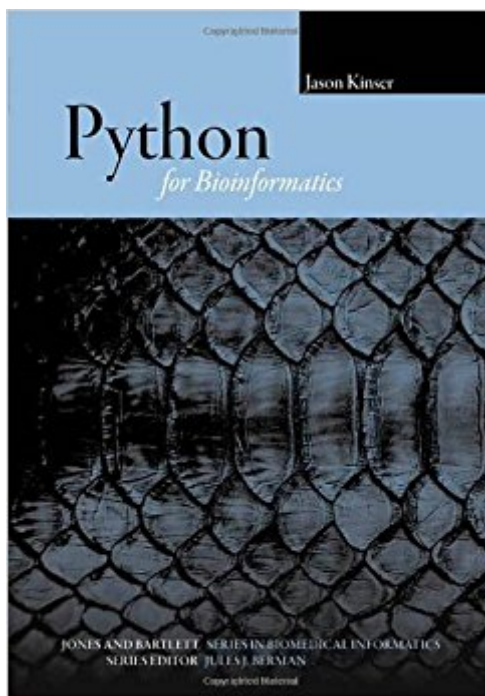The book was found

Python For Bioinformatics (Series In Biomedical Informatics)

Synopsis

Bioinformatics is a growing field that attracts researchers from many different backgrounds who are unfamiliar with the algorithms commonly used in the field. Python for Bioinformatics provides a clear introduction to the Python programming language and instructs beginners on the development of simple programming exercises . Ideal for those with some knowledge of computer programming languages, this book emphasizes Python syntax and methodologies. The text is divided into three complete sections; the first provides an explanation of general Python programming, the second includes a detailed discussion of the Python tools typically used in bioinformatics including clustering, associative memories, and mathematical analysis techniques, and the third section demonstrates how these tools are implemented through numerous applications.

Book Information

Average Customer Review: 4.5 out of 5 stars   5 customer reviews

Best Sellers Rank: #333,432 in Books (See Top 100 in Books)   #89 in Books > Computers & Technology > Computer Science > Bioinformatics   #345 in Books > Computers & Technology > Programming > Languages & Tools > Python   #429 in Books > Engineering & Transportation > Engineering > Bioengineering > Biochemistry

Customer Reviews

Bioinformatics is a growing field that attracts researchers from many different backgrounds who are unfamiliar with the algorithms commonly used in the field. Python for Bioinformatics provides a clear introduction to the Python programming language and instructs beginners on the development of simple programming exercises . Ideal for those with some knowledge of computer programming languages, this book emphasizes Python syntax and methodologies. The text is divided into three complete sections; the first provides an explanation of general Python programming, the second includes a detailed discussion of the Python tools typically used in bioinformatics including

clustering, associative memories, and mathematical analysis techniques, and the third section demonstrates how these tools are implemented through numerous applications.

The Author assumes a minimal background in bioinformatics, at least you must know what the field is about, a little of biology and have some ideas of programming (even better if you know Python). You only need to know little high school calculus and some algebra.The idea of the book is to teach algorithms that are useful for real bioinformatic applications, with the hope that you will be creating you own algorithms or applications in the future. Is not a book to learn BioPython (the preface clearly states that and explains why the skills learned in this book an BioPython could be used in a complementary fashion).The book uses Python 2, not Python 3. This is not a drawback as some people want to think, Python 2 is going to be the "standard" python for at least few year more and many (but not all) of the features of Python 3 are already present in Python 2.7. Even more important the book relies heavily in the NumPy library (as almost all scientific python programming) and NumPy is not, yet, compatible with Python 3, hence using Python 3 in a book like this will be, at least, non-sense.The only problem is that sometimes with some topics the author does not take too much time to explain the applications of some ideas, for example in the chapter on Hidden Markov Model (HMM) the Author just explain how to program different HMM implementations. Probably this is a mismatch between my background and the author's (I am closer to the a structural-biologist/biophysics) and some concepts are not used in the exactly same way in different scientific branchs, nothing that not can be solved by reading a Wikipedia entry.You should buy this book if you want to learn to develop bioinformatics solutions.

To be honest, I bought this book before I realized that what was out there for bioinformatics. I started a new job, and I knew Python, but I didn't know much about bioinformatics. I was a little disappointed that this book merely references biopython, and doesn't utilize it or show people how to use it. Why not use the tools that are available? In a classroom setting, I guess I can understand why you would want students to learn from the ground up, but this book is essentially teaching people Python in a bioinformatics way. For example, why does the book show how to parse fasta files in Chapter 6. This is merely a lesson in file parsing - something you should know if you understand Python, and why show it if biopython already does this for you.If you don't know much about Python or Bioinformatics, then this book is probably for you. If you have previous Python experience, I would skip this book.

I found it great reading

The author is a well-liked professor at George Mason University, and he has been teaching bioinformatics programming from beginning to advanced for several years. This book is formed somewhat like his lectures for those classes. He assumes you have a background in bioinformatics and that you already know some Python. From there he goes on to show you many of the problems you may be faced with in bioinformatics coded in Python. He actually says that he is trying to answer the question most commonly asked by his students - "How do I put what you just taught into code?".If you need to a good book on bioinformatics algorithms that is language agnostic may I suggestÂ An Introduction to Bioinformatics Algorithms (Computational Molecular Biology)Â as well asÂ Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology. The latter book is especially good for computer science students seeking bioinformatics knowledge. Let me also point out that this book is of use for people seeking Python solutions to non-bioinformatics problems. Since much of bioinformatics has to do with dealing with strings, trees, and statistical analysis of data, students of subjects other than biology can find uses for this book.Do note that the book's one great problem is that it is using Python 2 not Python 3. It is the fault of the designers of Python that most everything written for Python 2 becomes broken in a Python 3 interpreter rather than the fault of this author, yet the problem remains. Fortunately, Python looks enough like pseudocode that you can probably do any translations necessary without too much hair-pulling.

Python isn't as popular as some other languages amongst bioinformaticans , but it is probably gaining acceptance and this book is a result of it. The author is a practising bioinformatician. This is a good book. It discusses all the mathematical concepts that bioinformaticians usually use, and how they can be implemented in python. It requires, as the author himself says, a fairly good knowledge of mathematics and basic molecular biology. In my opinion, it also requires a good familiarity with the python language. There is a very small introduction to it in the first chapter but beginners will need more exposure to the language than that. Since I can code in python, and I needed a book that jumped straight into the bioinformatics part, I like it.

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