

INTERNATIONAL TABLES FOR CRYSTALLOGRAPHY

Volume B
RECIPROCAL SPACE

Edited by
U. SHMUELI

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Preface

BY URI SHMUELI

The purpose of Volume B of *International Tables for Crystallography* is to provide the user or reader with accounts of some well established topics, of importance to the science of crystallography, which are related in one way or another to the concepts of reciprocal lattice and, more generally, reciprocal space. Efforts have been made to extend the treatment of the various topics to include X-ray, electron, and neutron diffraction techniques, and thereby do some justice to the inclusion of the present Volume in the new series of *International Tables for Crystallography*.

An important crystallographic aspect of symmetry in reciprocal space, space-group-dependent expressions of trigonometric structure factors, already appears in Volume I of *International Tables for X-ray Crystallography*, and preliminary plans for incorporating this and other crystallographic aspects of reciprocal space in the new edition of *International Tables for Crystallography*, largely dedicated to the subject of reciprocal space, began over ten years later. The present structure of Volume B, as determined in the years preceding the 1984 Hamburg congress of the International Union of Crystallography (IUCr), is due to (i) computer-controlled production of concise structure-factor tables, (ii) the ability to introduce many more aspects of reciprocal space – as a result of reducing the effort of producing the above tables, as well as their volume, and (iii) suggestions by the National Committees and individual crystallographers of some additional interesting topics. It should be pointed out that the initial plans for the present Volume and Volume C (*Mathematical, Physical and Chemical Tables*, edited by Professor A. J. C. Wilson), were formulated and approved during the same period.

The obviously delayed publication of Volume B is due to several reasons. Some minor delays were caused by a requirement that potential contributors should be approved by the Executive Committee prior to issuing relevant invitations. Much more serious delays were caused by authors who failed to deliver their contributions. In fact, some invited contributions had to be excluded from this first edition of Volume B. Some of the topics here treated are greatly extended, considerably updated or modern versions of similar topics previously treated in the old Volumes I, II, and IV. Most of the subjects treated in Volume B are new to *International Tables*.

I gratefully thank Professor A. J. C. Wilson, for suggesting that I edit this Volume and for sharing with me his rich editorial experience. I am indebted to those authors of Volume B who took my requests and deadlines seriously, and to the Computing Center of Tel Aviv University for computing facilities and time. Special thanks are due to Mrs Z. Stein (Tel Aviv University) for skilful assistance in numeric and symbolic programming, involved in my contributions to this Volume.

I am most grateful to many colleagues—crystallographers for encouragement, advice, and suggestions. In particular, thanks are due to Professors J. M. Cowley, P. Goodman and C. J. Humphreys, who served as Chairmen of the Commission on Electron Diffraction during the preparation of this Volume, for prompt and expert help at all stages of the editing. The kind assistance of Dr J. N. King, the Executive Secretary of the IUCr, is also gratefully acknowledged. Last, but certainly not least, I wish to thank Mr M. H. Dacombe, the Technical Editor of the IUCr, and his staff for the skilful and competent treatment of the variety of drafts and proofs out of which this Volume arose.

Preface to the second edition

BY URI SHMUELI

The first edition of Volume B appeared in 1993, and was followed by a corrected reprint in 1996. Although practically all the material for the second edition was available in early 1997, its publication was delayed by the decision to translate all of Volume B, and indeed all the other volumes of *International Tables for Crystallography*, to Standard Generalized Markup Language (SGML) and thus make them available also in an electronic form suitable for modern publishing procedures.

During the preparation of the second edition, most chapters that appeared in the first edition have been corrected and/or revised, some were rather extensively updated, and five new chapters were added. The overall structure of the second edition is outlined below.

After an introductory chapter, Part 1 presents the reader with an account of structure-factor formalisms, an extensive treatment of the theory, algorithms and crystallographic applications of Fourier methods, and treatments of symmetry in reciprocal space. These are here enriched with more advanced aspects of representations of space groups in reciprocal space.

In Part 2, these general accounts are followed by detailed expositions of crystallographic statistics, the theory of direct methods, Patterson techniques, isomorphous replacement and anomalous scattering, and treatments of the role of electron

microscopy and diffraction in crystal structure determination. The latter topic is here enhanced by applications of direct methods to electron crystallography.

Part 3, *Dual Bases in Crystallographic Computing*, deals with applications of reciprocal space to molecular geometry and 'best'-plane calculations, and contains a treatment of the principles of molecular graphics and modelling and their applications; it concludes with the presentation of a convergence-acceleration method, of importance in the computation of approximate lattice sums.

Part 4 contains treatments of various diffuse-scattering phenomena arising from crystal dynamics, disorder and low dimensionality (liquid crystals), and an exposition of the underlying theories and/or experimental evidence. The new additions to this part are treatments of polymer crystallography and of reciprocal-space images of aperiodic crystals.

Part 5 contains introductory treatments of the theory of the interaction of radiation with matter, the so-called dynamical theory, as applied to X-ray, electron and neutron diffraction techniques. The chapter on the dynamical theory of neutron diffraction is new.

I am deeply grateful to the authors of the new contributions for making their expertise available to Volume B and for their excellent collaboration. I also take special pleasure in thanking

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those authors of the first edition who revised and updated their contributions in view of recent developments. Last but not least, I wish to thank all the authors for their contributions and their patience, and am grateful to those authors who took my requests seriously. I hope that the updating and revision of future editions will be much easier and more expedient, mainly because of the new format of *International Tables*.

Four friends and greatly respected colleagues who contributed to the second edition of Volume B are no longer with us. These are Professors Arthur J. C. Wilson, Peter Goodman, Verner Schomaker and Boris K. Vainshtein. I asked Professors Michiyoshi Tanaka, John Cowley and Douglas Dorset if they were prepared to answer queries related to the contributions of the late Peter Goodman and Boris K. Vainshtein to Chapter 2.5. I am most grateful for their prompt agreement.

This editorial work was carried out at the School of Chemistry and the Computing Center of Tel Aviv University. The facilities they put at my disposal are gratefully acknowledged on my behalf and on behalf of the IUCr. I wish to thank many colleagues for interesting conversations and advice, and in particular Professor Theo Hahn with whom I discussed at length problems regarding Volume B and *International Tables* in general.

Given all these expert contributions, the publication of this volume would not have been possible without the expertise and devotion of the Technical Editors of the IUCr. My thanks go to Mrs Sue King, for her cooperation during the early stages of the work on the second edition of Volume B, while the material was being collected, and to Dr Nicola Ashcroft, for her collaboration during the final stages of the production of the volume, for her most careful and competent treatment of the proofs, and last but not least for her tactful and friendly attitude.

Preface to the third edition

BY URI SHMUELI

The second edition of Volume B appeared in 2001. Plans for the third edition included the addition of new chapters and sections, the substantial revision of several chapters that existed in the second edition and minor revisions and updating of existing chapters. The overall structure of Volume B remained unchanged.

In Part 1, Chapter 1.5 on classifications of space-group representations in reciprocal space has been extensively revised.

In Part 2, Chapter 2.2 on direct methods has been considerably extended to include applications of these methods to macromolecular crystallography. Chapter 2.3 on Patterson and molecular replacement techniques has been updated and extended. Section 2.5.3 on convergent-beam electron diffraction has been completely rewritten by a newly invited author, and Section 2.5.6 on three-dimensional reconstruction has been updated and extended by a newly invited author, who has also added Section 2.5.7 on single-particle reconstruction. The Foreword to Chapter 2.5 on electron diffraction and microscopy has also been revised.

In Part 3, Chapter 3.3 on computer graphics and molecular modelling has been enriched by Section 3.3.4 on the implementation of molecular graphics to small and medium-sized molecules, and a comprehensive Chapter 3.5 on modern extensions of Ewald methods has been added, dealing with (i) inclusion of fast Fourier transforms in the computation of sums and (ii) departure from the point-charge model in Ewald summations.

In Part 4, Chapter 4.1 on thermal diffuse scattering of X-rays and neutrons has been updated, and Chapter 4.2 on disorder diffuse scattering of X-rays and neutrons has been extensively revised and updated.

Minor updates and corrections have also been made to several existing chapters and sections in all the parts of the volume.

My gratitude is extended to the authors of new contributions and to the authors of the first and second editions of the volume for significant revisions of their chapters and sections in view of new developments. I wish to thank all the authors for their excellent collaboration and for sharing with the *International Tables for Crystallography* their expertise. I hope that the tradition of keeping the contributions up to date will also persist in future editions of Volume B. This will be aided by significant improvements in various aspects of technical editing which were already apparent in the preparation of this edition.

Three greatly respected friends and colleagues who contributed to this and previous editions of Volume B passed away after the second edition of Volume B was published. These are Professors John Cowley, Boris Zvyagin and Donald Williams. I asked Professors John Spence, Douglas Dorset and Pawel Penczek to take care of any questions about the articles of the late John Cowley, Boris Zvyagin and Boris Vainshtein in Chapter 2.5, and Dr Bill Smith to answer any questions about Chapter 3.4 by the late Donald Williams. They all agreed promptly and I am most grateful for this.

My editorial work was carried out at the School of Chemistry of Tel Aviv University and I wish to acknowledge gratefully the facilities that were put at my disposal. I am grateful to many friends and colleagues for interesting conversations and exchanges related to this volume. Thanks are also due to my friends from the IUCr office in Chester for their helpful interest.

Finally, I think that the publication of the third edition of Volume B would not have been possible without the competent, tactful and friendly collaboration of Dr Nicola Ashcroft, the Technical Editor of this project during all the stages of the preparation of this edition.

SAMPLE PAGES

1.1. Reciprocal space in crystallography

By U. SHMUELI

1.1.1. Introduction

The purpose of this chapter is to provide an introduction to several aspects of reciprocal space, which are of general importance in crystallography and which appear in the various chapters and sections to follow. We first summarize the basic definitions and briefly inspect some fundamental aspects of crystallography, while recalling that they can be usefully and simply discussed in terms of the concept of the reciprocal lattice. This introductory section is followed by a summary of the basic relationships between the direct and associated reciprocal lattices. We then introduce the elements of tensor-algebraic formulation of such dual relationships, with emphasis on those that are important in many applications of reciprocal space to crystallographic algorithms. We proceed with a section that demonstrates the role of mutually reciprocal bases in transformations of coordinates and conclude with a brief outline of some important analytical aspects of reciprocal space, most of which are further developed in other parts of this volume.

1.1.2. Reciprocal lattice in crystallography

The notion of mutually reciprocal triads of vectors dates back to the introduction of vector calculus by J. Willard Gibbs in the 1880s (*e.g.* Wilson, 1901). This concept appeared to be useful in the early interpretations of diffraction from single crystals (Ewald, 1913; Laue, 1914) and its first detailed exposition and the recognition of its importance in crystallography can be found in Ewald's (1921) article. The following free translation of Ewald's (1921) introduction, presented in a somewhat different notation, may serve the purpose of this section:

To the set of \mathbf{a}_i , there corresponds in the vector calculus a set of 'reciprocal vectors' \mathbf{b}_i , which are defined (by Gibbs) by the following properties:

$$\mathbf{a}_i \cdot \mathbf{b}_k = 0 \quad (\text{for } i \neq k) \quad (1.1.2.1)$$

and

$$\mathbf{a}_i \cdot \mathbf{b}_i = 1, \quad (1.1.2.2)$$

where i and k may each equal 1, 2 or 3. The first equation, (1.1.2.1), says that each vector \mathbf{b}_k is perpendicular to two vectors \mathbf{a}_i , as follows from the vanishing scalar products. Equation (1.1.2.2) provides the norm of the vector \mathbf{b}_i : the length of this vector must be chosen such that the projection of \mathbf{b}_i on the direction of \mathbf{a}_i has the length $1/a_i$, where a_i is the magnitude of the vector \mathbf{a}_i ...

The consequences of equations (1.1.2.1) and (1.1.2.2) were elaborated by Ewald (1921) and are very well documented in the subsequent literature, crystallographic as well as other.

As is well known, the reciprocal lattice occupies a rather prominent position in crystallography and there are nearly as many accounts of its importance as there are crystallographic texts. It is not intended to review its applications, in any detail, in the present section; this is done in the remaining chapters and sections of the present volume. It seems desirable, however, to mention by way of an introduction some fundamental geometrical, physical and mathematical aspects of crystallography, and

try to give a unified demonstration of the usefulness of mutually reciprocal bases as an interpretive tool.

Consider the equation of a lattice plane in the direct lattice. It is shown in standard textbooks (*e.g.* Buerger, 1941) that this equation is given by

$$hx + ky + lz = n, \quad (1.1.2.3)$$

where h , k and l are relatively prime integers (*i.e.* not having a common factor other than +1 or -1), known as Miller indices of the lattice plane, x , y and z are the coordinates of any point lying in the plane and are expressed as fractions of the magnitudes of the basis vectors \mathbf{a} , \mathbf{b} and \mathbf{c} of the direct lattice, respectively, and n is an integer denoting the serial number of the lattice plane within the family of parallel and equidistant (hkl) planes, the interplanar spacing being denoted by d_{hkl} ; the value $n = 0$ corresponds to the (hkl) plane passing through the origin.

Let $\mathbf{r} = x\mathbf{a} + y\mathbf{b} + z\mathbf{c}$ and $\mathbf{r}_L = u\mathbf{a} + v\mathbf{b} + w\mathbf{c}$, where u , v , w are any integers, denote the position vectors of the point xyz and a lattice point uvw lying in the plane (1.1.2.3), respectively, and assume that \mathbf{r} and \mathbf{r}_L are different vectors. If the plane normal is denoted by \mathbf{N} , where \mathbf{N} is proportional to the vector product of two in-plane lattice vectors, the vector form of the equation of the lattice plane becomes

$$\mathbf{N} \cdot (\mathbf{r} - \mathbf{r}_L) = 0 \quad \text{or} \quad \mathbf{N} \cdot \mathbf{r} = \mathbf{N} \cdot \mathbf{r}_L. \quad (1.1.2.4)$$

For equations (1.1.2.3) and (1.1.2.4) to be identical, the plane normal \mathbf{N} must satisfy the requirement that $\mathbf{N} \cdot \mathbf{r}_L = n$, where n is an (unrestricted) integer.

Let us now consider the basic diffraction relations (*e.g.* Lipson & Cochran, 1966). Suppose a parallel beam of monochromatic radiation, of wavelength λ , falls on a lattice of identical point scatterers. If it is assumed that the scattering is elastic, *i.e.* there is no change of the wavelength during this process, the wavevectors of the incident and scattered radiation have the same magnitude, which can conveniently be taken as $1/\lambda$. A consideration of path and phase differences between the waves outgoing from two point scatterers separated by the lattice vector \mathbf{r}_L (defined as above) shows that the condition for their maximum constructive interference is given by

$$(\mathbf{s} - \mathbf{s}_0) \cdot \mathbf{r}_L = n, \quad (1.1.2.5)$$

where \mathbf{s}_0 and \mathbf{s} are the wavevectors of the incident and scattered beams, respectively, and n is an arbitrary integer.

Since $\mathbf{r}_L = u\mathbf{a} + v\mathbf{b} + w\mathbf{c}$, where u , v and w are unrestricted integers, equation (1.1.2.5) is equivalent to the equations of Laue:

$$\mathbf{h} \cdot \mathbf{a} = h, \quad \mathbf{h} \cdot \mathbf{b} = k, \quad \mathbf{h} \cdot \mathbf{c} = l, \quad (1.1.2.6)$$

where $\mathbf{h} = \mathbf{s} - \mathbf{s}_0$ is the diffraction vector, and h , k and l are integers corresponding to orders of diffraction from the three-dimensional lattice (Lipson & Cochran, 1966). The diffraction vector thus has to satisfy a condition that is analogous to that imposed on the normal to a lattice plane.

The next relevant aspect to be commented on is the Fourier expansion of a function having the periodicity of the crystal lattice. Such functions are *e.g.* the electron density, the density of nuclear matter and the electrostatic potential in the crystal, which are the operative definitions of crystal structure in X-ray, neutron and electron-diffraction methods of crystal structure determination. A Fourier expansion of such a periodic function may be

1.2. The structure factor

BY P. COPPENS

1.2.1. Introduction

The *structure factor* is the central concept in structure analysis by diffraction methods. Its modulus is called the *structure amplitude*. The structure amplitude is a function of the indices of the set of scattering planes h , k and l , and is defined as the amplitude of scattering by the contents of the crystallographic unit cell, expressed in units of scattering. For X-ray scattering, that unit is the scattering by a single electron (2.82×10^{-15} m), while for neutron scattering by atomic nuclei, the unit of scattering length of 10^{-14} m is commonly used. The complex form of the structure factor means that the phase of the scattered wave is not simply related to that of the incident wave. However, the observable, which is the scattered intensity, must be real. It is proportional to the square of the scattering amplitude (see, *e.g.*, Lipson & Cochran, 1966).

The structure factor is directly related to the distribution of scattering matter in the unit cell which, in the X-ray case, is the electron distribution, time-averaged over the vibrational modes of the solid.

In this chapter we will discuss structure-factor expressions for X-ray and neutron scattering, and, in particular, the modelling that is required to obtain an analytical description in terms of the features of the electron distribution and the vibrational displacement parameters of individual atoms. We concentrate on the most basic developments; for further details the reader is referred to the cited literature.

1.2.2. General scattering expression for X-rays

The total scattering of X-rays contains both elastic and inelastic components. Within the first-order Born approximation (Born, 1926) it has been treated by several authors (*e.g.* Waller & Hartree, 1929; Feil, 1977) and is given by the expression

$$I_{\text{total}}(\mathbf{S}) = I_{\text{classical}} \sum_n |\int \psi_n^* \exp(2\pi i \mathbf{S} \cdot \mathbf{r}_j) \psi_0 \, d\mathbf{r}|^2, \quad (1.2.2.1)$$

where $I_{\text{classical}}$ is the classical Thomson scattering of an X-ray beam by a free electron, which is equal to $(e^2/mc^2)^2(1 + \cos^2 2\theta)/2$ for an unpolarized beam of unit intensity, ψ is the n -electron space-wavefunction expressed in the $3n$ coordinates of the electrons located at \mathbf{r}_j and the integration is over the coordinates of all electrons. \mathbf{S} is the scattering vector of length $2 \sin \theta/\lambda$.

The coherent elastic component of the scattering, in units of the scattering of a free electron, is given by

$$I_{\text{coherent, elastic}}(\mathbf{S}) = |\int \psi_0^* \sum_j \exp(2\pi i \mathbf{S} \cdot \mathbf{r}_j) \psi_0 \, d\mathbf{r}|^2. \quad (1.2.2.2)$$

If integration is performed over all coordinates but those of the j th electron, one obtains after summation over all electrons

$$I_{\text{coherent, elastic}}(\mathbf{S}) = |\int \rho(\mathbf{r}) \exp(2\pi i \mathbf{S} \cdot \mathbf{r}) \, d\mathbf{r}|^2, \quad (1.2.2.3)$$

where $\rho(\mathbf{r})$ is the electron distribution. The scattering amplitude $A(\mathbf{S})$ is then given by

$$A(\mathbf{S}) = \int \rho(\mathbf{r}) \exp(2\pi i \mathbf{S} \cdot \mathbf{r}) \, d\mathbf{r} \quad (1.2.2.4a)$$

or

$$A(\mathbf{S}) = \hat{F}\{\rho(\mathbf{r})\}, \quad (1.2.2.4b)$$

where \hat{F} is the Fourier transform operator.

1.2.3. Scattering by a crystal: definition of a structure factor

In a crystal of infinite size, $\rho(\mathbf{r})$ is a three-dimensional periodic function, as expressed by the convolution

$$\rho_{\text{crystal}}(\mathbf{r}) = \sum_n \sum_m \sum_p \rho_{\text{unit cell}}(\mathbf{r}) * \delta(\mathbf{r} - n\mathbf{a} - m\mathbf{b} - p\mathbf{c}), \quad (1.2.3.1)$$

where n , m and p are integers, and δ is the Dirac delta function.

Thus, according to the Fourier convolution theorem,

$$A(\mathbf{S}) = \hat{F}\{\rho(\mathbf{r})\} = \sum_n \sum_m \sum_p \hat{F}\{\rho_{\text{unit cell}}(\mathbf{r})\} \hat{F}\{\delta(\mathbf{r} - n\mathbf{a} - m\mathbf{b} - p\mathbf{c})\}, \quad (1.2.3.2)$$

which gives

$$A(\mathbf{S}) = \hat{F}\{\rho_{\text{unit cell}}(\mathbf{r})\} \sum_h \sum_k \sum_l \delta(\mathbf{S} - h\mathbf{a}^* - k\mathbf{b}^* - l\mathbf{c}^*). \quad (1.2.3.3)$$

Expression (1.2.3.3) is valid for a crystal with a very large number of unit cells, in which particle-size broadening is negligible. Furthermore, it does not account for multiple scattering of the beam within the crystal. Because of the appearance of the delta function, (1.2.3.3) implies that $\mathbf{S} = \mathbf{H}$ with $\mathbf{H} = h\mathbf{a}^* + k\mathbf{b}^* + l\mathbf{c}^*$.

The first factor in (1.2.3.3), the scattering amplitude of one unit cell, is defined as the structure factor F :

$$F(\mathbf{H}) = \hat{F}\{\rho_{\text{unit cell}}(\mathbf{r})\} = \int_{\text{unit cell}} \rho(\mathbf{r}) \exp(2\pi i \mathbf{H} \cdot \mathbf{r}) \, d\mathbf{r}. \quad (1.2.3.4)$$

1.2.4. The isolated-atom approximation in X-ray diffraction

To a reasonable approximation, the unit-cell density can be described as a superposition of isolated, spherical atoms located at \mathbf{r}_j .

$$\rho_{\text{unit cell}}(\mathbf{r}) = \sum_j \rho_{\text{atom},j}(\mathbf{r}) * \delta(\mathbf{r} - \mathbf{r}_j). \quad (1.2.4.1)$$

Substitution in (1.2.3.4) gives

$$F(\mathbf{H}) = \sum_j \hat{F}\{\rho_{\text{atom},j}\} \hat{F}\{\delta(\mathbf{r} - \mathbf{r}_j)\} = \sum_j f_j \exp(2\pi i \mathbf{H} \cdot \mathbf{r}_j) \quad (1.2.4.2a)$$

or

$$\begin{aligned} F(h, k, l) &= \sum_j f_j \exp 2\pi i (hx_j + ky_j + lz_j) \\ &= \sum_j f_j \{\cos 2\pi (hx_j + ky_j + lz_j) \\ &\quad + i \sin 2\pi (hx_j + ky_j + lz_j)\}. \end{aligned} \quad (1.2.4.2b)$$

$f_j(S)$, the spherical atomic scattering factor, or form factor, is the Fourier transform of the spherically averaged atomic density $\rho_j(r)$, in which the polar coordinate r is relative to the nuclear position. $f_j(S)$ can be written as (James, 1982)

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Table 1.2.7.4. Closed-form expressions for Fourier transform of Slater-type functions (Avery & Watson, 1977; Su & Coppens, 1990)

$$\langle j_k \rangle \equiv \int_0^\infty r^N \exp(-Zr) j_k(Kr) dr, K = 4\pi \sin \theta / \lambda.$$

k	N							
	1	2	3	4	5	6	7	8
0	$\frac{1}{K^2 + Z^2}$	$\frac{2Z}{(K^2 + Z^2)^2}$	$\frac{2(3Z^2 - K^2)}{(K^2 + Z^2)^3}$	$\frac{24Z(Z^2 - K^2)}{(K^2 + Z^2)^4}$	$\frac{24(5Z^2 - 10K^2Z^2 + K^4)}{(K^2 + Z^2)^5}$	$\frac{240Z(K^2 - 3Z^2)(3K^2 - Z^2)}{(K^2 + Z^2)^6}$	$\frac{720(7Z^6 - 35K^2Z^4 + 21K^4Z^2 - K^6)}{(K^2 + Z^2)^7}$	$\frac{40320(Z^7 - 7K^2Z^5 + 7K^4Z^3 - K^6Z)}{(K^2 + Z^2)^8}$
1		$\frac{2K}{(K^2 + Z^2)^2}$	$\frac{8KZ}{(K^2 + Z^2)^3}$	$\frac{8K(5Z^2 - K^2)}{(K^2 + Z^2)^4}$	$\frac{48KZ(5Z^2 - 3K^2)}{(K^2 + Z^2)^5}$	$\frac{48K(35Z^4 - 42K^2Z^2 + 3K^4)}{(K^2 + Z^2)^6}$	$\frac{1920KZ(7Z^4 - 14K^2Z^2 + 3K^4)}{(K^2 + Z^2)^7}$	$\frac{5760K(21Z^6 - 63K^2Z^4 + 27K^4Z^2 - K^6)}{(K^2 + Z^2)^8}$
2			$\frac{8K^2}{(K^2 + Z^2)^3}$	$\frac{48K^2Z}{(K^2 + Z^2)^4}$	$\frac{48K^2(7Z^2 - K^2)}{(K^2 + Z^2)^5}$	$\frac{384K^2Z(7Z^2 - 3K^2)}{(K^2 + Z^2)^6}$	$\frac{1152K^2(21Z^4 - 18K^2Z^2 + K^4)}{(K^2 + Z^2)^7}$	$\frac{11520K^2Z(21Z^4 - 30K^2Z^2 + 5K^4)}{(K^2 + Z^2)^8}$
3				$\frac{48K^3}{(K^2 + Z^2)^4}$	$\frac{384K^3Z}{(K^2 + Z^2)^5}$	$\frac{384K^3(9Z^2 - K^2)}{(K^2 + Z^2)^6}$	$\frac{11520K^3Z(3Z^2 - K^2)}{(K^2 + Z^2)^7}$	$\frac{11520K^3(33Z^4 - 22K^2Z^2 + K^4)}{(K^2 + Z^2)^8}$
4					$\frac{384K^4}{(K^2 + Z^2)^5}$	$\frac{3840K^4Z}{(K^2 + Z^2)^6}$	$\frac{3840K^4(11Z^2 - K^2)}{(K^2 + Z^2)^7}$	$\frac{46080K^4Z(11Z^2 - 3K^2)}{(K^2 + Z^2)^8}$
5						$\frac{3840K^5}{(K^2 + Z^2)^6}$	$\frac{46080K^5Z}{(K^2 + Z^2)^7}$	$\frac{40680K^5(13Z^2 - K^2)}{(K^2 + Z^2)^8}$
6							$\frac{46080K^6}{(K^2 + Z^2)^7}$	$\frac{645120K^6Z}{(K^2 + Z^2)^8}$
7								$\frac{645120K^7}{(K^2 + Z^2)^8}$

$$P(u) = (2\pi\langle u^2 \rangle)^{-3/2} \exp\{-|u|^2/2\langle u^2 \rangle\}, \quad (1.2.10.1)$$

where $\langle u^2 \rangle$ is the mean-square displacement in any direction.

