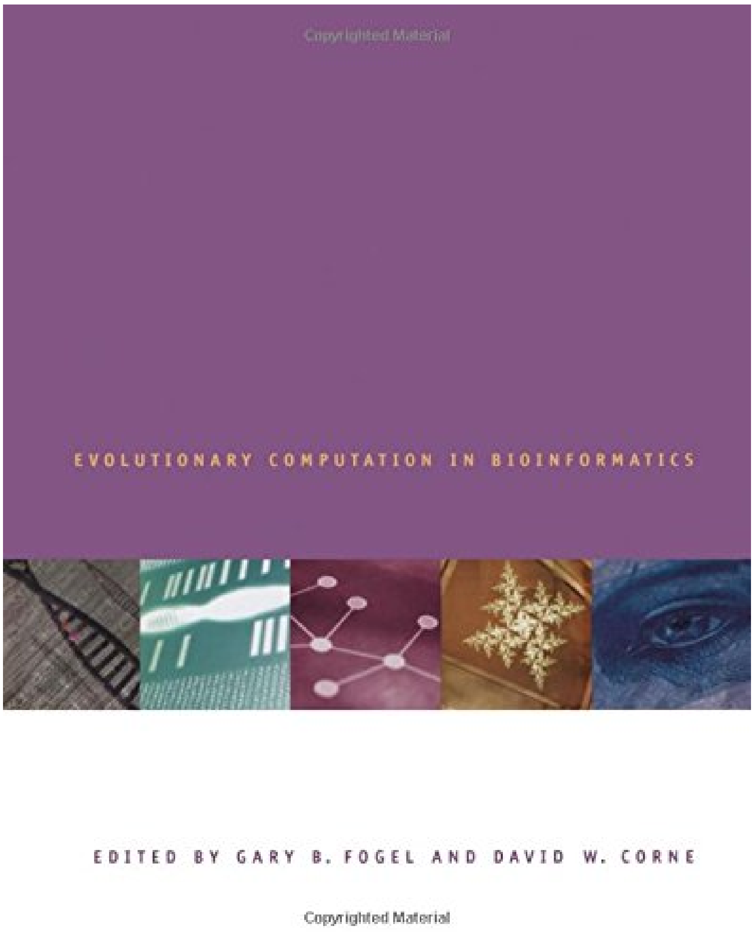
(Mobile library) Evolutionary Computation in Bioinformatics (The Morgan Kaufmann Series in Artificial Intelligence)

Evolutionary Computation in Bioinformatics (The Morgan Kaufmann Series in Artificial Intelligence)

From Brand: Morgan Kaufmann



#3967552 in Books Morgan Kaufmann 2002-09-30Ingredients: Example IngredientsOriginal language:EnglishPDF # 1 9.50 x 7.50 x 1.00l, 2.01 #File Name: 1558607978393 pages | File size: 44.Mb

From Brand: Morgan Kaufmann : Evolutionary Computation in Bioinformatics (The Morgan Kaufmann Series in Artificial Intelligence) before purchasing it in order to gage whether or not it would be worth my time, and all praised Evolutionary Computation in Bioinformatics (The Morgan Kaufmann Series in Artificial Intelligence):

14 of 17 people found the following review helpful. A good literature surveyBy Dr. Lee D. CarlsonThe subject of this book would seem a natural one, given the evolutionary paradigm in biology. Genetic algorithms and evolutionary programming have now found use in many different fields such as physics, financial engineering, network modeling, and computational radiology, to name a few. This use will no doubt continue as computer processing power increases in the future. Although genetic/evolutionary approaches are still much more effective from a computational point of view than strict combinatorial ones, they are still very time intensive, and for many problems have yet to compete with

