Phase Correction, a New Method to Solve Partially Known Structures*

BY W. HOPPE AND J. GASSMANN

Abteilung für Röntgenstrukturforschung am Max-Planck-Institut für Eiweiss- und Lederforschung,
München, Germany and Abteilung für Strukturforschung am Physikalisch-Chemischen Institut der Technischen
Hochschule, München, Germany

The aim of the method is to replace successive Fourier syntheses by a treatment in which the two discontinuous decisions of the Fourier method (determination of peaks and assignment of weights of either zero or one to them) is replaced by two more cautious continuous processes. This procedure has been fully automated and its application to hypothetical test structures and to two three-dimensional structures is reported.

1. Introduction

From the work of Luzzati (1953) and Ramachandran (1964) the characteristic features of a Fourier synthesis computed with phases from a partially known structure are well-known. If one compares the Fourier synthesis with phases from all atoms and that with phases from only some atoms of a structure, the different types of electron-density peak occurring in the latter Fourier synthesis are:

(a) Enhanced peaks at the sites of known atoms.
(b) Reduced peaks at the sites of unknown atoms.
(c) Reduced peaks at the sites of wrongly placed atoms.
(d) Background-peaks.

The method generally used to deduce the correct electron density ϱ_{corr} from the approximate density ϱ_{app} is the method of successive Fourier syntheses. A characteristic feature of this method is a twofold discontinuity (yes–no decision) in the determination of atoms. In principle one first determines all peak positions either manually or by computer. In a second step the peaks are given weight $g_j = 0$ to exclude or $g_j = 1$ to include them as possible atomic sites. The usual criterion for giving a peak unit weight is its height in the Fourier synthesis. This criterion is however, not always strictly followed and chemical evidence (bond length, molecular structure, packing considerations, *etc.*) and last but not least human intuition can help in making a more significant choice. A somewhat different procedure has recently been devised by Rollett & Hodgson (1962). Newly selected maxima in a Fourier synthesis are not immediately treated in the structure-factor calculations as atoms with weight $g_j = 1$, but are given an initial weight $g_j = 0$. These weights are varied by least-squares procedures. After a few cycles of least-squares refinement a peak that has attained a weight $g_j > 0$ is taken as a new atom (and given weight $g_j = 1$), whereas $g_j \leq 0$ indicates a background peak (and is given weight $g_j = 0$). The atomic sites thus determined are included in the calculation of phases for the next

Fourier synthesis, after which this 'double-looped' cycle (Fourier and least squares) repeats itself.

Some years ago we introduced a new method named *phase correction* for the determination of a structure, which like the procedure of successive Fourier syntheses starts from approximate phases (Hoppe, Huber & Gassmann, 1963; Gassmann, 1966; Hoppe, 1966). The name 'phase correction' indicates that this method is not intended to work as an ordinary refinement procedure,* but rather in the initial stage of the determination of the structure (*e.g.* approximate heavy atom phases in a heavy atom structure). The main difference between the method of 'phase correction' and both the successive Fourier analysis and the method of Rollett & Hodgson (1962) is that the twofold discontinuity (yes–no decision) is replaced by a continuous treatment. The first part of this treatment consists in working on the whole continuous electron density distribution (not on discrete peaks). The second consists in attaching to each point **r** of the electron density function $\varrho(\mathbf{r})$ a continuous weighting function $g(\mathbf{r})$ which depends on the electron density (instead of applying discontinuous weights $g_j = 0$ or $g_j = 1$ to selected peaks).

The advantages of this continuous treatment are as follows: (1) All the information contained in the electron density can be used. This is especially important in the case of diffuse and unresolved maxima where exact peak positions cannot be defined. (2) The small change in electron density per cycle due to the continuous weighting function $g(\mathbf{r})$ leads to a wider range of convergence than the more abrupt and discontinuous treatment of successive Fourier syntheses generally used.

This paper describes the theory and its application to hypothetical test structures and to two three-dimensional structure determinations. The method has also been successfully applied in four other structure determinations (to be published).

---

* Initially we called the method *phase refinement* but to avoid confusion with another method (Hoppe, 1963) we changed the name to *phase correction*.

2. Theory of phase correction

The initial electron density ϱ_{app} should be subjected to a modification with the following effects:

(a) Reduction of the enhanced maxima at known atomic sites.

(b) Enhancement of the reduced maxima at unknown atomic sites.

(c) Reduction of the reduced maxima at wrongly placed atomic sites.

(d) Reduction of background.

An improved electron density ϱ^* may be derived by subjecting each point in the unit cell to the process $\varrho(\mathbf{r})\rightarrow\varrho^*(\mathbf{r})$. If one assumes like atoms in the structure, this modification $\varrho\rightarrow\varrho^*$ is a unique function of ϱ and may be written as $\varrho^*=g(\varrho)\cdot\varrho$ (the case of unlike atoms is treated separately). The function $g(\varrho)$ may be developed as a Taylor series:

$$\varrho^*=\sum_{n=1}^{\infty}a_n\cdot\varrho^n\,.$$

The coefficient a_0 must be zero, since for $\varrho=0$, the condition is $\varrho^*=0$.

Initial calculations showed that phase correction using the first two powers $\varrho^*=a_1\cdot\varrho+a_2\cdot\varrho^2$ did not improve the electron density. An improvement was however achieved by using one more term:

$$\varrho^*=g(\varrho)\cdot\varrho=a\varrho+b\cdot\varrho^2+c\cdot\varrho^3\,. \tag{1}$$

A diagram of this function is given in Fig. 1. The peak height of the assumed like atoms has been defined as $\varrho=1$. The values of the parameters a, b and c depend on the conditions (a) to (d) for improving the electron density and on the threshold T which may be calculated by using the ratio 'known structure/total structure'. T is the threshold for increasing ($\varrho_{app}>T$) and decreasing ($\varrho_{app}<T$) the electron density. One determines T as the averaged relative peak height of an unknown atom. The value of T depends on the amount of known structure and has been calculated by Luzzati (1953), who used statistical arguments (see Fig. 2). We have used a different method, which calculates the relative peak height from convolution principles. To a good approximation the relative peak height for unknown atoms is found to be

$$T\propto\sigma_P$$

where

$$\sigma_P^2=\sum_{j=1}^{P}Z_j^2\bigg/\sum_{j=1}^{N}Z_j^2$$

($Z_j=$ atomic number, $P=$ number of known atoms, $N=$ total number of atoms).

Using Luzzati's result $T=\frac{1}{2}$ for the completely known structure (acentric case) we obtain $T=\frac{1}{2}\cdot\sigma_P$. This is in good agreement with Luzzati's result (see Fig. 2).

