2.3. PATTERSON AND MOLECULAR-REPLACEMENT TECHNIQUES

\[ |F_h|^2 + |F_{-h}|^2 = 2 \sum_{i,j} (f_i^{(i')'} + f_j^{(j')'}) \cos 2\pi \mathbf{h} \cdot (\mathbf{x}_i - \mathbf{x}_j) \]

and

\[ |F_h|^2 - |F_{-h}|^2 = 2 \sum_{i,j} (f_i^{(j')'} - f_j^{(i')'}) \sin 2\pi \mathbf{h} \cdot (\mathbf{x}_i - \mathbf{x}_j). \]

Let us now consider the significance of a Patterson in the presence of anomalous dispersion. The normal Patterson definition is given by

\[ P(u) = \int \rho'(x) \rho(x + u) \, dx \]

\[ = \frac{1}{V^2} \sum_{\mathbf{h}} |F_h|^2 \exp(-2\pi i \mathbf{h} \cdot \mathbf{u}) \]

\[ \equiv P_c(u) - iP_s(u), \]

where

\[ P_c(u) = \frac{2}{V} \sum_{\text{hemisphere}} (|F_h|^2 + |F_{-h}|^2) \cos 2\pi \mathbf{h} \cdot \mathbf{u} \]

and

\[ P_s(u) = \frac{2}{V} \sum_{\text{hemisphere}} (|F_h|^2 - |F_{-h}|^2) \sin 2\pi \mathbf{h} \cdot \mathbf{u}. \]

The \( P_c(u) \) component is essentially the normal Patterson, in which the peak heights have been very slightly modified by the anomalous-scattering effect. That is, the peaks of \( P_c(u) \) are proportional in height to \((f_i^{(i')'} + f_j^{(j')'})\).

The \( P_s(u) \) component is more interesting. It represents vectors between the normal atoms in the unit cell and the anomalous scatterers, proportional in height to \((f_i^{(j')'} - f_j^{(i')'})\) (Okaya et al., 1955). This function is antisymmetric with respect to the change of the direction of the diffraction vector. An illustration of the function is given in Fig. 2.3.4.1. In a unit cell containing \( N \) atoms, \( n \) of which are anomalous scatterers, the \( P_s(u) \) function contains only \( n(N-n) \) positive peaks and an equal number of negative peaks related to the former by antiprismatic symmetry. The analysis of a \( P_s(u) \) synthesis presents problems somewhat similar to those posed by a normal Patterson. The procedure has been used only rarely (cf. Moncrief & Lipscomb (1966) and Pepinsky et al. (1957)), probably because alternative procedures are available for small compounds and the solution of \( P_s(u) \) is too complex for large biological molecules.

2.3.4.3. The position of anomalous scatterers

Anomalous scatterers can be used as an aid to phasing, when their positions are known. But the anomalous-dispersion differences (Bijvoet differences) can also be used to determine or confirm the heavy atoms which scatter anomalously (Rossmann, 1961). Furthermore, the use of anomalous-dispersion information obviates the lack of isomorphism but, on the other hand, the differences are normally far smaller than those produced by a heavy-atom isomorphous replacement.

Consider a structure of many light atoms giving rise to the structure factor \( F_h(N) \). In addition, it contains a few heavy atoms which have a significant anomalous-scattering effect. The non-anomalous component will be \( F_h(H) \) and the anomalous component is \( F_h^*(H) = i(\Delta f_1/\Delta f_2)F_h(H) \) (Fig. 2.3.4.2a). The total structure factor will be \( F_h \). The Friedel opposite is constructed appropriately (Fig. 2.3.4.2a). Now reflect the Friedel opposite construction across the real axis of the Argand diagram (Fig. 2.3.4.2b). Let the difference in phase between \( F_h \) and \( F_h \) be \( \varphi \). Thus

\[ 4|F_h^*(H)|^2 = |F_h|^2 + |F_h|^2 - 2|F_h||F_h| \cos \varphi, \]

but since \( \varphi \) is very small

\[ |F_h^*(H)|^2 \approx \frac{1}{2}(|F_h| - |F_h|)^2. \]

Hence, a Patterson with coefficients \((|F_h| - |F_h|)^2\) will be

![Fig. 2.3.4.1](image)

![Fig. 2.3.4.2](image)
2. RECIPROCAL SPACE IN CRYSTAL-STRUCTURE DETERMINATION

2.3. Noncrystallographic symmetry

2.3.5.1. Definitions

The interpretation of Pattersons can be helped by using various types of chemical or physical information. An obvious example is the knowledge that one or two heavy atoms per crystallographic asymmetric unit are present. Another example is the exploitation of a rigid chemical framework in a portion of a molecule (Nordman & Nakatsu, 1963; Burnett & Rossmann, 1971). One extremely useful constraint on the interpretation of Pattersons is noncrystallographic symmetry. Indeed, the structural solution of large biological assemblies such as viruses is only possible because of the natural occurrence of this phenomenon. The term ‘molecular replacement’ is used for methods that utilize noncrystallographic symmetry in the solution of structures [for earlier reviews see Rossmann (1972) and Argos & Rossmann (1980)]. These methods, which are only partially dependent on Patterson concepts, are discussed in Sections 2.3.6–2.3.8.