Additions and Corrections

The First Stereoselective Total Synthesis of Quinine [*J. Am. Chem. Soc.* **2001**, *123* (14), 3239−3242]. GILBERT STORK,* DEQIANG NIU, ROGER A. FUJIMOTO, EMIL R. KOFT, JAMES M. BALKOVEC, JAMES R. TATA, AND GREGORY R. DAKE

Page 3239: The third author's name should be Roger A. Fujimoto.

JA015138B

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Computing Handedness: Quantized and Superposed Switch and Dynamic Memory of Helical Polysilylene [*J. Am. Chem. Soc.* **2001**, *123*, 6253−6261]. MICHIYA FUJIKI,* JULIAN R. KOE, MASAO MONTONAGA, HIROSHI NAKASHIMA, KEN TERAO, AND AKIO TERAMOTO

Pages 6258−6260, Figures 5b, 7, and 9b: "M-helix" of the left-side ordinate should read "P-helix", and conversely "P-helix" of the right-side ordinate should read "M-helix".

Page 6258, Figure 5a caption, line 2: "**PS-4** (filled squares)" should read "**PS-4** (crosses)".

Page 6257, right column, line 30: The percents given for P and M have been reversed, thus the two sentences should read as follows: In region 1, **PS-1** contains a constant 80% P and 20% M (60% P excess), but contrarily in region 3, it has 20% P and 80% M (60% M excess). However, **PS-2** invariably contains 80% P and 20% M (60% P excess) over the entire temperature range (−80 to +80 °C).

JA0151403

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Effect of Temperature and Composition on the Formation of Nanoscale Compartments in Phospholipid Membranes [*J. Am. Chem. Soc.* **2001**, *123*, 6951−6952]. ADRIAN S. MURESAN, HAIM DIAMANT, AND KA YEE C. LEE*

Page 6951, right column, line 8: distearoylphosphatidylcholine should be replaced by distearoylethylphosphatidylcholine.

All appearances of DSPC (except for that on p 6952, right column, line 3), should be replaced by DSEPC for clarity.

The conclusions of this study are not affected by these changes.

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Computer Software Reviews

Qsaris. SciVision, 200 Wheeler Road, Burlington, MA 01803. www.scivision.com. Suggested Retail Price: $1495.00; Mathematica 4.1 for Students Price: $139.95. Other Academic Pricing Available.

QSARIS is an integrated quantitative structure−activity relationship (QSAR) information system (IS) with multiple capabilities, including QSAR model building, molecular structure manipulation (including building and similarity searching), and storage of biological data. It is designed to run under Microsoft Windows on modest PC hardware. SciVision has done a good job of utilizing Windows functions, which gives the software a very familiar feel for those experienced with Windows. SciVision has attempted, with QSARIS, to bring QSAR model building to the medicinal chemist. To that end, there is a major emphasis throughout the software on "one-touch" features. Although an experienced user may consider these features as "black-box"

functionalities, suitable to be cast aside, the developers have put a great deal of effort into these default tools that makes them worthy of consideration, even for experts.

The current trend in the chemical software industry is to provide electronic manuals either online or on CD-ROM, and QSARIS follows this strategy. SciVision supplies the manual in Microsoft Word format; however, the pages are formatted for printing on customized paper sizes, which consequently requires some additional handling before printing. Despite this drawback, the manuals supplied for QSARIS are complete and fairly descriptive. The Getting Started and User Manuals are all one really needs to get running with minimal reading. SciVision has gone further by supplying a complete Reference Guide describing the methods and descriptors utilized by QSARIS. This is an excellent reference text for the uninitiated scientist striving to learn QSAR techniques and goes a long way toward making the black box features transparent.

QSARIS stores all data in a database (utilizing background Microsoft Access components), and as such, it is a powerful tool for organizing data while the user is in the process of devising QSAR models. Once a predictive model is found, it can be used to screen for compounds with good predicted activities with relative ease. QSARIS supports most popular molecule file formats (i.e., MDL mol, skc, and sdf; SMILES; PDB; Tripos mol2; Alchemy 2000.al2; etc.) for structure import, and molecules can be built or edited with the full-featured built-in sketcher. There is also a built-in link to start ChemDraw directly (not tested by reviewer). Structural and activity data can be loaded into QSARIS in multiple ways. Individual structure files can be imported or a batch facility will allow you to load all files of a particular type from a specified directory. There are some differences between file types; for example, in loading MDL skc files, there was an apparent conversion that took place upon importation of the structures, which resulted in the loss of the original filename. Once the files are loaded, data contained in a Microsoft Excel spreadsheet or a text file can then be added by mapping columns against the database (i.e., file names for the structure file). With the MDL skc file, the loss of the filename led to difficulties interfacing directly with an Excel spreadsheet. With the plethora of input tools available, however, this minor setback was easily circumvented. In general, the import and mapping of data is easy to use and powerful through a Wizard tool.