The corresponding trivariate normal distribution to be used for anisotropic harmonic motion is, in tensor notation,

$$P(\mathbf{u}) = \frac{|\sigma^{-1}|^{1/2}}{(2\pi)^{3/2}} \exp\{-\frac{1}{2}\sigma_{jk}^{-1}(u^j u^k)\}. \quad (1.2.10.2a)$$

Here σ is the variance-covariance matrix, with covariant components, and $|\sigma^{-1}|$ is the determinant of the inverse of σ . Summation over repeated indices has been assumed. The corresponding equation in matrix notation is

$$P(\mathbf{u}) = \frac{|\sigma^{-1}|^{1/2}}{(2\pi)^{3/2}} \exp\{-\frac{1}{2}(\mathbf{u})^T \sigma^{-1}(\mathbf{u})\}, \quad (1.2.10.2b)$$

where the superscript T indicates the transpose.

The characteristic function, or Fourier transform, of $P(\mathbf{u})$ is

$$T(\mathbf{H}) = \exp\{-2\pi^2 \sigma^{jk} h_j h_k\} \quad (1.2.10.3a)$$

or

$$T(\mathbf{H}) = \exp\{-2\pi^2 \mathbf{H}^T \sigma \mathbf{H}\}. \quad (1.2.10.3b)$$

With the change of variable $b^{jk} = 2\pi^2 \sigma^{jk}$, (1.2.10.3a) becomes

$$T(\mathbf{H}) = \exp\{-b^{jk} h_j h_k\}.$$

1.2.11. Rigid-body analysis

The treatment of rigid-body motion of molecules or molecular fragments was developed by Cruickshank (1956) and expanded into a general theory by Schomaker & Trueblood (1968). The theory has been described by Johnson (1970b) and by Dunitz (1979). The latter reference forms the basis for the following treatment.

The most general motions of a rigid body consist of rotations about three axes, coupled with translations parallel to each of the axes. Such motions correspond to screw rotations. A libration

around a vector λ ($\lambda_1, \lambda_2, \lambda_3$), with length corresponding to the magnitude of the rotation, results in a displacement $\delta \mathbf{r}$, such that

$$\delta \mathbf{r} = (\lambda \times \mathbf{r}) = \mathbf{D} \mathbf{r} \quad (1.2.11.1)$$

with

$$\mathbf{D} = \begin{bmatrix} 0 & -\lambda_3 & \lambda_2 \\ \lambda_3 & 0 & -\lambda_1 \\ -\lambda_2 & \lambda_1 & 0 \end{bmatrix}, \quad (1.2.11.2)$$

or in Cartesian tensor notation, assuming summation over repeated indices,

$$\delta r_i = D_{ij} r_j = -\varepsilon_{ijk} \lambda_k r_j \quad (1.2.11.3)$$

where the permutation operator ε_{ijk} equals +1 for i, j, k a cyclic permutation of the indices 1, 2, 3, or -1 for a noncyclic permutation, and zero if two or more indices are equal. For $i = 1$, for example, only the ε_{123} and ε_{132} terms occur. Addition of a translational displacement gives

$$\delta r_i = D_{ij} r_j + t_i. \quad (1.2.11.4)$$

When a rigid body undergoes vibrations the displacements vary with time, so suitable averages must be taken to derive the mean-square displacements. If the librational and translational motions are independent, the cross products between the two terms in (1.2.11.4) average to zero and the elements of the mean-square displacement tensor of atom n , U_{ij}^n , are given by

$$\begin{aligned} U_{11}^n &= +L_{22}r_3^2 + L_{33}r_2^2 - 2L_{23}r_2r_3 + T_{11} \\ U_{22}^n &= +L_{33}r_1^2 + L_{11}r_3^2 - 2L_{13}r_1r_3 + T_{22} \\ U_{33}^n &= +L_{11}r_2^2 + L_{22}r_1^2 - 2L_{12}r_1r_2 + T_{33} \\ U_{12}^n &= -L_{33}r_1r_2 - L_{12}r_3^2 + L_{13}r_2r_3 + L_{23}r_1r_3 + T_{12} \\ U_{13}^n &= -L_{22}r_1r_3 + L_{12}r_2r_3 - L_{13}r_2^2 + L_{23}r_1r_2 + T_{13} \\ U_{23}^n &= -L_{11}r_2r_3 + L_{12}r_1r_3 - L_{13}r_1r_2 - L_{23}r_1^2 + T_{23}, \end{aligned} \quad (1.2.11.5)$$

where the coefficients $L_{ij} = \langle \lambda_i \lambda_j \rangle$ and $T_{ij} = \langle t_i t_j \rangle$ are the elements of the 3×3 libration tensor \mathbf{L} and the 3×3 translation tensor \mathbf{T} , respectively. Since pairs of terms such as $\langle t_i t_j \rangle$ and $\langle t_j t_i \rangle$

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(5) *Parseval/Plancherel property*. If $\varphi, \psi, \Phi, \Psi$ are as above, then

$$\begin{aligned} (\mathcal{F}(\mathbf{N})[\Phi], \mathcal{F}(\mathbf{N})[\Psi])_W &= \frac{1}{|\det \mathbf{N}|} (\Phi, \Psi)_{W^*} \\ (\tilde{\mathcal{F}}(\mathbf{N})[\varphi], \tilde{\mathcal{F}}(\mathbf{N})[\psi])_W &= \frac{1}{|\det \mathbf{N}|} (\varphi, \psi)_W. \end{aligned}$$

(6) *Period 4*. When \mathbf{N} is symmetric, so that the ranges of indices k and k^* can be identified, it makes sense to speak of powers of $\mathcal{F}(\mathbf{N})$ and $\tilde{\mathcal{F}}(\mathbf{N})$. Then the ‘standardized’ matrices $(1/|\det \mathbf{N}|^{1/2})\mathcal{F}(\mathbf{N})$ and $(1/|\det \mathbf{N}|^{1/2})\tilde{\mathcal{F}}(\mathbf{N})$ are *unitary* matrices whose fourth power is the identity matrix (Section 1.3.2.4.3.4); their eigenvalues are therefore ± 1 and $\pm i$.

1.3.3. Numerical computation of the discrete Fourier transform

1.3.3.1. Introduction

The Fourier transformation’s most remarkable property is undoubtedly that of turning convolution into multiplication. As distribution theory has shown, other valuable properties – such as the shift property, the conversion of differentiation into multiplication by monomials, and the duality between periodicity and sampling – are special instances of the convolution theorem.

This property is exploited in many areas of applied mathematics and engineering (Campbell & Foster, 1948; Sneddon, 1951; Champeney, 1973; Bracewell, 1986). For example, the passing of a signal through a linear filter, which results in its being convolved with the response of the filter to a δ -function ‘impulse’, may be modelled as a multiplication of the signal’s transform by the transform of the impulse response (also called transfer function). Similarly, the solution of systems of partial differential equations may be turned by Fourier transformation into a division problem for distributions. In both cases, the formulations obtained after Fourier transformation are considerably simpler than the initial ones, and lend themselves to constructive solution techniques.

Whenever the functions to which the Fourier transform is applied are band-limited, or can be well approximated by band-limited functions, the discrete Fourier transform (DFT) provides a means of constructing explicit numerical solutions to the problems at hand. A great variety of investigations in physics, engineering and applied mathematics thus lead to DFT calculations, to such a degree that, at the time of writing, about 50% of all supercomputer CPU time is alleged to be spent calculating DFTs.

The straightforward use of the defining formulae for the DFT leads to calculations of size N^2 for N sample points, which become unfeasible for any but the smallest problems. Much ingenuity has therefore been exerted on the design and implementation of faster algorithms for calculating the DFT (McClellan & Rader, 1979; Nussbaumer, 1981; Blahut, 1985; Brigham, 1988). The most famous is that of Cooley & Tukey (1965) which heralded the age of digital signal processing. However, it had been preceded by the prime factor algorithm of Good (1958, 1960), which has lately been the basis of many new developments. Recent historical research (Goldstine, 1977, pp. 249–253; Heideman *et al.*, 1984) has shown that Gauss essentially knew the Cooley–Tukey algorithm as early as 1805 (before Fourier’s 1807 work on harmonic analysis!); while it has long been clear that Dirichlet knew of the basis of the prime factor algorithm and used it extensively in his theory of multiplicative characters [see *e.g.* Chapter I of Ayoub (1963), and Chapters 6 and 8 of Apostol (1976)]. Thus the computation of the DFT, far from being a purely technical and rather narrow piece of specialized numerical analysis, turns out to have very rich connections with such central areas of pure mathematics as number theory (algebraic and analytic), the representation

theory of certain Lie groups and coding theory – to list only a few. The interested reader may consult Auslander & Tolimieri (1979); Auslander, Feig & Winograd (1982, 1984); Auslander & Tolimieri (1985); Tolimieri (1985).

One-dimensional algorithms are examined first. The Sande mixed-radix version of the Cooley–Tukey algorithm only calls upon the additive structure of congruence classes of integers. The prime factor algorithm of Good begins to exploit some of their multiplicative structure, and the use of relatively prime factors leads to a stronger factorization than that of Sande. Fuller use of the multiplicative structure, *via* the group of units, leads to the Rader algorithm; and the factorization of short convolutions then yields the Winograd algorithms.

Multidimensional algorithms are at first built as tensor products of one-dimensional elements. The problem of factoring the DFT in several dimensions simultaneously is then examined. The section ends with a survey of attempts at formalizing the interplay between algorithm structure and computer architecture for the purpose of automating the design of optimal DFT code.

It was originally intended to incorporate into this section a survey of all the basic notions and results of abstract algebra which are called upon in the course of these developments, but time limitations have made this impossible. This material, however, is adequately covered by the first chapter of Tolimieri *et al.* (1989) in a form tailored for the same purposes. Similarly, the inclusion of numerous detailed examples of the algorithms described here has had to be postponed to a later edition, but an abundant supply of such examples may be found in the signal processing literature, for instance in the books by McClellan & Rader (1979), Blahut (1985), and Tolimieri *et al.* (1989).

1.3.3.2. One-dimensional algorithms

Throughout this section we will denote by $e(t)$ the expression $\exp(2\pi it)$, $t \in \mathbb{R}$. The mapping $t \mapsto e(t)$ has the following properties:

$$\begin{aligned} e(t_1 + t_2) &= e(t_1)e(t_2) \\ e(-t) &= \overline{e(t)} = [e(t)]^{-1} \\ e(t) &= 1 \Leftrightarrow t \in \mathbb{Z}. \end{aligned}$$

Thus e defines an isomorphism between the additive group \mathbb{R}/\mathbb{Z} (the reals modulo the integers) and the multiplicative group of complex numbers of modulus 1. It follows that the mapping $\ell \mapsto e(\ell/N)$, where $\ell \in \mathbb{Z}$ and N is a positive integer, defines an isomorphism between the one-dimensional residual lattice $\mathbb{Z}/N\mathbb{Z}$ and the multiplicative group of N th roots of unity.

The DFT on N points then relates vectors \mathbf{X} and \mathbf{X}^* in W and W^* through the linear transformations:

$$\begin{aligned} F(N) : \quad X(k) &= \frac{1}{N} \sum_{k^* \in \mathbb{Z}/N\mathbb{Z}} X^*(k^*) e(-k^*k/N) \\ \bar{F}(N) : \quad X^*(k^*) &= \sum_{k \in \mathbb{Z}/N\mathbb{Z}} X(k) e(k^*k/N). \end{aligned}$$

1.3.3.2.1. The Cooley–Tukey algorithm

The presentation of Gentleman & Sande (1966) will be followed first [see also Cochran *et al.* (1967)]. It will then be reinterpreted in geometric terms which will prepare the way for the treatment of multidimensional transforms in Section 1.3.3.3.

Suppose that the number of sample points N is composite, say $N = N_1 N_2$. We may write k to the base N_1 and k^* to the base N_2 as follows:

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Table A1.4.3.3. *Monoclinic space groups*

Each expression for A or B in the monoclinic system and for the space-group settings chosen in *IT* A is represented in terms of one of the following symbols:

$$\begin{aligned} c(hl)c(ky) &= \cos[2\pi(hx + lz)] \cos(2\pi ky), & c(hk)c(lz) &= \cos[2\pi(hx + ky)] \cos(2\pi lz), \\ c(hl)s(ky) &= \cos[2\pi(hx + lz)] \sin(2\pi ky), & c(hk)s(lz) &= \cos[2\pi(hx + ky)] \sin(2\pi lz), \\ s(hl)c(ky) &= \sin[2\pi(hx + lz)] \cos(2\pi ky), & s(hk)c(lz) &= \sin[2\pi(hx + ky)] \cos(2\pi lz), \\ s(hl)s(ky) &= \sin[2\pi(hx + lz)] \sin(2\pi ky), & s(hk)s(lz) &= \sin[2\pi(hx + ky)] \sin(2\pi lz), \end{aligned} \quad (\text{A1.4.3.1})$$

where the left-hand column of expressions corresponds to space-group representations in the second setting, with b taken as the unique axis, and the right-hand column corresponds to representations in the first setting, with c taken as the unique axis.

The lattice types in this table are P , A , B , C and I , and are all explicit in the full space-group symbol only (see below). Note that $s(hl)$, $s(hk)$, $s(ky)$ and $s(lz)$ are zero for $h = l = 0$, $h = k = 0$, $k = 0$ and $l = 0$, respectively.

No.	Group symbol		Parity	A	B	Unique axis
	Short	Full				
3	$P2$	$P121$		$2c(hl)c(ky)$	$2c(hl)s(ky)$	b
3	$P2$	$P112$		$2c(hk)c(lz)$	$2c(hk)s(lz)$	c
4	$P2_1$	$P12_11$	$k = 2n$	$2c(hl)c(ky)$	$2c(hl)s(ky)$	b
			$k = 2n + 1$	$-2s(hl)s(ky)$	$2s(hl)c(ky)$	
4	$P2_1$	$P112_1$	$l = 2n$	$2c(hk)c(lz)$	$2c(hk)s(lz)$	c
			$l = 2n + 1$	$-2s(hk)s(lz)$	$2s(hk)c(lz)$	
5	$C2$	$C121$		$4c(hl)c(ky)$	$4c(hl)s(ky)$	b
5	$C2$	$A121$		$4c(hl)c(ky)$	$4c(hl)s(ky)$	b
5	$C2$	$I121$		$4c(hl)c(ky)$	$4c(hl)s(ky)$	b
5	$C2$	$A112$		$4c(hk)c(lz)$	$4c(hk)s(lz)$	c
5	$C2$	$B112$		$4c(hk)c(lz)$	$4c(hk)s(lz)$	c
5	$C2$	$I112$		$4c(hk)c(lz)$	$4c(hk)s(lz)$	c
6	Pm	$P1m1$		$2c(hl)c(ky)$	$2s(hl)c(ky)$	b
6	Pm	$P11m$		$2c(hk)c(lz)$	$2s(hk)c(lz)$	c
7	Pc	$P1c1$	$l = 2n$	$2c(hl)c(ky)$	$2s(hl)c(ky)$	b
			$l = 2n + 1$	$-2s(hl)s(ky)$	$2c(hl)s(ky)$	
7	Pc	$P1n1$	$h + l = 2n$	$2c(hl)c(ky)$	$2s(hl)c(ky)$	b
			$h + l = 2n + 1$	$-2s(hl)s(ky)$	$2c(hl)s(ky)$	
7	Pc	$P1a1$	$h = 2n$	$2c(hl)c(ky)$	$2s(hl)c(ky)$	b
			$h = 2n + 1$	$-2s(hl)s(ky)$	$2c(hl)s(ky)$	
7	Pc	$P11a$	$h = 2n$	$2c(hk)c(lz)$	$2s(hk)c(lz)$	c
			$h = 2n + 1$	$-2s(hk)s(lz)$	$2c(hk)s(lz)$	
7	Pc	$P11n$	$h + k = 2n$	$2c(hk)c(lz)$	$2s(hk)c(lz)$	c
			$h + k = 2n + 1$	$-2s(hk)s(lz)$	$2c(hk)s(lz)$	
7	Pc	$P11b$	$k = 2n$	$2c(hk)c(lz)$	$2s(hk)c(lz)$	c
			$k = 2n + 1$	$-2s(hk)s(lz)$	$2c(hk)s(lz)$	
8	Cm	$C1m1$		$4c(hl)c(ky)$	$4s(hl)c(ky)$	b
8	Cm	$A1m1$		$4c(hl)c(ky)$	$4s(hl)c(ky)$	b
8	Cm	$I1m1$		$4c(hl)c(ky)$	$4s(hl)c(ky)$	b
8	Cm	$A11m$		$4c(hk)c(lz)$	$4s(hk)c(lz)$	c
8	Cm	$B11m$		$4c(hk)c(lz)$	$4s(hk)c(lz)$	c
8	Cm	$I11m$		$4c(hk)c(lz)$	$4s(hk)c(lz)$	c
9	Cc	$C1c1$	$l = 2n$	$4c(hl)c(ky)$	$4s(hl)c(ky)$	b
			$l = 2n + 1$	$-4s(hl)s(ky)$	$4c(hl)s(ky)$	
9	Cc	$A1n1$	$h + l = 2n$	$4c(hl)c(ky)$	$4s(hl)c(ky)$	b
			$h + l = 2n + 1$	$-4s(hl)s(ky)$	$4c(hl)s(ky)$	
9	Cc	$I1a1$	$h = 2n$	$4c(hl)c(ky)$	$4s(hl)c(ky)$	b
			$h = 2n + 1$	$-4s(hl)s(ky)$	$4c(hl)s(ky)$	
9	Cc	$A11a$	$h = 2n$	$4c(hk)c(lz)$	$4s(hk)c(lz)$	c
			$h = 2n + 1$	$-4s(hk)s(lz)$	$4c(hk)s(lz)$	
9	Cc	$B11n$	$h + k = 2n$	$4c(hk)c(lz)$	$4s(hk)c(lz)$	c
			$h + k = 2n + 1$	$-4s(hk)s(lz)$	$4c(hk)s(lz)$	
9	Cc	$I11b$	$k = 2n$	$4c(hk)c(lz)$	$4s(hk)c(lz)$	c
			$k = 2n + 1$	$-4s(hk)s(lz)$	$4c(hk)s(lz)$	
10	$P2/m$	$P12/m1$		$4c(hl)c(ky)$	0	b
10	$P2/m$	$P112/m$		$4c(hk)c(lz)$	0	c
11	$P2_1/m$	$P12_1/m1$	$k = 2n$	$4c(hl)c(ky)$	0	b
			$k = 2n + 1$	$-4s(hl)s(ky)$	0	

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Table A1.4.4.1 (*cont.*)

<i>P4</i> ₂ <i>2</i> No. 90 (143)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$: −110/2	(4) $\bar{k}hl$: −110/2
(5) $\bar{h}k\bar{l}$: −110/2	(6) $h\bar{k}l$: −110/2	(7) $kh\bar{l}$:	(8) $\bar{k}h\bar{l}$:
<i>P4</i> ₁ <i>22</i> No. 91 (144)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$: −001/2	(3) $k\bar{h}l$: −001/4	(4) $\bar{k}hl$: −003/4
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$: −001/2	(7) $kh\bar{l}$: −003/4	(8) $\bar{k}h\bar{l}$: −001/4
<i>P4</i> ₁ <i>2</i> ₁ <i>2</i> No. 92 (145)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$: −001/2	(3) $k\bar{h}l$: −221/4	(4) $\bar{k}hl$: −223/4
(5) $\bar{h}k\bar{l}$: −221/4	(6) $h\bar{k}l$: −223/4	(7) $kh\bar{l}$:	(8) $\bar{k}h\bar{l}$: −001/2
<i>P4</i> ₂ <i>22</i> No. 93 (146)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$: −001/2	(4) $\bar{k}hl$: −001/2
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $kh\bar{l}$: −001/2	(8) $\bar{k}h\bar{l}$: −001/2
<i>P4</i> ₂ <i>2</i> ₁ <i>2</i> No. 94 (147)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$: −111/2	(4) $\bar{k}hl$: −111/2
(5) $\bar{h}k\bar{l}$: −111/2	(6) $h\bar{k}l$: −111/2	(7) $kh\bar{l}$:	(8) $\bar{k}h\bar{l}$:
<i>P4</i> ₃ <i>22</i> No. 95 (148)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$: −001/2	(3) $k\bar{h}l$: −003/4	(4) $\bar{k}hl$: −001/4
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$: −001/2	(7) $kh\bar{l}$: −001/4	(8) $\bar{k}h\bar{l}$: −003/4
<i>P4</i> ₃ <i>2</i> ₁ <i>2</i> No. 96 (149)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$: −001/2	(3) $k\bar{h}l$: −223/4	(4) $\bar{k}hl$: −221/4
(5) $\bar{h}k\bar{l}$: −223/4	(6) $h\bar{k}l$: −221/4	(7) $kh\bar{l}$:	(8) $\bar{k}h\bar{l}$: −001/2
<i>I4</i> ₂₂ No. 97 (150)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$:	(4) $\bar{k}hl$:
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $kh\bar{l}$:	(8) $\bar{k}h\bar{l}$:
<i>I4</i> ₂₂ No. 98 (151)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$: −111/2	(3) $k\bar{h}l$: −021/4	(4) $\bar{k}hl$: −203/4
(5) $\bar{h}k\bar{l}$: −203/4	(6) $h\bar{k}l$: −021/4	(7) $kh\bar{l}$: −111/2	(8) $\bar{k}h\bar{l}$:

Point group: <i>4mm</i> Tetragonal Laue group: <i>4/mmm</i>			
<i>P4mm</i> No. 99 (152)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$:	(4) $\bar{k}hl$:
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $\bar{k}h\bar{l}$:	(8) $kh\bar{l}$:
<i>P4bm</i> No. 100 (153)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$:	(4) $\bar{k}hl$:
(5) $\bar{h}k\bar{l}$: −110/2	(6) $h\bar{k}l$: −110/2	(7) $\bar{k}h\bar{l}$: −110/2	(8) $kh\bar{l}$: −110/2
<i>P4</i> ₂ <i>cm</i> No. 101 (154)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$: −001/2	(4) $\bar{k}hl$: −001/2
(5) $\bar{h}k\bar{l}$: −001/2	(6) $h\bar{k}l$: −001/2	(7) $\bar{k}h\bar{l}$:	(8) $kh\bar{l}$:
<i>P4</i> ₂ <i>nm</i> No. 102 (155)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$: −111/2	(4) $\bar{k}hl$: −111/2
(5) $\bar{h}k\bar{l}$: −111/2	(6) $h\bar{k}l$: −111/2	(7) $\bar{k}h\bar{l}$:	(8) $kh\bar{l}$:
<i>P4cc</i> No. 103 (156)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$:	(4) $\bar{k}hl$:
(5) $\bar{h}k\bar{l}$: −001/2	(6) $h\bar{k}l$: −001/2	(7) $\bar{k}h\bar{l}$: −001/2	(8) $kh\bar{l}$: −001/2
<i>P4nc</i> No. 104 (157)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$:	(4) $\bar{k}hl$:
(5) $\bar{h}k\bar{l}$: −111/2	(6) $h\bar{k}l$: −111/2	(7) $\bar{k}h\bar{l}$: −111/2	(8) $kh\bar{l}$: −111/2

<i>P4</i> ₂ <i>mc</i> No. 105 (158)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$: −001/2	(4) $\bar{k}hl$: −001/2
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $\bar{k}h\bar{l}$: −001/2	(8) $kh\bar{l}$: −001/2
<i>P4</i> ₂ <i>bc</i> No. 106 (159)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$: −001/2	(4) $\bar{k}hl$: −001/2
(5) $\bar{h}k\bar{l}$: −110/2	(6) $h\bar{k}l$: −110/2	(7) $\bar{k}h\bar{l}$: −111/2	(8) $kh\bar{l}$: −111/2
<i>I4mm</i> No. 107 (160)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$:	(4) $\bar{k}hl$:
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $\bar{k}h\bar{l}$:	(8) $kh\bar{l}$:
<i>I4cm</i> No. 108 (161)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}l$:	(4) $\bar{k}hl$:
(5) $\bar{h}k\bar{l}$: −001/2	(6) $h\bar{k}l$: −001/2	(7) $\bar{k}h\bar{l}$: −001/2	(8) $kh\bar{l}$: −001/2
<i>I4</i> ₁ <i>md</i> No. 109 (162)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$: −111/2	(3) $k\bar{h}l$: −021/4	(4) $\bar{k}hl$: −203/4
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$: −111/2	(7) $\bar{k}h\bar{l}$: −203/4	(8) $kh\bar{l}$: −021/4
<i>I4</i> ₁ <i>cd</i> No. 110 (163)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$: −111/2	(3) $k\bar{h}l$: −021/4	(4) $\bar{k}hl$: −203/4
(5) $\bar{h}k\bar{l}$: −001/2	(6) $h\bar{k}l$: −110/2	(7) $\bar{k}h\bar{l}$: −201/4	(8) $kh\bar{l}$: −023/4

