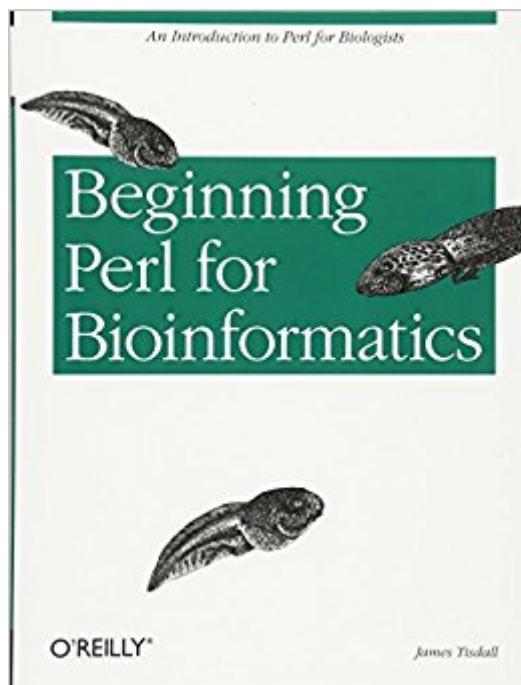The book was found

Beginning Perl For Bioinformatics

Synopsis

With its highly developed capacity to detect patterns in data, Perl has become one of the most popular languages for biological data analysis. But if you're a biologist with little or no programming experience, starting out in Perl can be a challenge. Many biologists have a difficult time learning how to apply the language to bioinformatics. The most popular Perl programming books are often too theoretical and too focused on computer science for a non-programming biologist who needs to solve very specific problems.Beginning Perl for Bioinformatics is designed to get you quickly over the Perl language barrier by approaching programming as an important new laboratory skill, revealing Perl programs and techniques that are immediately useful in the lab. Each chapter focuses on solving a particular bioinformatics problem or class of problems, starting with the simplest and increasing in complexity as the book progresses. Each chapter includes programming exercises and teaches bioinformatics by showing and modifying programs that deal with various kinds of practical biological problems. By the end of the book you'll have a solid understanding of Perl basics, a collection of programs for such tasks as parsing BLAST and GenBank, and the skills to take on more advanced bioinformatics programming. Some of the later chapters focus in greater detail on specific bioinformatics topics. This book is suitable for use as a classroom textbook, for self-study, and as a reference.The book covers:Programming basics and working with DNA sequences and strings Debugging your codeSimulating gene mutations using random number generatorsRegular expressions and finding motifs in dataArrays, hashes, and relational databasesRegular expressions and restriction mapsUsing Perl to parse PDB records, annotations in GenBank, and BLAST output

Book Information

Paperback: 400 pages

Publisher: O'Reilly Media; 1 edition (November 1, 2001)

Language: English

ISBN-10: 0596000804

ISBN-13: 978-0596000806

Product Dimensions: 7 x 0.8 x 9.2 inches

Shipping Weight: 1.2 pounds (View shipping rates and policies)

Average Customer Review: 4.2 out of 5 stars   46 customer reviews

Best Sellers Rank: #187,371 in Books (See Top 100 in Books)   #14 inÂ Books > Computers & Technology > Programming > Languages & Tools > Perl   #49 inÂ Books > Computers &