ordinary Monte Carlo techniques. This book gives a brief overview of how evolutionary algorithms are used in bioinformatics, with emphasis on genetic sequence alignment and protein folding. The book does not offer in-depth discussion on these algorithms, but does give references where more information can be obtained. Therefore the book could be described as a literature survey, at least for the chapters that I read, which did not include those on protein folding. The book is written for the computer scientist who wants to move into bioinformatics, and the biologist, who needs more background in these types of algorithms. Therefore, the editors of the book include two introductory chapters, one introducing bioinformatics for computer scientists, the other an introduction to evolutionary computation for biologists. The latter is more detailed, and the authors introduce the biologist to some of the elementary aspects of evolutionary computation. One interesting, but too short discussion is on the "No Free Lunch Theorem", which implies that evolutionary programs are not in any sense "universal", in that the choice of such a program will depend on the problem at hand, and in fact there may be many such programs for the problem, each with their own performance properties. The theorem is not proved in this book, but references to the proof are given. However, the proof involves a level of mathematics that a biologist would probably not have knowledge of, and so this reference would not be accessible to such a reader. In addition, the theorem has generated a lot of controversy, but the authors do point this out. The authors also discuss effectively the difference between the analytical and heuristic approaches to sequence alignment, setting the stage for later chapters in the book. The problem of local search algorithms getting "trapped" in local minima is also given a very intuitive and understandable treatment by the authors. The book also includes a discussion on the "DNA sequence reconstruction problem". Algorithms for dealing with this problem are recommended and the the problem is presented as one in integer programming. The authors present a hybrid evolutionary algorithm for dealing with this problem. They characterize this algorithm as being hybrid since it does make use of "crossover" operators and a heuristic "greedy-improvement" method. The discussion of this algorithm is only brief, but references are given. However the main reference is not yet available as it is very recent and in press, and, although the authors do include a fairly lengthy discussion of computational experiments, without a detailed description of the algorithm or source code, their results cannot be checked or validated. The contrast between optimization theory and evolutionary algorithms is a common theme in the book, with emphasis on the use of evolutionary algorithms to design scoring schemes for sequence alignment where optimization issues can be ignored. The difference between the optimal alignment obtained by various mathematical techniques and the correct (biological) alignment is carefully pointed out. Thus one must be able to tell whether an objective function is relevant from a biological standpoint. In chapter 5 of the book for example, the author introduces an alignment algorithm based on a combination of simulated annealing (SA), and genetic algorithms (GA), called appropriately SAGA. This chapter is the most helpful one in the book, for the author gives pseudocode for this algorithm, with Web links given for obtaining the source code. This allows the interested reader to study the efficacy of the SAGA algorithm in doing muliple sequence alignment. The use of simulated evolution to find optimal neural networks for identifying coding regions is discussed in chapter 9 of the book. The use of genetic algorithms to assign the weights in a neural network is well-known. The authors point out a further advantage in their use, namely that evolutionary neural networks can adapt to unexpected inputs on their own, and thus do not require any intervention on the part of the user. References are given that elaborate on the power of this approach. Readers who have worked with neural networks will understand fully the need for improvements over back-propagation and the need for automatic topology selection. The authors do not show however that the function-approximation ability of neural networks, so important from both a mathematical and applications standpoint, is improved by their approach.5 of 8 people found the following review helpful. Significant Addition to BiocomputingBy A CustomerI like this book. Bioinformatics is a ripe area for applying evolutionary algorithms and the book provides a good overview of many different applications. Some chapters are more polished than others, but that's to be expected. The editors do an excellent job of introducing both bioinformatics and evolutionary computation to their respective audiences. I can't think of another book that makes such an effort to integrate the two communities.I see another reviewer gave the book 3 stars. I've no idea why. The book is excellent, and has encouraged me to take a look at other papers in this area.

Bioinformatics has never been as popular as it is today. The genomics revolution is generating so much data in such rapid succession that it has become difficult for biologists to decipher. In particular, there are many problems in biology that are too large to solve with standard methods. Researchers in evolutionary computation (EC) have turned their attention to these problems. They understand the power of EC to rapidly search very large and complex spaces and return reasonable solutions. While these researchers are increasingly interested in problems from the biological sciences, EC and its problem-solving capabilities are generally not yet understood or applied in the biology community.This book offers a definitive resource to bridge the computer science and biology communities. Gary Fogel and David Corne, well-known representatives of these fields, introduce biology and bioinformatics to computer scientists, and evolutionary computation to biologists and computer scientists unfamiliar with these techniques. The fourteen chapters that follow are written by leading computer scientists and biologists who examine successful applications of evolutionary computation to various problems in the biological sciences. * Describes applications of

EC to bioinformatics in a wide variety of areas including DNA sequencing, protein folding, gene and protein classification, drug targeting, drug design, data mining of biological databases, and biodata visualization.* Offers industrial and academic researchers in computer science, biology, and bioinformatics an important resource for applying evolutionary computation.* Includes a detailed appendix of biological data resources.