Point group: <i>4̄2m</i> Tetragonal Laue group: <i>4/mmm</i>			
<i>P4̄2m</i> No. 111 (164)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $\bar{k}h\bar{l}$:	(8) $kh\bar{l}$:
<i>P4̄2c</i> No. 112 (165)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$: −001/2	(6) $h\bar{k}l$: −001/2	(7) $\bar{k}h\bar{l}$: −001/2	(8) $kh\bar{l}$: −001/2
<i>P4̄2</i> ₁ <i>m</i> No. 113 (166)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$: −110/2	(6) $h\bar{k}l$: −110/2	(7) $\bar{k}h\bar{l}$: −110/2	(8) $kh\bar{l}$: −110/2
<i>P4̄2</i> ₁ <i>c</i> No. 114 (167)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$: −111/2	(6) $h\bar{k}l$: −111/2	(7) $\bar{k}h\bar{l}$: −111/2	(8) $kh\bar{l}$: −111/2
<i>P4̄m</i> ₂ No. 115 (168)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $kh\bar{l}$:	(8) $\bar{k}h\bar{l}$:
<i>P4̄c</i> ₂ No. 116 (169)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$: −001/2	(6) $h\bar{k}l$: −001/2	(7) $kh\bar{l}$: −001/2	(8) $\bar{k}h\bar{l}$: −001/2
<i>P4̄b</i> ₂ No. 117 (170)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$: −110/2	(6) $h\bar{k}l$: −110/2	(7) $kh\bar{l}$: −110/2	(8) $\bar{k}h\bar{l}$: −110/2
<i>P4̄n</i> ₂ No. 118 (171)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$: −111/2	(6) $h\bar{k}l$: −111/2	(7) $kh\bar{l}$: −111/2	(8) $\bar{k}h\bar{l}$: −111/2
<i>I4̄m</i> ₂ No. 119 (172)			
(1) <i>hkl</i> :	(2) $\bar{h}\bar{k}l$:	(3) $k\bar{h}\bar{l}$:	(4) $\bar{k}\bar{h}l$:
(5) $\bar{h}k\bar{l}$:	(6) $h\bar{k}l$:	(7) $kh\bar{l}$:	(8) $\bar{k}h\bar{l}$:

1.5. CLASSIFICATION OF SPACE-GROUP REPRESENTATIONS

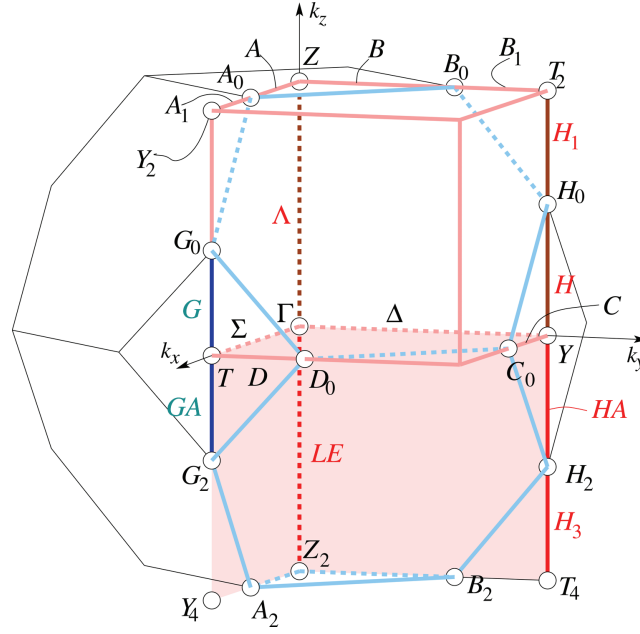


Fig. 1.5.5.5. Brillouin zone with asymmetric unit and representation domain of CDML for arithmetic crystal class $mm2F$: $a^{-2} < b^{-2} + c^{-2}$, $b^{-2} < c^{-2} + a^{-2}$ and $c^{-2} < a^{-2} + b^{-2}$. Space groups $Fmm2 - C_{2v}^{18}$ (42), $Fdd2 - C_{2v}^{19}$ (43). Reciprocal-space group $(Imm2)^*$, No. 44: $a^{*2} < b^{*2} + c^{*2}$, $b^{*2} < c^{*2} + a^{*2}$ and $c^{*2} < a^{*2} + b^{*2}$ (see Table 1.5.5.5). The representation domain of CDML is different from the asymmetric unit. Auxiliary points: T_4 : $0, \frac{1}{2}, -\frac{1}{2}$; Y_2 : $\frac{1}{2}, 0, \frac{1}{2}$; Y_4 : $\frac{1}{2}, 0, -\frac{1}{2}$; Z_2 : $0, 0, -\frac{1}{2}$. Flagpoles: $0, 0, z$: $-\frac{1}{2} < z < 0$; $0, \frac{1}{2}, z$: $-\frac{1}{2} < z < 0$. Wings: $x, 0, z$: $0 < x < \frac{1}{2}, -\frac{1}{2} < z < 0$; $0, y, z$: $0 < y < \frac{1}{2}, -\frac{1}{2} < z < 0$.

Table 1.5.5.5. List of \mathbf{k} -vector types for arithmetic crystal class $mm2F$: $a^{-2} < b^{-2} + c^{-2}$, $b^{-2} < c^{-2} + a^{-2}$ and $c^{-2} < a^{-2} + b^{-2}$

See Fig. 1.5.5.5. Parameter relations: $x = -\frac{1}{2}\alpha + \frac{1}{2}\beta + \frac{1}{2}\gamma$, $y = \frac{1}{2}\alpha - \frac{1}{2}\beta + \frac{1}{2}\gamma$, $z = \frac{1}{2}\alpha + \frac{1}{2}\beta - \frac{1}{2}\gamma$.

\mathbf{k} -vector label, CDML	Wyckoff position of IT A, cf. Section 1.5.4.3	Parameters
Γ $0, 0, 0$	ex 2 a $mm2$	$0, 0, 0$
Z $\frac{1}{2}, \frac{1}{2}, 0$	ex 2 a $mm2$	$0, 0, \frac{1}{2}$
Λ $\alpha, \alpha, 0$	ex 2 a $mm2$	$0, 0, z$: $0 < z < \frac{1}{2}$
LE $-\alpha, -\alpha, 0$	ex 2 a $mm2$	$0, 0, z$: $-\frac{1}{2} < z < 0$
$\Gamma \cup \Lambda \cup Z \cup LE$	2 a $mm2$	$0, 0, z$: $-\frac{1}{2} < z \leq \frac{1}{2}$
T $0, \frac{1}{2}, \frac{1}{2}$	ex 2 b $mm2$	$\frac{1}{2}, 0, 0$
$T \sim T_2$		$0, \frac{1}{2}, \frac{1}{2}$
Y $\frac{1}{2}, 0, \frac{1}{2}$	ex 2 b $mm2$	$0, \frac{1}{2}, 0$
G $\alpha, \frac{1}{2} + \alpha, \frac{1}{2}$	ex 2 b $mm2$	$\frac{1}{2}, 0, z$: $0 < z \leq g_0$
$G \sim H_3 = [H_2 T_4]$		$0, \frac{1}{2}, z$: $-\frac{1}{2} < z \leq -\frac{1}{2} + g_0 = h_2$
GA $-\alpha, \frac{1}{2} - \alpha, \frac{1}{2}$	ex 2 b $mm2$	$\frac{1}{2}, 0, z$: $g_2 = -g_0 < z < 0$
$GA \sim H_1 = [H_0 T_2]$		$0, \frac{1}{2}, z$: $\frac{1}{2} - g_0 = h_0 < z < \frac{1}{2}$
H $\frac{1}{2} + \alpha, \alpha, \frac{1}{2}$	ex 2 b $mm2$	$0, \frac{1}{2}, z$: $0 < z \leq h_0$
HA $\frac{1}{2} - \alpha, -\alpha, \frac{1}{2}$	ex 2 b $mm2$	$0, \frac{1}{2}, z$: $h_2 = -h_0 < z < 0$
$T_2 \cup H_1 \cup H \cup Y \cup HA \cup H_3$	2 b $mm2$	$0, \frac{1}{2}, z$: $-\frac{1}{2} < z \leq \frac{1}{2}$
Σ $0, \alpha, \alpha$	ex 4 c $.m.$	$x, 0, 0$: $0 < x < \frac{1}{2}$
A $\frac{1}{2}, \frac{1}{2} + \alpha, \alpha$	ex 4 c $.m.$	$x, 0, \frac{1}{2}$: $0 < x \leq a_0$
C $\frac{1}{2}, \alpha, \frac{1}{2} + \alpha$	ex 4 c $.m.$	$x, \frac{1}{2}, 0$: $0 < x < c_0 = \frac{1}{2} - a_0$
$C \sim A_1$		$x, 0, \frac{1}{2}$: $\frac{1}{2} - a_0 = c_0 < x < \frac{1}{2}$
J $\alpha, \alpha + \beta, \beta$	ex 4 c $.m.$	$x, 0, z$: $[\Gamma Z A_0 G_0 T]$
JA $-\alpha, -\alpha + \beta, \beta$	ex 4 c $.m.$	$x, 0, z$: $[\Gamma T G_2 A_2 Z_2]$
K $\frac{1}{2} + \alpha, \alpha + \beta, \frac{1}{2} + \beta$	ex 4 c $.m.$	$x, \frac{1}{2}, z$: $[Y H_0 C_0]$
$K \sim J_1$		$x, 0, z$: $[Y_4 G_2 A_2]$
KA $\frac{1}{2} - \alpha, -\alpha + \beta, \frac{1}{2} + \beta$	ex 4 c $.m.$	$x, \frac{1}{2}, z$: $[Y C_0 H_2]$
$KA \sim J_3$		$x, 0, z$: $[Y_2 G_0 A_0]$
$A \cup A_1 \cup J \cup J_3 \cup \Sigma \cup JA \cup J_1$	4 c $.m.$	$x, 0, z$: $0 < x < \frac{1}{2}, 0 < z \leq \frac{1}{2}$
Δ $\alpha, 0, \alpha$	ex 4 d $.m..$	$0, y, 0$: $0 < y < \frac{1}{2}$
B $\frac{1}{2} + \alpha, \frac{1}{2}, \alpha$	ex 4 d $.m..$	$0, y, \frac{1}{2}$: $0 < y < b_0$
D $\alpha, \frac{1}{2}, \frac{1}{2} + \alpha$	ex 4 d $.m..$	$\frac{1}{2}, y, 0$: $0 < y \leq d_0$
$D \sim B_1$		$0, y, \frac{1}{2}$: $\frac{1}{2} - d_0 = b_0 \leq y < \frac{1}{2}$
E $\alpha + \beta, \alpha, \beta$	ex 4 d $.m..$	$0, y, z$: $[\Gamma Y H_0 B_0 Z]$
EA $-\alpha + \beta, -\alpha, \beta$	ex 4 d $.m..$	$0, y, z$: $[\Gamma Z_2 B_2 H_2 Y]$
F $\alpha + \beta, \frac{1}{2} + \alpha, \frac{1}{2} + \beta$	ex 4 d $.m..$	$\frac{1}{2}, y, z$: $[T D_0 G_0]$
$F \sim E_3$		$0, y, z$: $[B_2 T_4 H_2]$
FA $-\alpha + \beta, \frac{1}{2} - \alpha, \frac{1}{2} + \beta$	ex 4 d $.m..$	$\frac{1}{2}, y, z$: $[T G_2 D_0]$
$FA \sim E_1$		$0, y, z$: $[T_2 B_0 H_0]$
$\Delta \cup B \cup B_1 \cup E \cup E_1 \cup EA \cup E_3$	4 d $.m..$	$0, y, z$: $0 < y < \frac{1}{2}, -\frac{1}{2} < z \leq \frac{1}{2}$
GP α, β, γ	8 e 1	x, y, z : $0 < x, y < \frac{1}{2}, 0 < z \leq \frac{1}{2}$

2. RECIPROCAL SPACE IN CRYSTAL-STRUCTURE DETERMINATION

tion to the structure factor as a random variable. This is of course a necessary requirement for any statistical treatment. If, however, the atomic composition of the asymmetric unit is widely heterogeneous, the structure factor is then a sum of unequally distributed random variables and the Lindeberg–Lévy version of the central-limit theorem (*cf.* Section 2.1.4.4) cannot be expected to apply. Other versions of this theorem might still predict a normal p.d.f. of the sum, but at the expense of a correspondingly large number of terms/atoms. It is well known that atomic heterogeneity gives rise to severe deviations from ideal behaviour (*e.g.* Howells *et al.*, 1950) and one of the aims of crystallographic statistics has been the introduction of a correct dependence on the atomic composition into the non-ideal p.d.f.'s [for a review of the early work on non-ideal distributions see Srinivasan & Parthasarathy (1976)]. A somewhat less well known fact is that the dependence of the p.d.f.'s of $|E|$ on space-group symmetry becomes more conspicuous as the composition becomes more heterogeneous (*e.g.* Shmueli, 1979; Shmueli & Wilson, 1981). Hence both the composition and the symmetry dependence of the intensity statistics are of interest. Other problems, which likewise give rise to non-ideal p.d.f.'s, are the presence of heavy atoms in (variable) special positions, heterogeneous structures with complete or partial noncrystallographic symmetry, and the presence of outstandingly heavy dispersive scatterers.

The need for theoretical representations of non-ideal p.d.f.'s is exemplified in Fig. 2.1.7.1, which shows the ideal centric and acentric p.d.f.'s together with a frequency histogram of $|E|$ values, recalculated for a centrosymmetric structure containing a platinum atom in the asymmetric unit of $P\bar{1}$ (Faggiani *et al.*, 1980). Clearly, the deviation from the Gaussian p.d.f., predicted by the central-limit theorem, is here very large and a comparison with the possible ideal distributions can (in this case) lead to wrong conclusions.

Two general approaches have so far been employed in derivations of non-ideal p.d.f.'s which account for the above-mentioned problems: the correction-factor approach, to be dealt with in the following sections, and the more recently introduced Fourier method, to which Section 2.1.8 is dedicated. In what follows, we introduce briefly the mathematical background of the correction-factor approach, apply this formalism to centric and acentric non-ideal p.d.f.'s, and present the numerical values of the moments of the trigonometric structure factor which permit an approximate evaluation of such p.d.f.'s for all the three-dimensional space groups.

2.1.7.2. Mathematical background

Suppose that $p(x)$ is a p.d.f. which accurately describes the experimental distribution of the random variable x , where x is related to a sum of random variables and can be assumed to obey (to some approximation) an ideal p.d.f., say $p^{(0)}(x)$, based on the central-limit theorem. In the correction-factor approach we seek to represent $p(x)$ as

$$p(x) = p^{(0)}(x) \sum_k d_k f_k(x), \quad (2.1.7.1)$$

where d_k are coefficients which depend on the cause of the deviation of $p(x)$ from the central-limit theorem approximation and $f_k(x)$ are suitably chosen functions of x . A choice of the set $\{f_k\}$ is deemed suitable, if only from a practical point of view, if it allows the convenient introduction of the cause of the above deviation of $p(x)$ into the expansion coefficients d_k . This requirement is satisfied – also from a theoretical point of view – by taking $f_k(x)$ as a set of polynomials which are orthogonal with respect to the ideal p.d.f., taken as their weight function (*e.g.* Cramér, 1951). That is, the functions $f_k(x)$ so chosen have to obey the relationship

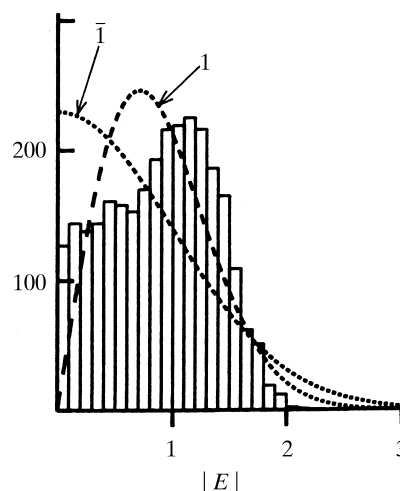


Fig. 2.1.7.1. Atomic heterogeneity and intensity statistics. The histogram appearing in this figure was constructed from $|E|$ values which were recalculated from atomic parameters published for the centrosymmetric structure of $C_6H_{18}Cl_2N_4O_4Pt$ (Faggiani *et al.*, 1980). The space group of the crystal is $P\bar{1}$, $Z = 2$, *i.e.* all the atoms are located in general positions. The figure shows a comparison of the recalculated distribution of $|E|$ with the ideal centric [equation (2.1.5.11)] and acentric [equation (2.1.5.8)] p.d.f.'s, denoted by $\bar{1}$ and 1, respectively.

$$\int_a^b f_k(x) f_m(x) p^{(0)}(x) dx = \delta_{km} = \begin{cases} 1, & \text{if } k = m \\ 0, & \text{if } k \neq m \end{cases}, \quad (2.1.7.2)$$

where $[a, b]$ is the range of existence of all the functions involved. It can be readily shown that the coefficients d_k are given by

$$d_k = \int_a^b f_k(x) p(x) dx = \langle f_k(x) \rangle = \sum_{n=0}^k c_n^{(k)} \langle x^n \rangle, \quad (2.1.7.3)$$

where the brackets $\langle \rangle$ in equation (2.1.7.3) denote averaging with respect to the *unknown* p.d.f. $p(x)$ and $c_n^{(k)}$ is the coefficient of the n th power of x in the polynomial $f_k(x)$. The coefficients d_k are thus directly related to the moments of the non-ideal distribution and the coefficients of the powers of x in the orthogonal polynomials. The latter coefficients can be obtained by the Gram–Schmidt procedure (*e.g.* Spiegel, 1974), or by direct use of the Szegő determinants (*e.g.* Cramér, 1951), for any weight function that has finite moments. However, the feasibility of the present approach depends on our ability to obtain the moments $\langle x^n \rangle$ without the knowledge of the non-ideal p.d.f., $p(x)$.

2.1.7.3. Application to centric and acentric distributions

We shall summarize here the non-ideal centric and acentric distributions of the magnitude of the normalized structure factor E (*e.g.* Shmueli & Wilson, 1981; Shmueli, 1982). We assume that (i) all the atoms are located in general positions and have rationally independent coordinates, (ii) all the scatterers are dispersionless, and (iii) there is no noncrystallographic symmetry. Arbitrary atomic composition and space-group symmetry are admitted. The appropriate weight functions and the corresponding orthogonal polynomials are

$p^{(0)}(E)$	$f_k(x)$	Non-ideal distribution
$(2/\pi)^{1/2} \exp(- E ^2/2)$	$He_{2k}(E)/[(2k)!]^{1/2}$	Centric
$2 E \exp(- E ^2)$	$L_k(E ^2)$	Acentric

(2.1.7.4)

2.2. Direct methods

By C. GIACOVAZZO

2.2.1. List of symbols and abbreviations

f_j	atomic scattering factor of j th atom
Z_j	atomic number of j th atom
N	number of atoms in the unit cell
m	order of the point group

$$[\sigma_r]_p, [\sigma_r]_q, [\sigma_r]_N, \dots = \sum_{j=1}^p Z_j^r, \sum_{j=1}^q Z_j^r, \sum_{j=1}^N Z_j^r, \dots$$

$[\sigma_r]_N$ is always abbreviated to σ_r when N is the number of atoms in the cell

$$\sum_p, \sum_q, \sum_N, \dots = \sum_{j=1}^p f_j^2, \sum_{j=1}^q f_j^2, \sum_{j=1}^N f_j^2, \dots$$

s.f.	structure factor
n.s.f.	normalized structure factor
cs.	centrosymmetric
ncs.	noncentrosymmetric
s.i.	structure invariant
s.s.	structure seminvariant
$\mathbf{C} = (\mathbf{R}, \mathbf{T})$	symmetry operator; \mathbf{R} is the rotational part, \mathbf{T} the translational part
$\varphi_{\mathbf{h}}$	phase of the structure factor $F_{\mathbf{h}} = F_{\mathbf{h}} \exp(i\varphi_{\mathbf{h}})$

2.2.2. Introduction

Direct methods are today the most widely used tool for solving small crystal structures. They work well both for equal-atom molecules and when a few heavy atoms exist in the structure. In recent years the theoretical background of direct methods has been improved to take into account a large variety of prior information (the form of the molecule, its orientation, a partial structure, the presence of pseudosymmetry or of a superstructure, the availability of isomorphous data or of data affected by anomalous-dispersion effects, ...). Owing to this progress and to the increasing availability of powerful computers, the phase problem for small molecules has been solved in practice: a number of effective, highly automated packages are today available to the scientific community.

The combination of direct methods with so-called direct-space methods have recently allowed the *ab initio* crystal structure solution of proteins. The present limit of complexity is about 2500 non-hydrogen atoms in the asymmetric unit, but diffraction data at atomic resolution (~ 1 Å) are required. Trials are under way to bring this limit to 1.5 Å and have shown some success.

The theoretical background and tables useful for origin specification are given in Section 2.2.3; in Section 2.2.4 the procedures for normalizing structure factors are summarized. Phase-determining formulae (inequalities, probabilistic formulae for triplet, quartet and quintet invariants, and for one- and two-phase s.s.'s, determinantal formulae) are given in Section 2.2.5. In Section 2.2.6 the connection between direct methods and related techniques in real space is discussed. Practical procedures for solving small-molecule crystal structures are described in Sections 2.2.7 and 2.2.8, and references to the most extensively used packages are given in Section 2.2.9. The integration of direct methods, isomorphous replacement and anomalous-dispersion techniques is briefly discussed in Section 2.2.10.

The reader interested in a more detailed description of the topic is referred to a recent textbook (Giacovazzo, 1998).

2.2.3. Origin specification

(a) Once the origin has been chosen, the symmetry operators $\mathbf{C}_s \equiv (\mathbf{R}_s, \mathbf{T}_s)$ and, through them, the algebraic form of the s.f. remain fixed.

A shift of the origin through a vector with coordinates \mathbf{X}_0 transforms $\varphi_{\mathbf{h}}$ into

$$\varphi'_{\mathbf{h}} = \varphi_{\mathbf{h}} - 2\pi \mathbf{h} \cdot \mathbf{X}_0 \quad (2.2.3.1)$$

and the symmetry operators \mathbf{C}_s into $\mathbf{C}'_s = (\mathbf{R}'_s, \mathbf{T}'_s)$, where

$$\mathbf{R}'_s = \mathbf{R}_s; \quad \mathbf{T}'_s = \mathbf{T}_s + (\mathbf{R}_s - \mathbf{I})\mathbf{X}_0 \quad s = 1, 2, \dots, m. \quad (2.2.3.2)$$

(b) *Allowed or permissible origins* (Hauptman & Karle, 1953, 1959) for a given algebraic form of the s.f. are all those points in direct space which, when taken as origin, maintain the same symmetry operators \mathbf{C}_s . The allowed origins will therefore correspond to those points having the same symmetry environment in the sense that they are related to the symmetry elements in the same way. For instance, if $\mathbf{T}_s = 0$ for $s = 1, \dots, 8$, then the allowed origins in *Pmmm* are the eight inversion centres.

To each functional form of the s.f. a set of permissible origins will correspond.

(c) A translation between permissible origins will be called a *permissible* or *allowed translation*. Trivial allowed translations correspond to the lattice periods or to their multiples. A change of origin by an allowed translation does not change the algebraic form of the s.f. Thus, according to (2.2.3.2), all origins allowed by a fixed functional form of the s.f. will be connected by translational vectors \mathbf{X}_p such that

$$(\mathbf{R}_s - \mathbf{I})\mathbf{X}_p = \mathbf{V}, \quad s = 1, 2, \dots, m, \quad (2.2.3.3)$$

where \mathbf{V} is a vector with zero or integer components.

In centred space groups, an origin translation corresponding to a centring vector \mathbf{B}_v does not change the functional form of the s.f. Therefore all vectors \mathbf{B}_v represent permissible translations. \mathbf{X}_p will then be an allowed translation (Giacovazzo, 1974) not only when, as imposed by (2.2.3.3), the difference $\mathbf{T}'_s - \mathbf{T}_s$ is equal to one or more lattice units, but also when, for any s , the condition

$$(\mathbf{R}_s - \mathbf{I})\mathbf{X}_p = \mathbf{V} + \alpha \mathbf{B}_v, \quad s = 1, 2, \dots, m; \quad \alpha = 0, 1 \quad (2.2.3.4)$$

is satisfied.

We will call any set of cs. or ncs. space groups having the same allowed origin translations a Hauptman-Karle group (H-K group). The 94 ncs. primitive space groups, the 62 primitive cs. groups, the 44 ncs. centred space groups and the 30 cs. centred space groups can be collected into 13, 4, 14 and 5 H-K groups, respectively (Hauptman & Karle, 1953, 1956; Karle & Hauptman, 1961; Lessinger & Wondratschek, 1975). In Tables 2.2.3.1–2.2.3.4 the H-K groups are given together with the allowed origin translations.

