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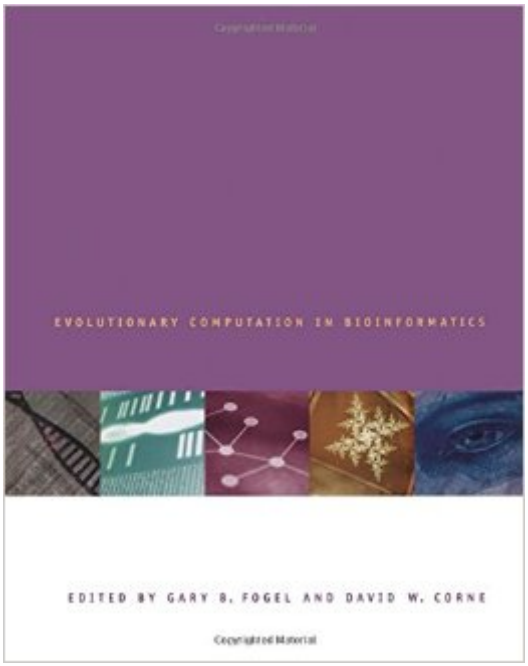
Evolutionary Computation In Bioinformatics (The Morgan Kaufmann Series In Artificial Intelligence)



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Synopsis

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.

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Bioinformatics

Customer Reviews

The 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.

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