The user can import all relevant data in one simple step if data are supplied in an MDL sdf file. This file type may contain not only the structural information but also all data directly extracted from another source (e.g., corporate database). Given that data can easily be exported to an sdf file as well, it is the most efficient way to interface external data sources and computational tools directly to QSARIS, strongly emphasizing the IS strengths of QSARIS.

A number of examples are shipped with QSARIS for investigating its features in an error-free environment while following the Getting Started manual. A set of carboquinones (anti-leukemic agents) (Gough, L.; Hall, L. H. *J. Chem. Inf. Comput. Sci.* **1999**, *39*, 356−361) and a set of HIV protease inhibitors (Holloway, M. K., et al. *J. Med. Chem.* **1995**, *38*, 305−317) are available, and their use is completely described. To test the strength and speed of QSARIS, HIV non-nucleoside reverse transcriptase inhibitors described in a recent article (Huuskonen, J. *J. Chem. Inf. Comput. Sci.* **2001**, *41*, 425−429) were treated as a comparative test.

QSARIS contains many parameters available for utilization, and although not tested, additional user-customized parameters can be added with some effort by way of dynamic link libraries. In any calculation, up to 250 individual descriptors, including those that are user defined, may be used, and standard descriptors that are available include simple and valence 2D connectivities, E-states, Kappa shapes, molecular moments, and other general parameters, such as calculated logP, charge, dipole moment, etc. QSARIS contains a classification tool that allows for straightforward and simple selection of desired individual descriptors or descriptor sets.

Forty-six training set compounds and 24 test set compounds were drawn with ISIS/Draw and saved as individual skc files. Activities were entered into Microsoft Excel, and the two sets of data were imported into a new database in QSARIS. Despite the small filename problem highlighted above, the whole exercise was quite rapid and the bulk of time was spent in ISIS/Draw.

One-touch analysis was performed on the training set, and within minutes, a reasonable five-component model could be obtained (n = 46, r^2 = 0.802, s = 0.594, F = 32.41, q^2 = 0.749). The one-touch genetic algorithm was able to identify a model of sufficient quality to rival the final model from the literature (n = 41, r^2 = 0.851, s = 0.525, F = 40.01, q^2 = 0.802) without requiring any additional user intervention. Utilizing the advanced tools allowed the building of different improved models. To investigate the one-touch model in more detail, simply removing outliers followed by rebuilding the model gave a model that was as good as the final model from the literature (above) (n = 41, r^2 = 0.896, s = 0.435, F = 60.24, q^2 = 0.8362). The QSARIS tools are quite intuitive, and all of the possible methodologies and descriptors could be evaluated in a short amount of time while building and testing new models. Detailed statistical information is supplied in a separate window after each model is generated, as is a text statement describing the "expert" opinion of QSARIS on the potential utility of the model. If a statistically poor model is generated or a model does not pass cross-validation tests, the user is given a detailed warning in real time. Graphical representations of the predicted and observed data are possible with histograms, predicted vs observed scatter plots, residual plots, etc. Since graphs are active, picking a point will select it both in the graph and the data table. Removing outliers can be done by an automated routine or manually.

The published 24-member test set was then analyzed by the improved one-touch model (r^2 = 0.80, s = 0.635, 3 outliers) and compared somewhat favorably with the literature prediction results (r^2 = 0.87, s = 0.52, 1 outlier), although more outliers were evident. This is one example, but it is important to point out that the generation of a reasonable QSAR model for a relatively small set of compounds by a nonexpert was undertaken in a very short amount of time. The whole process took less than half a day. Even the initial one-touch model would be a sufficiently good starting model for medicinal chemistry efforts.

QSARIS is distributed on a single CD-ROM, and the licensing is managed by an unlocking code, which allows it to run on a single machine. This could be a potential drawback in a fast-paced lab with frequent hardware upgrades, but SciVision quickly allowed the move of QSARIS to a new machine with no problem when a hardware upgrade occurred during the review period. A demo version is available that will run for a specific number of starts or a specific number of days.