(d) Let us consider a product of structure factors

$$\begin{aligned} F_{\mathbf{h}_1}^{A_1} \times F_{\mathbf{h}_2}^{A_2} \times \dots \times F_{\mathbf{h}_n}^{A_n} &= \prod_{j=1}^n F_{\mathbf{h}_j}^{A_j} \\ &= \exp\left(i \sum_{j=1}^n A_j \varphi_{\mathbf{h}_j}\right) \prod_{j=1}^n |F_{\mathbf{h}_j}|^{A_j}, \end{aligned} \quad (2.2.3.5)$$

A_j being integer numbers.

2.2. DIRECT METHODS

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XTAL3.6.1: Hall, S. R., du Boulay, D. J. & Olthof-Hazekamp, R. (1999). *Xtal3.6 crystallographic software*. <http://xtal.sourceforge.net/>.

2.2.10. Direct methods in macromolecular crystallography

2.2.10.1. Introduction

The smallest protein molecules contain about 400 non-hydrogen atoms, so they cannot be solved *ab initio* by the algorithms specified in Sections 2.2.7 and 2.2.8. However, traditional direct methods are applied for:

- (a) improvement of the accuracy of the available phases (refinement process);
- (b) extension of phases from lower to higher resolution (phase-extension process).

The application of standard tangent techniques to (a) and (b) has not been found to be very satisfactory (Coulter & Dewar, 1971; Hendrickson *et al.*, 1973; Weinzierl *et al.*, 1969). Tangent methods, in fact, require atomicity and non-negativity of the electron density. Both these properties are not satisfied if data do not extend to atomic resolution ($d > 1.2$ Å). Because of series termination and other errors the electron-density map at $d > 1.2$ Å presents large negative regions which will appear as false peaks in the squared structure. However, tangent methods use only a part of the information given by the Sayre equation (2.2.6.5). In fact, (2.2.6.5) express two equations relating the radial and angular parts of the two sides, so obtaining a large degree of overdetermination of the phases. To achieve this Sayre (1972) [see also Sayre & Toupin (1975)] suggested minimizing (2.2.10.1) by least squares as a function of the phases:

$$\sum_{\mathbf{h}} \left| a_{\mathbf{h}} F_{\mathbf{h}} - \sum_{\mathbf{k}} F_{\mathbf{k}} F_{\mathbf{h}-\mathbf{k}} \right|^2. \quad (2.2.10.1)$$

Even if tests on rubredoxin (extensions of phases from 2.5 to 1.5 Å resolution) and insulin (Cutfield *et al.*, 1975) (from 1.9 to 1.5 Å resolution) were successful, the limitations of the method are its high cost and, especially, the higher efficiency of the least-squares method. Equivalent considerations hold for the application of determinantal methods to proteins [see Podjarny *et al.* (1981); de Rango *et al.* (1985) and literature cited therein].

A question now arises: why is the tangent formula unable to solve protein structures? Fan *et al.* (1991) considered the question from a first-principle approach and concluded that:

- (1) the triplet phase probability distribution is very flat for proteins (N is very large) and close to the uniform distribution;

- (2) low-resolution data create additional problems for direct methods since the number of available phase relationships per reflection is small.

Sheldrick (1990) suggested that direct methods are not expected to succeed if fewer than half of the reflections in the range 1.1–1.2 Å are observed with $|F| > 4\sigma(|F|)$ (a condition seldom satisfied by protein data).

The most complete analysis of the problem has been made by Giacovazzo, Guagliardi *et al.* (1994). They observed that the expected value of α (see Section 2.2.7) suggested by the tangent formula for proteins is comparable with the variance of the α parameter. In other words, for proteins the signal determining the phase is comparable with the noise, and therefore the phase indication is expected to be unreliable.

Quite relevant results have recently been obtained by integrating direct methods with some additional experimental information. In particular, we will describe the combination of direct methods with:

- (a) direct-space techniques for the *ab initio* crystal structure solution of proteins;
- (b) isomorphous-replacement (SIR–MIR) techniques;
- (c) anomalous-dispersion (SAD–MAD) techniques;
- (d) molecular replacement.

Point (d) will not be treated here, as it is described extensively in *IT F*, Part 13.

2.2.10.2. *Ab initio* crystal structure solution of proteins

Ab initio techniques do not require prior information of any atomic positions. The recent tremendous increase in computing speed led to direct methods evolving towards the rapid development of multisolution techniques. The new algorithms of the program *Shake-and-Bake* (Weeks *et al.*, 1994; Weeks & Miller, 1999; Hauptman *et al.*, 1999) allowed an impressive extension of the structural complexity amenable to direct phasing. In particular we mention: (a) the minimal principle (De Titta *et al.*, 1994), according to which the phase problem is considered as a constrained global optimization problem; (b) the refinement procedure, which alternately uses direct- and reciprocal-space techniques; and (c) the parameter-shift optimization technique (Bhuiya & Stanley, 1963), which aims at reducing the value of the minimal function (Hauptman, 1991; De Titta *et al.*, 1994). An effective variant of *Shake-and-Bake* is *SHELXD* (Sheldrick, 1998) which cyclically alternates tangent refinement in reciprocal space with peak-list optimisation procedures in real space (Sheldrick & Gould, 1995). Detailed information on these programs is available in *IT F* (2001), Part 16.

A different approach is used by *ACORN* (Foadi *et al.*, 2000), which first locates a small fragment of the molecule (eventually by molecular-replacement techniques) to obtain a useful nonrandom starting set of phases, and then refines them by means of solvent-flattening techniques.

The program *SIR2004* (Burla *et al.*, 2005) uses the tangent formula as well as automatic Patterson techniques to obtain a first imperfect structural model; then direct-space techniques are used to refine the model. The Patterson approach is based on the use of the superposition minimum function (Buerger, 1959; Richardson & Jacobson, 1987; Sheldrick, 1992; Pavelčík, 1988; Pavelčík *et al.*, 1992; Burla *et al.*, 2004). It may be worth noting that even this approach is of multisolution type: up to 20 trial solutions are provided by using as pivots the highest maxima in the superposition minimum function.

It is today possible to solve structures up to 2500 non-hydrogen atoms in the asymmetric unit provided data at atomic (about 1 Å) resolution are available. Proteins with data at quasi-atomic resolution (say up to 1.5–1.6 Å) can also be solved, but with greater difficulties (Burla *et al.*, 2005). A simple evaluation of the potential of the *ab initio* techniques suggests that the structural complexity range and the resolution limits amenable to the *ab*

2.3. Patterson and molecular replacement techniques, and the use of noncrystallographic symmetry in phasing

BY L. TONG, M. G. ROSSMANN AND E. ARNOLD

2.3.1. Introduction

2.3.1.1. Background

Historically, the Patterson has been used in a variety of ways to effect the solutions of crystal structures. While some simple structures (Ketelaar & de Vries, 1939; Hughes, 1940; Speakman, 1949; Shoemaker *et al.*, 1950) were solved by direct analysis of Patterson syntheses, alternative methods have largely superseded this procedure. An early innovation was the heavy-atom method which depends on the location of a small number of relatively strong scatterers (Harker, 1936). Image-seeking methods and Patterson superposition techniques were first contemplated in the late 1930s (Wrinch, 1939) and applied sometime later (Beevers & Robertson, 1950; Clastre & Gay, 1950; Garrido, 1950a; Buerger, 1959). This experience provided the encouragement for computerized vector-search methods to locate individual atoms automatically (Mighell & Jacobson, 1963; Kraut, 1961; Hamilton, 1965; Simpson *et al.*, 1965) or to position known molecular fragments in unknown crystal structures (Nordman & Nakatsu, 1963; Huber, 1965). The Patterson function has been used extensively in conjunction with the isomorphous replacement method (Rossmann, 1960; Blow, 1958) or anomalous dispersion (Rossmann, 1961a) to determine the position of heavy-atom substitution. Pattersons have been used to detect the presence and relative orientation of multiple copies of a given chemical motif in the crystallographic asymmetric unit in the same or different crystals (Rossmann & Blow, 1962). Finally, the orientation and placement of known molecular structures ('molecular replacement') into unknown crystal structures can be accomplished *via* Patterson techniques.

The function, introduced by Patterson in 1934 (Patterson, 1934a,b), is a convolution of electron density with itself and may be defined as

$$P(\mathbf{u}) = \int_V \rho(\mathbf{x}) \cdot \rho(\mathbf{u} + \mathbf{x}) d\mathbf{x}, \quad (2.3.1.1)$$

where $P(\mathbf{u})$ is the 'Patterson' function at \mathbf{u} , $\rho(\mathbf{x})$ is the crystal's periodic electron density and V is the volume of the unit cell. The Patterson function, or F^2 series, can be calculated directly from the experimentally derived X-ray intensities as

$$P(\mathbf{u}) = \frac{2}{V^2} \sum_{\mathbf{h}}^{\text{hemisphere}} |\mathbf{F}_{\mathbf{h}}|^2 \cos 2\pi \mathbf{h} \cdot \mathbf{u}. \quad (2.3.1.2)$$

The derivation of (2.3.1.2) from (2.3.1.1) can be found in this volume (see Section 1.3.4.2.1.6) along with a discussion of the physical significance and symmetry of the Patterson function, although the principal properties will be restated here.

The Patterson can be considered to be a vector map of all the pairwise interactions between the atoms in a unit cell. The vectors in a Patterson correspond to vectors in the real (direct) crystal cell but translated to the Patterson origin. Their weights are proportional to the product of densities at the tips of the vectors in the real cell. The Patterson unit cell has the same size as the real crystal cell. The symmetry of the Patterson comprises the Laue point group of the crystal cell plus any additional lattice symmetry due to Bravais centring. The reduction of the real

space group to the Laue symmetry is produced by the translation of all vectors to the Patterson origin and the introduction of a centre of symmetry. The latter is a consequence of the relationship between the vectors \mathbf{AB} and \mathbf{BA} . The Patterson symmetries for all 230 space groups are tabulated in *IT A* (2005).

An analysis of Patterson peaks can be obtained by considering N atoms with form factors f_i in the unit cell. Then

$$\mathbf{F}_{\mathbf{h}} = \sum_{i=1}^N f_i \exp(2\pi i \mathbf{h} \cdot \mathbf{x}_i).$$

Using Friedel's law,

$$\begin{aligned} |\mathbf{F}_{\mathbf{h}}|^2 &= \mathbf{F}_{\mathbf{h}} \cdot \mathbf{F}_{\mathbf{h}}^* \\ &= \left[\sum_{i=1}^N f_i \exp(2\pi i \mathbf{h} \cdot \mathbf{x}_i) \right] \left[\sum_{j=1}^N f_j \exp(-2\pi i \mathbf{h} \cdot \mathbf{x}_j) \right], \end{aligned}$$

which can be decomposed to

$$|\mathbf{F}_{\mathbf{h}}|^2 = \sum_{i=1}^N f_i^2 + \sum_{i \neq j}^N \sum_{j=1}^N f_i f_j \exp[2\pi i \mathbf{h} \cdot (\mathbf{x}_i - \mathbf{x}_j)]. \quad (2.3.1.3)$$

On substituting (2.3.1.3) in (2.3.1.2), we see that the Patterson consists of the sum of N^2 total interactions of which N are of weight f_i^2 at the origin and $N(N-1)$ are of weight $f_i f_j$ at $\mathbf{x}_i - \mathbf{x}_j$.

The weight of a peak in a real cell is given by

$$w_i = \int_U \rho_i(\mathbf{x}) d\mathbf{x} = Z_i \quad (\text{the atomic number}),$$

where U is the volume of the atom i . By analogy, the weight of a peak in a Patterson (form factor $f_i f_j$) will be given by

$$w_{ij} = \int_U P_{ij}(\mathbf{u}) d\mathbf{u} = Z_i Z_j.$$

Although the maximum height of a peak will depend on the spread of the peak, it is reasonable to assume that heights of peaks in a Patterson are proportional to the products of the atomic numbers of the interacting atoms.

There are a total of N^2 interactions in a Patterson due to N atoms in the crystal cell. These can be represented as an $N \times N$ square matrix whose elements \mathbf{u}_{ij} , w_{ij} indicate the position and weight of the peak produced between atoms i and j (Table 2.3.1.1). The N vectors corresponding to the diagonal of this matrix are located at the Patterson origin and arise from the convolution of each atom with itself. This leaves $N(N-1)$ vectors whose locations depend on the relative positions of all of the atoms in the crystal cell and whose weights depend on the atom types related by the vector. Complete specification of the unique non-origin Patterson vectors requires description of only the $N(N-1)/2$ elements in either the upper or the lower triangle of this matrix, since the two sets of vectors represented by the two triangles are related by a centre of symmetry

2.4. Isomorphous replacement and anomalous scattering

BY M. VIJAYAN AND S. RAMASESHAN†

2.4.1. Introduction

Isomorphous replacement is among the earliest methods to be employed for crystal structure determination (Cork, 1927). The power of this method was amply demonstrated in the classical X-ray work of J. M. Robertson on phthalocyanine in the 1930s using centric data (Robertson, 1936; Robertson & Woodward, 1937). The structure determination of strychnine sulfate pentahydrate by Bijvoet and others provides an early example of the application of this method to acentric reflections (Bokhoven *et al.*, 1951). The usefulness of isomorphous replacement in the analysis of complex protein structures was demonstrated by Perutz and colleagues (Green *et al.*, 1954). This was closely followed by developments in the methodology for the application of isomorphous replacement to protein work (Harker, 1956; Blow & Crick, 1959) and rapidly led to the first ever structure solution of two related protein crystals, namely, those of myoglobin and haemoglobin (Kendrew *et al.*, 1960; Cullis *et al.*, 1961*b*). Since then isomorphous replacement has been the method of choice in macromolecular crystallography and most of the subsequent developments in and applications of this method have been concerned with biological macromolecules, mainly proteins (Blundell & Johnson, 1976; McPherson, 1982).

The application of anomalous-scattering effects has often developed in parallel with that of isomorphous replacement. Indeed, the two methods are complementary to a substantial extent and they are often treated together, as in this article. Although the most important effect of anomalous scattering, namely, the violation of Friedel's law, was experimentally observed as early as 1930 (Coster *et al.*, 1930), two decades elapsed before this effect was made use of for the first time by Bijvoet and his associates for the determination of the absolute configuration of asymmetric molecules as well as for phase evaluation (Bijvoet, 1949, 1954; Bijvoet *et al.*, 1951). Since then there has been a phenomenal spurt in the application of anomalous-scattering effects (Srinivasan, 1972; Ramaseshan & Abrahams, 1975; Vijayan, 1987). A quantitative formulation for the determination of phase angles using intensity differences between Friedel equivalents was derived by Ramachandran & Raman (1956), while Okaya & Pepinsky (1956) successfully developed a Patterson approach involving anomalous effects. The anomalous-scattering method of phase determination has since been used in the structure analysis of several structures, including those of a complex derivative of vitamin B₁₂ (Dale *et al.*, 1963) and a small protein (Hendrickson & Teeter, 1981). In the meantime, the effect of changes in the real component of the dispersion correction as a function of the wavelength of the radiation used, first demonstrated by Mark & Szillard (1925), also received considerable attention. This effect, which is formally equivalent to that of isomorphous replacement, was demonstrated to be useful in structure determination (Ramaseshan *et al.*, 1957; Ramaseshan, 1963). Protein crystallographers have been quick to exploit anomalous-scattering effects (Rossmann, 1961; Kartha & Parthasarathy, 1965; North, 1965; Matthews, 1966; Hendrickson, 1979) and, as in the case of the isomorphous replacement method, the most useful applications of anomalous scattering during the last two decades have been perhaps in the field of macromolecular crystallography (Kartha, 1975; Watenpugh *et al.*, 1975; Vijayan, 1981). In addition to anomalous scattering of X-rays, that of neutrons was also found to have

interesting applications (Koetzle & Hamilton, 1975; Sikka & Rajagopal, 1975). More recently there has been a further revival in the development of anomalous-scattering methods with the advent of synchrotron radiation, particularly in view of the possibility of choosing any desired wavelength from a synchrotron-radiation source (Helliwell, 1984).

It is clear from the foregoing that the isomorphous replacement and the anomalous-scattering methods have a long and distinguished history. It is therefore impossible to do full justice to them in a comparatively short presentation like the present one. Several procedures for the application of these methods have been developed at different times. Many, although of considerable historical importance, are not extensively used at present for a variety of reasons. No attempt has been made to discuss them in detail here; the emphasis is primarily on the state of the art as it exists now. The available literature on isomorphous replacement and anomalous scattering is extensive. The reference list given at the end of this part is representative rather than exhaustive.

During the past few years, rapid developments have taken place in the isomorphous replacement and anomalous-scattering methods, particularly in the latter, as applied to macromolecular crystallography. These developments are described in detail in *International Tables for Crystallography*, Volume F (2001). Therefore, they have not been dealt with in this chapter. Significant developments in applications of direct methods to macromolecular crystallography have also occurred in recent years. A summary of these developments as well as the traditional direct methods on which the recent progress is based are presented in Chapter 2.2.

2.4.2. Isomorphous replacement method

2.4.2.1. Isomorphous replacement and isomorphous addition

Two crystals are said to be isomorphous if (a) both have the same space group and unit-cell dimensions and (b) the types and the positions of atoms in both are the same except for a replacement of one or more atoms in one structure with different types of atoms in the other (isomorphous replacement) or the presence of one or more additional atoms in one of them (isomorphous addition). Consider two crystal structures with identical space groups and unit-cell dimensions, one containing N atoms and the other M atoms. The N atoms in the first structure contain subsets P and Q whereas the M atoms in the second structure contain subsets P , Q' and R . The subset P is common to both structures in terms of atomic positions and atom types. The atomic positions are identical in subsets Q and Q' , but at any given atomic position the atom type is different in Q and Q' . The subset R exists only in the second structure. If \mathbf{F}_N and \mathbf{F}_M denote the structure factors of the two structures for a given reflection,

$$\mathbf{F}_N = \mathbf{F}_P + \mathbf{F}_Q \quad (2.4.2.1)$$

and

$$\mathbf{F}_M = \mathbf{F}_P + \mathbf{F}_{Q'} + \mathbf{F}_R, \quad (2.4.2.2)$$

where the quantities on the right-hand side represent contributions from different subsets. From (2.4.2.1) and (2.4.2.2) we have

† Deceased.

2.5. Electron diffraction and electron microscopy in structure determination

BY J. M. COWLEY,[†] J. C. H. SPENCE, M. TANAKA, B. K. VAINSHTEIN,[†] B. B. ZVYAGIN,[†] P. A. PENCZEK
AND D. L. DORSET

2.5.1. Foreword

BY J. M. COWLEY AND J. C. H. SPENCE

Given that electrons have wave properties and the wavelengths lie in a suitable range, the diffraction of electrons by matter is completely analogous to the diffraction of X-rays. While for X-rays the scattering function is the electron-density distribution, for electrons it is the potential distribution which is similarly peaked at the atomic sites. Hence, in principle, electron diffraction may be used as the basis for crystal structure determination. In practice it is used much less widely than X-ray diffraction for the determination of crystal structures but is receiving increasing attention as a means for obtaining structural information not readily accessible with X-ray- or neutron-diffraction techniques.

Electrons having wavelengths comparable with those of the X-rays commonly used in diffraction experiments have energies of the order of 100 eV. For such electrons, the interactions with matter are so strong that they can penetrate only a few layers of atoms on the surfaces of solids. They are used extensively for the study of surface structures by low-energy electron diffraction (LEED) and associated techniques. These techniques are not covered in this series of volumes, which include the principles and practice of only those diffraction and imaging techniques making use of high-energy electrons, having energies in the range of 20 keV to 1 MeV or more, in transmission through thin specimens.

For the most commonly used energy ranges of high-energy electrons, 100 to 400 keV, the wavelengths are about 50 times smaller than for X-rays. Hence the scattering angles are much smaller, of the order of 10^{-2} rad, the recording geometry is relatively simple and the diffraction pattern represents, to a useful first approximation, a planar section of reciprocal space. Extinction distances are hundreds of ångströms, which, when combined with typical lattice spacings, produces rocking-curve widths which are, unlike the X-ray case, a significant fraction of the Bragg angle.

The elastic scattering of electrons by atoms is several orders of magnitude greater than for X-rays. This fact has profound consequences, which in some cases are highly favourable and in other cases are serious hindrances to structure analysis work. On the one hand it implies that electron-diffraction patterns can be obtained from very small single-crystal regions having thicknesses equal to only a few layers of atoms and, with recently developed techniques, having diameters equivalent to only a few interatomic distances. Hence single-crystal patterns can be obtained from microcrystalline phases.

However, the strong scattering of electrons implies that the simple kinematical single-scattering approximation, on which most X-ray diffraction structure analysis is based, fails for electrons except for very thin crystals composed of light-atom materials. Strong dynamical diffraction effects occur for crystals which may be 100 Å thick, or less for heavy-atom materials. As a consequence, the theory of dynamical diffraction for electrons has been well developed, particularly for the particular special diffracting conditions relevant to the transmission of fast electrons (see Chapter 5.2), and observations of dynamical diffraction effects are commonly made and quantitatively interpreted. The possibility has thus arisen of using the observation of

dynamical diffraction effects as the basis for obtaining crystal structure information. The fact that dynamical diffraction is dependent on the relative phases of the diffracted waves then implies that relative phase information can be deduced from the diffraction intensities and the limitations of kinematical diffraction, such as Friedel's law, do not apply. The most immediately practicable method for making use of this possibility is convergent-beam electron diffraction (CBED) as described in Section 2.5.3.

A further important factor, determining the methods for observing electron diffraction, is that, being charged particles, electrons can be focused by electromagnetic lenses. Many of the resolution-limiting aberrations of cylindrical magnetic lenses have now been eliminated through the use of aberration-correction devices, so that for weakly scattering samples the resolution is limited to about 1 Å by electronic and mechanical instabilities. This is more than sufficient to distinguish the individual rows of atoms, parallel to the incident beam, in the principal orientations of most crystalline phases. Thus 'structure images' can be obtained, sometimes showing direct representation of projections of crystal structures [see *IT C* (2004), Section 4.3.8]. However, the complications of dynamical scattering and of the coherent imaging processes are such that the image intensities vary strongly with crystal thickness and tilt, and with the defocus or other parameters of the imaging system, making the interpretation of images difficult except in special circumstances. Fortunately, computer programs are readily available whereby image intensities can be calculated for model structures [see *IT C* (2004), Section 4.3.6]. Hence the means exist for deriving the projection of the structure if only by a process of trial and error and not, as would be desirable, from a direct interpretation of the observations.

The accuracy with which the projection of a structure can be deduced from an image, or series of images, improves as the resolution of the microscope improves but is not at all comparable with the accuracy attainable with X-ray diffraction methods. A particular virtue of high-resolution electron microscopy as a structural tool is that it may give information on individual small regions of the sample. Structures can be determined of 'phases' existing over distances of only a few unit cells and the defects and local disorders can be examined, one by one.

The observation of electron-diffraction patterns forms an essential part of the technique of structure imaging in high-resolution electron microscopy, because the diffraction patterns are used to align the crystals to appropriate axial orientations. More generally, for all electron microscopy of crystalline materials the image interpretation depends on knowledge of the diffraction conditions. Fortunately, the diffraction pattern and image of any specimen region can be obtained in rapid succession by a simple switching of lens currents. The ready comparison of the image and diffraction data has become an essential component of the electron microscopy of crystalline materials but has also been of fundamental importance for the development of electron-diffraction theory and techniques. The development of the nanodiffraction method in the field-emission scanning transmission electron microscope (STEM) has allowed micro-diffraction patterns to be obtained from subnanometre-sized regions, and so has become the ideal tool for the structural analysis of the new microcrystalline phases important to nanoscience. The direct phasing of these coherent nanodiffraction patterns is an active field of research.

[†] Deceased.

