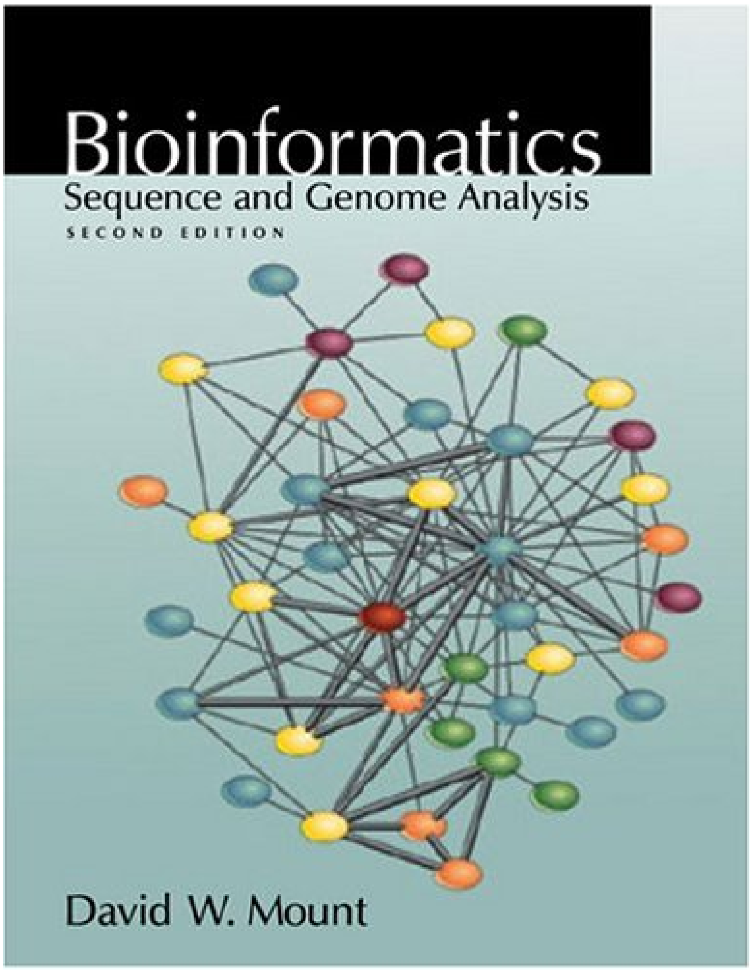
Bioinformatics: Sequence and Genome Analysis

David Mount



#457909 in Books Cold Spring Harbor Laboratory Press 2004-08-16Ingredients: Example IngredientsOriginal language:EnglishPDF # 1 8.30 x 1.20 x 11.00l, 4.40 #File Name: 0879697121692 pages | File size: 63.Mb

David Mount : Bioinformatics: Sequence and Genome Analysis before purchasing it in order to gage whether or not it would be worth my time, and all praised Bioinformatics: Sequence and Genome Analysis:

1 of 1 people found the following review helpful. Good in placesBy HThis is an interesting book! It is really good in places, for example the explanation of established alignment techniques. It is deficient in other areas such as post primary protein folding.0 of 1 people found the following review helpful. Very helpfulBy Pierre El Capitan de Castanets EnimigoWhen I was discovered as stowaway on Craig Venter's boat (long story), he put me to work. Well I had a choice of being a man of comfort or contribute to the research. I chose the former initally but I was better at the latter. This book really helps you get up to speed quickly and become a contribututor. Bayesian tree FTW!!!9 of 9 people found the following review helpful. Don't waste your timeBy Joseph A KnapkaI'm a graduate student in bioinformatics with an extensive background in software development. I am currently taking a class that uses this book

as its primary text. I will receive an A for the class, but this text was completely unhelpful in achieving that goal.This book is extremely frustrating. First, it has a lot of editing errors, some of which are critical to the descriptions of computational methods. This is really unacceptable in a second edition!More to the point, bioinformatics is fundamentally a computational pursuit, and discussion of the pertinent algorithms is inescapable. The author spends a great deal of text describing algorithms, in excruciating detail, in English. This is... I can't even describe how bad an idea this is. It can take several pages of text to describe an algorithm that could be succinctly coded in 100 lines of Python, which makes the text unnecessarily lengthy. Furthermore, the author's English descriptions of the algorithms are often ambiguous or misleading (sometimes due to the above-mentioned typographical errors, and sometimes due to the fact that English is much more ambiguous than any programming language). I cite specifically the description of the "expectation maximization" algorithm for sequence motif discovery in chapter 5, but that is only one of many examples.The result is that the author's descriptions are sufficiently detailed to be confusing, but NOT sufficiently clear to allow the algorithms to be implemented correctly. This approach does not serve students well: those who haven't yet been exposed to programming end up merely mystified, while those of us who have programming backgrounds end up dreadfully confused, or simply frustrated enough to go out and write 1-star reviews on .If you are an instructor looking for a bioinformatics text, please do your students a favor and choose a different one.

As more species' genomes are sequenced, computational analysis of these data has become increasingly important. The second, entirely updated edition of this widely praised textbook provides a comprehensive and critical examination of the computational methods needed for analyzing DNA, RNA, and protein data, as well as genomes. The book has been rewritten to make it more accessible to a wider audience, including advanced undergraduate and graduate students. New features include chapter guides and explanatory information panels and glossary terms. New chapters in this second edition cover statistical analysis of sequence alignments, computer programming for bioinformatics, and data management and mining. Practically oriented problems at the ends of chapters enhance the value of the book as a teaching resource. The book also serves as an essential reference for professionals in molecular biology, pharmaceutical, and genome laboratories.

This second edition is a qualified success. Every chapter in the second edition appears to be rewritten extensively, and three useful new chapters have been added. As a result, the new edition tops out at 692 pages, and many of the problems with the first edition have been rectified... Overall, this second edition is a considerable improvement over the first and will be popular on the desks of many scientists as well as many students....If you find that you need a reference that covers the entire breadth of bioinformatics, you need to buy this book. - DDLClinical ChemistryThe second edition of Bioinformatics: Sequence and Genome Analysis is an excellent textbook for bioinformatics introductory courses for both life sciences and computer science students, and a good reference for current problems in the field and the tools and methods employed in their solution. - Briefings in Bioinformatics