Although some aspects of QSARIS were not investigated in detail, principal functionalities of QSARIS are clearly an advance in the area of QSAR information systems. Functionality otherwise utilized by QSAR experts is available on desktop machines and one-touch expert system tools make model generation easy to attempt, validate, and refine in real-time. The built-in database tools allow easy storage of data and models. When further refinement of models is needed (for example, in a continuing medicinal chemistry project), the process is simple and straightforward.

These features, combined with the wealth of classical and new descriptors, as well as the ability to define new descriptors, make QSARIS a powerful tool that should find a home in every lab (academic, government, or industrial) needing this type of information. QSARIS is indeed a "turnkey solution", as advertised.

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The Chemical Thesaurus V2.0. Created by Mark R. Leach. Meta-Synthesis, 56 Downland Road, Brighton, BN2 6DJ, England. 2001. £ 19.95 (Approximately $29.00).

The Chemical Thesaurus is a reaction chemistry information system that extends traditional references by providing hyperlinks between related information. This program goes a long way toward meeting its ambitious goal of creating a nonlinear reference for reaction information. With its built-in connections, organizing themes, and multiple ways to sort and view data, *The Chemical Thesaurus* is much greater than the sum of the data in its database. The program does an excellent job of removing artificial barriers between different subdisciplinary areas of chemistry by presenting a unified vision of inorganic and organic reaction chemistry; however, *The Chemical Thesaurus* v2.0 does have a number of limitations.

The value of a database program arises from both the quality and completeness of its data, as well as the ways in which the data can be

accessed. *The Chemical Thesaurus* includes a database of species and reactions of moderate breadth, accessible in a novel manner. The database of species includes all elements (up to atomic number 108) and many isotopes and ions, as well as a more limited selection of organic and inorganic compounds and reactions for a total of 2600 unique species and 2600 reactions. There are virtually no literature references within the program, making searches unsuitable for many research purposes. The following three examples are illustrative of the limited content of the database. (1) Under the heading "substitution and elimination" only one example is given: a secondary cyclic iminium ion that cannot undergo E2 elimination owing to conformational restrictions. No mention is made of the competition between these reactions in less spatially restricted systems or of the more common competition between elimination and substitution reactions of alkyl halides and sulfonate esters. (2) The sigmatropic rearrangement category lists only the classic Claisen rearrangement (rearrangement of allyl phenyl ether); other reactions, such as the aliphatic Claisen (oxy-Cope) and Cope reactions, are omitted. (3) Only four reactions of the generic alkyllithium (RLi) are listed, addition reactions of RLi are not included, and *n*-butyllithium (a very common organic reagent) is not listed as a specific reagent at all. In other words, the database in *The Chemical Thesaurus* v2.0 is less extensive than common introductory organic chemistry textbooks. The use of generics, such as the RLi listed above, partially compensates for the missing data.

The greatest merits of *The Chemical Thesaurus* are the numerous ways in which the data (specifically species and reactions) can be extracted, sorted, and studied. The entire list of chemical species can be sorted by name, including synonyms, and by Hill formula. Elemental data can be accessed via tabular lists or by clicking on an element block on a periodic table. Lists of elemental data can be further sorted according to physical properties, crystal structure, abundance, and discovery information. Subsets of chemical species are also available as hyperlinked lists, an example being substances with similar applications or reactivities. Chemical species are also linked to reactions for which they are products, substrates, or reactants. Chemical reactions are grouped by mechanism and can be sorted according to reactants or products. Pre-defined subsets of reactions can be extracted, including name reactions, multistep reactions, synthetic routes, and biochemical reactions. In addition, reactions between substrates that are Lewis acids and Lewis bases are accessible through a novel frontier molecular orbital Lewis acid/base matrix developed by the author. The matrix describes 24 possible Lewis acid/Lewis base interactions, and each cell in the matrix is linked to a list of the corresponding reactions in the database.

