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modification based on satisfying the Sayre equation. In the event that the structure contains one type of heavy atom then a modified equation can be used which involves both squaring and cubing the current electron density (Woolfson, M M, 1958, *Acta Cryst* 11, 287-283).

A process has been devised, the ABC method, which enables density to be modified to satisfy the constraints of solvent flattening, histogram matching, Sayre's equation and the magnitudes of structure factors, all in terms of refining only a few (4-6) parameters. It may also be possible to introduce other constraints, for example a model distribution of atomic environments.

Preliminary results will be described and their potentiality discussed - in particular for *ab initio* phasing.

PS-02.01.11 A DENSITY MODIFICATION PROCEDURE FOR SOLVING SMALL & MIDDLE SIZE STRUCTURES AND PHASE REFINEMENT FOR PROTEINS. By M. Shiono, Y. Yada*, Department of Physics, Kyushu University, Higashi-ku, Fukuoka, Japan. L. S. Refaat and M. M. Woolfson, Department of Physics, University of York, Heslington, York, YO1 5DD.

The Low Density Elimination (LDE) procedure (Shiono, M. and Woolfson, M. M., *Acta Cryst.* (1992), **A48**, 451-456) which was developed for phase extension and refinement in order to solve macromolecules has been investigated regarding its power to solve small and middle size structures starting from random phase sets. In fact, the method is competitive against conventional direct methods. The LDE method, however, is time-consuming compared with conventional direct methods (e.g. MULTAN) since the procedure includes two Fourier transforms in one cycle. We have, therefore, combined MULTAN and LDE procedure. The LDE can be run in three different modes as follows.

Mode 1. Run the LDE with phases estimated by anomalous scatterings or isomorphous replacements. Mode 2. Employing multi-resolution strategy, run the LDE individually assigning all reflexions random phases. Mode 3. Run MULTAN and then proceed to the LDE using MULTAN phases as initial phase sets in order of figures of merit.

For small and middle size structures, mode 3 is most effective. We might eventually solve the structures with MULTAN trial. Even if MULTAN fails to find any useful structural configurations, MULTAN phases increase the power of the LDE in solving structures.

PS-02.01.12 DIRECT PHASING OF MACROMOLECULAR STRUCTURES BY MULTIPLE BEAM DIFFRACTION
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The feasibility of experimental phase determination of small protein structures using three-beam diffraction has already been demonstrated (K. Hümmer, W. Schwegle & E. Weckert (1991) *Acta Cryst.* **A47**, 60-62). It has been shown that triplet-phase invariants $\phi = -\varphi(\mathbf{h}) + \varphi(\mathbf{g}) + \varphi(\mathbf{h}-\mathbf{g})$ can be deduced from three-beam interference profiles (K. Hümmer, E. Weckert & H. Bondza (1989) *Acta Cryst.* **A45**, 182-187),

where the φ 's are the phases of individual structure factors of the involved reflections with reciprocal lattice vectors \mathbf{h} , \mathbf{g} , and $\mathbf{h}-\mathbf{g}$.

In experimental phase determination of macromolecular structure significant differences compared to small molecule structures occur. Among others they concern the weaker scattering power of individual reflections, increasing overlap of multiple-beam interference effects due to larger unit cells and in general higher sensitivity to radiation damage.

Because of the large number of overlapping multiple-beam interference patterns in protein crystal structures only three-beam cases of reflections with large structure factors are suitable for phase determination. It was possible to determine about 80 triplet phases of the small protein lysozyme in the low and medium resolution range with a mean phase error of about 17° .

Radiation damage can often be significantly reduced by using higher energy radiation, i.e. $\lambda = 0.7 \text{ \AA}$. Therefore, interference effects of lysozyme were systematically investigated in the range from 0.7 \AA to 1.58 \AA . As a result also in the short wavelength regime phase determination is possible.

