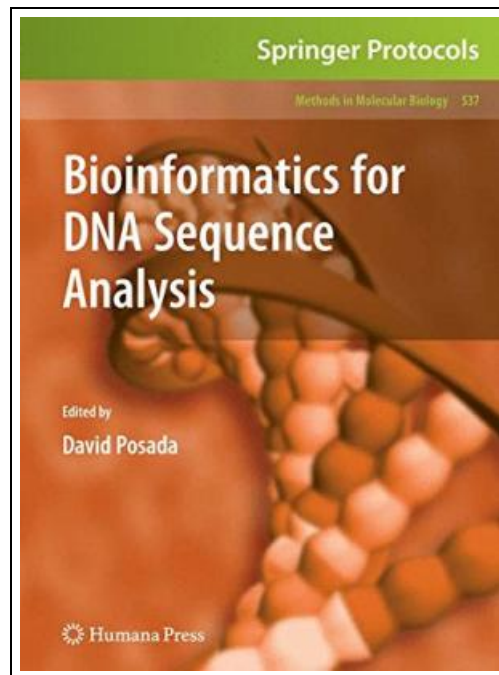


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Humana Press Inc., United States, 2009. Hardback. Condition: New. 2009 ed.. Language: English . Brand New Book \*\*\*\*\* Print on Demand \*\*\*\*\*. The recent accumulation of information from genomes, including their sequences, has resulted not only in new attempts to answer old questions and solve long-standing issues in biology, but also in the formulation of novel hypotheses that arise precisely from this wealth of data. The storage, processing, description, transmission, connection, and analysis of these data has prompted bioinformatics to become one of the most relevant applied sciences for this new century, walking hand-in-hand with modern molecular biology and clearly impacting areas like biotechnology and biomedicine. Bioinformatics skills have now become essential for many scientists working with DNA sequences. With this idea in mind, this book aims to provide practical guidance and troubleshooting advice for the computational analysis of DNA sequences, covering a range of issues and methods that unveil the multitude of applications and relevance that Bioinformatics has today. The analysis of protein sequences has been purposely excluded to gain focus. Individual book chapters are oriented toward the description of the use of specific bioinformatic tools, accompanied by practical examples, a discussion on the interpretation of results, and specific comments on strengths and limitations of the methods and tools. In a sense, chapters could be seen as enriched task-oriented manuals that will direct the reader in completing specific bioinformatics analyses. The target audience for this book is biochemists, and molecular and evolutionary biologists that want to learn how to analyze DNA sequences in a simple but meaningful fashion. Readers do not need a special background in statistics, mathematics, or computer science, just a basic knowledge of molecular biology and genetics. All the tools described in the book are free and all of them can be downloaded or accessed through the web. Most chapters could be used for practical advanced undergraduate or graduate-level courses in bioinformatics and molecular evolution.

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