There is no written documentation for the program, and in fact, none is needed. A brief tutorial is available on the Web site.[1] Navigation through the program occurs by clicking on any of the clearly labeled active regions of the screen. Most screens provide an option to return to the main menu, so it is impossible to get lost within the program. Database contents can be accessed in two ways: (1) by scrolling through sets of indexed terms, followed by clicking on a desired entry, or (2) by moving from one answer or set of answers to another by choosing one of the active areas on a given screen. The former method is somewhat like browsing through a customized index, then turning to the indexed page in a text; the latter resembles travelling between linked pages on the Internet or in a multimedia presentation or game. However, the simplicity of the interface is also a weakness. Many of the screens provide no way to go "back" to a previous screen, and the program lacks a "history" option or mapping of a path followed. The user cannot define customized searches, beyond those the author has chosen. There is no bookmark feature to allow one to return to a given screen, and information to be extracted must be hand written because the program lacks print and copy functions.

There were numerous other quirks, some intentionally built in, others in error. There were several misspellings, and one screen was found that was obviously not complete. Once during testing, an error message was generated stating that the disk was write-protected. The program starts up automatically when the CD-ROM disk is loaded; several times while loading the CD-ROM, a totally blank black screen appeared that forced a machine reboot. The program does not run in a multitasking mode; thus the only way to access another application is to close the program. There is also a button titled "Data Entry and Editing", a feature that is not included in the current program, but that would be a valuable edition in future versions.

Independent of and not linked to the main database are several additional modules: a glossary with many of the terms used in the tutorial, a database of congeneric species, and a tutorial on aromatic substitution. The aromatic tutorial can be used to explore the reactivity of benzene derivatives with a selection of nucleophiles and electrophiles. One error in this module is the lack of predicted reactivity of iodobenzene with electrophiles such as nitric acid/sulfuric acid. The congeneric series (120 total) are groups of elements, compounds, and ions that have linear structure/reactivity relationships. These series are particularly valuable in classifying chemical reactivity.

Many chemists will find *The Chemical Thesaurus* to be insightful, including educators and students interested in exploring a logical classification of reactivity across chemistry. *The Chemical Thesaurus* v2.0 will not replace any current text or reference, but it will augment the linear lists and units that the latter provides. Coupled with an appropriate workbook[2] or assignment, this database program could form an effective tutorial in reactivity; research in computer-assisted education suggests that database exploration has the potential to enhance learning significantly.[3] The Meta-Synthesis Web site[1] provides a brief history of the development of the organizing models for *The Chemical Thesaurus* v2.0 as well as free access to the raw data used to develop the software.

The program was tested on a Macintosh G3 266, running Mac OS 8.1, with 96 MB RAM. The software requires a Windows 95/98/NT or Mac OS computer with 16 MB of memory, a color screen, and a CD-ROM drive. On the machine tested, the program ran very quickly except for sorting large portions of the database, which took up to three minutes. No installation is required, making the product ideal for public computer laboratories having restricted write access to machines.

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(1) www.meta-synthesis.com.

(2) Version 1.5 of the product is sold with a workbook.

(3) Dillon, A.; Gabbard, R. *Rev. Educ. Res.* **1998**, *68*, 322−349.

Book Reviews[*]

Recent Theoretical and Experimental Advances in Hydrogen Bonded Clusters. NATO ASI Series C: Mathematical and Physical Sciences, Vol. 561. Edited by S. S. Xantheas (Pacific Northwest National Laboratory). Kluwer Academic Publishers: Dordrecht, Boston, London. 2000. x + 430 pp. $196.00. ISBN 0-7923-6703-0

This book arose out of a NATO Advanced Study Institute meeting of the same title held in Crete, Greece, in the summer of 1997. As the title suggests, the emphasis of the book is on the interaction between theory and experiment in hydrogen-bonded clusters. Thus, a variety of spectroscopic techniques as applied to hydrogen-bonded systems are reviewed, as are simulation techniques, such as the rigid-body diffusion Monte Carlo method to calculate various properties of weakly bonded clusters. Attention is also given to the study of water clusters as well as ammonia, methanol, and hydrogen fluoride molecules and cluster ions.

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10.1021/ja015244d

Combinatorial Chemistry. A Practical Approach. Edited by Willi Bannwarth (Universität Freiburg, Germany) and Eduard Felder (Pharmacia & Upjohn S.p.A., Nervino, Italy). Wiley-VCH: Weinheim. 2000. xx + 430 pp. $145.00. ISBN 3-527-30186-0.

[*]Unsigned book reviews are by the Book Review Editor.