The experimental results showed that the process of phase correction is not very sensitive to the exact value of the threshold T. This is important if one has postu-

lated false atomic sites at the beginning of phase correction and starts calculations with a too high value of T. In the experiments reported in this paper we have always used a value $T=0,3$ which corresponds to a known structure part σ_p^2 of about 40–50%. The modification of electron density [equation (1)] is also possible in reciprocal space. Here the equivalent relation reads:
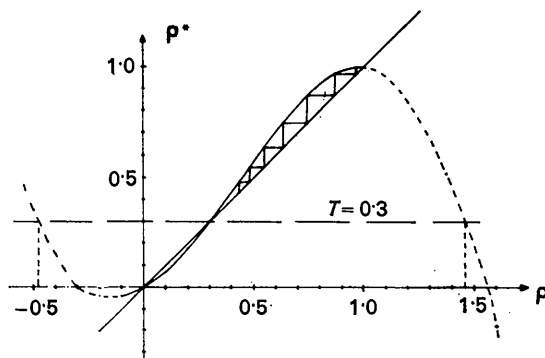

Fig. 1. Improved electron density: $\varrho^*=a\varrho+b\varrho^2+c\varrho^3$, where $a=(1-2T)/(1-T)$, $b=(1+T)(1-T)$, $c=-1/(1-T)$. T is the threshold for depressing or enhancing the electron density and may be calculated from the ratio 'known structure/total structure'. The stepwise curve shows the effect of equation (1) on a peak in repeated phase correction cycles. This step-curve gives schematically the effect of phase correction ($\varrho\rightarrow\varrho^*$) on the electron density. In the calculations only the phases from ϱ^* are used together with the experimental values of the structure factors.
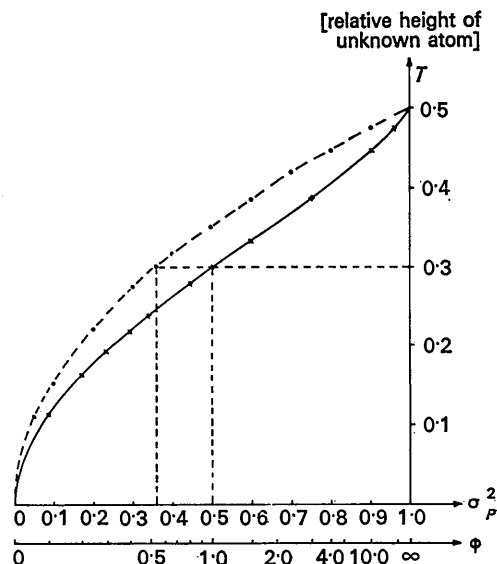

Fig. 2. Averaged relative peak height T of unknown atoms as a function of the amount of the known structure part (σ_P^2 and φ). The continuous curve gives Luzzati's result, the dashed curve represents the function we used. Since phase correction is not very sensitive to the exact value of T, a value of $T=0.3$ (broken line) was used in the experiments. The two abscissae result from the ratio 'known structure/total structure' (σ_P^2) and the ratio 'known structure/unknown structure' (φ). $\sigma_P^2=\sum^{P}Z_j^2\big/\sum^{N}Z_j^2$, $\varphi=\sigma_P^2/(1-\sigma_P^2)$.

$$\mathbf{F}_h = a\mathbf{F}_h^{\mathrm{app}} + bS_h \sum_{h'} \mathbf{F}_{h'}\mathbf{F}_{h-h'} + cS'_h \sum_{h'} \sum_{h''} \mathbf{F}_{h''}\mathbf{F}_{h'-h''}\mathbf{F}_{h-h'}$$

$$(2)$$

A new structure factor may then be derived consisting of the experimental value of $|F_{\mathrm{exp}}|$ and the phase φ_h calculated from relation (2):

$$\mathbf{F}_{\mathrm{corr}} = |F_{\mathrm{exp}}| \exp{(i\varphi_h)} .$$

$$(2a)$$

This phase correction process (relations 2, 2a) has been programmed to work continuously in cycles without calculating any intermediate Fourier synthesis.

Naturally the modification of the electron density in equation (1) could also be done in direct space. The phases of the modified electron density equivalent to equation (2) have then to be calculated by a Fourier transformation of the modified electron density ('reciprocal Fourier synthesis'). A special advantage of this combination of Fourier synthesis and reciprocal Fourier synthesis is that it allows the use of arbitrary and complicated weighting functions. In structures containing more than about 40 atoms calculation with the reciprocal Fourier synthesis requires less computing time. It is of vital importance for the method that the experimental structure factors be used in combination with the phases calculated from equation (2) [see § 3 *condition* (c)] or the equivalent reciprocal Fourier synthesis. In the following we propose to show how phase correction copes with requirements (a) to (d) for improving the electron density.
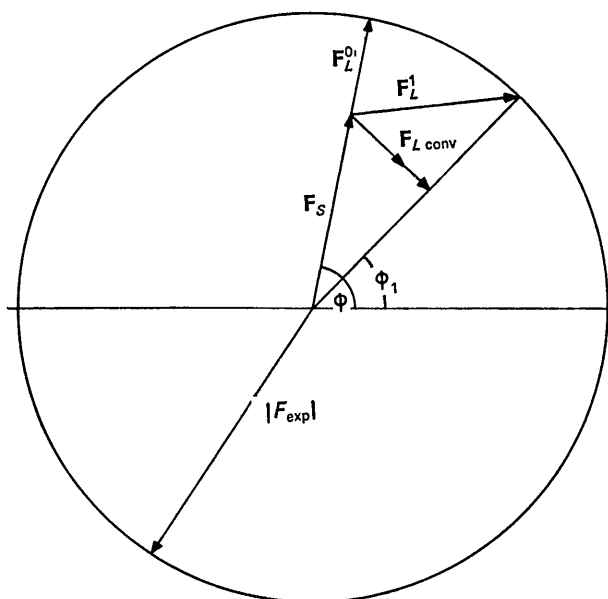

Fig. 3. Determination of the phase-corrected light atom contribution in a heavy-atom structure. The convolution of equation (2a) changes $\mathbf{F}_L^0$ into $\mathbf{F}_{L\ \mathrm{conv}}$, which after scaling gives a new structure factor phase φ_1. $\mathbf{F}_L^1$ can then be calculated, combining this new phase φ_1 with the value $|F_{\mathrm{exp}}|$.

3. Improvement of the electron density by phase correction

Reduction of known atomic peaks [condition (a)]

Fig. 1 explains in principle how peaks with $\varrho > 1$ are reduced by repeated phase correction $(\varrho \rightarrow \varrho^*)$ and ultimately reach $\varrho = 1$.

Enhancement of unknown atomic peaks [condition (b)]

In general, there are two types of unknown atomic maxima. Maxima of unknown atoms which are above the threshold T at the beginning of phase correction ('first order atoms') will increase steadily until they reach their full heights. Maxima of unknown atoms which initially have a height below the threshold T ('second order atoms') will be depressed in the first few cycles of phase correction. At a certain stage, the first order atoms will have increased so much that the 'known structure' (=initial structure + first order atoms) shifts the peaks of the second order atoms above the threshold T. From here on these peaks also increase steadily (see experimental results on phyllochlorine ester, § 5, and sulpholipid, § 6).

Reduction of wrongly placed atoms [condition (c)]

This is one of the most important features of phase correction which can best be explained by comparison with the enhancement of unknown atomic peaks: Equation (2a) $\mathbf{F}_h = |F_{\mathrm{exp}}| \exp{(i\varphi_h)}$ may be described in real space as a convolution of the 'Patterson-like' function with Fourier coefficients $|F_{\mathrm{exp}}|$ with a 'phase synthesis' with Fourier coefficients $\mathbf{F}_h/|F_h|$.

