Additions and Corrections

Theoretical Studies of Protium/Deuterium Fractionation Factors and Cooperative Hydrogen Bonding in Peptides [*J. Am. Chem. Soc.* **1995**, *117*, 9619−9624]. ARTHUR S. EDISON, FRANK WEINHOLD, AND JOHN L. MARKLEY*

Pages 9621−9622: Reference numbers 23 and 24 were repeated, leading to a two-number "slippage" for the final 12 references and footnotes.

Page 9623: The first monomer shown in Figure 2C should be labeled "AA-I."

Page 9624: In the acknowledgment, "Krevoy" should be "Kreevoy".

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Book Reviews

Advanced Computer-Assisted Techniques in Drug Discovery, Volume 3 (Methods and Principles in Medicinal Chemistry Series). Edited by Han van de Waterbeemd (Hoffman-LaRoche AG, Switzerland). VCH: New York. 1995. xx + 343 pp. DM168.00. ISBN 3-527-29248-9.

In the past 20 years, the art and science of drug design has changed immensely with computer-assisted molecular design exerting an ever-increasing influence. Indeed, some argue that computer-assisted molecular design is emerging as a biotechnology of the future. *Advanced Computer-Assisted Techniques in Drug Discovery* is Volume 3 in the series *Methods and Principles in Medicinal Chemistry* edited by the accomplished and experienced trio of R. Mannhold, P. Krogsgaard-Larsen, and H. Timmerman. All three volumes are dedicated to the application of specialized molecular modeling and computational tools to the analysis of complex pharmaceutical and medicinal chemistry data sets. Volume 1 focuses on the classical Hansch method of quantitative structure−activity relationship studies [QSAR]; Volume 2 considers the mature, well-established chemometric methods of molecular design and computer-assisted medicinal chemistry; Volume 3 concerns the newest emerging data analysis methods. Volume 1, and to a somewhat lesser extent Volume 2, is accessible to the bench chemist seeking tools to assist with the computer-aided unraveling of complex QSAR data sets. Volume 3, however, is designed for the specialist chemometrician performing applications at the cutting edge of the current technology; it is not designed for the medicinal or organic chemist looking for a ready-to-apply tool with which to understand experimental data.

Advanced Computer-Assisted Techniques in Drug Discovery is a well-compiled and -presented handbook of developing techniques in 3D-QSAR and advanced statistical analysis. It is a multiauthored text with contributions from 37 authors covering three continents. These authors come from a diversity of backgrounds, with 40% from the industrial sector and the remainder from either academic or government institutes. Despite this plethora of authors, any unevenness in presentation style has been minimized by excellent editing. At the beginning of each chapter there is a list of abbreviations and symbols which is useful for someone coming to terms with this "jargon-rich" area. All chapters are similarly organized, having an introduction, a well-organized and appropriately subtitled body, and then a brief series of cogent conclusions. The writing style is concise and informative. Figures are appropriate in number and content with high-quality reproduction. A number of excellent color figures have been included. A variety of worked examples have also been included. Unfortunately, many chapters have only 20−30 references with most of these being from 1990−1994. Referencing of the background basics for the methods being described is not as comprehensive as some readers may wish.

Advanced Computer-Assisted Techniques in Drug Discovery is divided into five sections. Section 1 is a brief, overview introduction. Section 2 focuses on the trendy, yet useful, three-dimensional QSAR methods including CoMFA (comparative molecular field analysis) and GOLPE (generating optimal linear partial least squares estimations). Section 3 explores the rational use of chemical and sequence databases using molecular similarity analysis, chemical structure database clustering, and phylogenetic clustering techniques. Section 4 is a nicely presented analysis of advanced statistical techniques with special emphasis on correspondence factorial analysis, single class discrimination, the fuzzy adaptive least squares algorithm, alternating conditional expectations, and the continuum regression algorithm. Finally, section 5 is a consideration of neural networks, expert systems, and other concepts from the field of artificial intelligence (AI) as future tools for drug design. This selection of topics provides a reasonably comprehensive survey of many important trends in computer-assisted drug discovery; the organization and presentation order of these topics is likewise logical. However, since the entire topic is covered in 330 pages, some areas are treated somewhat more superficially than others; it is at these points that one wishes that the reference citations were slightly more comprehensive. The mathematics are not extensive and are straightforward and easily understood. There are few errors, and these are minor. For example, the word "methodical" is used in one place where "methodological" was intended. In the chapter on molecular similarity analysis, the diol metabolites are carbamazepine are listed as anticonvulsant; in the pharmacological and clinical literature, the carbamazepine-10,11-diol is recognized as biologically inactive.

This book is aimed at the industrial or academic practitioner of computer-assisted drug discovery. It is useful to someone who has already worked in the area and is comfortable with statistics and theoretical conformational analysis. For the novice physical or computational chemist who is starting to work in this area, this is a useful handbook which is well worth acquiring. Although there is an emphasis on showing the user how to apply these methods, this a not a "cookbook". To successfully apply the techniques covered in this book requires a considerable amount of labor as well as consulting the original literature (and not merely relying on this handbook). Nevertheless, this monograph greatly facilitates understanding the techniques of computer-assisted drug design and will assist the practitioner in implementing them in a more effective and efficient manner. In many places, the strengths and weaknesses of the various methods are discussed candidly and accurately; this is very useful. However, for the bench organic or medicinal chemist, this book is only worth a glance, providing insights as to what lies down the road in computational drug design (an emerging biotechnology).

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