This text is the ninth in the Methods and Principles in Medicinal Chemistry series and concerns the practice of synthesizing and purifying combinatorial libraries. Although a relatively new area of pharmaceutical research, the synthesis of combinatorial libraries has been the subject of intense research for a sufficient number of years to warrant review and critical evaluation in a book. However, the field of combinatorial chemistry is changing so rapidly that textbooks risk containing outdated references and describing outmoded technology. Fortunately, many of the solution-phase (Chapter 2) and solid-phase (Chapter 3) synthetic strategies have matured into standardized technologies that will probably not become outdated in the near future. Many of these reactions are listed with citations in Chapter 8 as common organic reactions for solid-phase synthesis. Another feature of this text is the inclusion of brief experimental procedures within reviews of specific topics, which provide details regarding solvents, reagents, and reaction conditions for selected reactions. Altogether, these chapters would serve as a useful reference source to investigators just entering the field of combinatorial chemical synthesis.

However, the breadth, scope, utility, and timeliness of the information contained in different chapters are uneven. Juxtaposed with thorough chapters concerning solid-phase synthesis and polymer-supported reagents (Chapters 3 and 4), there are chapters simply cataloging commercial products for automated solid-phase synthesis (Chapter 6) and solid-phase reactions (Chapter 8). More critical evaluation of the reaction schemes and the synthetic instrumentation would have been welcome in these and other chapters. In the case of Chapter 7, on computer-aided library design, a broad overview of different approaches is presented with little detail. This is in contrast to the thorough 162-page chapter on solid-phase synthetic chemistry (excluding the additional 94-page chapter that lists chemical reactions). In some cases, such as Chapter 5, which describes encoding strategies for identifying organic compounds on solid supports, the information appears to be somewhat out-of-date. For example, although barcode encoding and radio frequency encoding are widely used today, the techniques of chemical encoding and mass spectrometric encoding are rarely used. This chapter would benefit from an updated critical evaluation of the literature. Another concern for the entire book is the timeliness of the references. Most of the citations are from 1997 and 1998, and few chapters cite references after 1998.

Overall, this book is thorough in that the important topics and issues in combinatorial chemical synthesis are addressed. In addition to chapters on solution-phase and solid-phase synthesis, computer-aided library design is included in a separate chapter, and another chapter is devoted to polymer-supported reagents for organic synthesis of combinatorial libraries. The chapter on solution-phase synthesis also addresses issues of product purification and polymer-assisted solution-phase synthesis. However, references and developments since 1998 are missing, the chapters are uneven in their depth, and many chapters lack a critical review of the literature and existing methods. In conclusion, this book is recommended to newcomers in the field of combinatorial chemical synthesis because of its broad scope.

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Self-Assembly in Supramolecular Systems. By Leonard F. Lindoy (University of Sydney) and Ian M. Atkinson (James Cook University). Monographs in Supramolecular Chemistry. Volume 7. Series edited by J. Fraser Stoddart. Royal Society of Chemistry: Cambridge. 2000. x + 224 pp. £69.70. ISBN 0-85404-512-0.

Although every area of chemistry can be traced back to a handful of (al)chemists a few centuries ago, supramolecular chemistry, the science of molecular interactions, took shape in the 1960s, culminating in the 1987 Nobel Award to Pedersen, Lehn, and Cram. This field grew out of the study of what has now become common knowledge: the crown ethers and their coordination chemistry. The study of the ability of this class of molecules to bind selectively to metals led to the formation of the concept of molecular recognition in artificial systems. For more than 30 years, this concept was refined and investigated kinetically and thermodynamically in increasingly sophisticated systems, such as the recognition of heavy metals, organic and inorganic molecules, biologically relevant small and large molecules, sensors, catalysts, carriers, and more. Fundamentally speaking, however, the most important and contemporary development of the field of molecular recognition is the phenomenon of self-assembly and self-organization.

This very active area of research crystallized from our ability to selectively recognize, transport, and transform a molecule by artificial hosts. But in most of these cases, the recognition process involves two or three molecules held by noncovalent forces (including coordination bonds). In self-assembly and self-organization (or self-processes to use Lehn's terminology), we are asking more from the molecules. Five, twenty, or even hundreds of molecules are instructed to organize themselves into well-defined discrete structures or infinite structures with sizes varying from the nanoscale to the macroscale. Like many areas of chemistry in their early development, self-processes are still at a very fundamental stage. The rules governing these processes, the design principles, and the resulting functional materials are not fully understood.

