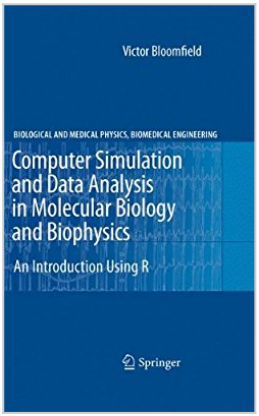

Computer Simulation and Data Analysis in Molecular Biology and Biophysics: An Introduction Using R (Biological and Medical Physics, Biomedical Engineering)

By Victor Bloomfield

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This book provides an introduction to two important aspects of modern biochistry, molecular biology, and biophysics: computer simulation and data analysis. My aim is to introduce the tools that will enable students to learn and use some fdamental methods to construct quantitative models of biological mechanisms, both deterministicandwithsomeelementsofrandomness;tolearnhowconceptsofprability can help to understand important features of DNA sequences; and to apply a useful set of statistical methods to analysis of experimental data. The availability of very capable but inexpensive personal computers and software makes it possible to do such work at a much higher level, but in a much easier way, than ever before.
TheExecutiveSummaryofthein?uential2003reportfromtheNationalAcademy of Sciences, “BIO 2010: Transforming Undergraduate Education for Future - search Biologists” [12], begins The interplay of the recombinant DNA, instrumentation, and digital revolutions has p- foundly transformed biological research. The con?uence of these three innovations has led to important discoveries, such as the mapping of the human genome. How biologists design, perform, and analyze experiments is changing swiftly. Biological concepts and models are becoming more quantitative, and biological research has become critically dependent on concepts and methods drawn from other scienti?c disciplines. The connections between the biological sciences and the physical sciences, mathematics, and computer science are rapidly becoming deeper and more extensive.

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Editorial Review

Review
From the reviews: “This book targets biochemistry and molecular biophysics students who have prior knowledge of a few subjects, including mathematics, statistics, and modeling, and possess very basic programming skills. Examples and illustrations are ample throughout the text, and the writing style is plain and efficient. … this book mostly appropriate for students or researchers who have prior exposure to the related subjects. Summing Up: Recommended. Upper-division undergraduates through researchers/faculty.” (D. Papamichail, Choice, Vol. 47 (5), January, 2010)

From the Back Cover

This book provides an introduction, suitable for advanced undergraduates and beginning graduate students, to two important aspects of molecular biology and biophysics: computer simulation and data analysis. It introduces tools to enable readers to learn and use fundamental methods for constructing quantitative models of biological mechanisms, both deterministic and with some elements of randomness, including complex reaction equilibria and kinetics, population models, and regulation of metabolism and development; to understand how concepts of probability can help in explaining important features of DNA sequences; and to apply a useful set of statistical methods to analysis of experimental data from spectroscopic, genomic, and proteomic sources.

These quantitative tools are implemented using the free, open source software program R. R provides an excellent environment for general numerical and statistical computing and graphics, with capabilities similar to Matlab®. Since R is increasingly used in bioinformatics applications such as the BioConductor project, it can serve students as their basic quantitative, statistical, and graphics tool as they develop their careers

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