of X-ray analysis in the study of chemical bonding, modular structures, ordering in liquid crystals, Langmuir–Blodgett films and stimulated phase transitions in ferroelectrics. There is a perfunctory listing of databases as of 1993 and a six-page 'update' on organic crystal chemistry.

The pattern of revision in this volume follows that adopted for the first. The bulk of the original material is left untouched and an extra chapter is added to 'complement' the original material. Whereas such an approach may be justified where the original material is well established and relatively unmodified by recent activity, it is much less satisfactory where that activity has changed or greatly modified our perspective. Thus, simply to add a few pages to supplement descriptions of views and models now more than two decades old, as has been done in Chapter 6 for several of the topics of Chapter 2, is to lose an opportunity at best, and to produce a quite misleading impression at worst. As an example, the supplementary material on liquid crystals, while a concise summary of some of the structural discoveries of the eighties, leaves in place the thoroughly outdated pictures of the nature of nematic and smectic phases used as illustrations in Chapter 2. A similar criticism may be made with respect to many of the illustrations of biological macromolecules in that same chapter. Plywood cross sections and glass contour maps, while of legitimate historical interest, scarcely qualify as 'modern' in the sense that the series title seeks to portray. The text remains one of the few generalized treatments of the structure of crystals. However, in the absence of a systematic integrated modernization of the work, it is difficult to recommend it over competing and more truly modern (and usually more specialized) treatments or, indeed, over the earlier edition that justifiably found a place in every scientific library.

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Structure correlation. Edited by J. D. DUNITZ and H. B. BÜRGI. Two Vols. Pp. xxvii + 888. Weinheim: Verlagsgesellschaft mbH, 1994. Price DM 398. ISBN 3-527-29042-7.

I remember the first time that I held the entire Cambridge Structural Database in the palm of my hand. The occasion was at a crystallographic meeting in the United States, some 25 years ago. Details of the 4500 or so structures then recorded in the database had been transferred to a thin stack of microfiche transparencies, the hypertext of the day. In some excitement, I drew the attention of a senior colleague to this small miracle. 'Look,' I said, 'every molecular structure known, here in this stack of celluloid!' Calmly, he regarded the transparencies. 'An impressive achievement;' he responded, 'what are you going to do with it?' The comment and question were fair then, and remain so today when we consider the mightily enlarged Cambridge files and their companion inorganic and protein databases, the last growing exponentially and soon to be supplemented with the results of NMR measurements. These volumes by Dunitz and Bürgi and their co-authors seek to describe the present state of the achievement and to provide contemporary answers to the question of how to interpret structural information. There is little that is new in the work, at least not to anyone who has followed the trail of plenary and invited lectures and presentations given by the editors and many of their collaborators at crystallographic, chemical and biological meetings over the last decade, but the books offer a timely review of the present status of this important and rapidly expanding branch of crystallography.

One of the strengths of the work is that it reminds us, as crystallographers, of the astonishing range of questions and, occasionally, answers that derive from diffraction measurements and the different ways of interpreting these measurements; and the book does not even begin to touch on materials! We tend to focus on our successes, not unnaturally, but the book also reminds us of the many unanswered problems that remain, some of which may be outside the power of our methodology to solve. The key to our sense of success, of course, is that the diffraction method remains, for the moment, the predominant method providing data on the three-dimensional structure of molecules, and a knowledge of the three-dimensional structure of molecules is, to the crystallographer at least, the beginning of all wisdom. If the power of the diffraction method occasionally blinds us to its limitations, there are chemists and spectroscopists all too ready to remind us of them. We have moved beyond the stage of obscurantist denial that the crystal structures (as opposed to conformations) of molecules need not be the same as those of the molecules in solution. The penicillin molecule does have a β-lactam ring; ribonuclease in the crystal state cleaves RNA. However, the structure of a molecule in the crystal remains just that – the time- and space-averaged structure attributable to that molecule in that particular crystalline environment. However, chemistry and biochemistry take place predominantly in solution. Reactions involve changes in molecular structure. How can diffractionists with their data banks of static models hope to compete with the spectroscopists probing the dynamics of solution chemistry and molecular reactivity? Surprisingly well, as this book makes clear. It is necessary, however, to separate the questions asked and answers provided in the different parts of the book. This is because structure and correlation have different meanings in the different parts of the work. The interpretation of fine detail, inseparable from the arguments presented in the parts of the work dealing with small molecules, is mostly impossible, and largely irrelevant, for the interpretation of macromolecular structure discussed in the later parts, although as the structures of the steroid receptor enzymes emerge, the symbolically blind authors of Chapter 14 will be able to gauge their success in trying to map active sites from the diet of small-molecule structures fed to the unseen elephants.