Lindoy and Atkinson's book is an excellent introduction to this field. The authors attempt to distill the essence of self-processes and describe it in very simple terms, a task that is often hard to accomplish in any state-of-the-art discipline. Because of the tremendous development this discipline had seen over the past decade, the authors wisely limited the scope of their book to self-assembled systems resulting in *discrete* as opposed to infinite structures.

Self-Assembly in Supramolecular Systems is composed of seven chapters. The first two introduce the basic concepts of self-assembly and the intermolecular interactions. A short Chapter 3 describes H-bonded systems. Chapters 4 and 5 discuss rotaxanes and catenanes that do not involve coordination bonds, while Chapter 6 covers metal-containing rotaxane, catananes, helicates, and molecular knots. The last chapter reviews a collection of inorganic and organometallic discrete assemblies. The authors illustrated these topics from recent work by a few leaders in this field. In fact, if an index of authors were included, all the topics described could be traced back to a dozen major research groups from around the world. The writing style is clear and concise. The authors managed to create continuity in their writing style despite the heterogeneous nature of the approaches and systems included in this monograph. The vast majority of the assemblies are in the nanoscale range and display unique chemical and physical properties. As such, they are relevant to the very timely field of nanoscale science and technology.

This book should certainly appeal to the novice at an advanced level and may even serve as a basis for an introductory course on self-processes. It is an excellent addition to the Monographs in Supramolecular Chemistry series edited by Stoddart.

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JA015233K

10.1021/ja015233k

Inductively Coupled Plasma-Mass Spectrometry: Practices and Techniques. By Howard E. Taylor (U.S. Geological Survey, Boulder, CO). Academic Press: San Diego. 2001. xii + 294 pp. $69.95. ISBN 0-12-683865.

This book represents the author's view of the operational characteristics of inductively coupled plasma mass spectrometry (ICP-MS). Since it starts with the Bohr model of the atom, it is aimed at the nonexpert. In general, it presents a fairly accurate description of the available instrumentation (including regular and alternative sample introduction systems) and of quantitation strategies (including the influence of spectroscopic and nonspectroscopic interferences).

There are a few typographical errors that would not be picked up by a spell-checker (such as "discreet" instead of "discrete" when discussing some sample introduction systems and 1998 instead of 1988 in the reference from Table 5.4) as well as some undefined acronyms. More importantly, some misleading inaccuracies can be found:

On p 24, the author states that the initial radiation zone (IRZ) is aligned with the radio frequency load coil. Yet, this would certainly not be the case in ICP-MS. First of all, the IRZ can be located anywhere within the plasma, depending on the power and aerosol carrier gas flow rate. It is simply the zone where analyte atoms are present. In ICP-MS, it would be above the load coil, so that its tip is fairly close

to the sampler in order to enable sampling of analyte ions from the normal analytical zone that is situated just above it.

On p 57, the use of a flow injection (FI) system to perform hydride generation is said to involve a complete reaction of the sample with reagents, which is rarely the case in FI. In fact, this would prevent the kinetic discrimination where the limited reaction time can be selected to prevent or reduce the occurrence of interfering reactions in favor of analyte vapor formation that is a definite feature of the FI mode.

Isotope dilution analysis is said to be a definitive method, i.e., standardless. Although this statement is true in MS, it is not the case in ICP-MS because of mass discrimination. A standardization (using standards of known isotopic composition) is therefore required to establish the mass bias and correct for it.

"Molecular ion" is used instead of "polyatomic ion", which would be confusing for someone with a background in MS. Indeed, the former implies the single ionization of a molecule, which would not be the case in ICP-MS since everything is atomized and then ionized. It is, however, possible for ions to recombine with atoms to form polyatomic ions.

The book is not comprehensive. For example, on p 94, only resins (by the way, 8-hydroxyquinoline is wrongly listed as a resin) are mentioned as a means of performing on-line matrix separation using FI. There is no mention of other methods that can also be used for on-line matrix separation, with or without preconcentration, such as hydride generation or liquid−liquid extraction. Similarly, electrothermal vaporization is not mentioned in the section on the analysis of solids.

In any case, by far the most important deficiency is that the text contains only 22 references. As a result, the usefulness of this book will be limited. Few people will indeed go through the 101 pages of supplemental references that have been compiled in an appendix, to guess from the titles where the additional information they are seeking can be found. Also, some of the appendices are provided without references: for instance, I doubt that the author has measured the atomic weight and ionization potentials of all the elements. Furthermore, the selection of these few references was somewhat unfair since the author did not fail to point out his invention but did not give credits for other inventions.

