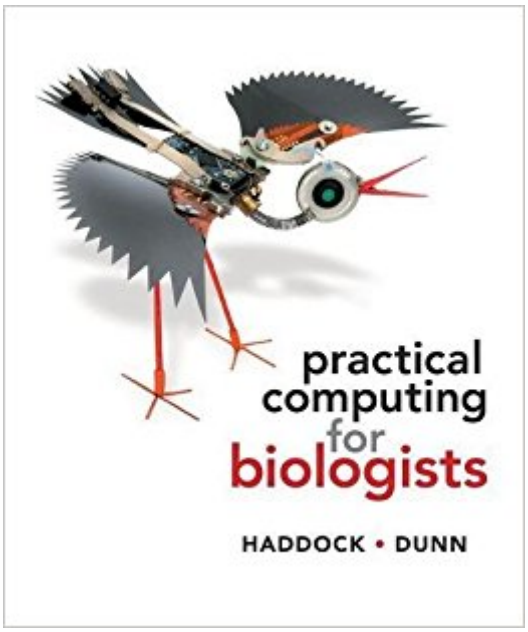
Practical Computing For Biologists



Synopsis

Increasingly, scientists find themselves facing exponentially larger data sets and analyses without suitable tools to deal with them. Many biologists end up using spreadsheet programs for most of their data-processing tasks and spend hours clicking around or copying and pasting, and then repeating the process for other data files.Practical Computing for Biologists shows you how to use many freely available computing tools to work more powerfully and effectively. The book was born out of the authors' own experience in developing tools for their research and helping other biologists with their computational problems. Although many of the techniques are relevant to molecular bioinformatics, the motivation for the book is much broader, focusing on topics and techniques that are applicable to a range of scientific endeavors. Twenty-two chapters organized into six parts address these topics (and more; see Contents): *Searching with regular expressions*The Unix command line *Python programming and debugging *Creating and editing graphics *Databases *Performing analyses on remote servers *Working with electronicsWhile most of the concepts and examples apply to any operating system, the main narrative focuses on Mac OS X. Where there are differences for Windows and Linux users, parallel instructions are provided in the margin and in an appendix. The book is designed to be used as a self-guided resource for researchers, a companion book in a course, or as a primary textbook. Practical Computing for Biologists will free you from the most frustrating and time-consuming aspects of data processing so you can focus on the pleasures of scientific inquiry.RESOURCESFor StudentsThe Companion Website includes downloads, community forums, tips and examples, and textbook errata and updates.For InstructorsThe Instructor's Resource Library features all of the textbook's figures and tables, provided in ready-to-use PowerPoint presentations.

Book Information

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Customer Reviews

"Practical Computing for Biologists is a clear guide to methods that unlock the power of the personal computer. Although the breadth of subjects covered is certainly an asset of this volume, what really makes the book stand out is how well the authors clearly describe each technique and its applicability to biological sciences. It is a great launching point for any necessary further investigation of computational techniques." --Matthew Aiello-Lammens, The Quarterly Review of Biology"The book covers a wide range of subjects that truly justifies the title of 'practical computing.' In addition to the usual programming-related topics, it also includes a thorough introduction to the programming environment, approaches to combining different programs together, a description of the basic text manipulation tools such as regular expressions, and even an introduction to dealing with digital art and images. As such the book is great value for the money, being at least three books in one." --Olga G. Troyanskaya, Cell"My copy of Practical Computing for Biologists arrived last week, and I've been very impressed. It is a well-written, well-paced guide to basic computing skills for scientists and engineers of all stripes (not just biologists). It is beautifully produced: full-color printing and great graphical design make this book a joy to read. If I ever do turn Software Carpentry into a book, I might skip the topics PCB covers and just tell people to go and buy it." --Greg Wilson, software-carpentry.org"When considering my research and use of time, this book has been the most important book I've read in the last year, and perhaps the last decade. Striking a perfect balance by guiding you through tutorials and nudging your own self-exploration, the book has just enough guided direction to not annoy or overwhelm. It has helped (and is still helping) me to do what I was doing before, but more efficiently." --Cyme & Cystidium

Steven H.D. Haddock is a Research Scientist at the Monterey Bay Aquarium Research Institute and adjunct Associate Professor at the University of California, Santa Cruz, studying bioluminescence and biodiversity of gelatinous zooplankton. He started programming in BASIC on an Apple][and began his undergraduate studies in engineering before deciding to change fields. He took this programming background with him to his graduate studies in Marine Biology, where he quickly realized the advantages that computing skills offered and felt compelled to help foster these abilities

