording/imaging and behaviour – each

have about ten or so chapters, and each is written by the experts, most of whom have contributed to the course. Each chapter includes a crisp introduction to the subject under scrutiny, usually in well under ten pages, followed by a number of protocols with some common troubleshooting advice, and finally a list of references. I was initially interested in inspecting those protocols that I knew something about, and so I turned to the final behaviour section. Here there are three chapters on conditioning in adults and larvae, one on aggression, two on courtship, one on circadian locomotor rhythms and sleep and, finally, one on feeding in larvae. The rhythms and sleep component, with which I am most familiar, was clearly written, and gives the reader an account of how to collect the data in the commercially available locomotor activity monitors and then, using a blow-by-blow idiots guide, how to process the data using ClockLab software (a MATLAB-based programme) and some custom-designed algorithms that are Excel-based from the senior author’s laboratory. Pretty useful, even for the beginner, I would say.

The chapters on courtship and aggression phenotypes were less easy to understand for a beginner because, unlike locomotor activity, which is totally automated, courtship and aggression require viewer observation which carries with it the element of subjectivity. A basic figure illustrating the courtship or aggression behavioural elements might have been helpful to go with the Web-based movie references provided for aggression (but not for courtship). However, assuming that you do know what you are looking for, the rest is reasonably helpful. Recently, fully automated observation methods for scoring these complex phenotypes have been reported. While their validation under different experimental conditions remains to be tested comprehensively, such developments are to be warmly welcomed in this traditionally thorny area of fly ethology.

I also read most of the chapters in the development section, selecting particularly those that described techniques of which I had little or no experience. I studied neuroblast development, embryonic cell fate, axon guidance, and mosaic analysis using the

modern methods of MARCM, and the larval neuromuscular junction (NMJ, nicely detailed this one). In the middle section, there are eight chapters that include methods of physiological recordings of various types, including eyes, ears (Johnstone's organ), noses (chemosensory sensillae), NMJ, Giant Fibre, and neuronal recordings from embryo, larva and adult. These tend to be the most detailed of the contributions. They were followed by the imaging chapters, including the main calcium and GFP methods with further contribution focusing on the many different ways one can manipulate neuronal excitability, transmission or signal transduction using various UAS constructs. While one cannot tell how good the protocols are without doing oneself the practical component, I found the chapters interesting for pointing out how much I did not know.

In conclusion, each chapter assumes that the reader already has a reasonably good knowledge of *Drosophila* biology in their research area and is pitched at the interface of the first/second year of PhD study. I felt that this manual will provide a substantial resource for the fly neurobiology community for the oncoming decade.

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Statistical Bioinformatics: For Biomedical and Life Science Researchers. Ed. J. K. Lee. Wiley-Blackwell. 2010. 370 pages. ISBN 9780471692720. Price £66.95 (paperback).

Statistical Bioinformatics, edited by Dr Jae Lee, is envisioned as a textbook for a one- or two-semester course. The book aims to provide a comprehensive introduction to statistical concepts and techniques relevant to the bioinformatics training of life scientists. The textbook is organized into four three-chapter blocks that cover statistical foundations (Chapters 2–4), high-dimensional analysis (Chapters 5–7), advanced topics (Chapters 8–10) and multigene systems analysis (Chapters 11–13). As befitting this breadth of topics, chapters were contributed by a diverse set of authors with expertise distributed through the field of bioinformatics.

Dedicated to statistical foundations, the first section of the book is arguably its most valuable. Chapters 2–4 touch on a wide variety of topics including probability concepts, hypothesis testing and an introduction to statistics and their sampling distributions. Also included are issues of special relevance to bioinformatics such as quality control, data normalization and the testing of multiple hypotheses.

The nature of *Statistical Bioinformatics* is such that none of these topics are treated in depth, but the coverage is appropriate, the content is valuable and students will benefit greatly from the aggregation of this foundational material into one text. The development of statistical inference is worth special mention: rather than relying on traditional concepts such as parametric estimation and confidence intervals, the focus is on sampling and resampling. This seems very much like the right choice even as it leaves a small gap between the foundations in Chapters 2–4 and the advanced topics in Chapters 8–10.

Chapters 5–13 build upon the statistical foundation established in the early part of the book. The second section of the book, spanning Chapters 5–7, focuses on the analysis of high-dimensional data. Chapters 5 and 6 are heavy on machine-learning techniques and cover unsupervised and supervised learning, respectively. After a useful introduction to similarity and dissimilarity metrics, Chapter 5 explores the problem of clustering in great detail. The discussion is logical and nicely complemented by figures that illustrate various clustering methods and their distinctions. Chapter 6 is more challenging than Chapter 5, perhaps because supervised learning is less intuitive than clustering, and perhaps because more background knowledge is required. The material is important but students may find it difficult in the absence of supplemental figures and examples. By contrast, the visualization of high-dimensional data as discussed in Chapter 7 is a more accessible topic.

Chapters 8–10 of *Statistical Bioinformatics* are reserved for advanced analysis topics that do not depend on the material in Chapters 5–7. These topics include statistical modelling (Chapter 8), experimental design (Chapter 9) and statistical resampling methods (Chapter 10). The statistical modelling chapter picks up where Chapter 2 left off and contains a concise survey of models and methods. The following chapter focuses on high-throughput biological experiments and discusses principles of design including replication and statistical power. While the emphasis of Chapter 9 is on microarray experiments, the principles discussed are quite general. Chapter 10 discusses resampling techniques for prediction, classification and model selection, again in the context of large biological data sets. Although Chapters 8–10 are meant to be independent of Chapters 5–7, there is synergy between Chapters 10 and 6, and while reading one, students should be cognizant of the other.

Chapters 11 and 12 of *Statistical Bioinformatics* address topics of relevance to systems biology. Chapter 11 is technically advanced and covers methods for statistical network analysis, whereas Chapter 12 presents a thorough discussion of trends and challenges in genome-wide association analysis (GWAS). Both topics are highly relevant, and the