For small-molecule structures, it is the particular contribution of the editors to have demonstrated how, by examining all the available structural data for a particular chemical fragment, correlations between the various structural parameters

may be used to suggest correlations between structure and energy that may mimic reaction pathways. Briefly stated, each related structure may be regarded as a single frame in a continuum, analogous to a motion picture reel. Properly arranged, the progression of single frames maps out the changing stereochemistry of the fragment in a progressively changing, if restricted, environment. The first two parts of the book are devoted to different aspects of this theme. In Part 1, two chapters by the editors show how to describe and define the structure of a molecule or molecular fragment, with particular emphasis on the role of symmetry. Two chapters by members of the Cambridge Crystallographic Data Centre review the development and present status of the various crystallographic data files, with particular emphasis on the Cambridge Structural Database, and the statistical and numerical tools needed to establish structure–structure correlations. The editors contribute a final chapter outlining the heart of the structure correlation method, the interpretation, in physical terms, of the observed correlations between the structural parameters. They conclude by describing their arguments for a principle of structure-energy correlation, relating structures to equilibrium and activation energies. The editors are frank about the limitations of their arguments. The method can suggest the detailed structural changes involved in passing from the ground state toward the transition state, but it does not allow detailed energetic deductions and can usually not distinguish between single step and multistep processes, nor can it distinguish early from late transition states.

Part 2 consists of four chapters describing applications of the structure correlation approach to a range of chemical problems. The first of these (Chapter 6, A. S. Cieplak) deals with organic addition and elimination reactions, with particular emphasis on carbonyl derivatives. This is a good review of this field through 1992, and Cieplak's opening sentence merits preservation! Chapter 7 (H.-B. Bürgi & V. Shklover) discusses reaction paths for nucleophilic substitution reactions at various metal centers in four-, five- and six-coordinate complexes and for certain first row elements. All of this is pretty well trodden ground, with no references beyond 1990, but it gives a good sense of what the structure correlation method is all about and how it has developed. Much the same can be said of Chapter 8 (T. Auf der Heyde), which deals with studies of ligand rearrangement and substitution reactions of transition metal complexes, reported through mid 1991. The first volume concludes with a review of conformational analysis of some organic systems, by Bernd Schweizer, with most of the examples cited being from the 1980's.

The first volume could well stand on its own as an authoritative exposition of the structure correlation method and its applications to specific molecular systems. The second volume begins (Part III, Chapter 10) with a review of bond-length–bond-valence relationships in inorganic solids, by I. D. Brown, although here the emphasis is primarily upon describing and illustrating the bond-valence model, rather than upon extensive correlation studies. In Chapter 11 (J. Bernstein, M. C. Etter & L. Leiserowitz) there is a review of the systematization of hydrogen-bonding patterns pioneered by Etter in her analyses of the Cambridge Structural Database. Here, predictive ability comes into play with the design of co-crystals and the use of crystal surfaces as growth modifiers. All good stuff, but rather far from from the thrust of Vol. 1. A. Gavezzotti, in Chapter 12, outlines the beginnings of an attempt to classify, rationalize and ultimately predict organic crystal structures. Here, a major challenge is to develop numerical definitions of the many complex molecular shapes that abound in the databases; part of the general problem of creating mathematical models of perception. Gavezzotti is candid on the difficulties, particularly when confronted with the phenomenon of polymorphism. His warning that 'huge amounts of computing times may be wasted when using a complex computational procedure whose key input data are of questionable accuracy' should be inscribed on the computer console of every amateur energy-minimizer.

