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

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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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