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Perl Programming For Biologists



Synopsis

Working on the assumption that the reader has no formal training in programming, Perl Programming for Biologists demonstrates how Perl is used to solve biological problems. Each chapter opens with a set of learning objectives, provides numerous review questions and self-study exercises, and concludes with a bulleted summary of key points. The author incorporates numerous real-life examples throughout the text. Upon completing the book, readers are able to quickly perform such tasks as correcting recurring errors in spreadsheets, scanning a Fasta sequence for every occurrence of an EcoRI site, adapting other writers' scripts to one's own purposes, and most important, writing reusable and maintainable scripts that spare the rote repetition of code.

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Customer Reviews

Although James Tisdall's Perl books (Beginning/Mastering Perl for Bioinformatics) could be a little scattered, I found that they offered more for the biologist learning Perl than this one; you could almost buy both those books for the price of this one! This book seems structured more along the lines of the (superior) Learning Perl and Intermediate Perl by Schwartz et al, with a few biological references thrown in as examples. Some of the most important aspects of biological sequence analysis were glossed over fairly quickly if at all. I found it somewhat amazing that file format parsing, restriction enzyme analysis, sequence conversion, transcription-translation, program output parsing, and other fundamental topics were either covered very briefly in passing or not covered at all. Disappointing! I believe one might find this book was a great read first time out (it is well written),

but that once they progressed to other texts (Learning Perl, Intermediate Perl, Programming Perl), they would rarely, if ever, refer back to this one. That's not good for a \$50 book. I can't see myself using it in the future when I have the Camel and Llama covering my back, along with Tisdall's texts. Basically a lot of sugar coating without much substance. Oh, and there's a major mistake in the Object-Oriented Programming section, one which really breaks your programs. In short : -> != => My advice: spend your money on those texts and use your imagination on what Perl can accomplish for you as a biologist. If you are an advanced Perl programmer and biologist, at least check out Tisdall's books and wait for the long-rumored BioPerl book. I would give it 3 stars for the writing but the price doesn't justify it, sorry. The review system won't let me change the rating though, so you lucked out this time!

I have taught Perl from Tisdall's "Beginning Perl for Bioinformatics", and was frankly frustrated by the seemingly random order of presentation of topics. The students in the class felt the same. This book, however, does it right: it is a clear, pedagogic introduction to Perl programming with applications in bioinformatics. Highly recommended for biologists who never programmed before.

Jamison's narrative is well thought out; he is a good teacher, provided you are attentive enough to initialize the variables, arrays and hashes in the required order without him reminding you. But he also needs a good editor. It is a shame his book is marred with so many typos. For instance, on p. 47, there are several typos. A couple are text typos, "when" instead of "we", which throw off the meaning of the text. More serious, however, is the statement after the print command, ""\$gene is on both maps\n";", when the code above really refers to three hashes, which contain three map keys. Unexplained is the fact that the RH map refers to the mouse radiation hybrid map, maintained by the Broad Institute. Still, for all its faults, it's the only game in town for biologists who are just cutting their teeth on Perl. It is essential to use a good Perl-friendly text editor/debugger with this book. Be savvy about using all the examples he mentions in passing, because the end-of-chapter exercises are inadequate to learning the language, and some of the programming challenges are mystifying. A major fault is that no answers are given. Another thing to note: Jamison may be an excellent software engineer, but he is no biologist. At one point, he confuses transcription and translation. Rely on your own biological knowledge.

It is a followable step-by-step introduction for biologists in perl programming. It is pity that the solutions of exercises are missing from the book.

Excellent book for the beginner programmer who is interested in Bioinformatics. However, an additional Perl reference book with examples is needed.

"...unique and I highly recommend it as a first book on programming for biology-oriented professionals interested in using perl...excellent for self-study...can also be a great resource as classroom material..." (Clinical Chemistry, Vol. 50, No. 2, 2004)

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