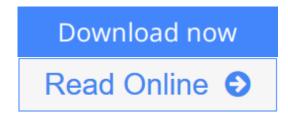


### **Bioinformatics: Problem Solving Paradigms**

By Volker Sperschneider



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This book presents fundamental principles for problem analysis and algorithm design used in bioinformatics. It includes numerous cause studies from the main fields of bioinformatics, from sequencing and mapping to pseudo-knot detection.



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Review

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"Computer science (CS) and molecular biology meet in the bioinformatics field. ... this book presents a CS perspective of the problems involved and considers some of the fundamental data structures and algorithms required for solving them. ... This book is appropriate for biologists who seek an overview of ways in which a computer scientist might approach the problems involved." (Jeffrey Putnam, ACM Computing Reviews, May, 2009)

From the Back Cover

There are fundamental principles for problem analysis and algorithm design that are continuously used in bioinformatics. This book concentrates on a clear presentation of these principles, presenting them in a self-contained, mathematically clear and precise manner, and illustrating them with lots of case studies from main fields of bioinformatics (e.g. sequencing and mapping, string storage and manipulation, pattern matching, alignment, gene identification, genome rearrangement, structure prediction, regulatory networks, pseudoknot detection). Emphasis is laid on algorithmic "pearls" of bioinformatics, showing that things may get rather simple when taking a proper view into them. The book closes with a thorough bibliography, ranging from classic research results to very recent findings, providing many pointers for future research. Overall, this volume is ideally suited for a senior undergraduate or graduate course on bioinformatics, with a strong focus on its mathematical and computer science background.

This book highlights basic paradigms of problem analysis and algorithm design in the context of core bioinformatics problems. Mathematically demanding themes are put across to the reader by properly chosen representations with the aid of lots of illustrations.

(Prof. Dr. Amitava Datta, UWA, Perth, Australia)

Written by a theoretical computer scientist, the book perfectly complements standard textbooks from the point of view of problem solving methods continuously applied in bioinformatics.

(Prof. Dr. Georg Fuellen, Univ. Greifswald, Germany)

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