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Determination of Angular Orientation of Rigid Group in Molecular Crystal: Vector-set Seeking Method

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In order to determine the angular orientation of the rigid atomic group, such as benzene ring, in a molecular crystal, a new method for interpreting a distribution of peaks near the origin of two-dimensional Patterson function has been described in this paper. Similar methods for solving the Patterson function by the aid of the rigid groups have been proposed by several authors, but the present method, vector-set seeking method, differs from them in the procedure to find a satisfactory fit of a vector-set of the rigid group on the Patterson function and in a criterion for a correct choice of the angular orientation. Satisfactory results for the known structures of salicylamide and α-pyridone and the unknown structure of *m*-hydroxybenzamide were quickly obtained by the application of this method.

In the early stage of crystal structure analysis, the orientation of a rigid atomic group in the unit cell provides useful information of the interpretation of the Patterson function. The optical transform method has been used for this purpose.[1] It has been realized that the interpretation of the Patterson peaks near the origin is also effective in some cases.[2] Recently, several systematic procedures for solving the Patterson function with the aid of the rigid group of known spatial atomic arrangement have been proposed and applied successfully to the practical crystal structure determinations.[3,4] However, a large scale computer would be required and even on such computer it might take rather long computational time.

We have developed on the same line somewhat different procedure, the vector-set seeking method, which is convenient to deal with two-dimensional Patterson function and could be done on the smaller computer. It was proved that this method worked well for some practical structure determinations. The present paper includes the procedure of the vector-set seeking method and its application.

Description of the Method

The angular orientation of the rigid group in a molecule is defined by θ, φ and ψ, which are the angles of the rotations with respect to the three mutually orthogonal reference axes, X, Y and Z respectively. In the application of the vector-set seeking method for the projection of the Patterson function, this expression of the rotation is more convenient than that by Eulerian angles.

The procedure of this method is as follows. A plausible model of the rigid group defined by the orthogonal coordinate system is first rotated about two axes, X and Y, and then finally about the third axis, Z. The model after such three independent rotations is projected along the axis of the final rotation, Z. The vector-set consisting of interatomic vectors in the projected model is superposed on the projected Patterson function, so that two systems coincide in the origin and the axis of projection. The relation of the crystallographic axes with the reference axes is indicated in the figure for each example. The summation of the values of the Patterson function at the ends of the vectors is carried out over all the vector-set. If necessary, the Patterson function may be modified by some function of the distance from the origin.

The sum obtained by this procedure would give a degree of the fitness between the vector-set having a given angular orientation and the Patterson function; we shall call it 'fit-factor'. In the practical applications, the fit-factor is computed at every point (θ, φ, ψ), with suitable intervals of the three angular coordinates. It is natural to assume that the angular coordinates which give the largest value, the best fitting, within a reasonable range of the rotation correspond to the correct orientation of the rigid group in the crystal.

1) C. A. Taylor and H. Lipson, "Optical Transforms," Bell and Son, London (1965).
2) W. Cochran, *Acta Cryst.*, **4**, 376 (1951).
3) P. Tollin and W. Cochran, ibid., **17**, 1322 (1964).
4) C. E. Nordman and K. Nakatsu, *J. Am. Chem. Soc.*, **85**, 353 (1963).

Application

This method was tested with the known structures of salicylamide[5] and α-pyridone[6], and with the unknown structure of *m*-hydroxybenzamide.[7] In these examples, the whole molecules were taken as the rigid group. The Patterson function computed for the grid points at suitable intervals was stored in the computer. The value of the function at the end of the vector was obtained by means of the interpolation by a second order equation.[8] In the case of the non-interpolation, the value on the nearest grid point from the end of the vector was taken. The angles, θ, φ and ψ, were stepwisely changed with intervals of 15° in the first stage, and of 5° to 10° in the search in the neighborhood of the maxima.

Salicylamide.—($a=12.92$, $b=4.98$, $c=21.04$ Å, $\beta=91.8°$, $I2_1/a$). The Patterson function projected on (010) was computed for the grid points at intervals of $a/64$ and $c/128$. A planar molecular model of salicylamide was set up with generally accepted bond lengths and angles. Only the Patterson function within 5.3 Å from the origin was stored in the computer, because all the intramolecular vectors of the model will be within this region. The value of the origin of the Patterson function was taken as zero. Both the seekings with the interpolation and with the non-interpolation were carried out. The difference between the results of these two seekings was very small, and the angular orientation of the molecule in the projection was uniquely determined. Figure 1 shows a part of the result. The highest peak appeared at $\theta=40°$, $\varphi=20°$ and $\psi=-20°$. In