Assuming two peaks of equal height in the initial Fourier synthesis, one resulting from an unknown correct atom, the other from a wrongly placed atom, phase correction treats these peaks as follows: According to equation (1) or (2), there is no difference in the enhancement of these two peaks. The phase factor $\exp{(i\varphi_h)}$ in equation (2a) therefore gives no indication as to the correctness of the peaks. However, the non-origin peaks of the 'Patterson-like' function calculated with the use of coefficients $|F_{\mathrm{exp}}|$, when convoluted with the function calculated with the phase factor $\exp{(i\varphi_h)}$ only give contributions to the correct atomic peaks. Thus in equation (2a) it is the magnitude of the experimental structure factors which enhances the height of the correct peak above the wrong peak. In the course of the phase correction cycles this finally leads to the elimination of the false peak (see experimental results, 18-C-test-structure, § 5).

Reduction of background [condition (d)]

Fig. 1 explains the elimination of background below the threshold T. Background peaks above the threshold show a behaviour similar to peaks due to wrongly placed atoms (see experimental results, phyllochlorine ester, § 5) and are finally eliminated. Holes $(-0,5 \le \varrho < 0)$ are also eliminated.

4. Extension of phase correction
to heavy-atom structures

Throughout the preceding section it has been assumed that all atoms have approximately the same scattering power. In this case the phase correction procedure may be looked upon as a continuous weighting scheme for the Fourier synthesis. Each point in the Fourier synthesis is given a weight g, which is a unique function of the existing electron density ϱ:

$$\varrho^* = g(\varrho) \cdot \varrho .$$

In the case of equation (1):

$$g(\varrho) = a + b\varrho + c\varrho^2 .$$

The uniqueness of $g(\varrho)$ results from the fact that for a structure containing only like atoms the structure factor is to a good approximation:

$$\mathbf{F}_h = f_h \sum_j g_j \exp (2\pi i \mathbf{h} \mathbf{r}_j) , \qquad (3)$$

f = form factor with the overall temperature factor included
g_j = weight for atom j
$g_j \geq 1$ for known atoms
$g_j < 1$ for unknown atoms .

If such a structure factor is modified by phase correction the relative weights g_j will be altered but not the common form factor. The heights of the atomic maxima change but their form remains constant. If different kinds of atom are present in a structure the continuous weight $g(\varrho)$ is not a unique function of ϱ any more but depends on the form factors of the various atoms. This type of phase correction is obviously possible in real space, but can also be undertaken in reciprocal space by using Woolfson's (1958) extension of Sayre's formula. This leads to multiple convolutions, which are very lengthy. The simplest method is therefore to exclude the heavy atoms and to start phase

correction with the light atom part of the structure. The positions of the heavy atoms can be obtained from a Patterson synthesis and their contributions φ_s to the phases calculated. The structure factor for the light atom part of the structure is then:
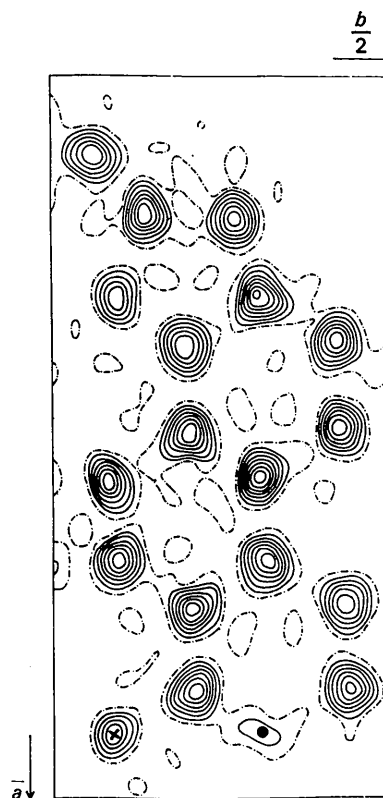

Fig. 5. Fourier synthesis of a two-dimensional 18-atom test structure, phases with 17 correct atoms and one wrongly placed atom (×). After 18 cycles, the missing atom (black dot) had nearly full height (95%), and the wrongly placed atom had disappeared (10%).
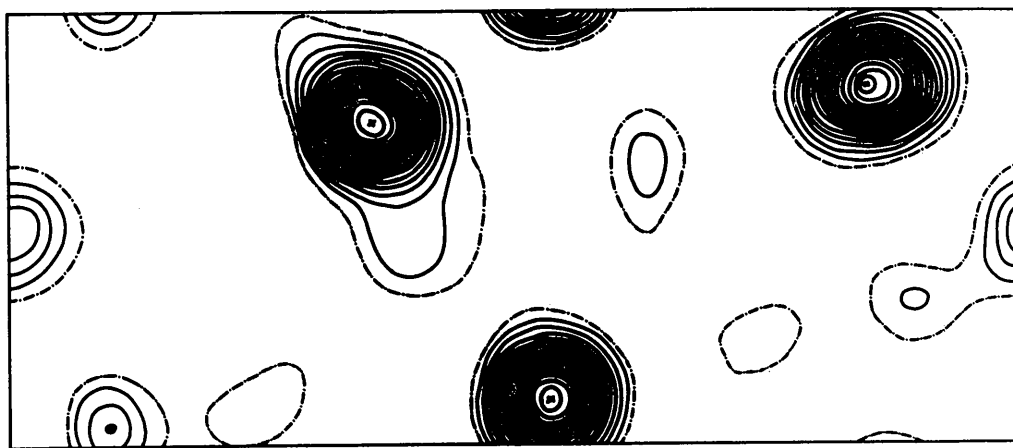