Customer Reviews

Biology, it seems, is a good showcase for the talents of Perl. Newcomers to Perl who understand biological information will find James Tisdall's Beginning Perl for Bioinformatics to be an excellent compendium of examples. Teachers of Perl will likewise find the text to be filled with fresh programming illustrations of growing scientific importance. Seasoned Perlmongers who want to learn biology, however, should search elsewhere, as Tisdall's emphasis is on Perl's logic rather than Mother Nature's. Departing from O'Reilly's earlier monograph Developing Bioinformatic Computer Skills, Tisdall's text is organized aggressively along didactic lines. Nearly all of the 13 chapters begin with twin bullet lists of Perl programming tools and the bioinformatic methods that require them. Likewise, the chapters end with exercises. String concatenation is illustrated with gene splicing, and regular expressions are taught with gene transcription and motif searching. Tisdall emphasizes sequence examples throughout, leading up to an introduction to a Perl interface for the NIH GenBank biological database and the widely used BLAST sequence alignment tool. After a brief discussion of three-dimensional protein structure, he returns to sequence extraction and secondary structure prediction. Tisdall's goal is to boost the beginning programmer into a domain of self-learning. He imparts essential etiquette for the success of programming newbies: use the wealth or resources available, from user documentation to Web site surveys to FAQs to How-To's to news groups and finally to direct personal appeals for help from a senior colleague. A well-plugged-in bioinformatics Perl student will soon discover Bioperl, an open-source effort to bring research-grade bioinformatic tools to the Perl community. Bioperl is described briefly at the end of Tisdall's book and will reportedly be a forthcoming title of its own in the O'Reilly bioinformatics series. Although he introduces bioinformatics as an academic discipline, Tisdall treats it as a trade throughout his book. He indicates that open questions and computational hard problems exist, but does not describe what they are or how they are being tackled. Ultimately, Tisdall presents bioinformatics as another arrow in a bench scientist's quiver, very much like HPLC, 2D-PAGE, and the various spectroscopies. As odd as a "bioinformatics-as-tool" book may be to its research proponents, the reduction of bioinformatics to trade status both deflates and vindicates the years of research, as Tisdall's work attests. --Peter Leopold

James Tisdall has worked as a musician, a programmer at Bell Labs (where he programmed for

speech research and discovered a formal language for musical rhythm), and as a bioinformaticist at Mercator Genetics in Menlo Park, California, and at Fox Chase Cancer Center in Philadelphia. He has a B.A. in mathematics from the City College of New York and an M.S. in computer science from Columbia University; he is working towards a Ph.D. in computer science at the University of Pennsylvania. In his spare time, Jim teaches computer music at the Settlement Music School in Philadelphia. He is also the author of O'Reilly's Beginning Perl for Bioinformatics.

Finally someone has written a beginning book on PERL for biologists, and has also done an excellent job of doing so. This book assumes no prior programming experience, and therefore suits the biologist who needs to concentrate on using computers to solve biological problems, and not have to become a computer scientist in the process. PERL can be a very cryptic language, but it is also extremely concise, and PERL programmers frequently and rightfully boast about their "one-liners" that accomplish complicated tasks with only one line of code.Since it is addressed to readers with no programming experience, the author introduces some elementary concepts of programming in the first three chapters. These include what text editor to use, how to install PERL, how run PERL programs, and other relevant elementary topics.The author then gets down to writing a program to store a DNA sequence in chapter 4. Very basic, it merely reads in a string and prints it out, but serves to start readers on their way to developing more useful programs. Later a program for the transcription of DNA to RNA is given, which illustrates nicely the binding, substitution and trace operators. Block diagrams are used here, and throughout the book, to illustrate basic PERL operators. The author shows in detail how to read protein sequence data from a file and how to use it in a PERL program. The reader is also introduced to the most ubiquitous data structure in all of computing: the array. Already the reader gets a taste of the power of PERL to manipulate arrays, using operations such as 'unshift', 'push', 'splice', etc.The next chapter introduces conditional statements in PERL, as a warm-up for the discussion on finding motifs in sequences. The reader can see why PERL is the language of choice in bioinformatics, with its ability to find substrings or patterns in strings. Things do become more cryptic in the discussion of regular expressions, but the reader can get through it with some effort. Interesting programs are given for determining the frequency of nucleotides.Since the programs have become more complicated to this point, a discussion of subroutines follows in the next chapter. And, for the same reason, the reader is introduced to debugging in PERL in this chapter also. The greater the complexity of the program, the harder it becomes to avoid making mistakes, and even more difficult to find them. The very important concepts of pass by value versus pass be reference are discussed briefly in this