2. RECIPROCAL SPACE IN CRYSTAL-STRUCTURE DETERMINATION

Table 2.5.3.9. Dynamical extinction lines appearing in ZOLZ reflections for all crystal space groups except Nos. 1 and 2

Point groups 2, m , $2/m$ (second setting, unique axis b)

Space group	Incident-beam direction		
	$[h0l]$		
3 $P2$			
4 $P2_1$	$0k0$ 2_1	A_2 B_3	B_2
5 $C2$			
6 Pm			
7 Pc	$h0l_o$ c	A_2 A_3	B_2
8 Cm			
9 Cc	h_e0l_o c	A_2 A_3	B_2
10 $P2/m$			
11 $P2_1/m$	$0k0$ 2_1	A_2 B_3	B_2
12 $C2/m$			
13 $P2/c$	$h0l_o$ c	A_2 A_3	B_2
14 $P2_1/c$	$0k0$ 2_1	A_2 B_3	B_2
	$h0l_o$ c	A_2 A_3	B_2
15 $C2/c$	h_e0l_o c	A_2 A_3	B_2

Point group 222

Space group	Incident-beam direction					
	$[100]$	$[010]$	$[001]$	$[hk0]$	$[0kl]$	$[h0l]$
16 $P222$						
17 $P222_1$	$00l$ 2_1	A_2 B_3	$00l$ 2_1	A_2 B_3	$00l$ 2_1	A_2 B_3
18 $P2_12_12$	$0k0$ 2_{12}	A_2 B_3	$h00$ 2_{11}	A_2 B_3	$h00$ 2_{11}	A_2 B_3
19 $P2_12_12_1$	$0k0$ 2_{12} $00l$ 2_{13}	A_2 B_3	$h00$ 2_{11} $00l$ 2_{13}	A_2 B_3	$00l$ 2_{13}	A_2 B_3
20 $C222_1$	$00l$ 2_1	A_2 B_3	$00l$ 2_1	A_2 B_3	$00l$ 2_1	A_2 B_3
21 $C222$						
22 $F222$						
23 $I222$						
24 $I2_12_12_1$						

Point group $mm2$

Space group	Incident-beam direction					
	$[100]$	$[010]$	$[001]$	$[hk0]$	$[0kl]$	$[h0l]$
25 $Pmm2$						
26 $Pmc2_1$	$00l$ $c, 2_1$	A_2 A_3	B_2 B_3	$00l$ 2_1	A_2 B_3	$h0l_o$ c
27 $Pcc2$	$00l$ c_2	A_3	$00l$ c_1	A_3	$0kl_o$ c_1	A_2 A_3
28 $Pma2$			$h00$ a	A_2 A_3	B_2	h_o0l a
29 $Pca2_1$	$00l$ 2_1	B_3	$00l$ $c, 2_1$	A_2 A_3	B_2 B_3	h_o0l a

2. RECIPROCAL SPACE IN CRYSTAL-STRUCTURE DETERMINATION

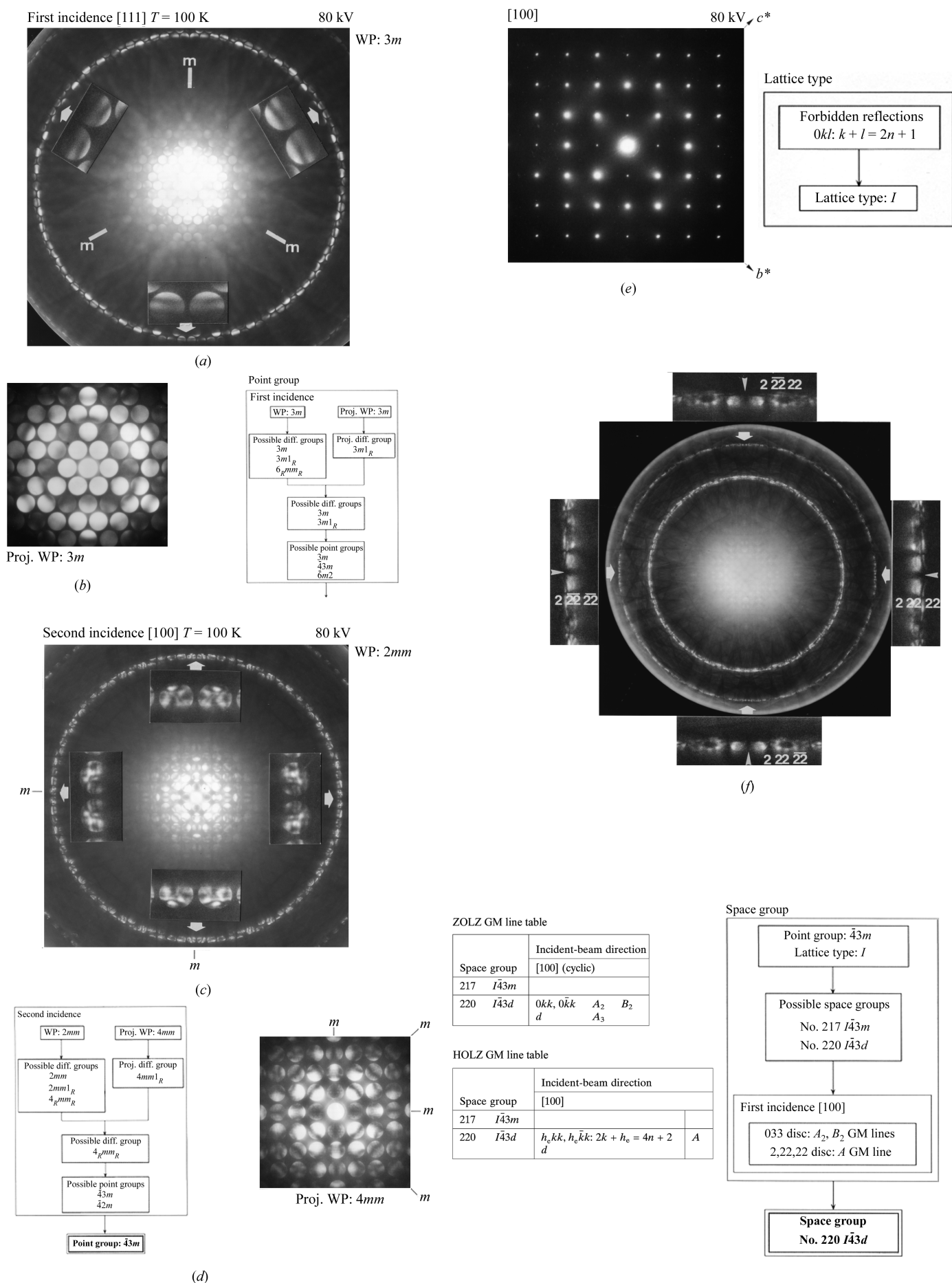


Fig. 2.5.3.16. CBED patterns of Sm_3Se_4 . The procedures for identifying the symmetry are also shown. (a, b) [111] incidence at 80 kV: the WP symmetry is $3m$ (a) and the projection (proj.) WP symmetry is $3m$ (b). (c, d) [100] incidence at 80 kV: the WP symmetry is $2mm$ (c) and the projection WP symmetry is $4mm$ (d). Dynamical extinction lines A_2 and A_3 are seen (d). The point group is determined to be $43m$. (e) Spot diffraction pattern taken with the [100] incidence at 80 kV shows the absence of $0kl$ reflections. The lattice type is determined to be I . (f) [100] incidence at 100 kV: dynamical extinction lines A in HOLZ reflections confirm the existence of a glide plane. The space group is determined to be $I\bar{4}3d$.

2.5. ELECTRON DIFFRACTION AND ELECTRON MICROSCOPY IN STRUCTURE DETERMINATION

cation second' approach. It is possible to reverse this order by using invariants with the supporting rationale that once approximately homogeneous classes of images were found, it should be easy to align them subsequently as within each class they will share the same motif.

A practical approach to reference-free alignment known as *alignment by classification* (Dube *et al.*, 1993) is based on the observation that for a very large data set and centred particles one can expect that although the in-plane rotation is arbitrary, there is a high chance that at least some of the similar images will be in the same rotational orientation. Therefore, in this approach the images are first (approximately) centred, then subjected to classification, and subsequently aligned.

In its simplest form, the *multireference alignment* belongs to the class of *supervised classification* methods: given a set of templates (*i.e.*, reference images; these can be selected unprocessed particle projections, or class averages that resulted from preceding analysis, or projections of a previously determined EM structure, or projections of an X-ray crystallographic structure), each of the images from the available data sets is compared (using a selected discrepancy measure) with all templates and assigned to the class represented by the most similar one. Equally often multireference alignment is understood as a form of *unsupervised classification*, more precisely *K-means* classification, even if the description is not formalized in terms of the latter. Given a number of initial 2D templates, the images are compared with all templates and assigned to the most similar one. New templates are calculated by averaging images assigned to their predecessors and the whole procedure is repeated until a stable solution is reached.

2.5.7.7. Initial determination of 3D structure using tilt experiments

The 2D analysis of projection images provides insight into the behaviour of the protein on the grid in terms of the structural consistency and the number and shape of projection images. In order to obtain 3D information, it is necessary to find geometrical relations between different observed 2D images. The most robust and historically the earliest approach is based on tilt experiments. By tilting the stage in the microscope and acquiring additional pictures of the same area of the grid it is possible to collect projection images of the same molecule with some of the required Eulerian angles determined accurately by the setting of the goniometer of the microscope.

In random conical tilt (RCT) reconstruction (Radermacher *et al.*, 1987), two micrographs of the same specimen area are collected: the first one is recorded at a tilt angle of $\sim 50^\circ$ while the second one is recorded at 0° (Fig. 2.5.7.3). If particles have preferred orientation on the support carbon film (or within the amorphous ice layer, if no carbon support is used), the projections of particles in the tilted micrographs form a conical tilt series. Since in-plane rotations of particles are random, the azimuthal angles of the projections of tilted particles are also randomly distributed; hence the name of the method. The untilted image is required for two reasons: (i) the particle projections from the untilted image are classified, thus a subset corresponding to possibly identical images can be selected ensuring that the projections originated from similar and similarly oriented structures; and (ii) the in-plane rotation angle found during alignment corresponds to the azimuthal angles in three dimensions (one of the three Eulerian angles needed). The second Eulerian angle, the tilt, is either taken from the microscope setting of the goniometer or calculated based on geometrical relations between tilted and untilted micrographs. The third Eulerian angle corresponds to the angle of the tilt axis of the microscope stage and is also calculated using the geometrical relations between two micrographs. In addition, it is necessary to centre the particle projections selected from tilted micrographs; although various correlation-based schemes have been proposed,

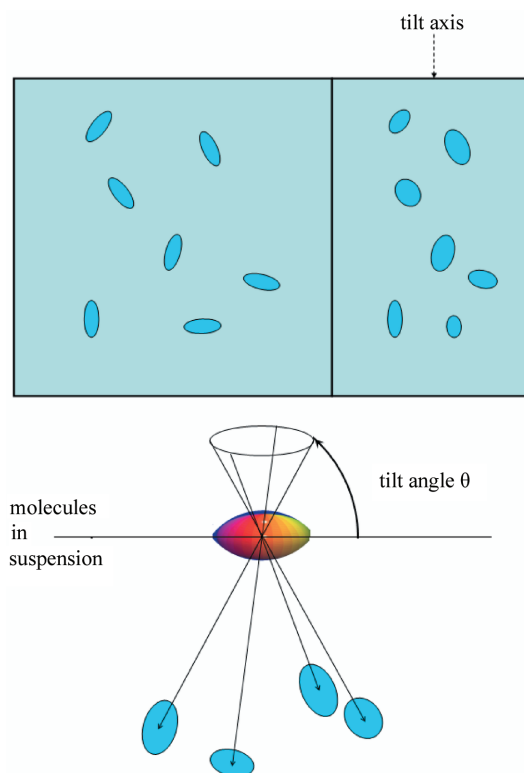


Fig. 2.5.7.3. Principle of random conical tilt reconstruction. A tilt pair of images of the same grid area is collected. By aligning the particle images in the untilted micrograph (left), the Eulerian angles of their counterparts in the tilted micrograph (right) are established. The particle images from the tilted micrograph are used for 3D reconstruction of the molecule (bottom). The set of projections form a cone in Fourier space; information within the cone remains undetermined.

the problem is difficult as the tilt data tend to be very noisy and have very low contrast.

Given three Eulerian angles and centred tilted projections, a 3D reconstruction is calculated. There are numerous advantages of the RCT method. (i) Assuming the sign of the tilt angle is read correctly (it can be confirmed by analysing the defocus gradient in the tilted micrographs), the method yields a correct hand of the structure. (ii) With the exception of the in-plane rotation of untilted projections, which can be found relatively easily using alignment procedures, the remaining parameters are determined by the experimental settings. Even if they are not extremely accurate, the possibility of a gross error is eliminated, which positively distinguishes the method from the *ab initio* computational approaches that use only untilted data. (iii) The computational analysis is entirely done using the untilted data, which have high contrast. (iv) The RCT method is often the only method of obtaining 3D information if the molecule has strongly preferential orientation and only one view is observed in untilted micrographs. The main disadvantage is that the conical projection series leaves a significant portion of the Fourier space undetermined. This follows from the central section theorem [equation (2.5.6.8) of Section 2.5.6]: as the tilt angle is less than 90° , the undetermined region can be thought to form a cone in three dimensions and is referred to as the missing cone. The problem can be overcome if the molecule has more than one preferred orientation. Subsets of particles that have similar untilted appearance (as determined by clustering) are processed independently and for each a separate 3D structure is calculated. If the preferred orientations are sufficiently different, *i.e.*, the orientations of the original particles in three dimensions are sufficiently different in terms of their angles with respect to the *z* axis, the 3D structures can be aligned and merged, all but eliminating the problem of the missing cone and yielding a robust, if resolution-limited, initial model of the molecule (Penczek *et al.*,

3.1. Distances, angles, and their standard uncertainties

By D. E. SANDS

3.1.1. Introduction

A crystal structure analysis provides information from which it is possible to compute distances between atoms, angles between interatomic vectors, and the uncertainties in these quantities. In Cartesian coordinate systems, these geometric computations require the Pythagorean theorem and elementary trigonometry. The natural coordinate systems of crystals, though, are determined by symmetry, and only in special cases are the basis vectors (or coordinate axes) of these systems constrained to be of equal lengths or mutually perpendicular.

It is possible, of course, to transform the positional parameters of the atoms to a Cartesian system and perform the subsequent calculations with the transformed coordinates. Along with the coordinates, the transformations must be applied to anisotropic thermal factors, variance–covariance matrices and other important quantities. Moreover, leaving the natural coordinate system of the crystal sacrifices the simplified relationships imposed by translational and point symmetry; for example, if an atom has fractional coordinates x^1, x^2, x^3 , an equivalent atom will be at $1 + x^1, x^2, x^3$, etc.

Fortunately, formulation of the calculations in generalized rectilinear coordinate systems is straightforward, and readily adapted to computer languages (Section 3.1.12 illustrates the use of Fortran for such calculations). The techniques for these computations are those of tensor analysis, which provides a compact and elegant notation. While an effort will be made to be self-sufficient in this chapter, some proficiency in vector algebra is assumed, and the reader not familiar with the basics of tensor analysis should refer to Chapter 1.1 and Sands (1982a).

3.1.2. Scalar product

The scalar product of vectors \mathbf{u} and \mathbf{v} is defined as

$$\mathbf{u} \cdot \mathbf{v} = uv \cos \varphi, \quad (3.1.2.1)$$

where u and v are the lengths of the vectors and φ is the angle between them. In terms of components,

$$\mathbf{u} \cdot \mathbf{v} = (u^i \mathbf{a}_i) \cdot (v^j \mathbf{a}_j) \quad (3.1.2.2)$$

$$\mathbf{u} \cdot \mathbf{v} = u^i v^j \mathbf{a}_i \cdot \mathbf{a}_j \quad (3.1.2.3)$$

$$\mathbf{u} \cdot \mathbf{v} = u^i v^j g_{ij}. \quad (3.1.2.4)$$

In all equations in this chapter, the convention is followed that summation is implied over an index that is repeated once as a subscript and once as a superscript in an expression; thus, the right-hand side of (3.1.2.4) implies the sum of nine terms

$$u^1 v^1 g_{11} + u^1 v^2 g_{12} + \dots + u^3 v^3 g_{33}.$$

The g_{ij} in (3.1.2.4) are the components of the metric tensor [see Chapter 1.1 and Sands (1982a)]

$$g_{ij} = \mathbf{a}_i \cdot \mathbf{a}_j. \quad (3.1.2.5)$$

Subscripts are used for quantities that transform the same way as the basis vectors \mathbf{a}_i ; such quantities are said to transform covariantly. Superscripts denote quantities that transform the same way as coordinates x^i ; these quantities are said to transform contravariantly (Sands, 1982a).

Equation (3.1.2.4) is in a form convenient for computer evaluation, with indices i and j taking successively all values from 1 to 3. The matrix form of (3.1.2.4) is useful both for symbolic manipulation and for computation,

$$\mathbf{u} \cdot \mathbf{v} = \mathbf{u}^T \mathbf{g} \mathbf{v}, \quad (3.1.2.6)$$

where the superscript italic T following a matrix symbol indicates a transpose. Written out in full, (3.1.2.6) is

$$\mathbf{u} \cdot \mathbf{v} = (u^1 u^2 u^3) \begin{pmatrix} g_{11} & g_{12} & g_{13} \\ g_{21} & g_{22} & g_{23} \\ g_{31} & g_{32} & g_{33} \end{pmatrix} \begin{pmatrix} v^1 \\ v^2 \\ v^3 \end{pmatrix}. \quad (3.1.2.7)$$

If \mathbf{u} is the column vector with components u^1, u^2, u^3 , \mathbf{u}^T is the corresponding row vector shown in (3.1.2.7).

3.1.3. Length of a vector

By (3.1.2.1), the scalar product of a vector with itself is

$$\mathbf{v} \cdot \mathbf{v} = (v)^2. \quad (3.1.3.1)$$

The length of \mathbf{v} is, therefore, given by

$$v = (v^i v^j g_{ij})^{1/2}. \quad (3.1.3.2)$$

Computation of lengths in a generalized rectilinear coordinate system is thus simply a matter of evaluating the double summation $v^i v^j g_{ij}$ and taking the square root.

3.1.4. Angle between two vectors

By (3.1.2.1) and (3.1.2.4), the angle φ between vectors \mathbf{u} and \mathbf{v} is given by

$$\varphi = \cos^{-1}[u^i v^j g_{ij}/(uv)]. \quad (3.1.4.1)$$

An even more concise expression of equations such as (3.1.4.1) is possible by making use of the ability of the metric tensor \mathbf{g} to convert components from contravariant to covariant (Sands, 1982a). Thus,

$$v_i = g_{ij} v^j, \quad u_j = g_{ji} u^i, \quad (3.1.4.2)$$

and (3.1.2.4) may be written succinctly as

$$\mathbf{u} \cdot \mathbf{v} = u^i v_i \quad (3.1.4.3)$$

3.2. The least-squares plane

BY R. E. MARSH AND V. SCHOMAKER†

3.2.1. Introduction

By way of introduction, we remark that in earlier days of crystal structure analysis, before the advent of high-speed computers and routine three-dimensional analyses, molecular planarity was often assumed so that atom coordinates along the direction of projection could be estimated from two-dimensional data [see, e.g., Robertson (1948)]. Today, the usual aim in deriving the coefficients of a plane is to investigate the degree of planarity of a group of atoms as found in a full, three-dimensional structure determination. We further note that, for such purposes, a crystallographer will often be served just as well by establishing the plane in an almost arbitrary fashion as by resorting to the most elaborate, nit-picking and pretentious least-squares treatment. The approximate plane and the associated perpendicular distances of the atoms from it will be all he needs as scaffolding for his geometrical and structural imagination; reasonable common sense will take the place of explicit attention to error estimates.

Nevertheless, we think it appropriate to lay out in some detail the derivation of the ‘best’ plane, in a least-squares sense, through a group of atoms and of the standard uncertainties associated with this plane. We see two cases: (1) The weights of the atoms in question are considered to be isotropic and uncorrelated (*i.e.* the weight matrix for the positions of all the atoms is diagonal, when written in terms of Cartesian axes, and for each atom the three diagonal elements are equal). In such cases the weights may have little or nothing to do with estimates of random error in the atom positions (they may have been assigned merely for convenience or convention), and, therefore, no one should feel that the treatment is proper in respect to the theory of errors. Nevertheless, it may be desired to incorporate the error estimates (variances) of the atom positions into the *results* of such calculations, whereupon these variances (which may be anisotropic, with correlation between atoms) need to be propagated. In this case the distinction between *weights* (or their inverses) and *variances* must be kept very clear. (2) The weights are anisotropic and are presumably derived from a variance–covariance matrix, which may include correlation terms between different atoms; the objective is to achieve a truly proper Gaussian least-squares result.

3.2.2. Least-squares plane based on uncorrelated, isotropic weights

This is surely the most common situation; it is not often that one will wish to take the trouble, or be presumptive enough, to assign anisotropic or correlated weights to the various atoms. And one will sometimes, perhaps even often, not be genuinely interested in the hypothesis that the atoms actually are rigorously coplanar; for instance, one might be interested in examining the best plane through such a patently nonplanar molecule as cyclohexane. Moreover, the calculation is simple enough, given the availability of computers and programs, as to be a practical realization of the off-the-cuff treatment suggested in our opening paragraph. The problem of deriving the plane’s coefficients is intrinsically nonlinear in the way first discussed by Schomaker *et al.* (1959; SWMB). Any formulation other than as an eigenvalue–eigenvector problem (SWMB), as far as we can tell, will some-

times go astray. As to the propagation of errors, numerous treatments have been given, but none that we have seen is altogether satisfactory.

We refer all vectors and matrices to Cartesian axes, because that is the most convenient in calculation. However, a more elegant formulation can be written in terms of general axes [e.g., as in Shmueli (1981)].

The notation is troublesome. Indices are needed for atom number and Cartesian direction, and the exponent 2 is needed as well, which is difficult if there are superscript indices. The best way seems to be to write all the indices as subscripts and distinguish among them by context – $i, j, 1, 2, 3$ for directions; k, l, p (and sometimes K, \dots) for atoms. In any case, *atom* first then *direction* if there are two subscripts; *direction*, if only one index for a vector component, but *atom* (in this section at least) if for a weight or a vector. And σ_{d_1} , e.g., for the standard uncertainty of the distance of atom 1 from a plane. For simplicity in practice, we use Cartesian coordinates throughout.

The first task is to find the plane, which we write as

$$0 = \mathbf{m} \cdot \mathbf{r} - d \equiv \mathbf{m}^T \mathbf{r} - d,$$

where \mathbf{r} is here the vector from the origin to any point on the plane (but usually represents the measured position of an atom), \mathbf{m} is a unit vector parallel to the normal from the origin to the plane, d is the length of the normal, and \mathbf{m} and \mathbf{r} are the column representations of \mathbf{m} and \mathbf{r} . The least-squares condition is to find the stationary values of $S \equiv [w_k(\mathbf{m}^T \mathbf{r}_k - d)^2]$ subject to $\mathbf{m}^T \mathbf{m} = 1$, with \mathbf{r}_k , $k = 1, \dots, n$, the vector from the origin to atom k and with weights, w_k , isotropic and without interatomic correlations for the n atoms of the plane. We also write S as $S \equiv [w(\mathbf{m}^T \mathbf{r} - d)^2]$, the subscript for atom number being implicit in the Gaussian summations (\sum) over all atoms, as it is also in the angle-bracket notation for the weighted average over all atoms, for example in $\langle \mathbf{r} \rangle$ – the weighted centroid of the groups of atoms – just below.

First solve for d , the origin-to-plane distance.

$$0 = -\frac{1}{2} \frac{\partial S}{\partial d} = [w(\mathbf{m}^T \mathbf{r} - d)] = 0,$$

$$d = [w\mathbf{m}^T \mathbf{r}] / [w] \equiv \mathbf{m}^T \langle \mathbf{r} \rangle.$$

Then

$$S \equiv [w(\mathbf{m}^T \mathbf{r} - d)^2] = [w\{\mathbf{m}^T (\mathbf{r} - \langle \mathbf{r} \rangle)\}^2]$$

$$\equiv [w(\mathbf{m}^T \mathbf{s})^2] \equiv \mathbf{m}^T [w\mathbf{s}\mathbf{s}^T] \mathbf{m} \equiv \mathbf{m}^T \mathbf{A} \mathbf{m}.$$

Here $\mathbf{s}_k \equiv \mathbf{r}_k - \langle \mathbf{r} \rangle$ is the vector from the centroid to atom k . Then solve for \mathbf{m} . This is the eigenvalue problem – to diagonalize \mathbf{A} (bear in mind that \mathbf{A}_{ij} is just $[w\mathbf{s}_i \mathbf{s}_j]$) by rotating the coordinate axes, *i.e.*, to find the 3×3 arrays \mathbf{M} and \mathbf{L} , \mathbf{L} diagonal, to satisfy

$$\mathbf{M}^T \mathbf{A} \mathbf{M} = \mathbf{L}, \quad \mathbf{M}^T \mathbf{M} = \mathbf{I}.$$

\mathbf{A} and \mathbf{M} are symmetric; the columns \mathbf{m} of \mathbf{M} are the direction cosines of, and the diagonal elements of \mathbf{L} are the sums of

† Deceased.

3.3. Molecular modelling and graphics

BY R. DIAMOND AND L. M. D. CRANSWICK

3.3.1. Graphics

BY R. DIAMOND

3.3.1.1. Coordinate systems, notation and standards

3.3.1.1.1. Cartesian and crystallographic coordinates

It is usual, for purposes of molecular modelling and of computer graphics, to adopt a Cartesian coordinate system using mutually perpendicular axes in a right-handed system using the ångström unit or the nanometre as the unit of distance along such axes, and largely to ignore the existence of crystallographic coordinates expressed as fractions of unit-cell edges. Transformations between the two are thus associated, usually, with the input and output stages of any software concerned with modelling and graphics, and it will be assumed after this section that all coordinates are Cartesian using the chosen unit of distance as the unit of coordinates. For a discussion of coordinate transformations and rotations without making this assumption see Chapter 1.1 in which formulations using co- and contravariant forms are presented.

The relationship between these systems may be written

$$\mathbf{X} = \mathbf{M}\mathbf{x} \quad \mathbf{x} = \mathbf{M}^{-1}\mathbf{X}$$

in which \mathbf{X} and \mathbf{x} are position vectors in direct space, written as column vectors, with \mathbf{x} expressed in crystallographic fractional coordinates (dimensionless) and \mathbf{X} in Cartesian coordinates (dimension of length).

There are two forms of \mathbf{M} in common use. The first of these sets the first component of \mathbf{X} parallel to \mathbf{a}^* and the third parallel to \mathbf{c} and is

$$\mathbf{M} = \begin{pmatrix} a\varphi/\sin\alpha & 0 & 0 \\ a(\cos\gamma - \cos\alpha\cos\beta)/\sin\alpha & b\sin\alpha & 0 \\ a\cos\beta & b\cos\alpha & c \end{pmatrix}$$

$$\mathbf{M}^{-1} = \begin{pmatrix} \sin\alpha/a\varphi & 0 & 0 \\ (\cos\alpha\cos\beta - \cos\gamma)/b\varphi\sin\alpha & 1/b\sin\alpha & 0 \\ (\cos\alpha\cos\gamma - \cos\beta)/c\varphi\sin\alpha & -1/c\tan\alpha & 1/c \end{pmatrix}$$

in which

$$\varphi = \sqrt{1 - \cos^2\alpha - \cos^2\beta - \cos^2\gamma + 2\cos\alpha\cos\beta\cos\gamma}$$

$$= \sin\alpha\sin\beta\sin\gamma^*.$$

φ is equal to the volume of the unit cell divided by abc , and is unchanged by cyclic permutation of α, β and γ and of α^*, β^* and γ^* . The Cartesian and crystallographic axes have the same chirality if the positive square root is taken.

