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Combining MAGEX with Random Phases

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Abstract

An algorithm is described which combines the magicinteger concept with that of representing a large number of phases by random numbers. The process, called *MAGEX* 89, is more economical than previous magicinteger approaches and in a number of tests its performance compares favourably with those of other commonly used methods of solving small structures.

Introduction

The magic-integer concept, introduced by White & Woolfson (1975), was utilized in a number of directmethod approaches to structure solution culminating in MAGEX (Hull, Viterbo, Woolfson & Zhang, 1981; Zhang & Woolfson, 1982) which was an option in earlier versions of MULTAN. In the original MAGEX procedure a number, q, of reflexions had their phases represented (in cycles) by

$$\varphi_j = m_j x \pmod{1}, \quad j = 1, 2, \dots, q, \quad (1)$$

where the m_j are integers based on the Fibonacci series. The relationships which linked the combination of these reflexions with those defining the origin and enantiomorph (O+E) became the foundation for a one-dimensional Fourier series, the ψ map, with space variable x. Peaks in the ψ map, translated into phases by (1), gave plausible starting points for phase extension. There was also a facility for carrying out multiple-pathway phase extension from each starting set of phases by further use of the ψ -map concept.

Although the general use of MAGEX has declined, in favour of the RANTAN approach (Yao, 1981) or SAYTAN (Debaerdemaeker, Tate & Woolfson, 1985, 1988) we have continued to develop the idea and would claim that, at least for small structures (≤ 100 independent atoms, say), what we have produced, *MAGEX*89, compares favourably in effectiveness and efficiency with other available methods.

MAGEX89

In the procedure *MAGEX* 89 we have combined the magic-integer concept with that of representing a large number of phases by random numbers. The algorithm we use to select the starting-set reflexions is that given by Zhang, Luo, Chen & Yao (1989). The O + E reflexions are chosen to have values of E and α_{est} as large as possible where

$$\alpha(\mathbf{h})_{est} = \sum_{k} \kappa(\mathbf{h}, \mathbf{k}) \frac{I_1\{\kappa(\mathbf{h}, \mathbf{k})\}}{I_0\{\kappa(\mathbf{h}, \mathbf{k})\}},$$
 (2)

where $\kappa(\mathbf{h}, \mathbf{k})$ is the usual direct-methods κ value and $I_1(x)$ and $I_0(x)$ are modified Bessel functions. A further 5-25 reflexions for the starting set are chosen so as to satisfy the following criteria as well as possible:

(i) these reflexions must be strongly linked with O+E so that the origin and enantiomorph are strongly defined by the phases of the complete starting set;

(ii) they should have values of E and α_{est} as large as possible.

These extra starting-set reflexions, q in number, have their phases allocated by (1) with multiple starting sets generated using random values in the range

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Table 1. Results of tests with three methods: S =SWTR (MULTAN82 version on PDP11/44); R =RANTAN (MULTAN82 version on PDP11/44); M = MAGEX89

A/B indicates that A out of B atoms were found in the best E map. A zero indicates that the default run found no solution.

	Space group		A/B		
Structure	and c	ontents	S	R	М
C12H16N2O5S	P21	Z = 4	0	27/40	23/40
C ₂₇ H ₄₃ NO ₄	P212121	Z = 4	0	0	22/32
C ₁₆ H ₁₂ ClN	P212121	Z = 4	17/18	17/18	17/18
$C_{16}H_{11}N_{3}O_{2}$	R3	Z = 6	21/21	0	21/21
C ₁₂ H ₁₄ N ₂ O ₄ S	ΡĪ	Z = 2	19/19	0	0
C14H15BNO4	$P2_1/c$	Z = 4	20/20	0	20/20
C ₂₈ H ₃₀ BN ₄	$P2_1/c$	Z = 4	15/33	0	15/33
C ₁₄ H ₂₈ B ₃ FeN	Pnma	Z = 4	6/13	6/13	6/13
$C_{18}H_{18}O_6 \cdot H_2O$	$Cmc2_1$	<i>Z</i> = 4	9/15	9/15	11/15

0 to 1 for the variable x. The default value of q is 15 but can be fixed by the user in the range 5 to 25 and the default number of trials, *i.e.* different values of x, equals the number of independent non-H atoms in the structure. A further N reflexions with large E and α_{est} values, where $N \approx 300$, are chosen by the program. These are allocated random values, a different set for each trial.