Part IV, entitled Proteins and Nucleic Acids, is a collection of half a dozen articles reviewing small-molecule–large-molecule interactions, structural patterns in proteins and nucleic acids, structural correlations in families of homologous proteins and the correlation of protein structure with local primary sequence patterns. The first chapter in this part (G. Klebe) discusses the factors governing ligand–receptor interactions with macromolecules and tries to identify common structural patterns. Here, the function of the databases is to provide a library of potential small-molecule conformers from which candidates may be selected to best fit the knobs and hollows of the presumed active site. Great is the joy when successful docking is achieved, but at the back of one's mind must surely echo that fundamental limitation on the determination of small-molecule structure: it is the minimum energy conformation for that particular molecule in that particular crystalline environment. Only rarely does that particular crystalline environment remotely resemble that into which the ligand is placed, a caveat that lies behind Klebe's acknowledgement that 'exclusive reliance on the crystal structures of a ligand itself may not be an infallible indicator of a biologically active conformation'.

The authors of the chapter on steroid molecular structure, protein interaction and biological function (W. L. Duax, J. F. Griffin & D. Ghosh) have no shortage of conformers in their cupboard. The steroid crystal structure analysis project in Buffalo is one of the oldest systematic biological structure projects. Begun in 1961, by the late Dorita Norton, when structure determination was not yet a routine activity, it is perhaps the ultimate statement of faith in the relevance of small-molecule structural data to the biological functioning of enzyme systems. The authors present the arguments in favor of their case. Now, with the arrival of the structures of several steroid receptor enzymes, comes the test of their faith.

The final four chapters review structural patterns in globular proteins (Chapter 15, E. G. Hutchinson, A. L. Morris and J. M. Thornton) and in nucleic acids (Chapter 18, M. Egli), and examine structural correlations in families of homologous proteins (Chapter 16, T. L. Blundell) and the correlation of protein structure with local amino acid sequence patterns (Chapter 17, C. Broger and K. Müller). It is not to denigrate the impressive achievements of crystallographers in establishing the wealth of structural information that we now have for biological macromolecules to point out that some of the most fundamental of questions remain unanswered. Despite valiant efforts, we still cannot predict the tertiary structure of a protein from its primary amino acid sequence, and the authors of Chapter 17 point out that mere accumulation of additional sequences and structures is unlikely to provide the answer. Indeed, these last chapters suggest that the classical structure correlation method described in the earlier parts of the book is likely to founder in the macromolecular area, both because of the inherent lower resolution of macromolecular structure

determinations and the immense variety and complexity of the biological reaction environment. The editors, perhaps taking a longer view, must be assumed to think differently, else there would be little to connect the later chapters to the earlier, save the common dependence on databases for their raw material. However, even if the connecting threads are occasionally tenuous, these volumes are still of great value and deserving of a place in every crystallographer's library. The frankness with which the various contributors acknowledge the limitations of their approaches makes refreshing reading at a time when even a hint of such reservations could doom a grant proposal. It is clear that small-molecule crystallography has entered a quite new phase with the maturing of the Cambridge project, just as it is clear that most of the obstacles to the accumulation of structural data for biological macromolecules have been removed. These two fields, and their interactions, lie at the cutting edges of contemporary crystallography, and the editors and their collaborators have provided us with an excellent guide to them.

It may seem carping to end with a criticism, but it is directed rather at the publisher than at the editors and contributors. VCH Verlag is now one of the foremost publishers of books on crystallography. Other reviewers in this journal have suggested that it would be both helpful and appropriate to list the authors of individual chapters in the Table of Contents, rather than only *in situ* after the actual chapter headings. I, too, believe this would be a useful change in policy.

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Books Received

The following books have been received by the Editor. Brief and generally uncritical notices are given of works of marginal crystallographic interest; occasionally, a book of fundamental interest is included under this heading because of difficulty in finding a suitable reviewer without great delay.

DNA structure and recognition. By S. NEIDLE. Pp. ix + 108. Oxford: IRL Press, 1994. Price £9.95. ISBN 0 19 963419. A review of this book, by Wolfram Saenger, has been published in the September 1995 issue of *Acta Crystallographica Section D*, page 858.