Modern Statistics for Modern Biology.

By Susan Holmes and Wolfgang Huber. Cambridge and New York: Cambridge University Press. $64.99 (paper). xxiii + 382 p.; ill.; index. ISBN: 978-1-108-70529-5. 2019.

This book is a tour de force through statistical methods that any biologist should be familiar with. The volume balances beautifully the introduction of both foundational and specialized knowledge. The scope ranges from basic statistical tests, experimental design, and fundamental plotting principles to advanced analyses, including clustering, supervised learning, networks, multivariate methods, and image analysis, among others. The book is written for biologists who are familiar with basic statistics, have some familiarity with the R working environment, and want to harness the strengths of R to expand their expertise to not only use modern statistical techniques, but also to understand their underlying principles. Graduate students, as well as established researchers, will learn from engaging with this volume.

Each statistical method is first introduced with examples and simulations to build intuition. After a thorough dive into the underlying principles of a method, analytic solutions are provided for those who want more information on the statistical machinery and formalism. Throughout the text, the authors bring illuminating examples, guiding questions, exercises, and sample code. Actively engaging with these materials will benefit any reader who truly wants to learn from the thoughtful exercises and elegant and concise R code. Examples and exercises come from a wide range of cutting-edge biological research, including genomics, transcriptomics (e.g., RNA-Seq and single-cell gene expression), microscopy (e.g., scanning electron microscopy and histology), metabolism, phylogenetics, and more.

One of the biggest perks of the volume is its online version (https://web.stanford.edu/class/bios221 /book/) that includes the book's text, R files, data files, and all of the example code, which can be easily copied into one own's R environment to test and experiment with. Most importantly, the online version is continuously updated to include new examples and keep up with developments in the ever-changing R universe. Engaging with the R code in the volume not only teaches statistics, but also establishes good coding practices and introduces R-specific perks that make code readable and efficient. Examples are in R and Bioconductor and plotting relies predominantly on the ggplot2 package.

Overall, the book is extremely readable and engaging, it explains complicated concepts in simple terms, and uses illuminating graphics and examples. Any researcher who wants to learn or teach up-to-date statistics to biologists will find this an es-

sential volume for modern teaching of modern statistics to modern biologists.

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Computing Skills for Biologists: A Toolbox.

By Stefano Allesina and Madlen Wilmes. Princeton (New Jersey): Princeton University Press. $110.00 (hardcover); $45.00 (paper). xxii + 417 p.; ill.; indexes of symbols; Unix commands; Git commands; Python functions, methods, properties, and libraries; LaTeX commands and libraries; R functions and libraries; SQLite commands; and general index. ISBN: 9780691167299 (hc); 9780691182759 (pb). 2019.

Computation is becoming an essential tool for biological researchers. Beyond bioinformaticians, biostatisticians, and computational biologists, even experimental biologists frequently must "wrangle" data or perform complex statistical analyses on large datasets. As a result, computing skills are now as essential as reading and writing. Unfortunately, the development of these skills has not yet been integrated into undergraduate and graduate coursework to the same extent that experimental techniques have. Trainees must often become self- (or book-) taught computational biologists. As such, *Computing Skills for Biologists: A Toolbox* is a must read for the next generation of biologists.

The authors summarize a practical introduction to computer science as applied to and relevant for the biological sciences. The text is inspired by Allesina's Introduction to Scientific Computing for Biologists course at the University of Chicago. It is broken into 10 semi-independent chapters to introduce key concepts in scientific computing, such as version control, basic programming, field-specific libraries and packages, resources for statistics, and data manipulation and storage. Allesina and Wilmes introduce the Unix operating system, several programming languages (R, python, and SQL), and useful tools such as Git and LaTeX.

Dedicated to "all biologists who think they can't code" (p. v), the authors know and care about their target audience. Code demonstrations and example problem sets are integrated into each chapter and chapters conclude with a list of additional resources. A companion website hosts downloadable code from the text, pseudocode (or, outlining in words what your code should aim to do), problem sets, and solutions, as well as clear instructions for how to download software and ensure your computing system is set up correctly. Importantly, every concept within the book is presented to a novice, including thoughtful and clear definitions of notation and terminology. Because the text is well written and organized, an experienced user can