Fig. 4. Fourier synthesis of a two-dimensional 5-atom test structure phased with 3 atoms. After 10 cycles of phase correction, all 5 atoms had equal heights.
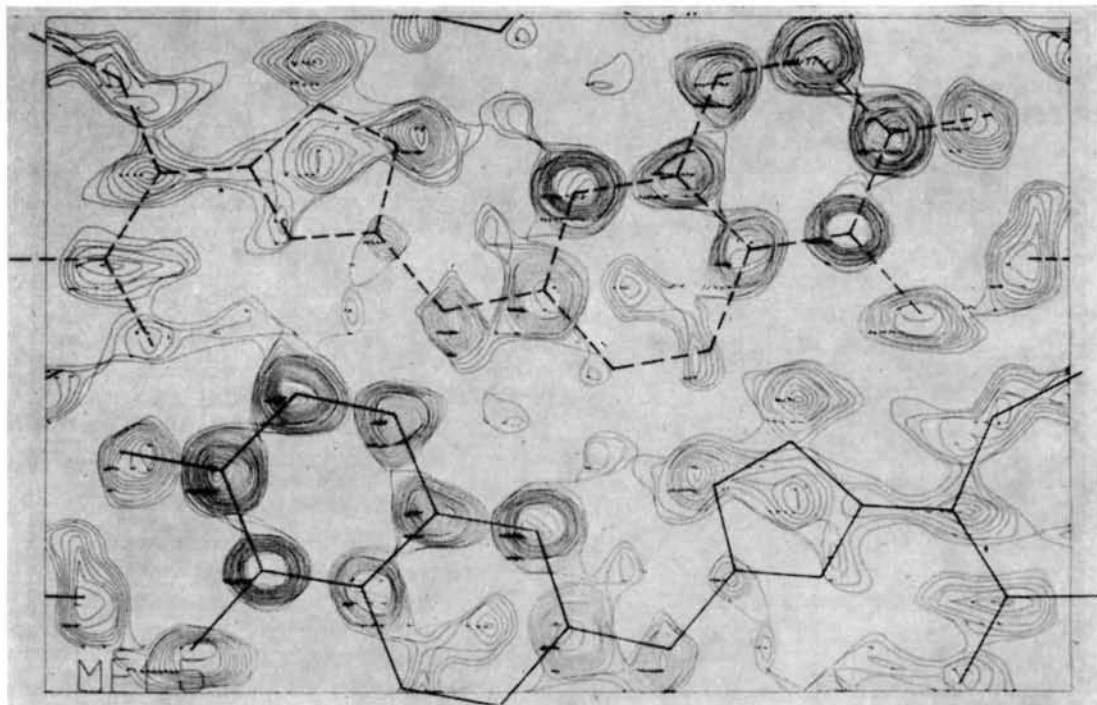
Fig. 6. Fourier synthesis of a 24-atom test structure phased with 8 atoms in approximately correct positions (deviation $\simeq$ 0·15 Å). The structure factor magnitudes were statistically wrong by $\pm$10%, and the atoms had temperature factors between 2·8 and 3·7. Only the largest structure factors (33%) inside the Cu sphere were used for the Fourier synthesis. Usual R index: $R = 58\%$.
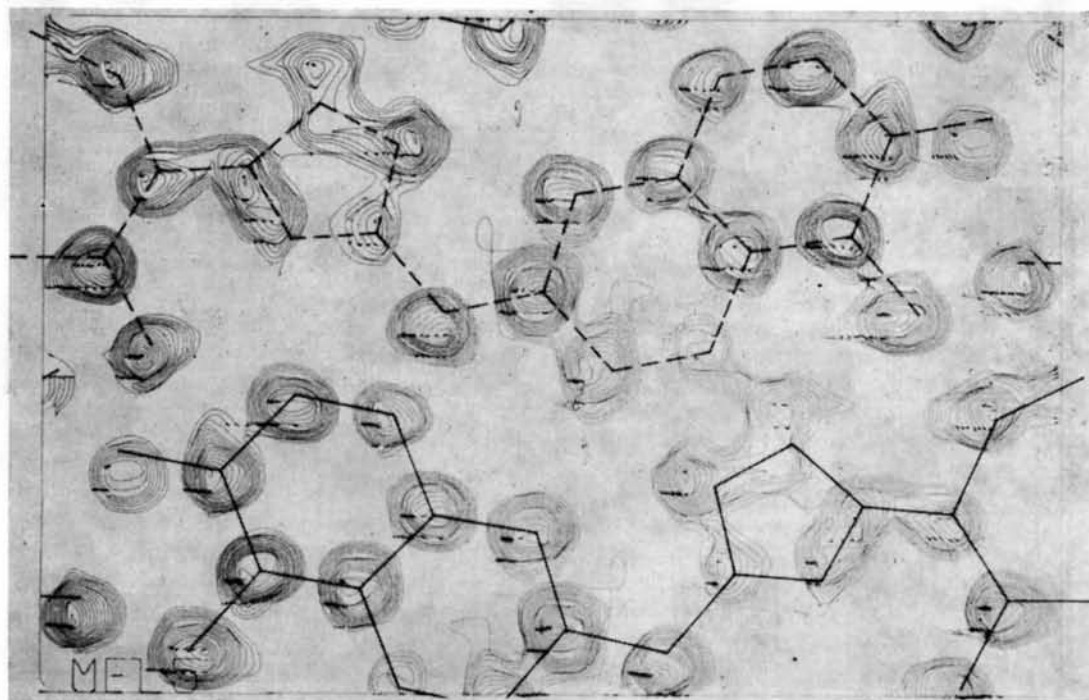
Fig. 7. Same structure as in Fig. 6 after 41 cycles of phase correction. Very high convergence to the correct structure has occurred.
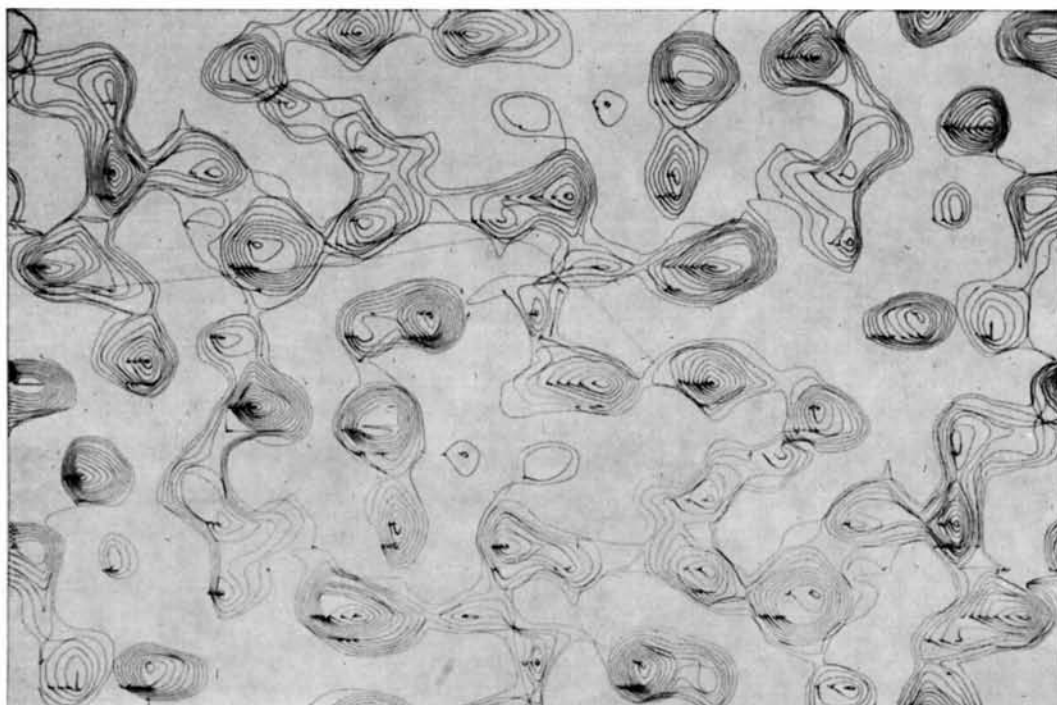
Fig. 8. Fourier synthesis of a 24-atom test structure phased with 2 P atoms in approximately correct positions (deviation $\simeq 0\cdot15$ Å).
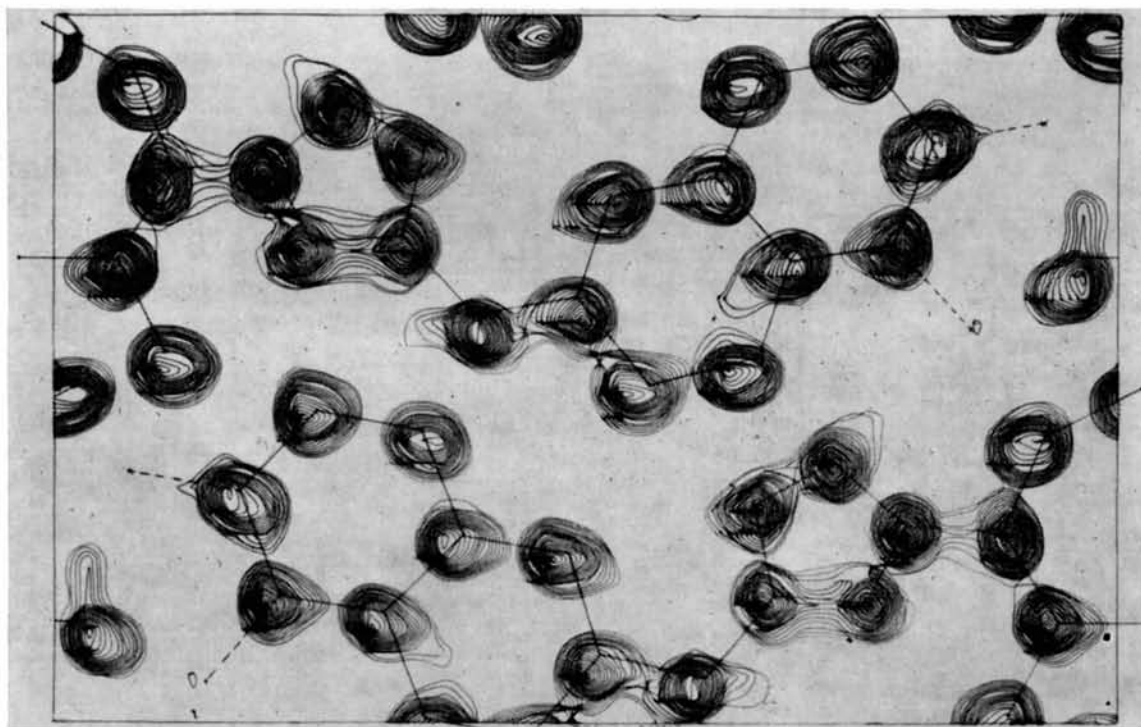