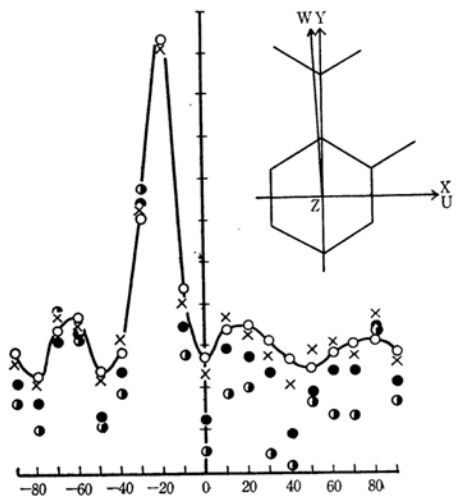

Fig. 1 (a)

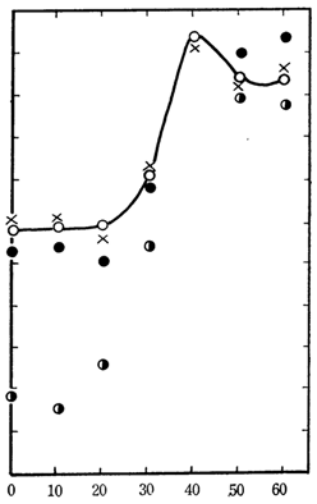

Fig. 1 (b)

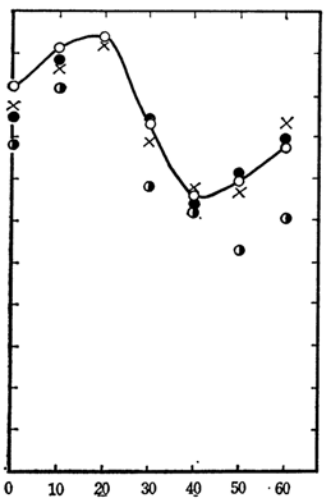

Fig. 1 (c)

Fig. 1. Variation of 'fit-factor,' in salicylamide,
(a) by the rotation of ψ at $\theta=40°$ and $\varphi=20°$,
(b) by that of θ at $\varphi=20°$ and $\psi=-20°$ and
(c) by that of φ at $\theta=40°$ and $\psi=-20°$.
○ interpolated, with equi-weighted vector-set.
× non-interpolated, with equi-weighted vector-set.
● non-interpolated, with weighted vector-set.
◑ non-interpolated, with weighted vector-set and Patterson function modified by distance from origin.
The values plotted by the other symbols than × were given by subtracting a constant from the fit-factors which were standardized so as to give the same value at the best fitting.

5) Y. Sasada, T. Takano and M. Kakudo, This Bulletin, **37**, 940 (1964).
6) B. R. Penford, *Acta Cryst.*, **6**, 591 (1953).
7) Y. Katsube, Y. Sasada and M. Kakudo, This Bulletin, **39**, 6107 (1966).
8) J. Ladell and J. L. Katz, *Acta Cryst.*, **7**, 460 (1954).

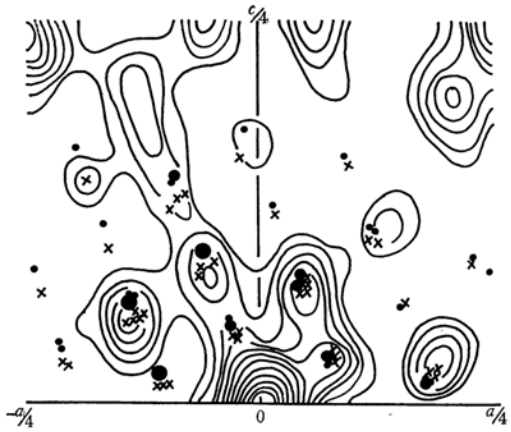

Fig. 2. Patterson projection of salicylamide and vector-set at the best fitting.
● model structure, × true structure

Fig. 2, the projected vector-set with this angula orientation of the model structure and that of th true structure are superposed on the Patterso projection. As seen from Fig. 2, the projecte vector-set obtained by this method is in good agreement with that of the correct structure already known, within the limits of error to be expected.