The second form sets the first component of \mathbf{X} parallel to \mathbf{a} and the third component of \mathbf{X} parallel to \mathbf{c}^* and is

$$\mathbf{M} = \begin{pmatrix} a & b\cos\gamma & c\cos\beta \\ 0 & b\sin\gamma & c(\cos\alpha - \cos\beta\cos\gamma)/\sin\gamma \\ 0 & 0 & c\varphi/\sin\gamma \end{pmatrix}$$

$$\mathbf{M}^{-1} = \begin{pmatrix} 1/a & -1/a\tan\gamma & (\cos\alpha\cos\gamma - \cos\beta)/a\varphi\sin\gamma \\ 0 & 1/b\sin\gamma & (\cos\beta\cos\gamma - \cos\alpha)/b\varphi\sin\gamma \\ 0 & 0 & \sin\gamma/c\varphi \end{pmatrix}.$$

A third form, suitable only for rhombohedral cells, is

$$\mathbf{M} = \frac{a}{3} \begin{pmatrix} p+2q & p-q & p-q \\ p-q & p+2q & p-q \\ p-q & p-q & p+2q \end{pmatrix}$$

$$\mathbf{M}^{-1} = \frac{1}{3a} \begin{pmatrix} \frac{1}{p} + \frac{2}{q} & \frac{1}{p} - \frac{1}{q} & \frac{1}{p} - \frac{1}{q} \\ \frac{1}{p} - \frac{1}{q} & \frac{1}{p} + \frac{2}{q} & \frac{1}{p} - \frac{1}{q} \\ \frac{1}{p} - \frac{1}{q} & \frac{1}{p} - \frac{1}{q} & \frac{1}{p} + \frac{2}{q} \end{pmatrix}$$

in which

$$p = \pm\sqrt{1+2\cos\alpha} \quad q = \pm\sqrt{1-\cos\alpha},$$

which preserves the equivalence of axes. Here the chiralities of the Cartesian and crystallographic axes are the same if p is chosen positive, and different otherwise, and the two sets of axes coincide in projection along the triad if q is chosen positive and are π out of phase otherwise.

3.3.1.1.2. Homogeneous coordinates

Homogeneous coordinates have found wide application in computer graphics. For some equipment their use is essential, and they are of value analytically even if the available hardware does not require their use.

Homogeneous coordinates employ four quantities, X, Y, Z and W , to define the position of a point, rather than three. The fourth coordinate has a scaling function so that it is the quantity X/W (as delivered to the display hardware) which controls the left-right positioning of the point within the picture. A point with $|X/W| < 1$ is in the picture, normally, and those with $|X/W| > 1$ are outside it, but see Section 3.3.1.3.5.

There are many reasons why homogeneous coordinates may be adopted, among them the following:

(i) X, Y, Z and W may be held as integers, thus enabling fast arithmetic whilst offering much of the flexibility of floating-point working. A single W value may be common to a whole array of X, Y, Z values.

(ii) Perspective transformations can be implemented without the need for any division. Only high-speed matrix multiplication using integer arithmetic is necessary, provided only that the drawing hardware can provide displacements proportional to the ratio of two signals, X and W or Y and W . Rotation, translation, scaling and the application of perspective are all effected by operations of the same form, namely multiplication of a four-vector by a 4×4 matrix. The hardware may thus be kept relatively simple since only one type of operation needs to be provided for.

(iii) Since kX, kY, kZ, kW represents the same point as X, Y, Z, W , the hardware may be arranged to maximize resolution without risk of integer overflow.

For analytical purposes it is convenient to regard homogeneous transformations in terms of partitioned matrices

$$\begin{pmatrix} \mathbf{M} & \mathbf{V} \\ \mathbf{U} & N \end{pmatrix} \begin{pmatrix} \mathbf{X} \\ W \end{pmatrix},$$

3.3. MOLECULAR MODELLING AND GRAPHICS

Table 3.3.4.1. *Functionality of software for crystal structure display*

Program	Ball and stick	ADPs	MSDA	Polyhedral display	Cartesian coordinates	Comparison/overlay of multiple structures	Extended structures/topology analysis	Magnetic structures	Incommensurate structures
<i>ATOMS</i>	Yes	Yes		Yes	Yes			Yes	
<i>Balls&Sticks</i>	Yes			Yes					
<i>BALSAC</i>	Yes				Yes				
<i>Cameron</i>	Yes	Yes							
<i>CaRIne</i>	Yes			Yes	Yes				
<i>Crystallographica</i>	Yes	Yes		Yes					
<i>CrystalMaker</i>	Yes			Yes	Yes			Yes	
<i>Crystal Studio</i>	Yes	Yes		Yes	Yes				
<i>CrystMol</i>	Yes	Yes			Yes	Yes			
<i>Diamond</i>	Yes	Yes		Yes	Yes			Yes	
<i>DrawXTL</i>	Yes	Yes		Yes				Yes	
<i>FpStudio</i>	Yes	Yes						Yes	Yes
<i>GRETEP</i>	Yes	Yes					Yes		
<i>Mercury</i>	Yes				Yes				
<i>MolXtl</i>	Yes	Yes			Yes				
<i>OLEX</i>	Yes				Yes		Yes		
<i>ORTEP-III</i>	Yes	Yes							
<i>ORTEP-3 for Windows</i>	Yes	Yes	Yes		Yes				
<i>ORTEX/Oscair X</i>	Yes	Yes							
<i>PEANUT</i>	Yes	Yes	Yes						
<i>Platon/Pluton</i>	Yes	Yes			Yes				
<i>PowderCell</i>	Yes								
<i>PRJMS</i>	Yes								Yes
<i>SCHAKAL</i>	Yes				Yes				
<i>STRUPLO</i>	Yes			Yes					
<i>STRUPLO for Windows</i>				Yes	Yes				
<i>STRUVIR</i>				Yes					
<i>VENUS</i>	Yes	Yes		Yes	Yes			Yes	
<i>XmLmctep</i>	Yes	Yes							
<i>X-Seed</i>	Yes	Yes			Yes				
<i>Xtal-3D</i>	Yes	Yes		Yes				Yes	
<i>XtalDraw</i>	Yes	Yes		Yes					

Crystallography Volume G (2005)] is slowly becoming a standard in this regard, displacing the single-crystal *SHELX* INS format, which has been a *de-facto* standard file format for much crystallographic data exchange. Entering crystallographic data by hand is slow and often introduces errors *via* typographical mistakes. Such mistakes can be minimized by importing structures using a known file type, or reformatting using a text editor or spreadsheet program into a known file type. A variety of software programs can be used for translating crystallographic structure files; however, the output (especially the handling of the symmetry operators and the space group) should be carefully checked. The CCP14 website (Cockroft & Stephenson, 2005) lists a variety of programs that can be used for this, of which a specialist program is *Cryscon* (Dowty, 2005).

3.3.4.2. Types of crystal structure display and functionality

The following information was current at the time of writing, but most software is continually changing with the insertion of new features. Thus occasional checks for updated functionality can be useful. Most software distributions include an 'updates' file containing new features and bug fixes. Detailed information on the software referred to in this section, including functionality, authorship, source and availability, is given in Tables 3.3.4.1 and 3.3.4.2.

3.3.4.2.1. Ball and stick

This is one of the most fundamental methods of displaying a crystal structure and almost all software supports this. The exceptions are *STRUVIR* and *STRUPLO for Windows* [a port of *STRUVIR* incorporating a graphical user interface (GUI)], which are both optimized for the polyhedral display of crystal structures.

3.3.4.2.2. Anisotropic displacement parameters

A subset of the programs that display ball-and-stick structures can also display surfaces related to anisotropic displacement parameters (ADPs) (also known colloquially as 'thermals', 'anisotropic thermal ellipsoids' or 'ORTEPS'). By default, most programs display the ellipsoid surfaces at a probability of 50% and normally allow this value to be changed to values between 1 and 99%. Programs that can draw ADPs include *ATOMS*, *Cameron*, *Crystallographica*, *CrystalMaker*, *Crystal Studio*, *CrystMol*, *Diamond*, *DrawXTL*, *FpStudio*, *GRETEP*, *MolXtl*, *ORTEP-III*, *ORTEP-3 for Windows*, *ORTEX*, *PEANUT*, *Platon*, *VENUS*, *XmLmctep*, *X-Seed* and *XtalDraw*.

3.3.4.2.3. Mean-square displacement amplitude

When a more thorough investigation of the ADPs would be informative (Hummel, Raselli & Bürgi, 1990), *PEANUT* can be used for plotting the mean-square displacement amplitude (MSDA), root-mean-square displacements (RMSDs) and difference surfaces. MSDA 'peanuts' can be displayed where the ADPs are non-positive-definite and the ellipsoids cannot be drawn. *ORTEP-3 for Windows* also has an option for plotting MSDAs. Care should be taken to ensure the resulting display is correct.

3.3.4.2.4. Polyhedral display

A method for understanding inorganic and intermetallic structures is the use of coordination polyhedra. The faces defined by the outer coordinated atoms generate a polyhedral object that is displayed instead of the individual atoms. This can aid in understanding the structures of polymeric inorganic materials involving both simple and complex tilt systems, and distorted

3. DUAL BASES IN CRYSTALLOGRAPHIC COMPUTING

Table 3.4.2.2. *Untreated lattice-sum results for the dispersion energy ($n = 6$) of crystalline benzene (kJ mol^{-1} , \AA)*

Truncation limit	Number of molecules	Number of terms	Calculated energy
6.0	26	524	-69.227
8.0	51	1313	-76.007
10.0	77	2631	-78.179
12.0	126	4718	-79.241
14.0	177	7531	-79.726
16.0	265	11274	-80.013
18.0	344	15904	-80.178
20.0	439	22049	-80.295
Converged value			-80.589

the original sum, which contains the difference terms, is not increased.

$$V_n = (1/2) \sum_j^{\text{one cell}} \sum_k^{\text{all cells}} Q_{jk} R_{jk}^{-n} W(R) + (1/2) \sum_j^{\text{one cell}} \sum_k^{\text{all cells}} Q_{jk} R_{jk}^{-n} [1 - W(R)].$$

In the accelerated-convergence method the difference terms are expressed as an integral of the product of two functions. According to Parseval's theorem (described below) this integral is equal to an integral of the product of the two Fourier transforms of the functions. Finally, the integral over the Fourier transforms of the functions is converted to a sum in reciprocal (or Fourier-transform) space. The choice of the convergence function $W(R)$ is not unique; an obvious requirement is that the relevant Fourier transforms must exist and have correct limiting behaviour. Nijboer and DeWette suggested using the incomplete gamma function for $W(R)$. More recently, Fortuin (1977) showed that this choice of convergence function leads to optimal convergence of the sums in both direct and reciprocal space:

$$W(R) = \Gamma(n/2, \pi w^2 R^2) / \Gamma(n/2),$$

where $\Gamma(n/2)$ and $\Gamma(n/2, \pi w^2 R^2)$ are the gamma function and the incomplete gamma function, respectively:

$$\Gamma(n/2, \pi w^2 R^2) = \int_{\pi w^2 R^2}^{\infty} t^{(n/2)-1} \exp(-t) dt$$

and

$$\Gamma(n/2) = \Gamma(n/2, 0).$$

The complement of the incomplete gamma function is

$$\gamma(n/2, \pi w^2 R^2) = \Gamma(n/2) - \Gamma(n/2, \pi w^2 R^2).$$

3.4.4. Preliminary derivation to obtain a formula which accelerates the convergence of an R^{-n} sum over lattice points $\mathbf{X}(\mathbf{d})$

The three-dimensional direct-space crystal lattice is specified by the origin vectors \mathbf{a}_1 , \mathbf{a}_2 and \mathbf{a}_3 . A general vector in direct space is defined as

$$\mathbf{X}(\mathbf{x}) = x_1 \mathbf{a}_1 + x_2 \mathbf{a}_2 + x_3 \mathbf{a}_3,$$

where x_1, x_2, x_3 are the fractional cell coordinates of \mathbf{X} . A lattice vector in direct space is defined as

$$\mathbf{X}(\mathbf{d}) = d_1 \mathbf{a}_1 + d_2 \mathbf{a}_2 + d_3 \mathbf{a}_3,$$

where d_1, d_2, d_3 are integers (specifying particular values of x_1, x_2, x_3) designating a lattice point. V_d is the direct-cell volume which is equal to $\mathbf{a}_1 \cdot \mathbf{a}_2 \times \mathbf{a}_3$. A general point in the direct lattice is $\mathbf{X}(\mathbf{x})$; the contents of the lattice are by definition identical as the components of \mathbf{x} are increased or decreased by integer amounts.

The reciprocal-lattice vectors are defined by the relations

$$\begin{aligned} \mathbf{a}_j \cdot \mathbf{b}_k &= 1 & j &= k \\ &= 0 & j &\neq k. \end{aligned}$$

A general vector in reciprocal space $\mathbf{H}(\mathbf{r})$ is defined as

$$\mathbf{H}(\mathbf{r}) = r_1 \mathbf{b}_1 + r_2 \mathbf{b}_2 + r_3 \mathbf{b}_3.$$

A reciprocal-lattice vector $\mathbf{H}(\mathbf{h})$ is defined by the integer triplet h_1, h_2, h_3 (specifying particular values of r_1, r_2, r_3) so that

$$\mathbf{H}(\mathbf{h}) = h_1 \mathbf{b}_1 + h_2 \mathbf{b}_2 + h_3 \mathbf{b}_3.$$

In other sections of this volume a shortened notation \mathbf{h} is used for the reciprocal-lattice vector. In this section the symbol $\mathbf{H}(\mathbf{h})$ is used to indicate that it is a particular value of $\mathbf{H}(\mathbf{r})$.

The three-dimensional Fourier transform $g(\mathbf{t})$ of a function $f(\mathbf{x})$ is defined by

$$g(\mathbf{t}) = FT_3[f(\mathbf{x})] = \int f(\mathbf{x}) \exp(2\pi i \mathbf{x} \cdot \mathbf{t}) d\mathbf{x}.$$

The Fourier transform of the set of points defining the direct lattice is the set of points defining the reciprocal lattice, scaled by the direct-cell volume. It is useful for our purpose to express the lattice transform in terms of the Dirac delta function $\delta(\mathbf{x} - \mathbf{x}_0)$ which is defined so that for any function $f(\mathbf{x})$

$$f(\mathbf{x}_0) = \int \delta(\mathbf{x} - \mathbf{x}_0) f(\mathbf{x}) d\mathbf{x}.$$

We then write

$$FT_3\{\sum_{\mathbf{d}} \delta[\mathbf{X}(\mathbf{x}) - \mathbf{X}(\mathbf{d})]\} = V_d^{-1} \sum_{\mathbf{h}} \delta[\mathbf{H}(\mathbf{r}) - \mathbf{H}(\mathbf{h})].$$

First consider the lattice sum over the direct-lattice points $\mathbf{X}(\mathbf{d})$, relative to a particular point $\mathbf{X}(\mathbf{x}) = \mathbf{R}$, with omission of the origin lattice point.

$$S'(n, \mathbf{R}) = \sum_{\mathbf{d} \neq 0} |\mathbf{X}(\mathbf{d}) - \mathbf{R}|^{-n}.$$

The special case with $\mathbf{R} = 0$ will also be needed:

$$S'(n, 0) = \sum_{\mathbf{d} \neq 0} |\mathbf{X}(\mathbf{d})|^{-n}.$$

3.5. Extensions of the Ewald method for Coulomb interactions in crystals

BY T. A. DARDEN

3.5.1. Introduction

High-precision single-crystal X-ray structural analysis of small organic molecules, yielding the space group, the unit-cell parameters and the fractional coordinates of the atoms making up the molecule(s) in the asymmetric unit, has become a routine matter as long as crystals of sufficient quality can be obtained. The thermodynamic stability of the crystal, as described by the enthalpy of sublimation ΔH_{sub} , can also be determined experimentally (although not always to high precision). Theoretical models for calculating intermolecular interaction energies can be used to connect the crystal structure to the molar enthalpy of sublimation using the relationship

$$\Delta H_{\text{sub}}(0 \text{ K}) = -E_{\text{lattice}},$$

where the lattice or packing energy E_{lattice} is the total (molar) intermolecular interaction energy between all the molecules in the crystal, which are treated as rigid entities with zero-point energies of intra- and intermolecular vibrations neglected. Connection to experimentally accessible heats of sublimation at higher temperatures involves thermodynamic corrections. Methods for calculating thermodynamic quantities of solids are discussed in Gavezzotti (2002a) and (in more detail) in Frenkel & Smit (2002).

Thus, given a parameterized intermolecular potential-energy function, or if computationally affordable a first-principles approach such as density-functional theory (or preferably, when it becomes feasible for crystals, a good-quality post-Hartree–Fock potential-energy surface that describes dispersion interactions), one can sum the intermolecular energies to obtain the lattice energy as a function of the above parameters defining the crystal structure. If such an energy function is used together with a method for systematic search of the crystal-structure parameters, one could in principle predict the minimum-lattice-energy crystal structure for a rigid organic molecule. To extend this approach to flexible molecules one would need to minimize the sum of the intramolecular energy plus the lattice energy. If the experimental crystal structure corresponds to the thermodynamic minimum-energy structure (*i.e.* it is not a metastable state determined by crystal-growth kinetics), one could in principle predict the experimental crystal structure of an organic compound through this minimization protocol. Moreover, one could ideally predict the additional metastable forms of the crystal.

Prediction of the structure of crystals of an organic molecule from its molecular structure is a difficult problem that has been compared to the protein folding problem (Dunitz, 2003; Dunitz & Scheraga, 2004). Like the protein folding problem, a solution of the crystal prediction problem has significant practical ramifications. A compound is often polymorphic, that is it has more than one crystal structure, and it may be difficult to characterize the conditions under which a particular crystal structure is formed (Dunitz & Bernstein, 1995). Polymorphs may have very different physical properties. An obvious example is diamond *versus* graphite, but other commercially important examples include food additives, various solid forms of explosives and the bio-availability of various forms of a drug such as ritonavir (Chemburkar *et al.*, 2000). A method for predicting the possible crystal structures of the compound, and ideally for predicting the dominant crystal structure given the experimental conditions, would thus be very valuable. Note that due to the subtleties of

crystallization, the lowest-free-energy polymorph at given temperature and pressure may not be the likeliest to form. The kinetics of growth of microcrystals may largely determine which low-energy polymorph appears (Dunitz, 2003). However, it is generally agreed that accurate calculation of the relative free energy of polymorphs is a prerequisite for predicting crystal structures.

To assess progress towards solving this latter problem, a series of blind tests of crystal-structure prediction has been undertaken (Day, Motherwell, Ammon *et al.*, 2005). The results of these tests have highlighted the need for continued improvements in sampling methods and intermolecular energy potentials. Since extensive sampling of the crystal-structure parameters is necessary [between 10^4 and 10^5 starting structures, each followed by parameter minimizations (Price & Price, 2005)], there is a trade-off in the computational cost *versus* accuracy of the intermolecular energy functions used. Calculating the work of transforming between polymorphs is yet more ambitious in terms of sampling. Consequently empirical force fields are likely to be needed for the near term at least.

In the remainder of the introduction we outline some of the approaches to empirical potentials used in the calculation of the lattice energy, and then, motivated by these developments, discuss techniques for efficient summation of the electrostatic and other slow-decaying interaction terms that occur in these potential functions.

Methodological developments in the intermolecular force fields used in crystal-structure prediction from early times to the present state of the art have been reviewed (Price & Price, 2005). Until recently, these force fields were made up of atom–atom interactions. The earliest involved only repulsion and dispersion, usually in the ‘exp-6’ form

$$U^{MN} = U_{\text{rep}}^{MN} + U_{\text{disp}}^{MN} = \sum_{i \in M, j \in N} A_{ij} \exp(-B_{ij} r_{ij}) - C_{ij} r_{ij}^{-6},$$

where U^{MN} denotes the intermolecular potential energy between molecules M and N and r_{ij} is the distance between atoms $i \in M$ and $j \in N$. Sometimes the exponential form in the above equation is replaced by a simpler power law, as in the Lennard–Jones potential. As was pointed out by Dunitz (2003), in comparison with more sophisticated force fields, this repulsion–dispersion form readily allows analysis of the significance of particular atom–atom interactions, since the interactions are short-ranged and thus can be localized. That is, the r^{-6} form of the attractive dispersion energy means that interaction energies are halved for every 12% increase in distance. In contrast, introduction of long-range Coulombic interactions not only entails subtleties in lattice summation (the subject of this contribution), but greatly complicates the assignment of ‘key’ atom–atom interactions. Gavezzotti and Fillipini systematically explored the use of the exp-6 potential in fitting organic crystal structures with and without hydrogen-bond interactions (Gavezzotti & Fillipini, 1994). They were surprisingly successful in accounting for weak hydrogen bonding in this way, but selective use of point charges improved the directionality of the potential. Earlier, Williams derived exp-6 parameters for the atoms C, H, N, O, Cl, F and polar H for use in organic crystal structures, but found it necessary (Williams & Cox, 1984) to supplement these with selected point charges, both atomic and at off-atom sites. Price and

4.1. Thermal diffuse scattering of X-rays and neutrons

By B. T. M. WILLIS

4.1.1. Introduction

Thermal motion of the atoms in a crystal gives rise to a reduction in the intensities of the Bragg reflections and to a diffuse distribution of non-Bragg scattering in the rest of reciprocal space. This distribution is known as thermal diffuse scattering (TDS). Measurement and analysis of TDS give information about the lattice dynamics of the crystal, *i.e.* about the small oscillatory displacements of the atoms from their equilibrium positions which arise from thermal excitations. Lattice-dynamical models form the basis for interpreting many physical properties – for example, specific heat and thermal conductivity – which cannot be explained by a static model of the crystal.

Reference to a lattice-dynamical model is found in Newton's *Principia*, which contains a discussion of the vibrations of a linear chain of equidistant mass points connected by springs. The model was used to estimate the speed of sound in air. The vibrational properties of a one-dimensional crystal treated as a linear chain of atoms provide the starting point for several modern treatises on the lattice dynamics of crystals.

The classical theory of the dynamics of three-dimensional crystals is based on the treatment of Born & von Kármán (1912, 1913). In this theory, the restoring force on an atom is determined not by the displacement of the atom from its equilibrium position, but by its displacement relative to its neighbours. The atomic motion is then considered in terms of travelling waves, or 'lattice vibrations', extending throughout the whole crystal. These waves are the normal modes of vibration, in which each mode is characterized by a wavevector \mathbf{q} , an angular frequency $\omega(\mathbf{q})$ and certain polarization properties.

For twenty years after its publication the Born–von Kármán treatment was eclipsed by the theory of Debye (1912). In the Debye theory the crystal is treated as a continuous medium instead of a discrete array of atoms. The theory gives a reasonable fit to the integral vibrational properties (for example, the specific heat or the atomic temperature factor) of simple monatomic crystals. It fails to account for the form of the frequency distribution function which relates the number of modes and their frequency.

An even simpler model than Debye's is due to Einstein (1907), who considered the atoms in the crystal to be vibrating independently of each other and with the same frequency ω_E . By quantizing the energy of each atom in units of $\hbar\omega_E$, Einstein showed that the specific heat falls to zero at $T = 0$ K and rises asymptotically to the Dulong and Petit value for T much larger than $\hbar\omega_E/k_B$. (\hbar is Planck's constant divided by 2π and k_B is Boltzmann's constant.) His theory accounts satisfactorily for the breakdown of equipartition of energy at low temperatures, but it predicts a more rapid fall-off of specific heat with decreasing temperature than is observed.

Deficiencies in the Debye theory were noted by Blackman (1937), who showed that they are overcome satisfactorily using the more rigorous Born–von Kármán theory. Extensive X-ray studies of Laval (1939) on simple structures such as sylvine, aluminium and diamond showed that the detailed features of the TDS could only be explained in terms of the Born–von Kármán theory. The X-ray work on aluminium was developed further by Olmer (1948) and by Walker (1956) to derive the phonon dispersion relations (see Section 4.1.5) along various symmetry directions in the crystal.

It is possible to measure the vibrational frequencies directly with X-rays, but such measurements are very difficult as lattice

vibrational energies are many orders of magnitude less than X-ray energies. The situation is much more favourable with thermal neutrons because their wavelength is comparable with interatomic spacings and their energy is comparable with a quantum of vibrational energy (or phonon). The neutron beam is scattered inelastically by the lattice vibrations, exchanging energy with the phonons. By measuring the energy change for different directions of the scattered beam, the dispersion relations $\omega(\mathbf{q})$ can be determined. Brockhouse & Stewart (1958) reported the first dispersion curves to be derived in this way; since then the neutron technique has become the principal experimental method for obtaining detailed information about lattice vibrations.

In this chapter we shall describe briefly the standard treatment of the lattice dynamics of crystals. There follows a section on the theory of the scattering of X-rays by lattice vibrations, and a similar section on the scattering of thermal neutrons. We then refer briefly to experimental work with X-rays and neutrons. The final section is concerned with the measurement of elastic constants: these constants are required in calculating the TDS correction to measured Bragg intensities (see Section 7.4.2 of *IT C*, 2004).