Fig. 9. Same structure as in Fig. 8 after 30 cycles of phase correction. The locations of the two P atoms used for initial phasing are marked by small crosses.

$$\mathbf{F}_L^0 = |F_{\mathrm{exp}}| \exp(i\varphi_s) - \sum_{js=1}^{s} f_{js} \exp(2\pi i\mathbf{hr}_{js}),\qquad(4)$$

S = number of heavy atoms.

The phase correction procedure will then modify $\mathbf{F}_L^0$ in both phase and amplitude to give a new light atom contribution $\mathbf{F}_{L\,\mathrm{conv.}}$. This value $\mathbf{F}_{L\,\mathrm{conv.}}$ is then scaled and added to the heavy atom contribution, resulting in a new phase φ_1. With this phase φ_1 and the total structure factor amplitude, the new light atom contribution $\mathbf{F}_L^1$ may be found (Fig. 3). The scaling of the light atom contribution $\mathbf{F}_{L\,\mathrm{conv.}}$ may become necessary as the initial light atom contributions are generally too small.

Several ways of determining the new light atom contribution $\mathbf{F}_L^1$ have been tried out. The method described above (Fig. 3) seems to work best. As can be seen from equation (4) the process of subtraction gives three limiting cases:

(a)

(b)

Fig. 10. (a) Fourier synthesis of phyllochlorine ester after 20 cycles of phase correction. 14 of the 15 unknown side-chain atoms have appeared. First contour line at 1 e.Å⁻³. (b) Final Fourier synthesis of phyllochlorine ester, $C_{33}N_4O_2H_{38}$. The detailed structure determination is given by Hoppe, Will, Gassmann & Weichselgartner (1967).

(a) The heavy atom contribution is small and the initial phases are very inaccurate.

(b) The heavy atom contribution is big and the accuracy of the remaining amplitudes is very low owing to experimental errors.

(c) The heavy atom contribution produces new symmetry elements.

All these limiting cases have been treated with two-dimensional test structures and real three-dimensional structures to demonstrate the range of application of phase correction.

5. Experimental results on light-atom structures

Two-dimensional test structures were first used to test the phase correction procedure. The results of the tests on various structures with the conditions imposed are given below.

(1) 5-*atom structure*: This structure was phased with three atoms in correct positions. The structure factor values were assumed to have been accurately determined and the temperature factor was taken as zero. Convergence to the correct structure occurred in 5–10 cycles (Fig. 4).

(2) 18-*atom structure*: This structure with exact $|F|$ and no temperature factor was phased with 17 atoms in correct positions and one atom in a wrong position (Fig. 5). The structure would not refine with ordinary least-squares methods. Phase correction gave the correct structure (18th atom 95% full height, wrong atom 10% full height) in 20 cycles.

(3) 24-*atom structure*: This structure had plane group pg and cell dimensions $a = 15$, $b = 10$ Å. The random errors in the structure factor amplitudes were $\pm 10\%$. Individual temperature factors between 2·7 and 3·5 were assigned to the atoms: Only one-third of all data inside the Cu sphere were used. The part of the structure taken as initially known consisted of 8 atoms randomly displaced by about 0·15 Å from their correct positions. Phase correction gave convergence to the correct structure (Fig. 6). The convergence improved if only the largest normalized structure factors were used (Fig. 7).

The first real structure to which phase correction was applied was phyllochlorine ester, $C_{33}N_4O_2H_{38}$. This structure (Fig. 10) was a severe test for phase correction as

(a) the observed structure factors had an average error of about 10%. Only 1744 of the 3000 independent reflexions inside the Cu sphere were observed,

(b) the porphyrine ring structure $C_{20}N_4$ had been determined by the convolution molecule technique with an average deviation of 0·24 Å from the final atomic sites, and

(c) the assumed flat conformation of the porphyrine ring with an orientation nearly perpendicular to the symmetry axis ($P2_1$) produced partial pseudosymmetry.

After 20 cycles of phase correction 14 of the 15 unknown atoms appeared quite clearly (Figs. 10(a) and 11)
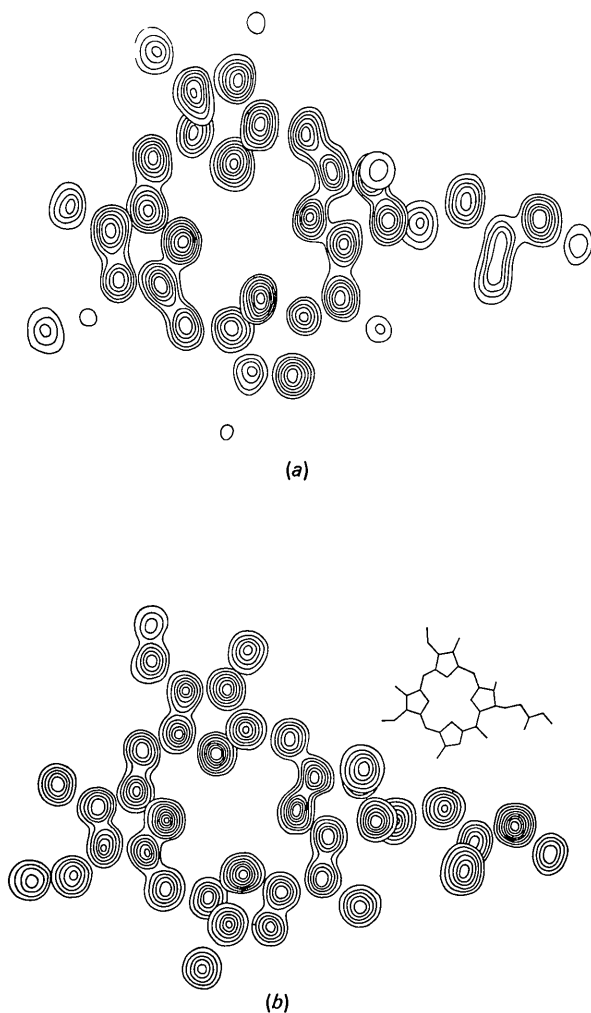
and the background peaks had been reduced in height and number. At this stage phase correction was stopped. The missing 15th atom was later found to have a temperature factor of $B = 6.5$ Å².

