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Book Review

Computational Chemistry Workbook: Learning through Examples. By Thomas Heine, Jan-Ole Joswig, and Achim Gelessus.. Wiley-VCH, Weinheim, Germany. 2009. xvii + 232 pp. 17 × 24 cm. ISBN 978-3-527-32442-2. $65.00.

This is a welcome book, providing computer exercises to students taking a course in theoretical or computational chemistry. The book will help students gain a better understanding of the corresponding material in lectures and textbooks. The exercises complement any of the well-known textbooks on computational chemistry and quantum chemistry that have been published in the past 20 years.

The book is organized into 16 chapters covering the following topics: putting molecules in the form that computer software can understand and process; describing diatomics with harmonic oscillator and Morse potentials; describing diatomics quantum mechanically; atomic orbitals; ionization potentials and electron affinities; Hückel molecular orbital theory; geometry optimization; electron spin; vibrational spectroscopy; thermochemistry; molecular dynamics; thermostats; simulated annealing. All the chapters are useful, and the last three are especially valuable because they cover material not found in other introductory workbooks. Each chapter clearly states its aim, the theoretical background, a worked example or two, a short set of problems for the students to perform, a summary, and finally the briefest of bibliographies.

A great attribute of the book is that it is self-contained. Software needed to work the examples is on the accompanying CD. The software is free for academics to use as provided with this book; no expensive commercial software packages need be purchased to use the book in a class. Most of the quantum chemical exercises are based on using the density functional theory program deMon of Prof. Dennis R. Salahub (University of Calgary, Canada), who also supplied the Foreword to the book. Other software on the CD includes a Linux operating system, Molden (molecular editor), Hückel (π-electron systems), CaGe (fullerenes), and Xmgrace and gnuplot (data analyses). In addition, the CD has character tables related to determining molecular symmetry.

Input data sets for deMon are shown so that all that the student has to do is add the atomic coordinates or internal molecular geometry (**Z**-matrix). The data sets for deMon have the program options, basis set, and other flags already set up for the student to run. The book gives only the barest of explanations of what these flags mean. The concept of basis sets is not explained, so to some extent the students will be using deMon as a black box. Likewise, density functional theory itself is beyond the purview of this book. The quantum chemical exercises could also be implemented for some of the other widely used programs such as Gaussian, ADF, and so on.

Most of the exercises deal with diatomic or small polyatomic molecules so that the students can perform the computer experiments in a reasonable time on their own laptop computers. No high-end computers are necessary. The exercise on Hückel theory involves annulenes and C_{76} fullerenes. The exercises in molecular dynamics are designed for implementation on a spreadsheet program, such as Excel. A spreadsheet program is not included on the CD, but most students will have Excel or other spreadsheet program on their laptops. Independent of the book, the student will have to know how to program formulas in a spreadsheet in order to be able to perform the exercises.

The CD should work on common Intel x86-compatible computers running Windows, Linux, or Macintosh operating system. The CD that came with the reviewer's copy of the book worked okay on a Macintosh, but was not readable on a couple of modern PCs with standard Windows setups. However, links to an image of the CD and the software are available at http://www.compchem.jacobs-university.de/workbook.html. The authors plan updates of this Web site.

The seven-page index will help students locate most of what they will seek. The computer programs on the CD are not indexed. The authors state that their intention was to minimize difficult mathematics, which they do for the most part. However, they introduce the mathematical terms erf, trace, and tensor without definition and without background. The book has a few minor scientific errors and some terminological and grammatical rough spots that could easily be fixed in a second edition. An instructor can spot these and help the students avoid confusion. The publisher composed the book with extra wide margins that are convenient for students who like to make notes. However, the composition occasionally compresses lines, so there is almost no space between the words. The equations in a couple chapters lack spaces between the terms, which makes them less easy to interpret.

The book will help instructors easily give students meaningful laboratory experiments or homework to be done with computers. Use of the workbook in courses on theoretical or computation chemistry is highly recommended.