4.1.2. Dynamics of three-dimensional crystals

For modes of vibration of very long wavelength, the crystal can be treated as a homogeneous elastic continuum without referring to its crystal or molecular structure. The theory of the propagation of these elastic waves is based on Hooke's law of force and on Newton's equations of motion. As the wavelength of the vibrations becomes shorter and shorter and approaches the separation of adjacent atoms, the calculation of the vibrational properties requires a knowledge of the crystal structure and of the nature of the forces between adjacent atoms. The three-dimensional treatment is based on the formulation of Born and von Kármán, which is discussed in detail in the book by Born & Huang (1954) and in more elementary terms in the books by Cochran (1973) and by Willis & Pryor (1975).

Before setting up the equations of motion, it is necessary to introduce three approximations:

(i) *The harmonic approximation.* When an atom is displaced from its equilibrium position, the restoring force is assumed to be proportional to the displacement, measured relative to the neighbouring atoms. The approximation implies no thermal expansion and other properties not possessed by real crystals; it is a reasonable assumption in the lattice-dynamical theory provided the displacements are not too large.

(ii) *The adiabatic approximation.* We wish to set up a potential function for the crystal describing the binding between the atoms. However, the binding involves electronic motions whereas the dynamics involve nuclear motions. The adiabatic approximation, known as the Born–Oppenheimer approximation in the context of molecular vibrations, provides the justification for adopting the same potential function to describe both the binding and the dynamics. Its essence is that the electronic and nuclear motions may be considered separately. This is possible if the nuclei move very slowly compared with the electrons: the electrons can then instantaneously take up a configuration appropriate to that of the displaced nuclei without changing their quantum state. The approximation holds well for insulators, where electronic transition energies are high owing to the large energy gap between filled and unfilled electron states. Surprisingly, it even works for

4.2. Disorder diffuse scattering of X-rays and neutrons

BY F. FREY, H. BOYSEN AND H. JAGODZINSKI

4.2.1. Introduction

Diffuse scattering of X-rays, neutrons and other particles is an accompanying effect in all diffraction experiments aimed at structure analysis with the aid of elastic scattering. In this case, the momentum exchange of the scattered photon or particle includes the crystal as a whole; the energy transfer involved becomes negligibly small and need not be considered in diffraction theory. Static distortions as a consequence of structural changes cause typical elastic diffuse scattering. Many structural phenomena and processes contribute to diffuse scattering, and a general theory has to include all of them. Hence the exact treatment of diffuse scattering becomes very complex.

Inelastic scattering is due to dynamical fluctuations or ionization processes and may become observable as a 'diffuse' contribution in a diffraction pattern. A separation of elastic from inelastic diffuse scattering is generally possible, but difficulties may result from small energy exchanges that cannot be resolved for experimental reasons. The latter is true for scattering of X-rays by phonons, which have energies of the order of 10^{-2} – 10^{-3} eV, values which are considerably smaller than 10 keV, a typical value for X-ray quanta. Another equivalent explanation, frequently forwarded in the literature, is the high speed of X-ray photons, such that the rather slow motion of atoms cannot be 'observed' by them during diffraction. Hence, all movements appear as static displacement waves of atoms, and temperature diffuse scattering is pseudo-elastic for X-rays. This is not true in the case of thermal neutrons, which have energies comparable to those of phonons. Phonon-related or thermal diffuse scattering is discussed separately in Chapter 4.1, *i.e.* the present chapter is mainly concerned with the elastic (or pseudo-elastic other than thermal) part of diffuse scattering. A particularly important aspect concerns diffuse scattering related to phase transitions, in particular the critical diffuse scattering observed at or close to the transition temperature. In simple cases, a satisfactory description may be given with the aid of a 'soft phonon', which freezes at the critical temperature, thus generating typical temperature-dependent diffuse scattering. If the geometry of the lattice is maintained during the transformation (*i.e.* there is no breakdown into crystallites of different cell geometry), the diffuse scattering is very similar to diffraction phenomena described in this chapter. Sometimes, however, very complicated interim stages (ordered or disordered) are observed, demanding a complicated theory for their full explanation (see, *e.g.*, Dorner & Comes, 1977).

Obviously, there is a close relationship between thermodynamics and diffuse scattering in disordered systems representing a stable or metastable thermal equilibrium. From the thermodynamical point of view, the system is then characterized by its grand partition function, which is intimately related to the correlation functions used in the interpretation of diffuse scattering. The latter is nothing other than a kind of 'partial partition function' where two atoms, or two cell occupancies, are fixed such that the sum of all partial partition functions represents the grand partition function. This fact yields the useful correlation between thermodynamics and diffuse scattering mentioned above, which may well be used for a determination of thermodynamical properties of the crystal. This important subject shall not be included here for the following reason: real three-dimensional crystals generally exhibit diffuse scattering by defects and/or disordering effects that are not in thermal equilibrium. They are created during crystal growth, or are frozen-in defects formed at

higher temperatures. Hence a thermodynamical interpretation of diffraction data needs a careful study of diffuse scattering as a function of temperature or some other thermodynamical parameters. This can be done in very rare cases only, so the omission of this subject seems justified.

As shown in this chapter, electron-density fluctuations and distribution functions of defects play an important role in the complete interpretation of diffraction patterns. Both quantities may best be studied in the low-angle scattering range. Hence many problems cannot be solved without a detailed interpretation of low-angle diffraction (also called small-angle scattering).

Disorder phenomena in magnetic structures are also not specifically discussed here. Magnetic diffuse neutron scattering and special experimental techniques constitute a large subject by themselves. Many aspects, however, may be analysed along similar lines to those given here.

Glasses, liquids or liquid crystals show typical diffuse diffraction phenomena. Particle-size effects and strains have an important influence on the diffuse scattering. The same is true for dislocations and point defects such as interstitials or vacancies. These defects are mainly described by their strain field, which influences the intensities of sharp reflections like an artificial temperature factor: the Bragg peaks diminish in intensity while the diffuse scattering increases predominantly close to them. These phenomena are less important from a structural point of view, at least in the case of metals or other simple structures. This statement is true as long as the structure of the 'kernel' of defects may be neglected when compared with the influence of the strain field. Whether dislocations in more complicated structures meet this condition is not yet known.

Commensurate and incommensurate modulated structures and quasicrystals frequently show a typical diffuse scattering, a satisfactory explanation of which demands extensive experimental and theoretical study. A reliable structure determination becomes very difficult in cases where the interpretation of diffuse scattering has not been incorporated. Many erroneous structural conclusions have been published in the past. The solution of problems of this kind needs careful thermodynamical consideration as to whether a plausible explanation of the structural data can be given.

For all of the reasons mentioned above, this article cannot be complete. It is hoped, however, that it will provide a useful guide for those who need a full understanding of the crystal chemistry of a given structure.

The study of disorder in crystals by diffuse-scattering techniques can be performed with X-rays, neutrons or electrons. Each of these methods has its own advantages (and disadvantages) and they often can (or have to) be used in a complementary way (*cf.* Chapter 4.3 of this volume). Electron diffraction and microscopy are usually restricted to relatively small regions in space and thus supply information on a local scale, *i.e.* local defect structures. Moreover, electron-microscopy investigations are carried out on thin samples (films), where the disorder could be different from the bulk, and, in addition, could be affected by the high heat load deposited by the impinging electron beam. X-rays and neutrons sample larger crystal volumes and thus provide thermodynamically more important information on *averages* of the disorder. These methods are also better suited to the analysis of long-range correlated cooperative disorder phenomena. On the other hand, electron microscopy and diffraction often allow more direct access to disorder and can therefore provide valuable

4.3. Diffuse scattering in electron diffraction

BY J. M. COWLEY† AND J. K. GJØNNES

4.3.1. Introduction

The origins of diffuse scattering in electron-diffraction patterns are the same as in the X-ray case: inelastic scattering due to electronic excitations, thermal diffuse scattering (TDS) from atomic motions, scattering from crystal defects or disorder. For diffraction by crystals, the diffuse scattering can formally be described in terms of a nonperiodic deviation $\Delta\varphi$ from the periodic, average crystal potential, $\bar{\varphi}$:

$$\varphi(\mathbf{r}, t) = \bar{\varphi}(\mathbf{r}) + \Delta\varphi(\mathbf{r}, t), \quad (4.3.1.1)$$

where $\Delta\varphi$ may have a static component from disorder in addition to time-dependent fluctuations of the electron distribution or atomic positions.

In the kinematical case, the diffuse scattering can be treated separately. The intensity I_d as a function of the scattering variable \mathbf{u} ($|\mathbf{u}| = 2 \sin \theta / \lambda$) and energy transfer $h\nu$ is then given by the Fourier transform \mathcal{F} of $\Delta\varphi$

$$I(\mathbf{u}, \nu) = |\Delta\Phi(\mathbf{u}, \nu)|^2 = |\mathcal{F}\{\Delta\varphi(\mathbf{r}, t)\}|^2 = \mathcal{F}\{P_d(\mathbf{r}, \nu)\} \quad (4.3.1.2)$$

and may also be written as the Fourier transform of a correlation function P_d representing fluctuations in space and time (see Cowley, 1981). When the energy transfers are small – as with TDS – and hence not measured, the observed intensity corresponds to an integral over ν :

$$\begin{aligned} I(\mathbf{u}) &= I_d(\mathbf{u}) + I_{av}(\mathbf{u}) \\ I_d(\mathbf{u}) &= \int I_d(\mathbf{u}, \nu) d\nu = \mathcal{F}\{P_d(\mathbf{r}, \mathbf{0})\} \end{aligned}$$

and also

$$I_d(\mathbf{u}) = \langle |\Phi(\mathbf{u})|^2 \rangle - |\langle \Phi(\mathbf{u}) \rangle|^2, \quad (4.3.1.3)$$

where the brackets may indicate a time average, an expectation value, or a spatial average over the periodicity of the lattice in the case of static deviations from a periodic structure.

The considerations of TDS and static defects and disorder of Chapters 4.1 and 4.2 thus may be applied directly to electron diffraction in the kinematical approximation when the differences in experimental conditions and diffraction geometry are taken into account.

The most prominent contribution to the diffuse background in electron diffraction, however, is the inelastic scattering at low angles arising mainly from the excitation of outer electrons. This is quite different from the X-ray case where the inelastic ('incoherent') scattering, $S(\mathbf{u})$, goes to zero at small angles and increases to a value proportional to Z for high values of $|\mathbf{u}|$. The difference is due to the Coulomb nature of electron scattering, which leads to the kinematical intensity expression S/u^4 , emphasizing the small-angle region. At high angles, the inelastic scattering from an atom is then proportional to Z/u^4 , which is considerably less than the corresponding elastic scattering $(Z - f)^2/u^4$ which approaches Z^2/u^4 (Section 2.5.2) (see Fig. 4.3.1.1).

The kinematical description can be used for electron scattering only when the crystal is very thin (10 nm or less) and composed of light atoms. For heavy atoms such as Au or Pb, crystals of thickness 1 nm or more in principal orientations show strong deviations from kinematical behaviour. With increasing thickness, dynamical scattering effects first modify the sharp Bragg reflections and then have increasingly significant effects on the diffuse scattering. Bragg scattering of the diffuse scattering produces Kikuchi lines and other effects. Multiple diffuse scattering broadens the distribution and smears out detail. As the thickness increases further, the diffuse scattering increases and the Bragg beams are reduced in intensity until there is only a diffuse 'channelling pattern' where the features depend in only a very indirect way on the incident-beam direction or on the sources of the diffuse scattering (Uyeda & Nonoyama, 1968).

The multiple-scattering effects make the quantitative interpretation of diffuse scattering more difficult and complicate the extraction of particular components, *e.g.* disorder scattering. Much of the multiple scattering involves inelastic scattering processes. However, electrons that have lost energy of the order of 1 eV or more can be subtracted experimentally by use of electron energy filters (Krahl *et al.*, 1990; Krivanek *et al.*, 1992) which are commercially available. Measurement can be made also of the complete scattering function $I(\mathbf{u}, \nu)$, but such studies have been rare. Another significant improvement to quantitative measurement of diffuse electron scattering is offered by new recording devices: slow-scan charge-couple-device cameras (Krivanek & Mooney, 1993) and imaging plates (Mori *et al.*, 1990).

There are some advantages in the use of electrons which make it uniquely valuable for particular applications.

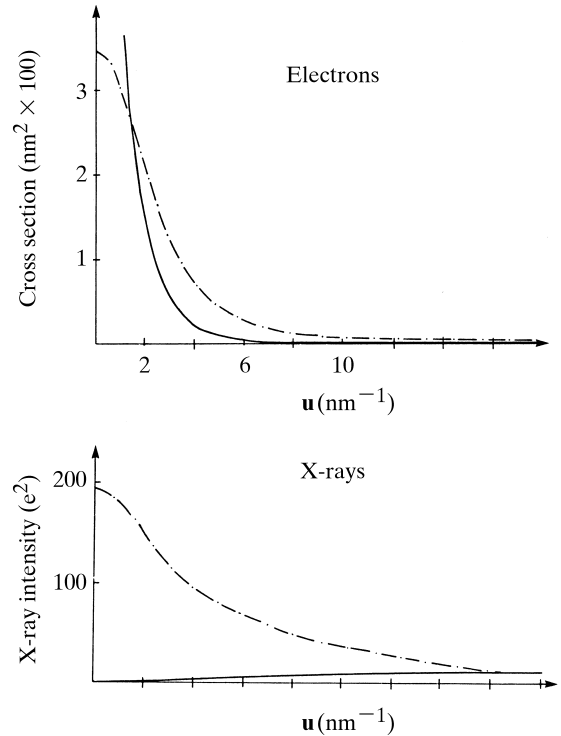


Fig. 4.3.1.1. Comparison between the kinematical inelastic scattering (full line) and elastic scattering (broken) for electrons and X-rays. Values for silicon [Freeman (1960) and *IT C* (2004)].

† Deceased.

4.4. Scattering from mesomorphic structures

BY P. S. PERSHAN

4.4.1. Introduction

The term mesomorphic is derived from the prefix 'meso-', which is defined in the dictionary as 'a word element meaning middle', and the term '-morphic', which is defined as 'an adjective termination corresponding to morph or form'. Thus, mesomorphic order implies some 'form', or order, that is 'in the middle', or intermediate between that of liquids and crystals. The name liquid crystalline was coined by researchers who found it to be more descriptive, and the two are used synonymously. It follows that a mesomorphic, or liquid-crystalline, phase must have more symmetry than any one of the 230 space groups that characterize crystals.

A major source of confusion in the early liquid-crystal literature was concerned with the fact that many of the molecules that form liquid crystals also form true three-dimensional crystals with diffraction patterns that are only subtly different from those of other liquid-crystalline phases. Since most of the original mesomorphic phase identifications were performed using a 'miscibility' procedure, which depends on optically observed changes in textures accompanying variation in the sample's chemical composition, it is not surprising that some three-dimensional crystalline phases were mistakenly identified as mesomorphic. Phases were identified as being either the same as, or different from, phases that were previously observed (Liebert, 1978; Gray & Goodby, 1984), and although many of the workers were very clever in deducing the microscopic structure responsible for the microscopic textures, the phases were labelled in the order of discovery as smectic-A, smectic-B *etc.* without any attempt to develop a systematic nomenclature that would reflect the underlying order. Although different groups did not always assign the same letters to the same phases, the problem is now resolved and the assignments used in this article are commonly accepted (Gray & Goodby, 1984).

Fig. 4.4.1.1 illustrates the way in which increasing order can be assigned to the series of mesomorphic phases in three dimensions listed in Table 4.4.1.1. Although the phases in this series are the

most thoroughly documented mesomorphic phases, there are others not included in the table which we will discuss below.

The progression from the completely symmetric isotropic liquid through the mesomorphic phases into the crystalline phases can be described in terms of three separate types of order. The first, or the molecular orientational order, describes the fact that the molecules have some preferential orientation analogous to the spin orientational order of ferromagnetic materials. In the present case, the molecular quantity that is oriented is a symmetric second-rank tensor, like the moment of inertia or the electric polarizability, rather than a magnetic moment. This is the only type of long-range order in the nematic phase and as a consequence its physical properties are those of an anisotropic fluid; this is the origin of the name liquid crystal. Fig. 4.4.1.2(a) is a schematic illustration of the nematic order if it is assumed that the molecules can be represented by oblong ellipses. The average orientation of the ellipses is aligned; however, there is no long-range order in the relative positions of the ellipses. Nematic phases are also observed for disc-shaped molecules and for clusters of molecules that form micelles. These all share the common properties of being optically anisotropic and fluid-like, without any long-range positional order.

The second type of order is referred to as bond orientational order. Consider, for example, the fact that for dense packing of spheres on a flat surface most of the spheres will have six neighbouring spheres distributed approximately hexagonally around it. If a perfect two-dimensional triangular lattice of indefinite size were constructed of these spheres, each hexagon on the lattice would be oriented in the same way. Within the last few years, we have come to recognize that this type of order, in which the hexagons are everywhere parallel to one another, is possible even when there is no lattice. This type of order is referred to as bond orientational order, and bond orientational order in the absence of a lattice is the essential property defining the hexatic phases (Halperin & Nelson, 1978; Nelson & Halperin, 1979; Young, 1979; Birgeneau & Litster, 1978).

The third type of order is the positional order of an indefinite lattice of the type that defines the 230 space groups of conven-

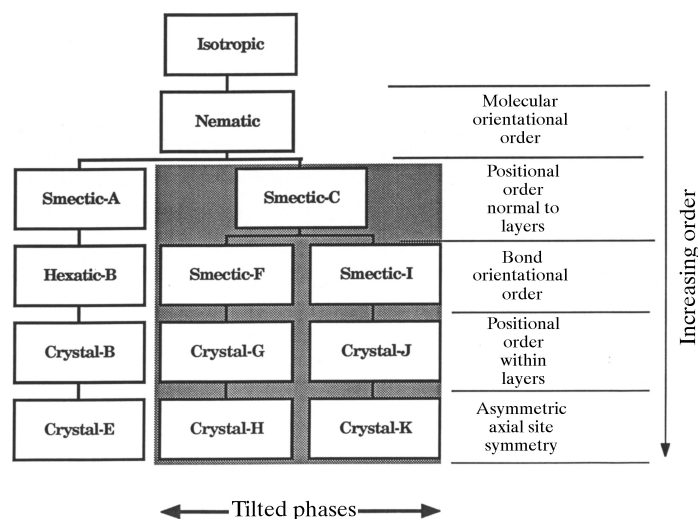


Fig. 4.4.1.1. Illustration of the progression of order throughout the sequence of mesomorphic phases that are based on 'rod-like' molecules. The shaded section indicates phases in which the molecules are tilted with respect to the smectic layers.

Table 4.4.1.1. Some of the symmetry properties of the series of three-dimensional phases described in Fig. 4.4.1.1

The terms LRO and SRO imply long-range or short-range order, respectively, and QLRO refers to 'quasi-long-range order' as explained in the text.

Phase	Molecular orientation order within layer	Bond orientation order	Positional order	
			Normal to layer	Within layer
Smectic-A (SmA)	SRO	SRO	SRO	SRO
Smectic-C (SmC)	LRO	LRO†	SRO	SRO
Hexatic-B	LRO†	LRO	QLRO	SRO
Smectic-F (SmF)	LRO	LRO	QLRO	SRO
Smectic-I (SmI)	LRO	LRO	QLRO	SRO
Crystalline-B (CrB)	LRO	LRO	LRO	LRO
Crystalline-G (CrG)	LRO	LRO	LRO	LRO
Crystalline-J (CrJ)	LRO	LRO	LRO	LRO
Crystalline-E (CrE)	LRO	LRO	LRO	LRO
Crystalline-H (CrH)	LRO	LRO	LRO	LRO
Crystalline-K (CrK)	LRO	LRO	LRO	LRO

† Theoretically, the existence of LRO in the molecular orientation, or tilt, implies that there must be some LRO in the bond orientation and *vice versa*.

for the intensities $I_l(R_{hk})$ from the data $I(R, Z)$ on the diffraction pattern. The parameters l_{lat} , l_{axial} and α_0 , as well as the cell constants and possibly other parameters, can also be refined as part of the profile-fitting procedure using nonlinear optimization.

A suite of programs for processing fibre diffraction data is distributed (and often developed) by the Collaborative Computational Project for Fibre and Polymer Diffraction (CCP13) in the UK (<http://www.ccp13.ac.uk/>) (Shotton *et al.*, 1998).

4.5.2.6. Structure determination

4.5.2.6.1. Overview

Structure determination in fibre diffraction is concerned with determining atomic coordinates or some other structural parameters, from the measured cylindrically averaged diffraction data. Fibre diffraction analysis suffers from the phase problem and low resolution (diffraction data rarely extend beyond 3 Å resolution), but this is no worse than in protein crystallography where phases derived from, say, isomorphous replacement or molecular replacement, coupled with the considerable stereochemical information usually available on the molecule under study, together contribute enough information to lead to precise structures. What makes structure determination by fibre diffraction more difficult is the loss of information owing to the cylindrical averaging of the diffraction data. However, in spite of these difficulties, fibre diffraction has been used to determine, with high precision, the structures of a wide variety of biological and synthetic polymers, and other macromolecular assemblies. Because of the size of the repeating unit and the resolution of the diffraction data, methods for structure determination in fibre diffraction tend to mimic those of macromolecular (protein) crystallography, rather than small-molecule crystallography (direct methods).

For a noncrystalline fibre one can determine only the molecular structure from the continuous diffraction data, whereas for a polycrystalline fibre one can determine crystal structures from the Bragg diffraction data. However, there is little fundamental difference between methods used for structure determination with noncrystalline and polycrystalline fibres. For partially crystalline fibres, little has so far been attempted with regard to rigorous structure determination.

As is the case with protein crystallography, the precise methods used for structure determination by fibre diffraction depend on the particular problem at hand. A variety of tools are available and one selects from these those that are appropriate given the data available in a particular case. For example, the structure of a polycrystalline polynucleotide might be determined by using Patterson functions to determine possible packing arrangements, molecular model building to define, refine and arbitrate between structures, difference Fourier synthesis to locate ions or solvent molecules, and finally assessment of the reliability of the structure. As a second example, to determine the structure of a helical virus, one might use isomorphous replacement to obtain phase estimates, calculate an electron-density map, fit a preliminary model and refine it using simulated annealing alternating with difference Fourier analysis, and assess the results. The various tools available, together with indications of where and how they are used, are described in the following sections.

Although a variety of techniques are used to solve structures using fibre diffraction, most of the methods do fall broadly into one of three classes that depend primarily on the size of the helical repeat unit. The first class applies to molecules whose repeating units are small, *i.e.* are represented by a relatively small number of independent parameters or degrees of freedom (after all stereochemical constraints have been incorporated). The

structure can then be determined by an exhaustive exploration of the parameter space using molecular model building. The first example above would belong to this class. The second class of methods is appropriate when the size of the helical repeating unit is such that its structure is described by too many variable parameters for the parameter space to be explored *a priori*. It is then necessary to phase the fibre diffraction data and construct an electron-density map into which the molecular structure can be fitted and then refined. The second example above would belong to this class. The second class of methods therefore mimics conventional protein crystallography quite closely. The third class of problems applies when the structure is large, but there are too few diffraction data to attempt phasing and the usual determination of atomic coordinates. The solution to such problems varies from case to case and usually involves modelling and optimization of some kind.

An important parameter in structure determination by fibre diffraction is the degree of overlap (that results from the cylindrical averaging) in the data. This parameter is equal to the number of significant terms in equation (4.5.2.17) or the number of independent terms in equation (4.5.2.24), and depends on the position in reciprocal space and, for a polycrystalline fibre, the space-group symmetry. The number of degrees of freedom in a particular datum is equal to twice this number (since each structure factor generally has real and imaginary parts), and is denoted in this section by m . Determination of the $G_{nl}(R)$ from the cylindrically averaged data $I_l(R)$ therefore involves separating the $m/2$ amplitudes $|G_{nl}(R)|$ and assigning phases to each. The electron density can be calculated from the $G_{nl}(R)$ using equations (4.5.2.7) and (4.5.2.11).

4.5.2.6.2. Helix symmetry, cell constants and space-group symmetry

The first step in analysis of any fibre diffraction pattern is determination of the molecular helix symmetry u_v . Only the zero-order Bessel term contributes diffracted intensity on the meridian, and referring to equation (4.5.2.6) shows that the zero-order term occurs only on layer lines for which l is a multiple of u . Therefore, inspection of the distribution of diffraction along the meridian allows the value of u to be inferred. This procedure is usually effective, but can be difficult if u is large, because the first meridional maximum may be on a layer line that is difficult to measure. This difficulty was overcome in one case by Franklin & Holmes (1958) by noting that the second Bessel term on the equator is $n = u$, estimating $G_{00}(R)$ using data from a heavy-atom derivative (see Section 4.5.2.6.6), subtracting this from $I_0(R)$, and using the behaviour of the remaining intensity for small R to infer the order of the next Bessel term [using equation (4.5.2.14)] and thence u .

Referring to equations (4.5.2.6) and (4.5.2.14) shows that the distribution of R_{\min} for $0 < l < u$ depends on the value of v . Therefore, inspection of the intensity distribution close to the meridian often allows v to be inferred. Note, however, that the distribution of R_{\min} does not distinguish between the helix symmetries u_v and u_{u-v} . Any remaining ambiguities in the helix symmetry need to be resolved by steric considerations, or by detailed testing of models with the different symmetries against the available data.

For a polycrystalline system, the cell constants are determined from the (R, Z) coordinates of the spots on the diffraction pattern as described in Section 4.5.2.6.4. Space-group assignment is based on analysis of systematic absences, as in conventional crystallography. However, in some cases, because of possible overlap of systematic absences with other reflections, there may be some ambiguity in space-group assignment. However, the space group can always be limited to one of a few possibilities, and ambiguities can usually be resolved during structure determination (Section 4.5.2.6.4).

