

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

GWAS chapter is a must-read for students today. The final chapter of *Statistical Bioinformatics* highlights the book's greatest strength: the consistent inclusion of statistical programming examples. The statistical programming language R is used throughout the text, and Chapter 13 discusses at length the use of R and its Bioconductor package for bioinformatics applications.

Statistical Bioinformatics is noteworthy for its breadth of coverage and use of descriptive examples. It will find use both as a graduate textbook and as a guide to self-study. Statistics is a large field, and the foundational chapters will help guide students to what they need to know. The remaining chapters introduce topics of relevance to bioinformatics students in such a way that more specialized knowledge can easily be sought.

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Statistics at the Bench: A Step-by-Step Handbook for Biologists. M. Bremer & R. W. Doerge. Cold Spring Harbor Laboratory Press. 2010. 167 pages. ISBN 9780879698577. Price \$59 (hardback).

In recent years, there has been an increase in the number of elementary statistical textbooks based on a statistical package such as SAS, Minitab or S-Plus. The idea behind this approach is that the availability of such packages allows computational details to be skimmed in order to free the reader to concentrate on interpretation.

Statistics at the Bench, a handbook from Cold Spring Harbor Laboratory Press, is an example of the genre, with Excel (the spreadsheet application from Microsoft) as the chosen program. The authors describe the book as providing 'a quick refresher or a big-picture overview of a statistical procedure', and address the typical reader as the kind of biologist for whom 'it has been a long time (if ever) since you last took a course in mathematics or statistics, or even considered thinking quantitatively about your data'. The motivation for the book is that 'biology is becoming increasingly computational ... Large amounts of quantitative information need to be organized, displayed and understood'.

The writing style is light and breezy, designed to reassure the biologist who has a dislike or fear of mathematics. Cartoons illustrate some of the examples, which are varied and relevant for a biological audience. Some examples: Mendel's data on colour

and shape of peas, the iron content of spinach, life-span of English gentry, the number of petals on an *Arabidopsis* plant, the effectiveness of contraception, length of *Drosophila* sperm cells, candidate genes for alcoholism and a BLAST search. Explanations are given verbally as far as possible. Mathematical terminology is basic and kept to a minimum.

Standard topics are covered (descriptive statistics, design of experiments, confidence intervals, hypothesis testing, regression and ANOVA), as well as some topics not usually included in a text at this level (classification, clustering, principal components, microarray data analysis, maximum likelihood and Bayesian statistics). A typical chapter introduces a topic by describing the aim of the analysis and the type of data to which it applies. Parameter estimation and hypothesis testing are described briefly (generally without detail or formulas), and instructions given for analysis in Excel. A small worked example is used to illustrate the technique. The reader is shown how to examine diagnostic plots and check the assumptions of the model.

This approach works reasonably well for the simpler applications, but breaks down for more complex cases. As the authors explain, 'we chose Excel because it ... is widely used by biologists today. This said, we recognize the limitations of Excel and acknowledge that it is not an advanced statistical program. For applications that exceed the scope of this text (and Excel), there are other statistical programs that may be more appropriate'.

The treatment of most topics is rather superficial, but as an introduction for the target audience (biologists with a weak background in statistics) the level is about right. The reader will have to look elsewhere for an in-depth treatment. References given at the end of the book might usefully have included some standard texts, such as Sokal & Rohlf (1995).

The authors describe their aim as 'to assist biologists in becoming fluent and comfortable in the language of quantitative reasoning and to facilitate open and informed communication between the biological and quantitative sciences'. This book represents a small step in that direction.

Reference

Sokal, R. R. & Rohlf, F. J. (1995). *Biometry: the Principles and Practice of Statistics in Biological Research*, 3rd edn. New York: Freeman.

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