# An error in space group $\mathbf{P 6}_{\mathbf{2}} \mathbf{2 2}$ in International Tables for $\boldsymbol{X}$-ray Crystallography. By Fusao Takusagawa <br> and Shintaro Misaki, Department of Chemistry, University of Kansas, Lawrence, KS 66045, USA 

(Received 24 August 1989; accepted 6 February 1990)


#### Abstract

An error in the structure-factor expression for space group $P_{2} 22$ (No. 180) has been found in International Tables for $X$-ray Crystallography, Volume I, 1st through 3rd editions. The minus sign of the second sine function in the $B$ part of the equation for $l=3 n \pm 1$ should be a plus sign.

An error in the $B$ part of the equation for $l=3 n \pm 1$ for space group $\mathrm{P6}_{2} 22$ (No. 180) on p. 481 of International Tables for X-ray Crystallography $(1952,1965,1969)$ has been found. The minus sign of the second sine function


should be a plus sign. The correct equation is

$$
\begin{aligned}
B= & 4\{\sin 2 \pi l z \sin \pi h(2 x-y) \sin \pi(i-k) y \\
& +\sin 2 \pi\left(l z \mp \frac{1}{3}\right) \sin \pi h(x+y) \sin \pi(i-k)(y-x) \\
& \left.+\sin 2 \pi\left(l z \pm \frac{1}{3}\right) \sin \pi h(x-2 y) \sin \pi(i-k) x\right\} .
\end{aligned}
$$

## Reference

International Tables for X-ray Crystallography (1952, 1965, 1969). Vol. I. Birmingham: Kynoch Press.

Acta Cryst. (1990). A46, 625-626

Determination of the correct reference frame from an atomic coordinate list. By T. O. Yeates, Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, CA 92037, USA

(Received 26 June 1989; accepted 22 February 1990)


#### Abstract

A simple method is described for determining the reference coordinate system of a list of atomic coordinates. The reference system is characterized by finding the optimal metric tensor on the basis of the expected bond lengths. The ability to identify the correct frame of reference is important for structures solved in non-orthogonal unit cells.


Atomic coordinates are commonly described with respect to three different reference coordinate systems: (1) basis vectors given by the crystallographic unit-cell axes (coordinates referred to as 'fractional'); (2) basis vectors taken to be $1 \AA$ vectors parallel to the unit-cell axes (coordinates referred to here as 'axial'); and (3) mutually orthogonal $1 \AA$ basis vectors (coordinates referred to as 'orthogonal'). In non-orthogonal unit cells, the 'axial' and 'orthogonal' systems are distinct, but usually cannot be distinguished by inspection of the coordinate list. Since the coordinates of macromolecular structures are frequently converted back and forth between reference frames, uncertainty occasionally arises, especially when receiving coordinates from an external source. The following algebraic analysis is sufficient to resolve any ambiguity.

The coordinate list is used to form a list of interatomic vectors between pairs of atoms that are bonded and whose expected bond length is known. Let $x^{i}$ be the usual (contravariant) components of an interatomic vector in the given (unknown) coordinate system. The corresponding bond length is given by

$$
\begin{equation*}
\|\mathbf{x}\|=\left(\sum_{i=1}^{3} \sum_{j=1}^{3} \mathbf{G}_{i j} x^{i} x^{j}\right)^{1 / 2} \tag{1}
\end{equation*}
$$

where $\mathbf{G}$, which is to be determined, is the covariant metric tensor for the unknown reference frame.* In more familiar terms of matrices, $\|\mathbf{x}\|=\left(\mathbf{x}^{\mathrm{T}} \mathbf{G} \mathbf{x}\right)^{1 / 2}$. If $d$ is the expected bond length (in $\AA$ ), then the equation

$$
\begin{equation*}
\|\mathbf{x}\|^{2}=d^{2} \tag{2}
\end{equation*}
$$

provides a linear equation in terms of the variables $G_{i j}$. Since $\mathbf{G}$ may be taken to be symmetric, the equation for the unique components of $\mathbf{G}$ is

$$
\begin{align*}
& \left(x^{1}\right)^{2} G_{11}+2 x^{1} x^{2} G_{12}+2 x^{1} x^{3} G_{13} \\
& \quad+\left(x^{2}\right)^{2} G_{22}+2 x^{2} x^{3} G_{23}+\left(x^{3}\right)^{2} G_{33}=d^{2} \tag{3}
\end{align*}
$$

Given a large number of interatomic vectors, the $G_{i j}$ can be accurately determined by least squares. The metric tensor obtained is the one which minimizes the sum over the bonds of the squared differences between $\|\mathbf{x}\|^{2}$ and $d^{2}$. Alternatively, the metric tensor which minimizes the sum of the squared differences between $\|\mathbf{x}\|$ and $d$ may be obtained by iteration.

The reference frame may be described in crystallographic terms ( $a, b, c, \alpha, \beta, \gamma$ ) by equating the values obtained for the $G_{i j}$ with the crystallographic metric tensor (Patterson, 1985; Sands, 1982)

$$
\left(\begin{array}{ccc}
a^{2} & a b \cos \gamma & a c \cos \beta  \tag{4}\\
a b \cos \gamma & b^{2} & b c \cos \alpha \\
a c \cos \beta & b c \cos \alpha & c^{2}
\end{array}\right) .
$$

If $a=b=c=1$, and $\alpha=\beta=\gamma=90^{\circ}$, then the reference

[^0](C) 1990 International Union of Crystallography
frame for the coordinates is 'orthogonal'. If $a=b=c=1$, but $\alpha, \beta$ or $\gamma \neq 90^{\circ}$, then the reference frame is 'axial'.

If the reference frame is 'fractional', then the values obtained for $a, b, c, \alpha, \beta$ and $\gamma$ should be those of the crystallographic unit cell. For macromolecular structures, where the number of vectors is large, the statistical significance is high and the cell parameters obtained provide an independent evaluation of the experimentally measured cell parameters.

A Fortran program ELAST has been written to perform the above analysis on protein structures, considering only bonds between backbone atoms. For a protein of average size, the number of bonds included is about 2000 . The time
required for the analysis is approximately 4 s on a Convex C2.

This work was supported in part by NIH grant T32NS07078. This is manuscript No. 5953-MB of the Research Institute of Scripps Clinic.

## References

Patterson, A. L. (1985). In International Tables for X-ray Crystallography, Vol. II, edited by J. S. Kasper \& K. Lonsdale, pp. 52-64. Birmingham: Kynoch Press. (Present distributor Kluwer Academic Publishers, Dordrecht.)
SANDS, D. E. (1982). Vectors and Tensors in Crystallography. Reading, MA: Addison-Wesley.

Acta Cryst. (1990). A46, 626
Bloch waves and multislice in transmission and reflection diffraction. Erratum. By Y. MA* and L. D. Marks, Materials Research Center, Northwestern University, Evanston, IL 60208, USA
(Received 14 April 1990)

[^1]
(i)

Fig. 11. Corresponding results under the same conditions as for Fig. 8, except that the incidence angle is 10 mrad.


[^0]:    * In the case of an ordinary Euclidean reference frame, $\mathbf{G}$ is the identity matrix and $\|\mathbf{x}\|=\left(\mathbf{x}^{T} \mathbf{x}\right)^{1 / 2}$.

[^1]:    Abstract
    Owing to a printer's error, Fig. 11(i) of the paper by Ma \& Marks [Acta Cryst. (1990). A46, 11-32] was published in the wrong orientation. The correct figure is given.

    * Present address: Department of Materials Science and Engineering, University of Utah, Salt Lake City, UT 84112, USA.