chapter.Random number generators, so important in any consideration of mutations, are discussed in chapter 7. It is shown, via some straightforward programs, how to select a random location in DNA and mutate it with some other nucleotide. In addition, the author shows how to use random numbers to generate DNA sequences and mutate them in order to study the effect of mutations over time.The next chapter is the most interesting in the book, for it shows how PERL can be used to simulate how the genetic code directs the translation of DNA into protein, the hash data structure being used extensively for this purpose. The author shows how to read DNA from files in FASTA format, and discusses in detail reading frames. He gives a useful subroutine to translate reading frames.The author returns to regular expressions in chapter 9, wherein they are used as 'wildcards' to search for a particular string in a collection of strings. In addition, the range operator is used to find restriction sites. Regular expressions are also used in the next chapter to manipulate GenBank 'flat files'. The author does however give URLs for more sophisticated bioinformatics software. This is followed in chapter 11 by a discussion of the use of PERL to work with files in the Protein Data Bank. Recursion, one of the most powerful techniques in programming, is introduced here.Chapter 12 covers the Basic Local Alignment Search Tool (BLAST), wherein readers get a taste of the field of computational biology. This extremely popular software package is used to find similarity between a given sequence and a library of known sequences. The author does discuss some of the basic rudiments of string matching and homology, and encourages the reader to consult the BLAST documentation for further details. In addition, the author briefly discusses the Bioperl project in this chapter, and shows the reader how to run some elementary computations using it.This book definitely is a timely one and it will serve the needs of biologists who need to obtain some programming expertise in PERL. There are helpful exercises at the end of each chapter that serve to solidify the understanding of the concepts introduced in the chapter. After a thorough study of it, readers will be well-equipped to use PERL in bioinformatics. With more mathematical background, readers after finishing it will be able to enter the exciting field of computational biology, a field that is exploding, and one in which will require imaginative programming skill in the future.

If you haven't programmed in perl before, this book is perfect for learning. It also teaches very low level bioinformatics skills that'd probably help an undergraduate get their next internship. I was clueless to perl, and programming for that matter, when I got this book a long time ago. I painfully flipped each page from front to back, because it 'is' a technical book, and absorbed everything as much as possible. This book set me off in a direction that I never imagined. Although we're on the brink of version six of the language, this book will do you right in any aspect of computer

programming. For a 'beginner' looking to get into any language, this book is for you. It's painful, but try and take the time to really learn the information the book presents. It not only teaches you perl, but gives you a peek into the numerous databases and resources that exist as well as a terrific job of teaching you how to use regular expressions. In the end, you'll have the foundation to become whatever kind of perl programmer you desire. If you're looking into bioinformatics, or a bioinformatician looking to learn, I recommend this book as well as 'Programming Perl', 'Mastering Perl for Bioinformatics', and 'BLAST'. 'BLAST' is fairly easy to breeze through and does a good job of explaining everything you would need to know. 'Mastering Perl...' picks up where this book left off, and 'Programming Perl' is one of the best buys I ever made, in regards to perl. I know these are all O REILLY books, but they're probably the best source for perl books out there. I'm not pitching their books either. Lastly, if you have the time I recommend you crunch on through 'CGI Programming with Perl'. Although the book is a bit out of date, it's definitely another 'piece' of the puzzle for someone to become a LAMP programmer.

I bought this book knowing nothing about Perl. I'm not sorry I bought it, but it didn't get me very far.Pros:- clear descriptions of how to do many of the very basic things you need to do- explains regexes pretty well to the uninitiated (I do still look up how to do some regex things in it)Cons:- not very deep, you'll exhaust it quicklyAt this point I rarely look back at this book even as a reference. It was a stepping stone that I've now left behind.

This is a fantastic book for the beginners. This was actually a textbook for our first bioinformatics class. This book helped me lot and was able to learn programming. It was easy to start and follow. Examples in the book are easy to understand and text explanation obviously helped to understand the concept. Recommended for those who are beginners in perl and bioinformatics.

I have a MS degree in Bioinformatics and I bought this book to help me learn Perl for my job. During my training at the University, I wasn't taught Perl, because most programs assumed Perl would have become obsolete. The truth is that many jobs still list Perl as a desired skill. This book was a little too easy for me, because of my background, but I think it is a great start for the newbie in Bioinformatics who wants to learn to program. It is definitely a very practical tool for learning how to develop practical Bioinformatics solutions.

I bought this book to create a working knowledge of programming, especially in the light of

bioinformatics (I'm a biology grad student). I have no prior programming experience but this book is extremely easy to follow and I feel as if I am actually learning how to use each of the commands in a way to create my own programs. I have yet to completely get through the book, but from what I have been through I highly recommend this book to any who are interested in gaining an understanding of this science.

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