α-Pyridone.—($a=13.63$, $b=5.89$, $c=5.67$ Å, $P2_12_12_1$) The Patterson function projected on (001) was computed for the grid points at intervals of $a/60$ and $b/30$. In the seeking with the interpolation, there appeared some broad peaks with the shoulders, and it was unable to determine uniquely the angular orientation. However, it was not so difficult to find out the most probable angular orientation to be $\theta=-15°$, $\varphi=65°$ and $\psi=-45°$,

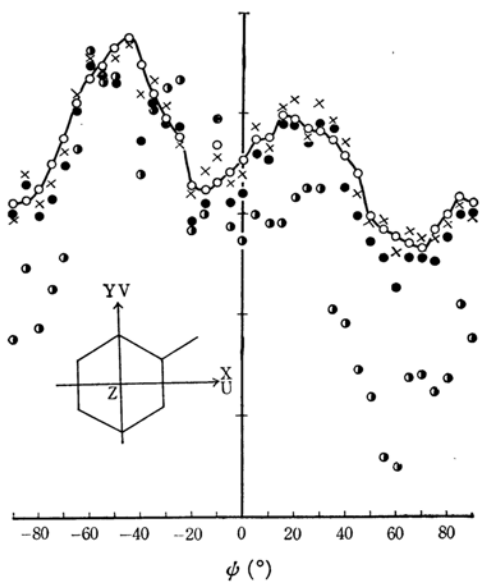

Fig. 3 (a)

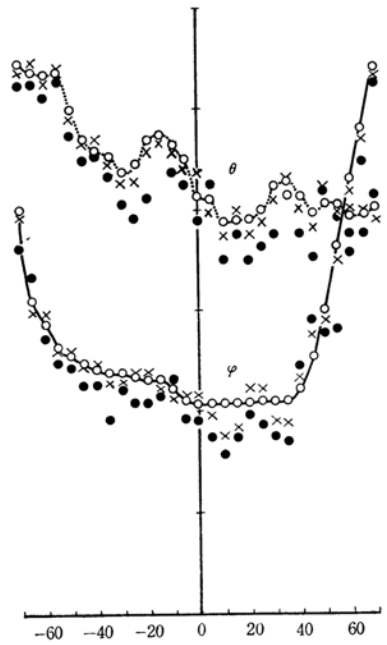

Fig. 3 (b)

Fig. 3. Variation of 'fit-factor,' in α-pyridone,
(a) by the rotation of ψ at $\theta=-15°$ and $\varphi=65°$,
(b) by that of θ at $\varphi=65°$ and $\psi=-45°$ (dotted curve) and by that of φ at $\theta=-15°$ and $\psi=-45°$ (full curve).

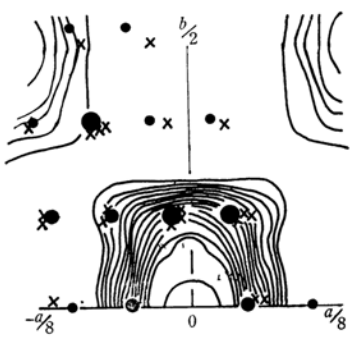

Fig. 4. Patterson projection of α-pyridone and vector-set at the best fitting.

through the inspection of the Patterson function superposed on the possible vector-sets given by the seeking within a limit of rotations due to the unit cell dimensions. This was in good agreement with the orientation of the true structure in the projection. The result of seeking in every five degree of the rotation is shown in Fig. 3, and the vector-set of the model with the orientation corresponding to these angles and that of the true structure superposed on the Patterson projection is also shown in Fig. 4.

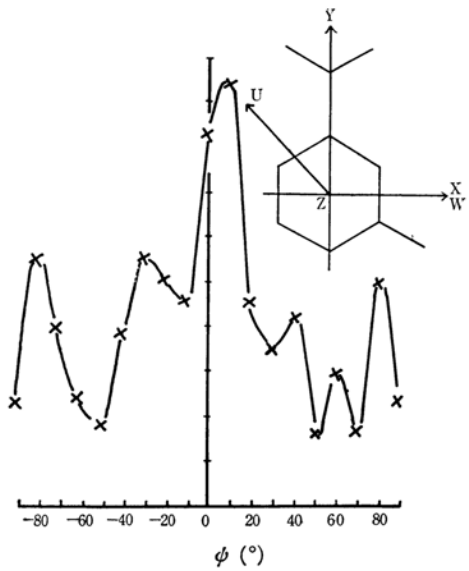

Fig. 5. Variation of 'fit-factor,' in *m*-hydroxybenzamide, by the rotation of ϕ at $\theta=0°$ and $\varphi=45°$.

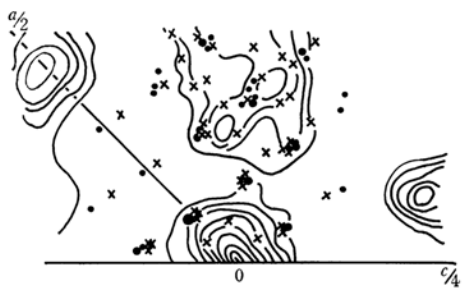

Fig. 6. Patterson projection of *m*-hydroxybenzamide and vector-set at the best fitting.