Overall, this book should be useful to nonspecialists who want to learn about the capabilities of ICP-MS without having to go through specialized papers or books. The supplemental references could perhaps be useful to people wishing to tabulate a database of ICP-MS papers (although several abstracting services are available for this purpose). If these supplemental references had been included in the text, then this book would have likely become a source book for all newcomers to ICP-MS, as it would have served not only as a tutor but also as a guide to more information.

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JA0152308

10.1021/ja0152308

Reviews in Computational Chemistry. Volume 16. Edited by Kenny B. Lipkowitz and Donald B. Boyd (Indiana University−Purdue University). Wiley-VCH: New York. 2000. xxviii + 342 pp. $135.00. ISBN 0-471-38667-7.

This volume continues the tradition of up-to-date and insightful reviews in all areas of computational chemistry. It contains four chapters: (1) "Computer-Aided Molecular Diversity Analysis and Combinatorial Library Design", by R. A. Lewis, S. D. Pickett and D. E. Clark; (2) "Artificial Neural Networks and Their Use in Chemistry", by K. L. Peterson; (3) "Use of Force Fields in Material Modeling", by J.-R. Hill, C. M. Freeman, and L. Subramanian; and (4) "Free Energy Calculations: Use and Limitations in Predicting Ligand Binding Affinities", by M. R. Reddy, M. D. Erion, and A. Agarwal. Although each chapter is written by acknowledged experts in the field, each also contains tutorial information that serves to ground one not familiar with the methods and jargon. The chapters are also well-referenced, containing more than 200 citations.

Chapter 1 focuses on molecular similarity and diversity, the reduction to practice of these concepts, and the use of these concepts and algorithms. The types of 2D and 3D molecular descriptors that have been used in diversity analysis are well described, as are guidelines for choosing a descriptor set for a particular application. The chapter then moves on to discuss applications that use diversity analysis: e.g., selecting subsets for screening in a biological assay or selecting compounds to enhance a compound collection and combinatorial library design. The chapter concludes with the caveat that one must consider properties other than diversity when selecting compounds for biological testing.

Chapter 2 provides an expert's evaluation of the complicated and frequently confusing field of artificial neural networks. Throughout the chapter, thoughtful comments guide the reader to an understanding of the significance of the material. The author begins with a basic tutorial on neural networks in general and then describes why and when one should consider using a neural network. Applications are found for classification, modeling, and mapping, and the question, "When will a neural network be a better way to solve a problem than traditional statistical methods?" is addressed. The individual processing elements of a network and collections of them are then described. Also offered in this chapter is a description of 11 different types of networks, how each is assembled, the types of problems appropriate for them, and their strengths and weaknesses. The chapter then covers practical considerations in using, evaluating, and analyzing a network.

Chapter 3 introduces the reader to computational approaches used in modeling materials, such as metal oxides and ceramics, superconductors, zeolites, glasses, and polymers. In particular, the authors discuss the utility of ion-pair and shell-model potentials, which describe ionic systems in which there is no directionality of bonding, versus molecular mechanics force fields commonly used in protein and nucleic acid modeling, which describe covalently bonded systems with strong directionality of bonds. The authors discuss which are appropriately applied to what type of problem, how the force fields are parametrized, and how well they predict the properties of materials. The most detailed simulations appear to have been done on zeolites, which require that one use both types of modeling approaches to investigate behavior.

The final chapter covers the theory of free energy perturbation, computational details, and calculations for small molecules and macromolecules and offers a guide to structure-based ligand optimization and a discussion of the optimization of ligands to HIV-1 protease. Especially helpful is a table that summarizes approximately 90 free-energy perturbation studies on the relative binding of two ligands for either a protein or DNA (two examples are given). Nineteen proteins are reported in this table, which lists the force field and some details of the calculations. Of the 62 complexes, for which experimental data on the relative binding of the two ligands are also available, the difference between the observed and calculated change in binding energy is within 1.0 kcal/mol for 22 of the pairs and greater than 3.0 kcal/mol for 15. The errors are roughly divided between under- and overestimation of the relative binding affinity. Each of the studies is then discussed in some detail. Although the accuracy of the current calculations is not particularly encouraging, the authors point out that most of the limitations are related to either the computational requirements or the inadequacies in the force fields used. Both types of limitations should be overcome in the near future.

The volume concludes with a 20-page index of cited authors and a 15-page subject index. Both of these add substantially to the value of the book.

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