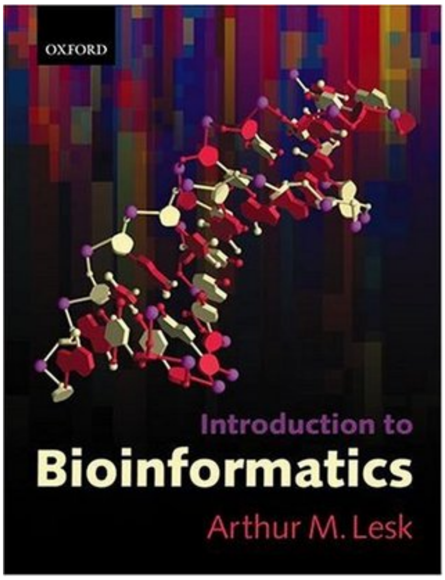

Introduction to Bioinformatics

Arthur M. Lesk

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Introduction to Bioinformatics by Arthur Lesk is a timely and much-needed textbook which provides an accessible and thorough introduction to a subject which is becoming a fundamental part of biological science today. As a pioneer of the use of bioinformatics techniques in research, Dr Lesk brings unrivalled experience and expertise to the study of this field. The aim of the book is to generate an understanding of the biological background of bioinformatics, and to integrate this with an introduction to the use of computational skills. Without describing computer science or sophisticated programming skills in detail, the book supports and encourages the application of the many powerful computational tools of bioinformatics in a way that is both relevant to and stimulating for the reader.
The book contains numerous problems and innovative Weblems (for Web-based Problems) to encourage students to engage with the subject and with the accompanying web site and to develop a working understanding and appreciation of the power of bioinformatics as a research tool.
Web site www.oup.co.uk/best.textbooks/biochemi...

Introduction to Bioinformatics Details

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Genre : Science, Biology, Reference, Chemistry, Mathematics, Computer Science, Nonfiction

From Reader Review Introduction to Bioinformatics for online ebook

Tiffany says

Not the best bioinformatics textbook I've seen ... Mount is better. But not bad, and actually has quite a bit of Perl code in it.

Twitter-Kun says

Pretty good intro. Some problems with the layout were quite annoying though

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Eric 'siggy' says

Lesk's introduction is an excellent guide for the newcomer to the world of large-scale genomic data. It is my opinion that you can end your search here for an entry point to the modern field of bioinformatics. It's organized around tools of the trade rather than grandiose theory (systems biology discussions left off till the last chapter), and will serve better as a introduction for undergraduates or researchers new to the field than a reference book for experts. It's biggest perk is the lucidness of discussion and readability.

As best I can tell, the target audience is undergraduate biology students who have basic familiarity with computer programming. Virtually no mathematical sophistication is required -- there is not a proof in sight, and complex mathematical topics like Hidden Markov Models and Monte Carlo algorithms are explained in an unintimidating, intuitive manner. Computer science knowledge such as graph theory, dynamic programming, and computational complexity are introduced minimally and only when they are needed.

Biological concepts are also sufficiently explained, except for perhaps a term here and there, and as a computer scientist I found the book a cinch to read.

Lesk's writing style is lucid and motivated. You know not only what you're learning, but why you're learning it and what you can do with it. Therefore, the book is self-contained and is excellent for self-study.

The first half of the book (Chapter 1-4) are a high-level overview, and a practical summary of existing databases of genetic and proteomic data. This serves an excellent guide for those who A) need to become familiar with the websites that "everybody" in the field knows about, or B) are eager to get their paws on sequence data and start playing! Chapter 3 even gives a (very) brief introduction to data mining and natural language processing for extracting information from the literature.

Chapters 5-7 are the meat of the matter. Sequence alignment (chapter 5) is "THE basic tool of bioinformatics" (p. 243), and is what much of the technical material is organized around. Dotplots, single and multiple sequence alignment, profiling, BLAST, PSI-BLAST, Hidden Markov Models, and phylogenetic trees are all discussed and situated so that the read knows the advantages and disadvantages of each tool, and their limitations used to motivated future chapters on protein structure.

Chapter 6 covers protein folding, structure prediction, classification, and function prediction, as well as applications to drug discovery.

Chapter 7 ends the book with a more theoretical, big-picture discussion of systems biology, information theory, and regulatory networks.

Overall, I think this book is great. It will give you a solid, if low-resolution understanding of the field, and the writing style ensures that you have a genuine understanding of the tools' relationship to scientific questions. The book is full of practical tips like "Visual examination of multiple sequence alignment tables is one of the most profitable activities that a molecular biologist can undertake away from the lab bench. Don't even THINK about not displaying them with different colors for amino acids of different physiochemical type" (p. 271). He also is careful to emphasize difficulties in, for instance, inferring homology from sequence similarity, and in making assumptions about mutation rate. And if you are a biologist who doesn't need more than a basic understanding of the most effective tools, maybe this is sufficient.

Perhaps best of all, you can actually *read* a book like this from cover to cover! And you will actually *remember* what you read!

That said, as a computer scientist with a math degree under my belt, I did miss the presence of rigorous mathematics. The academic field of bioinformatics is much more technical than this introduction-for-mathophobes would imply, as other books like Waterman's (now outdated) Introduction to Computational Biology: Maps, Sequences and Genomes (Chapman & Hall/CRC Interdisciplinary Statistics) makes painfully clear. Then again, that's probably why I didn't ever finish reading Waterman!

That said, I should point out that I was never bored with Lesk's description of algorithms.

Tim Verstraete says

Find it a fascinating topic and it appeared that the book was written in a very accessible style and content. some things were not always as easy explained but when then looking on the internet or using the links mentioned in the book you could always connect all the info and understand what was being said. next time I want a book on this topic I will definitely check if the author has written something about it.