***m*-Hydroxybenzamide.** — ($a=11.59$, $b=5.03$, $c=15.53$ Å, $\beta=136.1°$, $P2_1/c$). The Patterson function projected on (010) was computed for the grid points at intervals of $a/64$ and $c/64$. In the seeking with the non-interpolation, the angular orientation of the benzene ring in the projection was determined with the planar molecular model consisting of the atoms of equal weight. A complete analysis of the crystal structure has been carried out with the knowledge on the angular orientation of the benzene ring obtained by this method. The result of the seeking is shown in Fig. 5, and the vector-set of the model with the orientation at the best fitting and that of the true structure is also shown in Fig. 6.

Discussion

In the crystals mentioned above, it was possible to find the orientation of the molecule in the projection by the application of this method. Since the maxima corresponding to the best fittings in the crystals of salicylamide and of *m*-hydroxybenzamide were sharp, the angular orientations of these molecules were quickly determined.

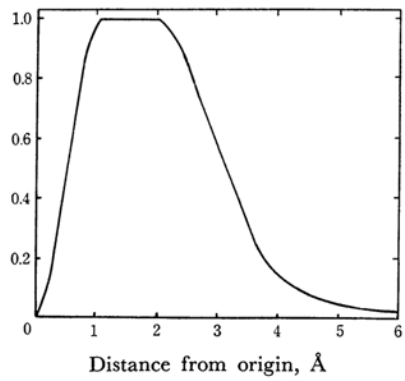

Fig. 7. Modification function against Patterson function to avoid the disturbance from the neighboring molecules.

When a part of the molecule, say the benzene ring, was taken as a rigid group, the peak in the fit-factor distribution became broader and lower. Although it was difficult, in general, to assign the orientation of the group, this method still worked well in some cases.

The fit-factor, especially in the seeking with the non-interpolation, was greatly affected by the rotation about the axis of the projection. Therefore, it may lead to a false orientation unless the rotation about this axis is carried out at relatively close intervals; the interval of the rotation angle should be decided by a correlation between the longest vector in the set and the size of the mesh of the Patterson function calculated. When there is the ambiguity in the estimation of the best fitting, as seen in the case of α-pyridone, the angular orientation may be estimated by the search of the largest fit-factor within the allowable angular region of the rotation; the dimension of the axis of the projection limits correlatively the ranges of θ and φ. However, in such a case, it may be difficult to find out the correct orientation by only the application of this method.

In the crystal of the molecule composed of the atoms of approximately equal weight, as seen from the present examples, it may be not necessary to use the weighted vector-set.

It is not always the case, even in that of the rigid molecule, that the angular coordinates for the best fitting give the correct angular orientation, because of the difference in geometries between the model used and the true molecule. In the crystal of *m*-hydroxybenzamide, in spite of the twist between a carboxyamide group and benzene ring, the angular coordinates obtained from the best fitting was very close to those of the benzene

ring in the true structure. The difference between their geometries was suggested by the disagreement between the vector-set of the model structure and that of the true structure, as shown in Fig. 6. It seems that the small difference between their geometries does not give rise to a serious problem for the determination of the approximate angular orientation of the molecule.

Different orientations due to the symmetry of the projected Patterson function may also influence the correct choice of the angular orientation. In the case of α-pyridone, two vector-sets related by the symmetry may overlap to some extent, and the Patterson peaks may not appear exactly in the positions corresponding to the points of the vector-sets; in fact, the peaks near the origin were mostly unresolved. It seems that the difficulty in the determination of the angular orientation of the α-pyridone molecule arose from this fact.

The intermolecular vectors may disturb the determination of the angular orientation. In order to minimize such obstruction, the values of the Patterson function were modified by a function of the distance from the origin, because the probability that the Patterson function at a point is due to only the intramolecular interactions decreases with increasing distance from the origin. In the present work, the modification as shown in Fig. 7 was used; the modification of this type also corresponded to the removal of the origin peak in the Patterson function. But the removal of the effects from the intermolecular vector and the origin peak was not greatly going to help the search of the best fitting; the latter resulted in the low background in the fit-factor distribution.

The vector-set seeking method was also applied to the crystal of salicylamide with the Patterson function sharpened by the factors of $\{3.5\exp 2\sin^2\theta/\lambda^2)\}$. This brought almost a similar result to the seeking with the unsharpened Patterson function. However, this helped the identification of the angular coordinates for the best fitting, because the maximum peak became sharper than that with the unsharpened Patterson function.

In the present work, a program was written in the machine language of NEAC 2230 computer. The computing time for the seeking with the interpolation is about 3.5 sec. per evaluation of a fit-factor' for a given angular orientation of the model containing ten atoms, while that for the non-interpolation is about 2.5 sec.