The enhancement of the correct peaks and the depression of the false peaks in the course of phase correction is shown in Figs. 11 and 12. The theoretical curves for improving atomic peaks and depressing background peaks are not reproduced in the experiment. This is probably due to the fact that the initial structure was only very approximately known and the new atomic peaks are diffused and contract only after some cycles of phase correction. In the initial Fourier synthesis seven other peaks that turned out to be real atomic peaks were smaller than the background peaks and the highest unknown atomic peak was only 30% above the highest background peak.

6. Experimental results on heavy-atom structures

The first set of structures consisted of two-dimensional hypothetical test structures P_2C_6 and P_2C_{14}. Assuming known positions of the P atoms, phase correction pro-

duced the correct structure in 10–15 cycles. Structure factor amplitudes were taken as exact, no temperature factor applied and all reflexions inside the Cu sphere were used. The new phases were calculated in the manner indicated in § 3 [equation (4)].

The next test structure was P_2C_{22}, which has the same form as the test structure C_{24} (Fig. 7) but with two C atoms replaced by P atoms. All experimental errors occurring in a real structure determination were taken into account:

(a) *Incorrect structure factor amplitudes.* The amplitudes deviated by $\pm 10\%$ from the correct values, only part ($\simeq \frac{1}{3}$) of all reflexions inside the Cu sphere were used.

(b) *Approximate heavy atom positions.* The P atoms were displaced by approximately 0.10 Å from their correct sites.

(c) *Individual temperature factors.* For structure factor calculations all atoms had isotropic temperature factors ranging from 2.2 to 3.5.

In applying these errors individually, it was possible to show that the inaccurate heavy atom positions

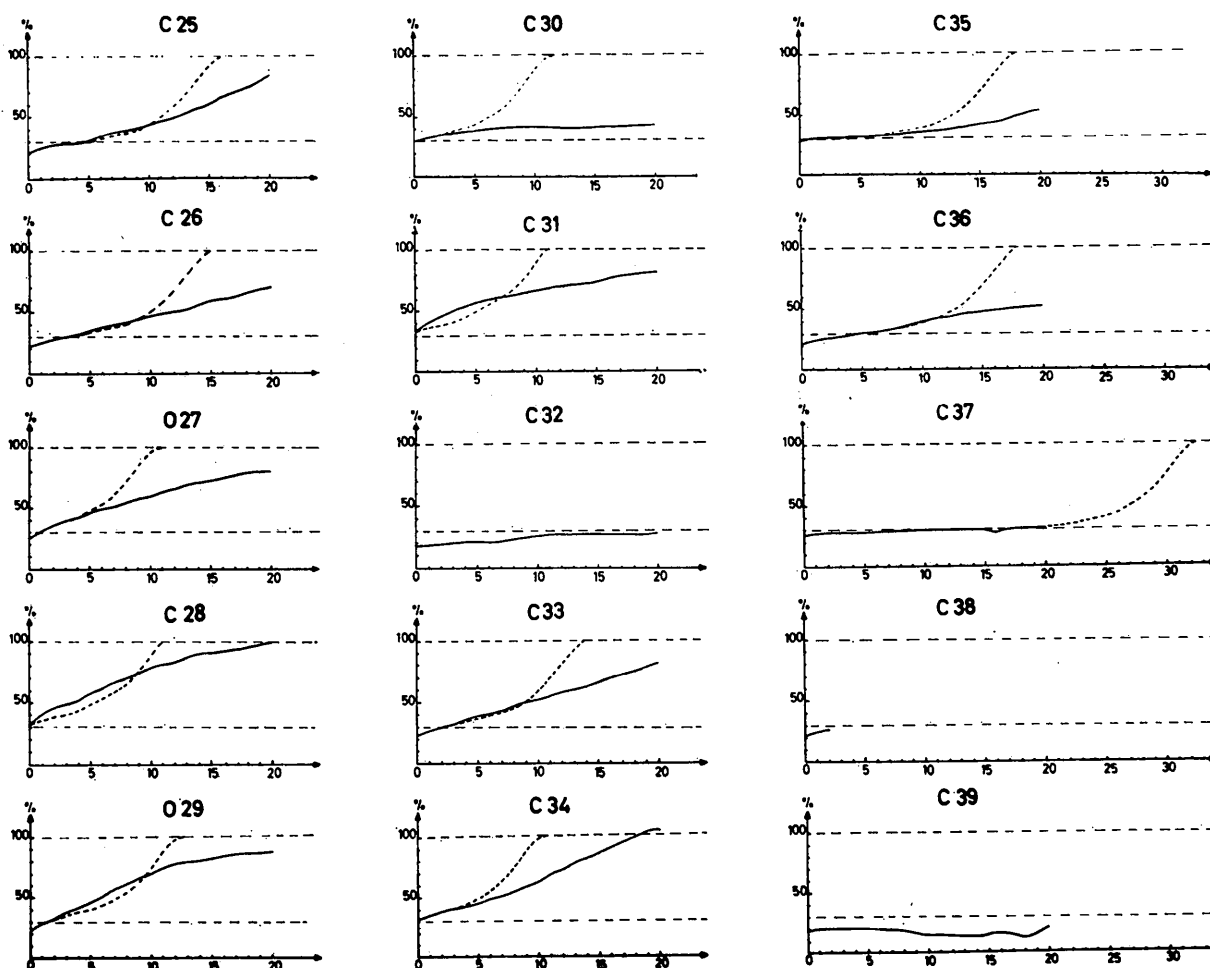Fig. 11. Increasing peak height of the unknown atoms in phyllochlorine ester in the course of phase correction. The dashed curves give the theoretical increase calculated from equation (1).
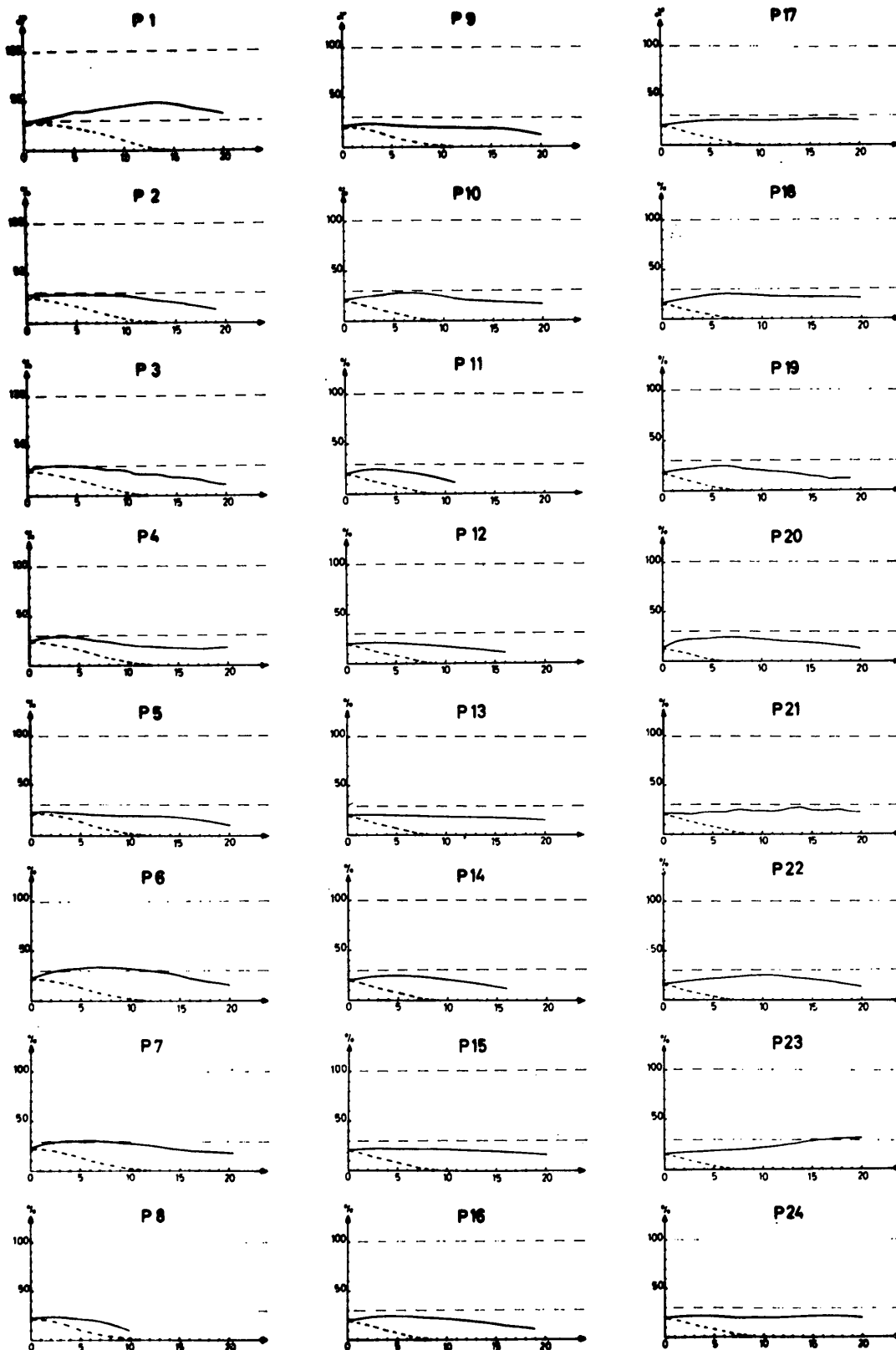
Fig. 12. Reduction of background peaks in phyllochlorine ester in the course of phase correction. Peak P1 was initially higher than the peaks of 7 of the unknown atoms. The dashed curves give the theoretical reduction expected from equation (1).

