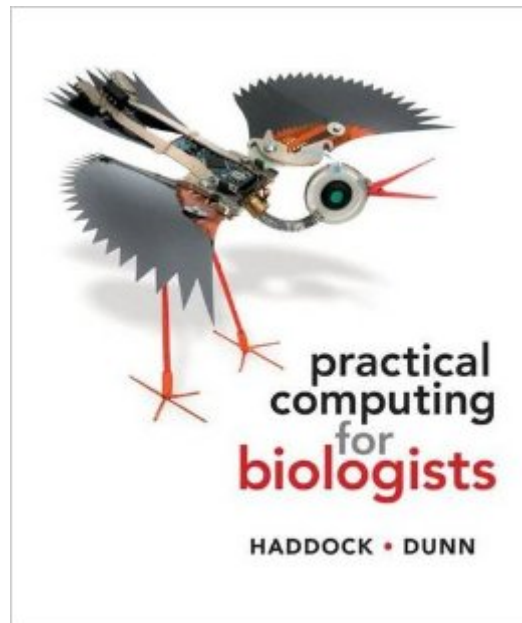# Practical Computing For Biologists

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: Searching with regular expressions The Unix command line Python programming and debugging Creating and editing graphics Databases Performing analyses on remote servers Working with electronics   While 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.

Book Information

Paperback: 538 pages

Publisher: Sinauer Associates, Inc.; First edition (November 5, 2010)

Language: English

ISBN-10: 0878933913

ISBN-13: 978-0878933914

Product Dimensions: 7.6 x 1 x 9.1 inches

Shipping Weight: 2.5 pounds (View shipping rates and policies)

Average Customer Review: 4.7 out of 5 stars See all reviews (51 customer reviews)

Best Sellers Rank: #56,992 in Books (See Top 100 in Books)   #10 in Books > Computers & Technology > Computer Science > Bioinformatics   #77 in Books > Computers & Technology > Programming > Languages & Tools > Python   #158 in Books > Computers & Technology > Programming > Web Programming

Customer Reviews

More than any other book I've read, Practical Computing for Biologists delivers exactly what the title promises. I've tried several tutorials for both Python and R over the last few years, and even just the first 2 chapters of PCFB were more helpful than any of that (I'm now on chapter 9 and the book continues to please). I think it fills a huge need for biologists who want to be able to deal with data sets that are quickly growing in size, but who don't necessarily want to or have the time to become computer scientists themselves. I couldn't recommend this book more highly for any scientist who has experienced frustration dealing with large data sets (like high-throughput DNA sequences), or just wants to cut down time spent on repetitive computer tasks. I'm sure I'll be referencing it often, and for a long time.

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.

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!

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