

2.3. PATTERSON AND MOLECULAR-REPLACEMENT TECHNIQUES

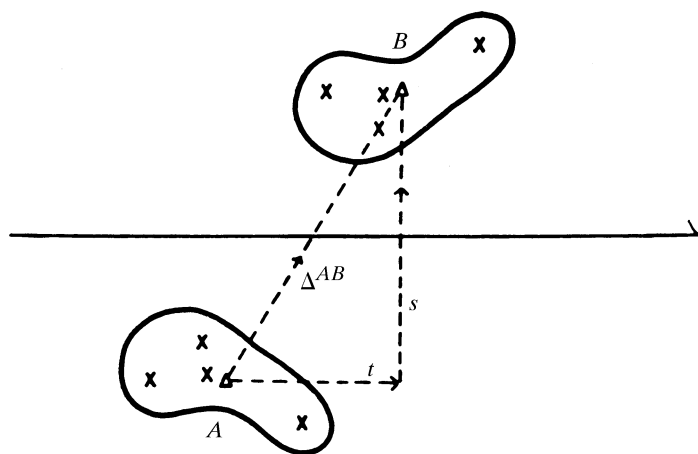


Fig. 2.3.7.1. Crosses represent atoms in a two-dimensional model structure. The triangles are the points chosen as approximate centres of molecules *A* and *B*. Δ^{AB} has components *t* and *s* parallel and perpendicular, respectively, to the screw rotation axis. [Reprinted from Rossmann *et al.* (1964).]

$$T(\mathbf{S}_x, \mathbf{S}_{x'}) = \frac{2}{V_h V_p} \sum_{\mathbf{h}} \sum_{\mathbf{p}} |\mathbf{F}_h| |\mathbf{F}_p| G_{\mathbf{h}\mathbf{p}} \times \cos[\alpha_{\mathbf{h}} + \alpha_{\mathbf{p}} - 2\pi(\mathbf{h} \cdot \mathbf{S}_x + \mathbf{p} \cdot \mathbf{S}_{x'})]. \quad (2.3.7.1)$$

2.3.7.2. Position of a noncrystallographic element relating two unknown structures

The function (2.3.7.1) is quite general. For instance, the rotation function corresponds to a comparison of Patterson functions P_1 and P_2 at their origins. That is, the coefficients are F^2 , phases are zero and $\mathbf{S}_x = \mathbf{S}_{x'} = 0$. However, the determination of the translation between two objects requires the comparison of cross-vectors away from the origin.

Consider, for instance, the determination of the precise translation vector parallel to a rotation axis between two identical

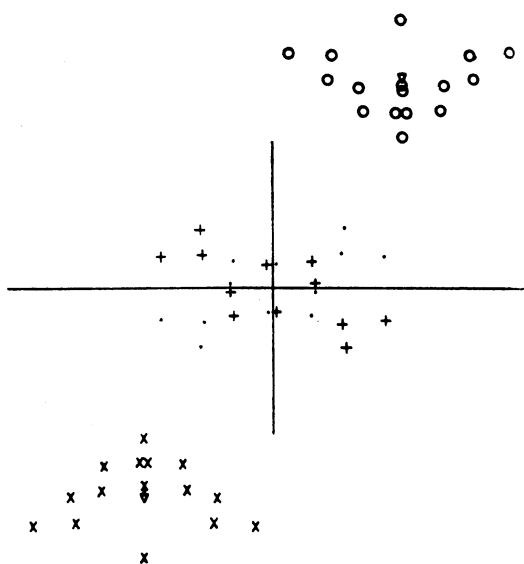


Fig. 2.3.7.2. Vectors arising from the structure in Fig. 2.3.7.1. The self-vectors of molecules *A* and *B* are represented by + and ·; the cross-vectors from molecules *A* to *B* and *B* to *A* by × and ○. Triangles mark the position of $+\Delta^{AB}$ and $-\Delta^{AB}$. [Reprinted from Rossmann *et al.* (1964).]