hindered the convergence of phase correction most strongly. Fig.8 shows the initial Fourier synthesis of P_2C_{22} phased with 2 P atoms. Fig.9 shows the same Fourier synthesis after 30 cycles of phase correction. The P atoms have been subtracted in both cases.

After these test structures the method was tried on the sulpholipid rubidium salt, $RbSO_{10}C_9H_{17}$, solved by Okaya (1964). This structure has a very high heavy atom contribution and the positions of the Rb atom ($y=0·25$) and the S atom ($y=0·22$) from the Patterson synthesis give a partial pseudo-symmetry. This gives an opportunity to test phase correction in cases with big heavy atom contributions and pseudo-symmetry.

Table 1 gives the peaks in an initial Fourier synthesis phased with approximate Rb and S positions. The scaling factor and overall temperature factor were taken from Wilson statistics. Background peaks, residual Rb and S peaks, and mirror atom peaks are found which are considerably higher than the unknown atomic peaks.

Phase correction proceeded quite fast and the peaks found in a Fourier synthesis after 7 cycles of phase correction are given in Table 2. At this stage no background peak was higher than an atomic peak and it was even possible to distinguish oxygen from carbon.

7. Discussion

The method of phase correction enables one to solve the whole structure if some information on the structure is available. This may consist of phases determined by direct methods or of the positions of heavy atoms or some chemically known group deduced from a Patterson synthesis and/or by the convolution molecule technique of Hoppe (1957). No intermediate Fourier syntheses and no human intervention are needed in the course of phase determination right up to the completion of the structure determination. The test examples calculated show that phase correction works in cases where wrong atomic sites had been postulated.

Table 1. *Peaks in the Fourier synthesis of the sulpholid rubidium salt*, $RbSO_{10}C_9H_{17}$, *phased with* Rb *and* S *contributions* (*from Patterson synthesis*)

Owing to the relative positions of the Rb ($y=0,25$) and the S atom ($y=0,22$) in the space group $P2_1$ high false peaks occur as a result of pseudosymmetry.

230 PEAKS LOCATED AMONG THE 51300 POINTS SUPPLIED   **O. cycle**   **Sulfolipid**

93 UNIQUE PEAKS WERE PICKED

50 PEAKS OF HIGHEST DENSITY ARE PLOTTED

X	Y	Z	VALUE OF FUNCTION AT POINT	PLOT CHARACTER	identified atom peaks	mirror atom peaks
0.5908	0.2451	0.5692	16.9807	A	O2	
0.7778	0.3406	0.9300	16.7114	B	(S)	
0.1840	0.2403	0.5119	13.2557	C	O2'	
0.7133	0.2449	0.3733	12.9349	D	C1	
0.4777	0.2584	0.3246	11.7754	E	C3	
0.5970	0.2251	0.9218	11.1711	F		
0.3886	0.3195	0.0737	11.0953	G	O4	
0.7867	0.1460	0.9391	10.9646	H	OII	
0.3665	0.3517	0.3687	10.4946	J	O3	
0.7545	0.3681	0.7764	10.4287	K	OIII	
0.7203	0.3157	0.2428	10.0407	L	O5	
0.6150	0.2676	0.1293	9.9329	M	C5	
0.8791	0.3912	0.	9.2144	N	OI	
0.9542	0.4998	0.3156	9.1480	P	O3'	
0.3669	0.1403	0.3661	9.1158	Q		(O3)
0.1852	0.2726	0.6650	9.0540	R	C2'	
0.7101	0.0456	0.3634	8.7312	S	O1	
0.0949	0.2122	0.1496	8.3072	T	(Rb)	
0.1813	0.4878	0.6825	8.1425	U	C1'	
0.8778	0.1124	-0.0000	7.9879	V		(O1)
0.7189	0.1743	0.2446	7.9772	W		(O5)
0.5950	0.3030	0.4308	7.9475	X	C2	
0.2521	0.2580	-0.0000	7.5699	Y		
0.0551	0.2125	0.6902	7.4738	Z	C3'	
0.9449	0.7125	0.3098	7.4738	A1		(C2')
0.3875	0.1733	0.0794	7.1519	B1		(O4)
0.7542	0.1356	0.7757	7.0565	C1		(OIII)
0.0502	0.4974	0.6709	6.9991	D1		(O3')
0.4992	0.3638	0.1776	6.9546	E1	C4	
0.7088	0.4451	0.3590	6.5022	F1		(O1)
0.3490	0.2197	0.9547	5.8960	G1		
0.7293	0.2463	0.4779	5.7818	H1		
0.2916	0.2779	0.1395	5.5691	J1		
0.5908	0.1700	0.4292	5.4603	K1		(C2)
0.6348	0.3798	1.0000	5.1084	L1	C6	
0.9839	0.2460	0.4033	4.9582	M1		
0.1709	0.2495	0.8947	4.9309	N1		
0.5006	0.2506	0.0419	4.9023	P1		
0.4985	0.1495	0.1706	4.8959	Q1		(C4)
0.5536	0.6667	0.5249	4.8616	R1		
0.4464	0.1667	0.4751	4.8616	S1		
0.8153	0.2651	0.3763	4.7204	T1		
0.6288	0.1065	0.	4.6514	U1		(C6)
-0.0000	0.2029	0.0893	4.5143	V1		
0.7223	0.2331	0.8124	4.4204	W1		
0.7765	0.2425	0.0497	4.3346	X1		
0.4085	0.3110	0.5047	4.2238	Y1		
0.8228	0.5117	0.3265	4.0385	Z1		(C1')
0.0223	0.2885	0.9560	4.0293	A2		
0.3950	0.1447	0.1750	4.0189	B2		