Theoretical calculations by dynamical theory and experimental results confirm the existence of three-beam interference effects even for crystal sizes smaller than the "Pendellösung" lengths. Further investigations show that it is this range where a unique correlation exists between the interference profiles and the triplet phases independent whether the primary reflection is in Bragg- or Laue-diffraction geometry. In general the crystal size of proteins is smaller than the "Pendellösung" length.

Due to the weak reflectivity of protein crystals "Aufhellung" effects are weaker compared to the higher reflectivity of small molecule structures. Therefore, the high number of overlapping three-beam cases does not severely affect the phase exploitation in proteins.

First experiments with catalase crystals (space group $P4_22_12$, $a = 106.7 \text{ \AA}$, $c = 106.3 \text{ \AA}$) indicate that even for large proteins experimental phase determination may be feasible.

The possibilities to integrate measured triplet-phase invariants into statistical structure solution methods are discussed. First results to extend this phase information by an approach using maximum entropy will be presented.

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PS-02.01.13 FOURIER SERIES PROBABILITY DISTRIBUTION OF STRUCTURE FACTORS AND ITS RELATION WITH OTHER DISTRIBUTIONS.

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In his pioneering work, Wilson (*Acta Cryst.* 1949, 2, 318), showed that the distribution of structure factor components was Gaussian. Later, introduction of Edgeworth series (Mitra and

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Belgaumkar, Proc. Ind. Nat. Sci. Acad., 1973, 39, 95), the Gram-Charlier Series (Shmueli and Wilson, Acta Cryst, 1981, A37, 342) and Cauchy distribution (Mitra and Das, Acta Cryst, 1989, A45, 314) were ushered in. Meanwhile Hauptman and Karle (Acta Cryst, 1952, 5, 48) and Karle and Hauptman (Acta Cryst, 1953, 6, 31) invoked, for this purpose, the theory of random walk developed by Rayleigh. They showed that, for a centrosymmetric crystal, the probability density function P(F) for the structure factor F becomes

$$P(F) = (2\pi)^{-1} \left[\int_0^{\infty} A(x) \cos F(x) dx \right] \quad (1)$$

where $A(x) = \prod_{j=1}^{N/m} q(f_j, x)$ with $m =$ symmetry numbers

and $q(f_j, x) = 2 \int_0^{\infty} p(c) \cos(cf_j x) dc$

Again, shmueli, Weiss, Kieffer and Wilson (Acta Cryst, 1984, A40, 651-666) expressed P(F) as a Fourier series

$$P(F) = (2S)^{-1} \left\{ 1 + 2 \sum_{m=1}^{\infty} A(m) \cos(2\pi m F/s) \right\} \quad (2)$$

where $A(m) = \prod_{j=1}^{N/m} J_0(2\pi m f_j/s)$ and $s = \sum_{j=1}^N f_j$

when $J_0(R)$ signifies the Bessel function of first kind and order zero with argument R and f_j being the atomic scattering factor of the jth atom.

Changing over to $E = F / (\sum_{j=1}^N f_j^2)^{1/2}$ eq. (2) becomes

$$P(E) = \alpha \left\{ 1 + 2 \sum_{m=1}^{\infty} A(m) \cos(2\pi m \alpha E) \right\} \quad (3)$$

where

$$\alpha = \left(\sum_{j=1}^N f_j^2 \right)^{1/2} / \left(\sum_{j=1}^N f_j \right)$$

For equal atom case eq. (3) is given by

$$P(E) = N^{-1/2} \left\{ 1 + 2 \sum_{m=1}^{\infty} A(m) \cos 2\pi m E N^{-1/2} \right\} \quad (4)$$

when $A(m)$ reduces to $[J_0(2\pi m N^{-1})]^{N/2}$

Changing from the standardised amplitude E to the corresponding intensity $Z = E^2$, eq. (4) may be written as

$$p(Z) = N^{-1/2} Z^{-1/2} \left[1 + 2 \sum_{m=1}^{\infty} A(m) \cos 2\pi m Z^{1/2} N^{-1/2} \right] \quad (5)$$