in others. He has developed many utilities and devices for research, including instruments to monitor bioluminescence from fireflies, a freezer monitoring system, a web-based conference registration database, and a PCR calculator for smartphones. In addition to teaching invertebrate zoology and writing a booklet to teach the technique of blue-water scuba diving, he has given tutorials in computing to students and administrators. His interest in education extends to his Bioluminescence Web Page (http://lifesci.ucsb.edu/~biolum/) and the Jellywatch.org citizen-science website (www.jellywatch.org).Casey W. Dunn, a Professor at Yale University, does research that has a large computational component but always in conjunction with work in the field and lab. His first interest in computers stemmed from building electronics, and he further developed his computational skills working in Silicon Valley while an undergraduate. As his data sets grew larger and larger during grad school and his postdoc, he found himself reaching back to his computer background more often. In the course of his own research and helping other biologists with their computational challenges, he became concerned about the mismatch between training opportunities and the real day-to-day computational problems biologists face. In addition to teaching invertebrate biology, evolution, and development, his educational activities include the websites siphonophores.org and creaturecast.org. Dr. Dunn is the recipient of the National Science Foundation’s 2011 Alan T. Waterman Award, recognizing an outstanding young researcher in any field of science or engineering supported by NSF.

Update:THIS BOOK MADE ME SHINE!One of the exercises in the book involves using building a program using regular expressions to modify the format of lat/lon data into a .kml-readable format.Guess what my employer asked me to do today?Yup, manually reformat hundreds of lines of lat/lon data.It took me 20 minutes instead of tedious hours, and I was paid for completion of the job, not the hours.In science, it is all about efficiency and building a better mouse-trap. This book teaches you all the great shortcuts to stand out in a competitive field of study.THANK YOU PCfB!!!!!My Background:I am a biochemistry and molecular biology graduate who is learning BioPy and R to aid in my ability to process and understand large data sets. I’ve been reading books on python and bioinformatics, but they are often either too cryptic or too basic. Until I found PCfB, I couldn’t find a book that got to the real meat of bioinformatics and biological data processing/management.Review:If you are pursuing higher education in science, buy this book. Seriously, put this book into your cart now.Now that advanced computer skills are in great demand by employers in scientific disciplines, I really think a course involving this material should be mandatory in any undergraduate chemistry or biology department. But it isn’t, so buy this book and

catch up. This is the information they should have taught you in college.PCfB is probably best for people who have a basic understanding of computers. The book is neither written for experts nor for novices and fits well at the college level. It provides sufficient detail and complex examples without interjecting excess esoteric programming theory.The only downside is that the book is catered towards OSX/UNIX, but to be fair, the authors include how to run commands on windows and linux.

This is an invaluable text for anyone looking to demystified computing. While the examples tend to be biological, for instance dealing with DNA sequences or specimen collection data, I think this textbook will be useful to readers in many different fields of science. In fact, a lot of the text focuses on data acquisition, organization, and management, and is applicable to readers from a variety of fields.This book was recommended to me by a number of biology graduate students that used in it seminar-style courses on bioinformatics. I had no previous experience with programming and was pretty intimidated by programming and computing in general. However, this book helped me get over that fear quickly! It builds a strong foundation in a variety of computational methods (particularly programming in python). With this foundation I was able to take advantage of a lot of online resources that were previously beyond my understanding. In this book, I quickly learned a number of basic strategies for data collection and analysis that would have saved me weeks of work had I known how to employ them earlier in my graduate career. I’m glad I know them now and I look forward to building on the skills I developed with this book!

This is one of the most valuable and useful books that I have read in a very long time. This book is also extremely timely - given how reliant on computers the analysis of biological data is becoming. The authors clearly and concisely walk the reader through a broad range of extremely useful computational processes that will increase the efficiency of how any biologist stores, analyzes, and/or manipulates their data. Most of my colleagues know that they could be using their computers, and analyzing their data, more efficiently; but many do not know where to start, or are intimidated by the vast "computer programming" section of their local bookstore. This book acts as an excellent intermediate step - providing clear (and biologically relevant) examples of how a few key skills can immediately alter daily tasks. The authors then point the reader in the necessary direction for those who wish to learn more. Briefly, some topics that I found particularly helpful were: (1) the use of regular expressions to quickly modify text files (who hasn’t suffered through manually doing this to convert the output from one program to the input of another?); (2) the fairly extensive introduction to Python programming and some of its uses; (3) the friendly introduction to MySQL

(which can otherwise be very intimidating); and (4) the information on vector art. I also appreciate that the authors focused on Open Source programs; which makes all of the examples/programs available to anyone. I would highly recommend this book to all biologists - full stop. I also want to thank the authors for writing it - it has been a huge help to me, and couldn't have come at a better time.

Fantastic book. Clear, accessible presentation that wastes no time honing in on the subset of computer skills guaranteed to deliver the most bang for the buck for the average biologist/ecologist. I was using this stuff literally the next day after I read it and have enjoyed major gains in productivity + decreases in frustration. I wish I'd read it the moment I stepped out of undergrad. It's worth mentioning that the focus is on data management/preparation, and not so much on analysis, for which the authors refer the user to R or Matlab. This book coupled with a good one on the stats program of your choice is all you'd need to get churning on your analysis.

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