Table 2. *Peaks in the Fourier synthesis of the sulpholid rubidium salt after 7 cycles phase correction*
The mirror atoms and background peaks have disappeared.

194 PEAKS LOCATED AMONG THE 51300 POINTS SUPPLIED   7 cycle Sulfolipid

79 UNIQUE PEAKS WERE PICKED

50 PEAKS OF HIGHEST DENSITY ARE PLOTTED

X	Y	Z	VALUE OF FUNCTION AT POINT	PLOT CHARACTER	identified atom peaks
0.7778	0.3337	0.9291	23.9683	A	(s)
0.5859	0.2202	0.5669	22.4215	B	O2
0.7194	0.3225	0.2453	21.9191	C	O5
0.3955	0.3190	0.0726	21.7311	D	O4
0.7553	0.3689	0.7790	20.6253	E	OIII
0.3665	0.3445	0.3695	20.5517	F	O3
0.9568	0.4974	0.3181	18.7581	G	O3'
0.1868	0.2091	0.5126	18.5467	H	O2'
0.7177	0.0448	0.3668	18.3507	J	O1
0.7857	0.1155	0.9405	18.3199	K	OII
0.8784	0.4019	-0.0000	17.7959	L	OI
0.6116	0.2762	0.1288	17.6457	M	C5
0.1799	0.2809	0.6615	17.2656	N	C2'
0.7104	0.2395	0.3784	16.9420	P	C1
0.1771	0.4777	0.6652	16.7232	Q	C1'
0.4787	0.2678	0.3237	16.3725	R	C3
0.4986	0.3651	0.1775	16.3156	S	C4
0.1118	0.2307	0.1756	15.1690	T	(Rb)
0.5931	0.3090	0.4269	14.0831	U	C2
0.0629	0.2031	0.6831	10.6879	V	C3'
0.6433	0.3817	-0.0000	9.9116	W	C6
0.5958	0.2010	0.9763	7.9210	X	
0.	0.3195	0.9263	6.7348	Y	
0.2522	0.2601	-0.0000	6.3955	Z	
0.7454	0.1966	0.8153	5.9400	A1	
0.5006	0.2399	0.0545	5.8379	B1	
0.9585	0.8751	0.8080	5.5189	C1	
0.1304	0.2451	0.3471	5.1204	D1	
0.3510	0.1834	0.2703	5.0231	E1	
0.0552	0.4120	0.1831	5.0227	F1	
0.3612	0.2152	0.9490	4.9455	G1	
0.8377	0.3134	0.4204	4.6169	H1	
0.0469	0.3284	0.6544	4.4846	J1	
0.4151	0.1803	0.5055	4.1814	K1	
0.2126	0.1309	0.1261	4.1316	L1	
0.8818	0.1710	0.3175	3.9598	M1	
0.9324	0.4312	0.6697	3.9565	N1	
1.0000	0.1761	0.2486	3.8304	P1	
0.2363	0.	0.8334	3.6289	Q1	
0.2868	0.2750	0.1387	3.4333	R1	
0.6009	0.0173	-0.0000	3.3889	S1	
0.7444	0.0333	0.8343	3.3507	T1	
0.7256	0.4965	0.8717	3.3445	U1	
0.0675	0.1000	0.2662	3.2385	V1	
0.6708	0.2346	0.8898	3.1676	W1	
0.9050	0.1000	0.8039	3.1396	X1	
0.7928	0.2344	0.0570	3.1293	Y1	
0.1779	0.2679	0.7068	3.0420	Z1	
0.3778	0.2572	0.8070	3.0385	A2	
0.8651	0.2647	0.6971	3.0168	B2	

This particular feature gives the method a distinct advantage over least-squares procedures. The basic difference between the least-squares and phase-correction techniques is that phase correction takes into account all information contained in the structure amplitudes and phases, whereas least squares reduces the amount of information by observing only the peaks occurring in a Fourier synthesis and selecting from these peaks probable atomic sites. It is assumed therefore, that phase correction should work in many cases, where least-squares methods fail in the automatic structure determination of a partially known molecule.

Variants of the method are feasible. One possibility for a Fourier synthesis with resolved peaks is to select an initial set of peak positions (analogous to the normal successive Fourier analysis) and to attach to them weights, determined from the peak height in the Fourier synthesis. These weights are then continuously changed according to the weighting function of our method. Another variant would be to apply some least-squares cycles (similar to the method of Rollett & Hodgson), not starting with initial weights $g_j=0$ for unknown atoms, but with weights set after the heights in the initial Fourier synthesis. After applying the weighting procedure of phase correction, a selection of significant peaks should be easier.

References

GASSMANN, J. (1966). *Acta Cryst.* **21**, A6.
HOPPE W. (1957). *Acta Cryst.* **10**, 750.
HOPPE, W., HUBER, R. & GASSMANN, J. (1963). *Acta Cryst.* **16**, A4.
HOPPE, W. (1963). *Z. Kristallogr.* **118**, 121.
HOPPE, W. (1966). *Angew. Chem.* **5**, 267.
HOPPE, W., WILL, G., GASSMANN, J. & WEICHSELGARTNER, H. (1967). *Z. Kristallogr.* In the press.
LUZZATI, V. (1953). *Acta Cryst.* **6**, 142.
OKAYA, J. (1964). *Acta Cryst.* **17**, 1276.
RAMACHANDRAN, G. N. (1964). *Advanced Methods of Crystallography*, pp. 25–65.
ROLLETT, J. & HODGSON, L. (1962). Symposium 50 Jahre Röntgeninterferenzen, München.
WOOLFSON, M. M. (1958). *Acta Cryst.* **11**, 277.