replaced to advantage by others on areas of glycochemistry and glycobiology that have not been discussed at all. For example, I would have liked to find a separate contribution on carbohydrate analysis, as many of the results described would not have been possible without the remarkable developments that have occurred in NMR spectroscopy and mass spectrometry.

For readers who are not very familiar with glycochemistry the book offers a good way of quickly gaining a sound appreciation of the many different aspects of the field. As already mentioned, the amount of experimental detail in some chapters is probably too much for that purpose, but despite that I recommend the book to those readers, and therefore I answer yes to the above question. On the other hand, of course, the book does not go far enough for specialist readers. Their general needs are better served by other (mainly multivolume) works that are already available. Also, in cases where a specific area of development is described in a short article in this book, the specialist reader will instead go to a relevant monograph where the topic is treated more thoroughly. Therefore, for those readers the answer to the question must be no.

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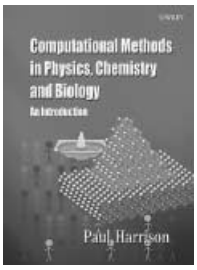
Computational Methods in Physics, Chemistry and Biology. By *Paul Harrison.* John Wiley & Sons, Inc., New York 2001. 201 pp., softcover £ 24.95.—ISBN 0-471-49563-8



Numerical experimentation, that is, the computational modeling of physical phenomena, has become established as a third pillar, next to laboratory experiment and theory, in the investigation of the natural world. The present book attempts to provide undergraduate students in physics, chemistry, biology, and related areas with the basic techniques underlying many of the computational models used in these numerical experiments. The nine chapters cover topics such as numerical and approximate solutions for the Schrödinger equation (e.g., perturbation methods and the variational principle), technical applications such as matrix methods and the use of basis sets to expand state functions, deterministic and stochastic simulation techniques, percolation theory, evolutionary methods and genetic algorithms, and finally molecular dynamics.

The fundamental physics which the various numerical methods attempt to model is introduced in a very brief and often superficial manner. Constructs such as the Kronecker δ or divergence are used with no further explanation. Without solid prior knowledge the reader will certainly have difficulties in understanding this important background information. The numerical techniques themselves are explained in more detail, and are accompanied by examples of the use of the corresponding algorithms in computer programs written in C (one example in Fortan is also included). All chapters end with a summary and a set of tasks and projects. The source code examples, as well as hints and outline answers to the problems, are available through the Internet from the author's website.

As the title suggests, the author defines the audience of this book as computational physicists, chemists, mathematicians, and biologists. However, the examples and the overall style of treatment are strongly biased towards physics. Chemistry and biology related aspects are only very rarely touched upon. This becomes evident, for example, when Monte Carlo simulations are introduced with the words: "Monte Carlo simulations are usually associated with electron scattering processes in semiconductors". While this mirrors the author's background in quantum electronics and semiconductor physics, it completely neglects the important role of these techniques in other areas. For example, Monte Carlo methods have important applications in chemistry and are used for molecular mechanics simulations, an aspect which is not mentioned at all in the book. Similarly, the chapter on molecular dynamics focuses almost exclusively on applications in solid-state physics. The great importance of these methods in many areas of chemistry is noted only very briefly, even though molecular dynamics simulations are nowadays frequently used in many academic and industrial laboratories for the prediction of properties of reagents, potential new drugs, and other chemicals. Moreover, some of the information regarding chemical aspects is even incorrect, for example in Figure 8.12 where C–H and H–H bonds are shown as being weaker than a C–C single bond.

To sum up, this book is certainly of value for students interested in computational physics. On the other hand, chemists, and probably also biologists, will find it less suitable because much physical background knowledge is required, and direct ties to applications in these disciplines are missing.

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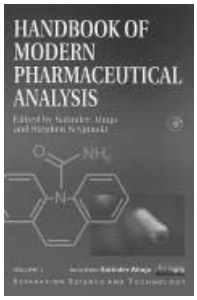
Handbook of Modern Pharmaceutical Analysis. By *Satinder Ahuja* and *Stephen Scypinski*. Academic Press, San Diego 2001. 566 pp., hardcover $ 124.95.—ISBN 0-12-045555-2



Pharmaceutical analysis can be considered from several aspects: the analytical methods that are available, the areas of application, and the regulatory requirements. The structure of a book on pharmaceutical analysis is determined essentially by the kinds of readers for whom it is intended. In the case of the *Handbook of Modern Pharmaceutical Analysis* those readers are analysts working in industry. Accordingly, the book places the areas of application and the regulatory aspects in the foreground, whereas the reader is assumed to be already largely familiar with the analytical methods.

After an introductory chapter giving a good overview of the main areas of

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