4.6. Reciprocal-space images of aperiodic crystals

By W. STEURER[‡] AND T. HAIBACH

4.6.1. Introduction

The discovery of materials with icosahedral diffraction symmetry (Shechtman *et al.*, 1984) was the main reason for the reassessment of the definition of *crystallinity* and for the introduction of the concept of *aperiodic crystals*. The first aperiodic crystal, *i.e.* a material with Bragg reflections not located only at reciprocal-lattice nodes, was identified long before (Dehlinger, 1927). In the following decades a wealth of incommensurately modulated phases and composite crystals were discovered. Nevertheless, only a few attempts have been made to develop a crystallography of aperiodic crystals; the most powerful of these was the higher-dimensional approach (see de Wolff, 1974, 1977; Janner & Janssen, 1979, 1980a,b; de Wolff *et al.*, 1981). In fact, incommensurate structures can be easily described using the higher-dimensional approach and also, fully equivalently, in a dual way: as a three-dimensional (3D) combination of one or more periodic basic structures and one or several modulation waves (de Wolff, 1984). However, with the discovery of quasicrystals and their noncrystalline symmetries, the latter approach failed and geometrical crystallography including the higher-dimensional approach received new attention. For more recent reviews of the crystallography of all three types of aperiodic crystals see van Smaalen (1995), of incommensurately modulated structures see Cummins (1990), of quasicrystals see Steurer (1990, 1996), of quasicrystals and their crystalline approximants see Goldman & Kelton (1993) and Kelton (1995). Textbooks on quasicrystals have been written by Janot (1994) and Senechal (1995).

According to the traditional crystallographic definition, an *ideal crystal* corresponds to an infinite 3D periodic arrangement of identical structure motifs. Its symmetry can be described by one of the 230 3D space groups. Mathematically, a periodic structure can be generated by the convolution of a function representing the structure motif with a lattice function. The structure motif can be given, for instance, by the electron-density distribution $\rho(\mathbf{r})$ of one primitive unit cell of the structure. The lattice function $g(\mathbf{r})$ is represented by a set of δ functions at the nodes $\mathbf{r} = \sum_{i=1}^3 k_i \mathbf{a}_i$ of a 3D lattice Λ with basis \mathbf{a}_i , $i = 1, \dots, 3$, and $k_i \in \mathbb{Z}$ (\mathbb{Z} is the set of integer numbers). In reciprocal space, this convolution corresponds to the product of the Fourier transform $G(\mathbf{H})$ of the lattice function $g(\mathbf{r})$ and the Fourier transform $F(\mathbf{H}) = \int_V \rho(\mathbf{r}) \exp(2\pi i \mathbf{H} \cdot \mathbf{r}) d\mathbf{r}$ of the structure motif $\rho(\mathbf{r})$. $G(\mathbf{H})$ is represented by the reciprocal lattice Λ^* decorated with δ functions on the reciprocal-lattice nodes $\mathbf{H} = \sum_{i=1}^3 h_i \mathbf{a}_i^*$, with the reciprocal-basis vectors \mathbf{a}_i^* , $i = 1, \dots, 3$, defined by $\mathbf{a}_i \cdot \mathbf{a}_j^* = \delta_{ij}$ and $h_i \in \mathbb{Z}$. The product $G(\mathbf{H}) \times F(\mathbf{H})$ is called the weighted reciprocal lattice; the weights are given by the structure factors $F(\mathbf{H})$. Thus, the characteristic feature of an ideal crystal in direct and reciprocal space is the existence of a lattice. In direct space, this lattice is decorated with identical structure motifs preserving translational and point symmetry in the framework of *space-group symmetry*. In reciprocal space, only the point symmetry between structure factors is maintained. The *Fourier spectrum* (or *Fourier image*, *i.e.* the Fourier transform) of the electron-density distribution of an ideal crystal consists of a countably infinite set of discrete Bragg peaks with a strictly defined minimum distance.

This crystal definition can be generalized to $n > 3$ dimensions. A d -dimensional (dD) *ideal aperiodic crystal* can be defined as a dD irrational section of an n -dimensional (nD , $n > d$) crystal with

nD lattice symmetry. The intersection of the nD *hypercrystal* with the dD physical space is equivalent to a projection of the weighted nD reciprocal lattice $\Sigma^* = \{\mathbf{H} = \sum_{i=1}^n h_i \mathbf{d}_i^* | h_i \in \mathbb{Z}\}$ onto the dD physical space. The resulting set (Fourier module) $M^* = \{\mathbf{H}^\parallel = \sum_{i=1}^n h_i \mathbf{a}_i^* | h_i \in \mathbb{Z}\}$ is countably dense. *Countably dense* means that the dense set of Bragg peaks can be mapped one-to-one onto the set of natural numbers. Hence, the Bragg reflections can be indexed with integer indices on an appropriate basis. The Fourier module of the projected reciprocal-lattice vectors \mathbf{H}^\parallel has the structure of a \mathbb{Z} module of rank n . A \mathbb{Z} module is a free Abelian group, its rank n is given by the number of free generators (rationally independent vectors). The dimension of a \mathbb{Z} module is that of the vector space spanned by it. The vectors \mathbf{a}_i^* are the images of the vectors \mathbf{d}_i^* projected onto the physical space \mathbf{V}^\parallel . Thus, by definition, the 3D reciprocal space of an ideal *aperiodic crystal* consists of a countably dense set of Bragg reflections only. Contrary to an ideal *crystal*, a minimum distance between Bragg reflections does not exist in an aperiodic one. In summary, it may be stressed that the terms *aperiodic* and *periodic* refer to properties of crystal structures in dD space. In nD space, as considered here, lattice symmetry is always present and, therefore, the term *crystal* is used.

Besides the *aperiodic crystals* mentioned above, other classes of *aperiodic structures* with strictly defined construction rules exist (see Axel & Gratias, 1995). Contrary to the kind of aperiodic crystals dealt with in this chapter, the Fourier spectra of aperiodic structures considered in the latter reference are continuous and contain only in a few cases additional sharp Bragg reflections (δ peaks).

Experimentally, the borderline between aperiodic crystals and their periodic approximations (*crystalline approximants*) is not sharply defined. Finite crystal size, static and dynamic disorder, chemical impurities and defects broaden Bragg peaks and cause diffuse diffraction phenomena. Furthermore, the resolution function of the diffraction equipment is limited.

However, the concept of describing an aperiodic structure as a dD physical-space section of an nD crystal (see Section 4.6.2) is only useful if it significantly simplifies the description of its structural order. Thus, depending on the shape of the *atomic surfaces*, which gives information on the atomic ordering, incommensurately modulated structures (IMSS, Sections 4.6.2.2 and 4.6.3.1), composite structures (CSs, Sections 4.6.2.3 and 4.6.3.2), or quasiperiodic structures (QSs, Sections 4.6.2.4 and 4.6.3.3) can be obtained from irrational cuts. The atomic surfaces are continuous $(n - d)$ -dimensional objects for IMSS and CSs, and discrete $(n - d)$ -dimensional objects for QSs. A class of aperiodic crystals with discrete fractal atomic surfaces also exists (Section 4.6.2.5). In this case the Hausdorff dimension (Hausdorff, 1919) of the atomic surface is not an integer number and smaller than $n - d$. The most outstanding characteristic feature of a fractal is its scale invariance: the object appears similar to itself 'from near as from far, that is, whatever the scale' (Gouyet, 1996).

To overcome the problems connected with experimental resolution, the translational symmetry of periodic crystals is used as a hard constraint in the course of the determination of their structures. Hence, space-group symmetry is taken for granted and only the local atomic configuration in a unit cell (actually, asymmetric unit) remains to be determined. In reciprocal space, this assumption corresponds to a condensation of Bragg reflections with finite full width at half maximum (FWHM) to δ peaks

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5.1. Dynamical theory of X-ray diffraction

BY A. AUTHIER

5.1.1. Introduction

The first experiment on X-ray diffraction by a crystal was performed by W. Friedrich, P. Knipping and M. von Laue in 1912 and Bragg's law was derived in 1913 (Bragg, 1913). Geometrical and dynamical theories for the intensities of the diffracted X-rays were developed by Darwin (1914*a,b*). His dynamical theory took into account the interaction of X-rays with matter by solving recurrence equations that describe the balance of partially transmitted and partially reflected amplitudes at each lattice plane. This is the first form of the dynamical theory of X-ray diffraction. It gives correct expressions for the reflected intensities and was extended to the absorbing-crystal case by Prins (1930). A second form of dynamical theory was introduced by Ewald (1917) as a continuation of his previous work on the diffraction of optical waves by crystals. He took into account the interaction of X-rays with matter by considering the crystal to be a periodic distribution of dipoles which were excited by the incident wave. This theory also gives the correct expressions for the reflected and transmitted intensities, and it introduces the fundamental notion of a wavefield, which is necessary to understand the propagation of X-rays in perfect or deformed crystals. Ewald's theory was later modified by von Laue (1931), who showed that the interaction could be described by solving Maxwell's equations in a medium with a continuous, triply periodic distribution of dielectric susceptibility. It is this form which is most widely used today and which will be presented in this chapter.

The geometrical (or kinematical) theory, on the other hand, considers that each photon is scattered only once and that the interaction of X-rays with matter is so small it can be neglected. It can therefore be assumed that the amplitude incident on every diffraction centre inside the crystal is the same. The total diffracted amplitude is then simply obtained by adding the individual amplitudes diffracted by each diffracting centre, taking into account only the geometrical phase differences between them and neglecting the interaction of the radiation with matter. The result is that the distribution of diffracted amplitudes in reciprocal space is the Fourier transform of the distribution of diffracting centres in physical space. Following von Laue (1960), the expression *geometrical theory* will be used throughout this chapter when referring to these geometrical phase differences.

The first experimentally measured reflected intensities were not in agreement with the theoretical values obtained with the more rigorous dynamical theory, but rather with the simpler geometrical theory. The integrated reflected intensities calculated using geometrical theory are proportional to the square of the structure factor, while the corresponding expressions calculated using dynamical theory for an infinite perfect crystal are proportional to the modulus of the structure factor. The integrated intensity calculated by geometrical theory is also proportional to the volume of the crystal bathed in the incident beam. This is due to the fact that one neglects the decrease of the incident amplitude as it progresses through the crystal and a fraction of it is scattered away. According to geometrical theory, the diffracted intensity would therefore increase to infinity if the volume of the crystal was increased to infinity, which is of course absurd. The theory only works because the strength of the interaction is very weak and if it is applied to very small crystals. How small will be shown quantitatively in Sections 5.1.6.5 and 5.1.7.2. Darwin (1922) showed that it can also be applied to large imperfect crystals. This is done using the model of mosaic crystals

(Bragg *et al.*, 1926). For perfect or nearly perfect crystals, dynamical theory should be used. Geometrical theory presents another drawback: it gives no indication as to the phase of the reflected wave. This is due to the fact that it is based on the Fourier transform of the electron density limited by the external shape of the crystal. This is not important when one is only interested in measuring the reflected intensities. For any problem where the phase is important, as is the case for multiple reflections, interference between coherent blocks, standing waves *etc.*, dynamical theory should be used, even for thin or imperfect crystals.

Until the 1940s, the applications of dynamical theory were essentially intensity measurements. From the 1950s to the 1970s, applications were related to the properties (absorption, interference, propagation) of wavefields in perfect or nearly perfect crystals: anomalous transmission, diffraction of spherical waves, interpretation of images on X-ray topographs, accurate measurement of form factors, lattice-parameter mapping. In recent years, they have been concerned mainly with crystal optics, focusing and the design of monochromators for synchrotron radiation [see, for instance, Batterman & Bilderback (1991)], the location of atoms at crystal surfaces and interfaces using the standing-waves method, determination of phases using multiple reflections [for reviews of *n*-beam diffraction, see Weckert & Hümmel (1997) and Chang (2004); for recent determinations of phases, see Chang *et al.* (2002), Mo *et al.* (2002), Weckert *et al.* (2002), Shen & Wang (2003)], characterization of the crystal perfection of epilayers and superlattices by high-resolution diffractometry [see, for instance, Tanner (1990) and Fewster (1993)], *etc.*

Modern developments include the extension of dynamical theory to time-dependent phenomena (Chukhovskii & Förster, 1995; Shastri *et al.*, 2001; Graeff, 2002*a,b*, 2004; Malgrange & Graeff, 2003; Sondhauss & Wark, 2003; Adams, 2004) and the study of the influence of the coherence of the source (Yamazaki & Ishikawa, 2002, 2004).

For reviews of dynamical theory, see Zachariasen (1945), von Laue (1960), James (1963), Batterman & Cole (1964), Authier (1970), Kato (1974), Brümmer & Stephanik (1976), Pinsker (1978), Authier *et al.* (1996), Authier & Malgrange (1998), and Authier (2005). Topography is described in Chapter 2.7 of *IT C* (2004), in Tanner (1976) and in Tanner & Bowen (1992). For the use of Bragg-angle measurements for accurate lattice-parameter mapping, see Hart (1981). For online calculations in the case of multiple diffraction, grazing incidence or for strained crystals, see <http://sergey.gmca.aps.anl.gov>.

A reminder of some basic concepts in electrodynamics is given in Section A5.1.1.1 of the Appendix.

5.1.2. Fundamentals of plane-wave dynamical theory

5.1.2.1. Propagation equation

The wavefunction Ψ associated with an electron or a neutron beam is *scalar* while an electromagnetic wave is a *vector* wave. When propagating in a medium, these waves are solutions of a *propagation equation*. For electrons and neutrons, this is Schrödinger's equation, which can be rewritten as

$$\Delta\Psi + 4\pi^2k^2(1 + \chi)\Psi = 0, \quad (5.1.2.1)$$

5.2. Dynamical theory of electron diffraction

BY A. F. MOODIE, J. M. COWLEY† AND P. GOODMAN†

5.2.1. Introduction

Since electrons are charged, they interact strongly with matter, so that the single scattering approximation has a validity restricted to thin crystals composed of atoms of low atomic number. Further, at energies of above a few tens of keV, the wavelength of the electron is so short that the geometry of two-beam diffraction can be approximated in only small unit cells.

It is therefore necessary to develop a scattering theory specific to electrons and, preferably, applicable to imaging as well as to diffraction. The development, started by Born (1926) and Bethe (1928), and continuing into the present time, is the subject of an extensive literature, which includes reviews [for instance: Howie (1978), Humphreys (1979)] and historical accounts (Goodman, 1981), and is incorporated in Chapter 5.1. Here, an attempt will be made to present only that outline of the main formulations which, it is hoped, will help the nonspecialist in the use of the tables. No attempt will be made to follow the historical development, which has been tortuous and not always logical, but rather to seek the simplest and most transparent approach that is consistent with brevity. Only key points in proofs will be sketched in an attempt to display the nature, rather than the rigorous foundations of the arguments.

5.2.2. The defining equations

No many-body effects have yet been detected in the diffraction of fast electrons, but the velocities lie well within the relativistic region. The one-body Dirac equation would therefore appear to be the appropriate starting point. Fujiwara (1962), using the scattering matrix, carried through the analysis for forward scattering, and found that, to a very good approximation, the effects of spin are negligible, and that the solution is the same as that obtained from the Schrödinger equation provided that the relativistic values for wavelength and mass are used. In effect a Klein-Gordon equation (Messiah, 1965) can be used in electron diffraction (Buxton, 1978) in the form

$$\nabla^2 \psi_b + \frac{8\pi^2 m |e| \varphi}{h^2} \psi_b + \frac{8\pi^2 m_0 |e| W}{h^2} \left(1 + \frac{|e| W}{2m_0 c^2}\right) \psi_b = 0.$$

Here, W is the accelerating voltage and φ , the potential in the crystal, is defined as being positive. The relativistic values for mass and wavelength are given by $m = m_0(1 - v^2/c^2)^{-1/2}$, and taking ' e ' now to represent the modulus of the electronic charge, $|e|$,

$$\lambda = h[2m_0 e W(1 + eW/2m_0 c^2)]^{-1/2},$$

and the wavefunction is labelled with the subscript b in order to indicate that it still includes back scattering, of central importance to LEED (low-energy electron diffraction).

In more compact notation,

$$[\nabla^2 + k^2(1 + \varphi/W)]\psi_b = (\nabla^2 + k^2 + 2k\sigma\varphi)\psi_b = 0. \quad (5.2.2.1)$$

Here $k = |\mathbf{k}|$ is the scalar wavenumber of magnitude $2\pi/\lambda$, and the interaction constant $\sigma = 2\pi m e \lambda / h^2$. This constant is approximately 10^{-3} for 100 kV electrons.

For fast electrons, φ/W is a slowly varying function on a scale of wavelength, and is small compared with unity. The scattering will therefore be peaked about the direction defined by the incident beam, and further simplification is possible, leading to a forward-scattering solution appropriate to HEED (high-energy electron diffraction).

5.2.3. Forward scattering

A great deal of geometric detail can arise at this point and, further, there is no generally accepted method for approximation, the various procedures leading to numerically negligible differences and to expressions of precisely the same form. Detailed descriptions of the geometry are given in the references.

The entrance surface of the specimen, in the form of a plate, is chosen as the x, y plane, and the direction of the incident beam is taken to be close to the z axis. Components of the wavevector are labelled with suffixes in the conventional way; $\mathbf{K}_0 = \mathbf{k}_x + \mathbf{k}_y$ is the transverse wavevector, which will be very small compared to \mathbf{k}_z . In this notation, the excitation error for the reflection is given by

$$\zeta_h = \frac{K_0^2 - |\mathbf{K}_0 + 2\pi\mathbf{h}|^2}{4\pi|\mathbf{k}_z|}.$$

An intuitive method argues that, since $\varphi/W \ll 1$, then the component of the motion along z is little changed by scattering. Hence, making the substitution $\psi_b = \psi \exp\{ik_z z\}$ and neglecting $\partial^2 \psi / \partial z^2$, equation (5.2.2.1) becomes

$$\frac{\partial \psi}{\partial z} = i \left[\frac{1}{2k_z} (\nabla_{x,y}^2 + K_0^2) + \sigma \varphi \right] \psi, \quad (5.2.3.1)$$

where

$$\nabla_{x,y}^2 \equiv \frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2},$$

and $\psi(x, y, 0) = \exp\{i(k_x x + k_y y)\}$.

Equation (5.2.3.1) is of the form of a two-dimensional time-dependent Schrödinger equation, with the z coordinate replacing time. This form has been extensively discussed. For instance, Howie (1966) derived what is essentially this equation using an expansion in Bloch waves, Berry (1971) used a Green function in a detailed and rigorous derivation, and Goodman & Moodie (1974), using methods due to Feynman, derived the equation as the limit of the multislice recurrence relation. A method due to Coronas *et al.* (1982) brings out the relationship between the HEED and LEED equations. Equation (5.2.2.1) is cast in the form of a first-order system,

$$\frac{\partial}{\partial z} \begin{pmatrix} \psi_b \\ \frac{\partial \psi_b}{\partial z} \end{pmatrix} = \begin{pmatrix} 0 & 1 \\ -(\nabla_{x,y}^2 + k^2 + 2k\sigma\varphi) & 0 \end{pmatrix} \begin{pmatrix} \psi_b \\ \frac{\partial \psi_b}{\partial z} \end{pmatrix}.$$

† Deceased.

5.3. Dynamical theory of neutron diffraction

BY M. SCHLENKER AND J.-P. GUIGAY

5.3.1. Introduction

Neutron and X-ray scattering are quite similar both in the geometry of scattering and in the orders of magnitude of the basic quantities. When the neutron spin is neglected, *i.e.* when dealing with scattering by perfect nonmagnetic crystals, the formalism and the results of the dynamical theory of X-ray scattering can be very simply transferred to the case of neutrons (Section 5.3.2). Additional features of the neutron case are related to the neutron spin and appear in diffraction by magnetic crystals (Section 5.3.3). The low intensities available, coupled with the low absorption of neutrons by most materials, make it both necessary and possible to use large samples in standard diffraction work. The effect of extinction in crystals that are neither small nor bad enough to be amenable to the kinematical approximation is therefore very important in the neutron case, and will be discussed in Section 5.3.4 together with the effect of crystal distortion. Additional possibilities arise in the neutron case because the neutrons can be manipulated from outside through applied fields (Section 5.3.5). Reasonably extensive tests of the predictions of the dynamical theory of neutron diffraction have been performed, with the handicap of the very low intensities of neutron beams as compared with X-rays: these are described in Section 5.3.6. Finally, the applications of the dynamical theory in the neutron case, and in particular neutron interferometry, are reviewed in Section 5.3.7.

5.3.2. Comparison between X-rays and neutrons with spin neglected

5.3.2.1. The neutron and its interactions

An excellent introductory presentation of the production, properties and scattering properties of neutrons is available (Scherm & Fåk, 1993, and other papers in the same book). A stimulating review on neutron optics, including diffraction by perfect crystals, has been written by Klein & Werner (1983). X-rays and neutrons are compared in terms of the basic quantities in Table 4.1.3.1 of *IT C* (2004), where Chapter 4.4 is devoted to neutron techniques.

The neutron is a massive particle for which the values relevant to diffraction are: no electric charge, rest mass $m = 1.675 \times 10^{-27}$ kg, angular momentum eigenvalues along a given direction $\pm \hbar/2$ (spin $\frac{1}{2}$) and a magnetic moment of -1.913 nuclear magneton, meaning that its component along a quantization direction z can take eigenvalues $\mu_z = \mp 0.996 \times 10^{-26}$ A m². The de Broglie wavelength is $\lambda = h/p$ where h is Planck's constant ($h = 2\pi\hbar = 6.625 \times 10^{-34}$ J s) and p is the linear momentum; $p = mv$ in the nonrelativistic approximation, which always applies in the context of this chapter, v being the neutron's velocity. The neutron's wavelength, λ , and kinetic energy, E_c , are thus related by $\lambda = h/(2mE_c)^{1/2}$, or, in practical units, $\lambda [\text{\AA}] = 9.05/(E_c [\text{meV}])^{1/2}$. Thus, to be of interest for diffraction by materials, neutrons should have kinetic energies in the range 10^0 to 10^2 meV. In terms of the velocity, $\lambda [\text{\AA}] = 3.956/(v [\text{km s}^{-1}])$.

Neutron beams are produced by nuclear reactors or by spallation sources, usually pulsed. In either case they initially have an energy in the MeV range, and have to lose most of it before they can be used. The moderation process involves inelastic interactions with materials. It results in statistical distributions of

energy, hence of velocity, close to the Maxwell distribution characteristic of the temperature T of the moderator. Frequently used moderators are liquid deuterium (D_2 , *i.e.* 2H_2) at 25 K, heavy water (D_2O) at room temperature and graphite allowed to heat up to 2400 K; the corresponding neutron distributions are termed cold, thermal and hot, respectively.

The interaction of a neutron with an atom is usually described in terms of scattering lengths or of scattering cross sections. The main contribution corresponding to the nuclear interaction is related to the strong force. The interaction with the magnetic field created by atoms with electronic magnetic moments is comparable in magnitude to the nuclear term.

5.3.2.2. Scattering lengths and refractive index

The elastic scattering amplitude for scattering vector \mathbf{s} , $f(\mathbf{s})$, is defined by the wave scattered by an object placed at the origin when the incident plane wave is $\Psi_i = A \exp[i(\mathbf{k}_0 \cdot \mathbf{r} - \omega t)]$, written as $\Psi_s = A[f(\mathbf{s})/r] \exp[i(kr - \omega t)]$ with $k = |\mathbf{k}_0| = |\mathbf{k}_0 + \mathbf{s}| = 2\pi/\lambda$. In the case of the strong-force interaction with nuclei, the latter can be considered as point scatterers because the interaction range is very small, hence the scattering amplitude is isotropic (independent of the direction of \mathbf{s}). It is also independent of λ except in the vicinity of resonances. It is conventionally written as $-b$ so that most values of b , called the scattering length, are positive. A table of experimentally measured values of the scattering lengths b is given in *IT C* for the elements in their natural form as well as for many individual isotopes. It is apparent that the typical order of magnitude is the fm (femtometre, *i.e.* 10^{-15} m, or fermi), that there is no systematic variation with atomic number and that different isotopes have very different scattering lengths, including different signs. The first remark implies that scattering amplitudes of X-rays and of neutrons have comparable magnitudes, because the characteristic length for X-ray scattering (the scattering amplitude for forward scattering by one free electron) is $R = 2.8$ fm, the classical electron radius. The second and third points explain the importance of neutrons in structural crystallography, in diffuse scattering and in small-angle scattering. Scattering of neutrons by condensed matter implies the use of the bound scattering lengths, as tabulated in *IT C*. The 'free' scattering length, used in some presentations, is obtained by multiplying the bound scattering lengths by $A/(A+1)$, where A is the mass of the nucleus in atomic units.

A description in terms of an interaction potential is possible using the Fermi pseudo-potential, which in the case of the nuclear interaction with a nucleus at \mathbf{r}_0 can be written as $V(\mathbf{r}) = (h^2/2\pi m)b\delta(\mathbf{r} - \mathbf{r}_0)$, where δ denotes the three-dimensional Dirac distribution.

Refraction of neutrons at an interface can be conveniently described by assigning a refractive index to the material, such that the wavenumber in the material, k , is related to that in a vacuum, k_0 , by $k = nk_0$. Here

$$n = \left(1 - \frac{\lambda^2}{\pi V} \sum_i b_i\right)^{1/2},$$

where the sum is over the nuclei contained in volume V . With typical values, n is very close to 1 and $1 - n = (\lambda^2/2\pi V) \sum_i b_i$ is