"This is a fine book that clearly discusses the applications of evolutionary computation techniques to a variety of different areas. It covers most topics a bioinformatician will find interesting."--Santosh Mishra, Eli LillyFrom the Back Cover"This is a fine book that clearly discusses the applications of evolutionary computation techniques to a variety of different areas. It covers most topics a bioinformatician will find interesting."--Santosh Mishra, Eli LillyBioinformatics has never been as popular as it is today. The genomics revolution is generating so much data in such rapid succession that it has become difficult for biologists to decipher. In particular, there are many problems in biology that are too large to solve with standard methods. Researchers in evolutionary computation (EC) have turned their attention to these problems. They understand the power of EC to rapidly search very large and complex spaces and return reasonable solutions. While these researchers are increasingly interested in problems from the biological sciences, EC and its problem-solving capabilities are generally not yet understood or applied in the biology community.This book offers a definitive resource to bridge the computer science and biology communities. Gary Fogel and David Corne, well-known representatives of these fields, introduce biology and bioinformatics to computer scientists, and evolutionary computation to biologists and computer scientists unfamiliar with these techniques. The fourteen chapters that follow are written by leading computer scientists and biologists who examine successful applications of evolutionary computation to various problems in the biological sciences.FeaturesDescribes applications of EC to bioinformatics in a wide variety of areas including DNA sequencing, protein folding, gene and protein classification, drug targeting, drug design, data mining of biological databases, and biodata visualization.Offers industrial and academic researchers in computer science, biology, and bioinformatics an important resource for applying evolutionary computation.Includes a detailed appendix of biological data resources.About the AuthorGary B. Fogel is a senior staff scientist at Natural Selection, Inc., in La Jolla, California.His research interests include the application of evolutionary computationto problems in the biomedical sciences and evolutionary biology. He received aB.A. in biology from the University of California, Santa Cruz, in 1991 and a Ph.D.in biology from the University of California, Los Angeles, in 1998 with a focus onevolutionary biology. While at UCLA, Dr. Fogel was a fellow of the Center for theStudy of Evolution and the Origin of Life and earned several teaching and researchawards. He is a current member of the International Society for the Studyof the Origin of Life, the Society for the Study of Evolution, IEEE, Sigma Xi, andthe Evolutionary Programming Society. He currently serves as an associate editorfor IEEE Transactions on Evolutionary Computation and BioSystems and was a technicalco-chair for the recent 2000 Congress on Evolutionary Computation. He is alsoa senior staff scientist at the Center for Excellence in Evolutionary Computation,a nonprofit organization that promotes scientific research and development ofevolutionary algorithms.David W. Corne is a reader in evolutionary computation (EC) at the University of Reading. His early research on evolutionary timetabling (with Peter Ross) resultedin the first freely available and successful EC-based general timetabling programfor educational and other institutions. His later EC work has been in suchareas as DNA pattern mining, promoter modeling, phylogeny, scheduling, layoutdesign, telecommunications, data mining, algorithm comparison issues, and multiobjectiveoptimization. Recent funded work (with Douglas Kell) applies EC directlyto the in vivo optimization of proteins. He is an associate editor of the IEEETransactions on Evolutionary Computation and a founding co-editor of the Journal ofScheduling. Dr. Corne is on the editorial boards of Applied Soft Computing and the InternationalJournal of Systems Science, and he serves on a host of international conferenceprogram committees. Other recent edited books include New Ideas in Optimization(with Marco Dorigo and Fred Glover), Telecommunications Optimization: Heuristic andAdaptive Techniques (with Martin Oates and George Smith), and Creative EvolutionarySystems (with Peter Bentley). He is also a director of Evosolve (United Kingdomregistered charity number 1086384, with Jeanne Lynch-Aird, Paul Marrow, GlenysOates, and Martin Oates), a nonprofit organization that promotes the use of advancedcomputation technologies to enhance the quality of life.