The single isomorphous-replacement method: a correction. By D. M. Blow and Michael G. Rossmann, *M.R.C. Laboratory of Molecular Biology, Hills Road, Cambridge, England*

We wish to correct a fallacy contained in section 5 of our paper (Blow & Rossmann, 1961). It is stated there that it will be possible to decide the absolute configuration of the heavy atoms, so as to utilise the anomalous scattering effect, by correlation of the two Fourier syntheses, one based on single isomorphous replacement only, the other on anomalous scattering effects only. It is shown below that the correlation between these syntheses is exactly zero.

Let the electron-density distribution due to the single isomorphous replacement alone be given by

$$\varrho_{is}(\mathbf{x}) = \sum_h |\xi_h| \exp i(\alpha_h + 2\pi \mathbf{h} \cdot \mathbf{x});$$

and the electron density distribution due to the anomalous scattering effects alone be given by

$$\varrho_{AD}(\mathbf{x}) = \sum_p |\eta_p| \exp i(\beta_p + 2\pi \mathbf{p} \cdot \mathbf{x}).$$

(Notation as in our paper.) The correlation between ϱ_{is} and ϱ_{AD} over the whole unit cell may now be defined as

$$C = \int_{\text{unit cell}} \varrho_{is}(\mathbf{x})\varrho_{AD}(\mathbf{x})d\mathbf{x}.$$

Substituting the above Fourier expressions for ϱ_{is} and ϱ_{AD} we obtain

$$C = \sum_h \sum_p |\xi_h||\eta_p| \exp i(\alpha_h + \beta_p) \int_{\text{unit cell}} \exp 2\pi i(\mathbf{h} + \mathbf{p})\mathbf{x} \cdot d\mathbf{x}.$$

The integral is zero unless $h + p = 0$, when it becomes unity. Hence, making use of the Friedel relationship,

$$C = 2 \sum_h |\xi_h||\eta_h| \cos(\alpha_h - \beta_h).$$

Fig. 4 of Blow & Rossmann (1961) shows that

$$\alpha_h - \beta_h = \pm \tfrac{1}{2}\pi. \text{ Hence } C = 0 \text{ always.}$$

The Fourier synthesis calculated with the correct configuration of heavy atoms will, of course, be more accurate than the one with incorrect absolute configuration. If only a single isomorphous pair is available, then the only criterion for determining the absolute configuration of the heavy atoms is the actual examination of the two possible Fourier syntheses for reasonable features.

Reference

Blow, D. M. & Rossmann, M. G. (1961). *Acta Cryst.* **14**, 1195.

Variable weighting and the solution of the false structure of rubrofusarin. By George H. Stout, *Department of Chemistry* and L. H. Jensen, *Department of Anatomy, University of Washington, Seattle 5, Washington, U.S.A.*

The molecular structure of rubrofusarin, a natural product, has been determined (Stout & Jensen, 1962) by a modification of Sayer's method (Sayer, 1952; Zachariasen, 1952). The unit cell parameters are

$$a = 7 \cdot 52, \ b = 23 \cdot 14, \ c = 7 \cdot 20 \text{ Å}; \ \beta = 98 \cdot 2°.$$

The space group is $P2_1/c$, four molecules per unit cell. Fig. 1 shows the skeleton formula and numbering of the atoms.
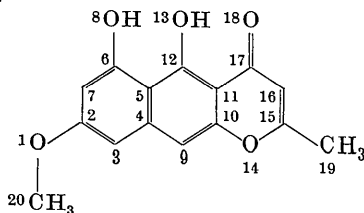

Fig. 1. Skeleton formula and numbering of the atoms.

In determining signs for 123 of the largest structure factors, it was found that they fell into two groups. For one, signs could be determined absolutely; for the other, they could be determined relative to a parameter $a = \pm$. Calculation of a three-dimensional F_0 synthesis with a taken $(-)$ led to a structure that refined by one F_0 synthesis from $R = 46\%$ to $R = 30\%$ for 358 of the most intense reflections. At this point the structure ap-

peared to have 'locked in', but several cycles of ΔF syntheses including only these terms for which $F_c > F_0/2$ did not decrease R below 22%. A determined effort to refine further using 1835 hkl data and again including only terms for which $F_c > F_0/2$ was without success. The molecular structure was reasonable, but inspection of the calculated structure factors revealed a few outstanding discrepancies that left no doubt the structure was incorrect.

Calculation of a three-dimensional F_0 synthesis with a taken $(+)$ gave what appeared on first sight to be the same structure. Closer inspection proved, however, that it differed essentially in the displacement of the molecule with an average deviation between corresponding atoms in the two structures less than 0·25 Å. This structure refined normally by ΔF syntheses and a final full matrix least squares cycle (Busing & Levy, 1959).

Since the shortest Fourier component for complete Cu $K\alpha$ data has a period of 0·8 Å, one might reasonably question the reality of a false minimum corresponding to a structure with the average deviation of the atoms less than 0·25 Å from their true positions. The validity of such a minimum has been tested further using the full matrix least squares program of Busing & Levy on 1835 hkl reflections. Table 1 summarizes the results. In column 2 are listed for each atom in the incorrect structure the deviations from its position in the true structure