molecules of unknown structure. For simplicity, let the noncrystallographic axis be a dyad (Fig. 2.3.7.1). Fig. 2.3.7.2 shows the corresponding Patterson of the hypothetical point-atom structure. Opposite sets of cross-Patterson vectors in Fig. 2.3.7.2 are related by a twofold rotation and a translation equal to twice the precise vector in the original structure. A suitable translation function would then compare a Patterson at \mathbf{S} with the rotated Patterson at $-\mathbf{S}$. Hence, substituting $\mathbf{S}_x = \mathbf{S}$ and $\mathbf{S}_{x'} = -\mathbf{S}$ in (2.3.7.1),

$$T(\mathbf{S}) = \frac{2}{\sqrt{2}} \sum_{\mathbf{h}} \sum_{\mathbf{p}} |\mathbf{F}_h|^2 |\mathbf{F}_p|^2 G_{\mathbf{h}\mathbf{p}} \cos[2\pi(\mathbf{h} - \mathbf{p}) \cdot \mathbf{S}]. \quad (2.3.7.2)$$

The opposite cross-vectors can be superimposed only if an evenfold rotation between the unknown molecules exists. The translation function (2.3.7.2) is thus applicable only in this special situation. There is no published translation method to determine the interrelation of two unknown structures in a crystallographic asymmetric unit or in two different crystal forms. However, another special situation exists if a molecular evenfold axis is parallel to a crystallographic evenfold axis. In this case, the position of the noncrystallographic symmetry element can be easily determined from the large peak in the corresponding Harker section of the Patterson.

In general, it is difficult or impossible to determine the positions of noncrystallographic axes (or their intersection at a molecular centre). However, the position of heavy atoms in isomorphous derivatives, which usually obey the noncrystallographic symmetry, can often determine this information.

2.3.7.3. Position of a known molecular structure in an unknown unit cell

The most common type of translation function occurs when looking for the position of a known molecular structure in an unknown crystal. For instance, if the structure of an enzyme has previously been determined by the isomorphous replacement method, then the structure of the same enzyme from another species can often be solved by molecular replacement [*e.g.* Grau *et al.* (1981)]. However, there are some severe pitfalls when, for instance, there are gross conformational changes [*e.g.* Moras *et al.* (1980)]. This type of translation function could also be useful in the interpolation of *E* maps produced by direct methods. Here there may often be confusion as a consequence of a number of molecular images related by translations (Karle, 1976; Beurskens, 1981; Egert & Sheldrick, 1985).

Tollin's (1966) *Q* function and Crowther & Blow's (1967) translation function are essentially identical (Tollin, 1969) and depend on a prior knowledge of the search molecule as well as its orientation in the unknown cell. The derivation given here, however, is somewhat more general and follows the derivation of Argos & Rossmann (1980), and should be compared with the method of Harada *et al.* (1981).

If the known molecular structure is correctly oriented into a cell (\mathbf{p}) of an unknown structure and placed at \mathbf{S} with respect to a defined origin, then a suitable translation function is

$$T(\mathbf{S}) = \sum_{\mathbf{p}} |\mathbf{F}_{\mathbf{p}, \text{obs}}|^2 |\mathbf{F}_{\mathbf{p}}(\mathbf{S})|^2. \quad (2.3.7.3)$$

This definition is preferable to one based on an *R*-factor calculation as it is more amenable to computation and is independent of a relative scale factor.

The structure factor $\mathbf{F}_{\mathbf{p}}(\mathbf{S})$ can be calculated by modifying expression (2.3.8.9) (see below). That is,

$$\mathbf{F}_{\mathbf{p}}(\mathbf{S}) = \frac{U}{V_h} \sum_{n=1}^N \exp(2\pi i \mathbf{p} \cdot \mathbf{S}_n) \left[\sum_{\mathbf{h}} \mathbf{F}_h G_{\mathbf{h}\mathbf{p}_n} \exp(-2\pi i \mathbf{h} \cdot \mathbf{S}) \right],$$