Let the cumulative probability function Q(z) be

$$Q(z) = \int_0^z p(z) dz$$

Then

$$Q(z) = 2z^{1/2} N^{-1/2} + 4N^{-1/2} + 4N^{-1/2} \sum_{m=1}^{\infty} B(m) \sin 2\pi m Z^{1/2} N^{-1/2} \dots \quad (6)$$

..... (6)

$$\dots \dots \dots \quad (7)$$

where $B(m) = A(m) / 2\pi m N^{-1/2}$ (7)
A plot of Q(z) against z, based on eq. (6) and (7) for different values of N shows that for N = 60, Q(z) is very nearly equal to the Gaussian distribution (Howells, Philips and Rogers, Acta Cryst., 1950, 3, 210) and that for N = 30 corresponds very closely to the Cauchy bicentric case (Mitra and Das, Ind. J. Phys., 1992, 66A (3), 375). Relations with other distributions are under study.

02.02 – Anomalous Dispersion Methods

MS-02.02.01 THE FORM FACTOR FORMALISM : SHOULD HIGHER ORDER TENSOR REPRESENTATIONS BE USED?
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In its normal usage by crystallographers the form factor of an atom describes the scattering by an isolated spherical atom of the incident x radiation. Using this single formalism it has been possible to solve a wide range of problems in crystallography. The formalism works equally as well for powdered as for single crystal samples.

It does, however, have deficiencies, and these arise from the assumption that each atom scatters independently of its neighbours. The existence of XAFS and XANES demonstrates that this simplistic assumption fails near absorption edges. This modulation due to the interaction of the ejected photo-electrons with the crystalline structure is, however, a small modulation to the total scattering power of the atom. For most atomic species the overall scattering by an atom in the neighbourhood is approximated well by theory (Creagh & McAuley, 1992, International Tables for Crystallography, Vol. C, Section 4.2.6) as seen in Figure 1.

The difference in scattering is due to XAFS and may be accounted for by the scalar addition of the XAFS amplitude calculated using Rehr's FEFF Code.

For most materials no angular distribution of scattering is observed: the atomic form factor behaves as if it were a scalar quality. However, in some types of crystal dichroic effects occur, and these may be explained by the addition of a second rank tensor to the scalar form factor tensor (Templeton & Templeton, 1986, Acta Cryst., A42, 478-86). This second rank tensor has its elements determined by the crystalline charge distributions of the dichroic crystals under investigation.

For some rare earth magnetic materials such as holmium and erbium, magnetic scattering can give rise to additional points in the reciprocal lattice, and the position and dynamics of these lattice points can be described in terms of a fourth order tensor as shown by Blume (Blume, 1992, ICAS Meeting, Malente).

This paper will discuss the tensor form of the atomic scattering factor formalism and its use in solving problems in crystallography.

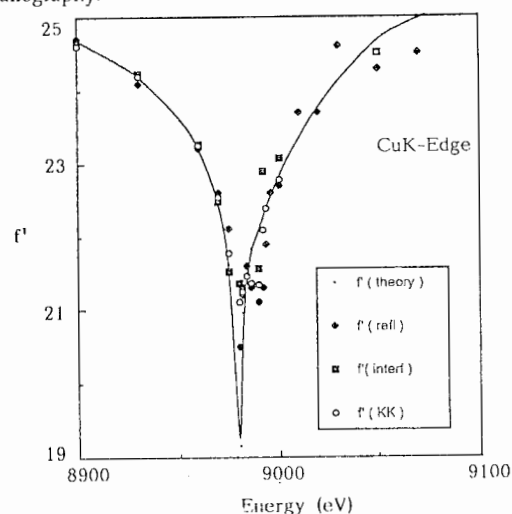


Figure 1. Comparison of a variety of experimental results with theory.