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Lead Generation Approaches in Drug Discovery. Edited by Zoran Rankovic and Richard Morphy.. Wiley, Hoboken, NJ. 2010. xi + 295 pp. 16 × 24 cm. ISBN 978-0-470-25761-6. $99.95.

Although high throughput screening is a strategy for drug discovery that has been embraced by the pharmaceutical industry over the past 20 years or more, the way in which it is practiced has been refined significantly. That is the subject of this volume, which covers the major aspects of the process and points out the problems that are inherent in the system and how some of them have been overcome. There are nine chapters by authors from both industry and academia, and the chapter titles give a good idea of what is covered: Lead Discovery: The Process; High Throughput Screening Approach to Lead Discovery; In Silico Screening; Fragment-Based Lead Discovery; Design of Multitarget Ligands; De Novo Drug Design; Role of Natural Products in Drug Discovery; Early Screening for ADMET Properties; Role of Chemistry in Lead Discovery.

A few of the chapters deserve special mention. The first chapter gives a good overview of high throughput screening and points out that the idea of ever being able to synthesize and test all possible druglike molecules is "utterly and completely impossible". It has been estimated that the available chemical space is so vast that a collection of one molecule of each type would exceed the mass of the universe many times over. Therefore, as explained in the second chapter, one of the main problems in high throughput screening is to critically focus the library of compounds to be assayed. The last chapter will be of special interest to medicinal chemists, as it covers synthetic strategies with many structural flow sheets and cites specific case studies of hit-to-lead development.

Overall, this volume is well-written and it usually gives specific examples of the concepts covered. One annoying feature is the overuse of acronyms. Although they are often defined early in a chapter, there are so many that it is difficult to keep track of them. This problem can sometimes be rectified by consulting the index, which seems to be quite useful. Although most medicinal chemists use such terms as SAR, ADMET, and GPCR, other acronyms used throughout the book are more familiar to practitioners of HTS (high throughput screening).

This volume is recommended to chemists and biologists who wish to learn about the practice of high throughput screening and about the concepts involved in making the method a successful route to drug discovery. Some will view the idea of making and testing very large libraries of compounds (to generate millions of pieces of data) as exciting, like a treasure hunt. Others will take the view that too much of the effort seems wasted and that the art of a finely crafted synthetic scheme, usually associated with natural products synthesis, is lacking.

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The Biochemistry of Drug Metabolism: Conjugations, Consequences of Metabolism, Influencing Factors. Edited by Bernard Testa and Stephanie D. Krämer.. Verlag Helvetica Chimica Acta, Zurich, Switzerland, and Wiley-VCH, Weinheim, Germany. 2010. xiii + 588 pp. 17 × 24 cm. ISBN 3906390543. $75.00. Two-volume set: 950 pp. ISBN 3906390550. $130.00

This is Volume 2 of an excellent two-volume set with a unique but very effective presentation style, being a series of excellently designed color figures laid out as presentation formatted slides. Each figure is accompanied by text elaborating on each concept and providing links to the original literature. The work is extraordinarily detailed and comprehensive, yet presented in a clear and attractive manner. I recommend it for faculty and graduate student readership and to advanced industrial scientists. The authors are expert teachers and scientists in the field. This work represents a refinement of their extensive teaching materials into a single up-to-date package. As a metabolism scientist and instructor of introductory and advanced drug metabolism to pharmacy students and to biomedical sciences graduate students, I appreciate the expert combination of clarity and detail. Students will find the slides and notes an ideal accompaniment for independent study. Instructors and metabolism scientists will find that the text provides a vast, accurate, and up-to-date resource. The coverage includes the recent explosion of knowledge in the field of metabolism including genetic and molecular mechanisms that cause variation in metabolism of drugs, toxicants, carcinogens, and other exogenous compounds. The reference lists for each chapter are noteworthy for completeness and relevance, with many citations listing multiple sources so that readers can easily find the original research supporting each concept described. The material has also been published as individual articles available in electronic format (pdf) from the journal *Chemistry and Biodiversity*. However, I encourage all to purchase the two-volume set to have the complete package easily accessible in full color and high resolution.

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