With all phases having initial values a process of phase refinement is started using the standard *MULTAN* weighted tangent formula. Weights are associated with the initial phases as follows: O + E: weight = 1.0 and the phases are kept fixed; q extra starting-set phases: weight = 0.95; other phases: weight = 0.20. At the end of the refinement figures of merit are found and the process continues as for *MULTAN*.

We have investigated the average error obtained when a number of phases are generated by using a random variable x. For example, with q = 10 and using 30 trial values of x one trial would give a lowest average deviation from true phases of about 50°. To illustrate this, for a set of true phases 46, 78, 160, 315, 130, 35, 245, 348, 4, 88° and with a magic-integer sequence 177, 176, 175, 173, 170, 165, 157, 144, 123, 89 with 30 random values of x, one of them gave a mean average error of $52 \cdot 3^\circ$. This process is far less demanding of computer time than calculating a ψ map. In addition, we have found no advantage in taking equally spaced values of x in the range 0 to 1 $\frac{1}{2}$ which is sometimes better and sometimes worse than taking random values. The advantage of using random values is that, if one has been unsuccessful with a first run and wishes to try again, the following batch of trial values of x can be completely different from the previous ones.

Tests of MAGEX89

We have developed MAGEX 89 to run on the computer available to us, a PDP 11/44. We also have

Table 2. The best figures of merit found by default runs for the structure $C_{27}H_{43}NO_4$

The MAGEX89 phase set led to the structure solution. The figures of merit are the conventional ones used by MULTAN.

Method	ABSFOM	PSIZERO	RESID
SWTR	0.707	2.340	27.74
RANTAN	0.755	2.294	28.03
MAGEX89	0.835	1.723	22.51

available MULTAN82, which runs on the same machine and contains RANTAN and SWTR, which uses the statistically weighted tangent formula developed by Hull & Irwin (1978). In Table 1 we show the results of applying MAGEX89, RANTANand SWTR, all run with default parameters, to nine structures and the relative computing times used with these three methods are 91, 100 and 58, respectively. These structures were previously unknown and all eventually refined to R factors of less than 0.08 by conventional least-squares methods.

The structure with formula $C_{27}H_{43}NO_4$ was solved only by *MAGEX* 89 and we give details of the solution here. As shown in the table the space group is $P2_12_12_1$ with Z = 4. Data were collected on an Enraf-Nonius CAD-4 diffractometer with Mo $K\alpha$ radiation,



Fig. 1. The finally deduced chemical structure of $C_{27}H_{43}NO_4$ and the *E* map found from *MAGEX*89 which gave the solution.

graphite monochromator and $\omega/2\theta$ scan mode in the range $1 \le \theta \le 25^\circ$. Table 2 gives the figures of merit of the best sets for all three methods; that of *MAGEX89* gave an *E* map showing 22 atoms and is reproduced in Fig. 1. Fourier calculations revealed the remaining atoms and least-squares refinement gave a final residual of 0.055 for the observed reflexions.

Discussion

It will be seen from Table 1 that for the trial structures the MAGEX89 method performed somewhat better than the other two and the computer resources used by MAGEX89 were 9% less than those of RANTAN. Not too much should be made of that since by modifying parameters all three methods are probably capable of solving all the structures. What we do say is that it is worthwhile having MAGEX89 available. While any individual method may not succeed for a particular structure, the probability of failure is far lower with many methods available.

The version of *MAGEX*89 we have used has been programmed for a PDP11/44 but should be able to

run on most standard personal computers. It can handle all 230 space groups in the standard orientations, including alternative settings, as given in *International Tables for Crystallography* (1987).

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A Method for Multiple Superposition of Structures

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Abstract

The study of families of protein structures is important in analysing the results of NMR structure determinations and in investigating mechanisms of molecular evolution at the level of conformation. A method is discussed for finding the transformations that mutually superpose an arbitrary number of structures in the least-squares sense given specified atomto-atom correspondence.

1. Introduction

Superposition has become an important tool for comparing protein structures and for deriving an 'average' structure from a family of conformations of a protein. The problem arises regularly in the determination of the three-dimensional structure of a protein in solution using nuclear magnetic resonance, which typically produces an ensemble of conformations (Wuethrich, 1986). Sets of interproton distances

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