its structure is described by too many variable parameters for the parameter space to be explored *a priori*. It is then necessary to phase the fibre diffraction data and construct an electron-density map into which the molecular structure can be fitted and then refined. The second example above would belong to this class. The second class of methods therefore mimics conventional protein crystallography quite closely. The third class of problems applies when the structure is large, but there are too few diffraction data to attempt phasing and the usual determination of atomic coordinates. The solution to such problems varies from case to case and usually involves modelling and optimization of some kind.

An important parameter in structure determination by fibre diffraction is the degree of overlap (that results from the cylindrical averaging) in the data. This parameter is equal to the number of significant terms in equation (4.5.2.17) or the number of independent terms in equation (4.5.2.24), and depends on the position in reciprocal space and, for a polycrystalline fibre, the space-group symmetry. The number of degrees of freedom in a particular datum is equal to twice this number (since each structure factor generally has real and imaginary parts), and is denoted in this section by m. Determination of the $G_{nl}(R)$ from the cylindrically averaged data $I_l(R)$ therefore involves separating the $m/2$ amplitudes $|G_{nl}(R)|$ and assigning phases to each. The electron density can be calculated from the $G_{nl}(R)$ using equations (4.5.2.7) and (4.5.2.11).

4.5.2.6.2. *Helix symmetry, cell constants and space-group symmetry*

The first step in analysis of any fibre diffraction pattern is determination of the molecular helix symmetry u_v. Only the zero-order Bessel term contributes diffracted intensity on the meridian, and referring to equation (4.5.2.6) shows that the zero-order term occurs only on layer lines for which l is a multiple of u. Therefore, inspection of the distribution of diffraction along the meridian allows the value of u to be inferred. This procedure is usually effective, but can be difficult if u is large, because the first meridional maximum may be on a layer line that is difficult to measure. This difficulty was overcome in one case by Franklin & Holmes (1958) by noting that the second Bessel term on the equator is $n = u$, estimating $G_{00}(R)$ using data from a heavy-atom derivative (see Section 4.5.2.6.6), subtracting this from $I_0(R)$, and using the behaviour of the remaining intensity for small R to infer the order of the next Bessel term [using equation (4.5.2.14)] and thence u.

Referring to equations (4.5.2.6) and (4.5.2.14) shows that the distribution of $R_{\min}$ for $0 < l < u$ depends on the value of v. Therefore, inspection of the intensity distribution close to the meridian often allows v to be inferred. Note, however, that the distribution of $R_{\min}$ does not distinguish between the helix symmetries u_v and u_{u-v}. Any remaining ambiguities in the helix symmetry need to be resolved by steric considerations, or by detailed testing of models with the different symmetries against the available data.

For a polycrystalline system, the cell constants are determined from the (R, Z) coordinates of the spots on the diffraction pattern as described in Section 4.5.2.6.4. Space-group assignment is based on analysis of systematic absences, as in conventional crystallography. However, in some cases, because of possible overlap of systematic absences with other reflections, there may be some ambiguity in space-group assignment. However, the space group can always be limited to one of a few possibilities, and ambiguities can usually be resolved during structure determination (Section 4.5.2.6.4).

4.5.2.6.3. *Patterson functions*

In fibre diffraction, the conventional Patterson function cannot be calculated since the individual structure-factor intensities are not available. However, MacGillavry & Bruins (1948) showed that the *cylindrically averaged Patterson function* can be calculated from fibre diffraction data. Consider the function $\hat{Q}(r, z)$ defined by

$$\hat{Q}(r,z) = \sum_{l=0}^{\infty} \int_0^{\infty} \varepsilon_l I_l(R) J_0(2\pi R r) \cos(2\pi l z/c) 2\pi R \, \mathrm{d}R, \quad (4.5.2.58)$$

where $\varepsilon_l = 1$ for $l = 0$ and 2 for $l > 0$, which can be calculated from the intensity distribution on a continuous fibre diffraction pattern. Using equations (4.5.2.7), (4.5.2.10), (4.5.2.17) and (4.5.2.58) shows that $\hat{Q}(r, z)$ is the cylindrical average of the Patterson function, $\hat{P}(r, \varphi, z)$, of one molecule, *i.e.*

$$\hat{Q}(r,z) = (1/2\pi) \int_0^{2\pi} \hat{P}(r,\varphi,z) \, \mathrm{d}\varphi. \quad (4.5.2.59)$$

The $\hat{}$ symbols on $\hat{P}(r, \varphi, z)$ and $\hat{Q}(r, z)$ indicate that these are Patterson functions of a single molecule, as distinct from the usual Patterson function of a crystal, which contains intermolecular interatomic vectors and is periodic with the same periodicity as the crystal. $\hat{P}(r, \varphi, z)$ is periodic only along z and is therefore, strictly, a Patterson function along z and an autocorrelation function along x and y (Millane, 1990*b*). The cylindrically averaged Patterson contains information on interatomic separations along the axial direction and in the lateral plane, but no information on orientations of the vectors in the lateral plane.

For a polycrystalline system; consider the function $Q(r, z)$ given by

$$Q(r,z) = \sum_l \sum_{h,k} R_{hk} I_l(R_{hk}) J_0(2\pi R_{hk} r) \cos(2\pi l z/c), \quad (4.5.2.60)$$

where the sums are over all the overlapped reflections $I_l(R_{hk})$ on the diffraction pattern, given by equation (4.5.2.24). It is easily shown that $Q(r, z)$ is related to the Patterson function $P(r, \varphi, z)$ by

$$Q(r,z) = (1/2\pi) \int_0^{2\pi} P(r,\varphi,z) \, \mathrm{d}\varphi, \quad (4.5.2.61)$$

where, in this case, $P(r, \varphi, z)$ is the usual Patterson function (expressed in cylindrical polar coordinates), *i.e.* it contains all intermolecular (both intra- and inter-unit cell) interatomic vectors and has the same translational symmetry as the unit cell. The cylindrically averaged Patterson function for polycrystalline fibres therefore contains the same information as it does for noncrystalline fibres (*i.e.* no angular information in the lateral plane), except that it also contains information on intermolecular separations.

Low resolution and cylindrical averaging, in addition to the usual difficulties with interpretation of Patterson functions, has resulted in the cylindrically averaged Patterson function not playing a major role in structure determination by fibre diffraction. However, information provided by the cylindrically averaged Patterson function has, in a number of instances, been a useful component in fibre diffraction analyses. A good review of the application of Patterson functions in fibre diffraction is given by Stubbs (1987). Removing data from the low-resolution part (or all) of the equator when calculating the cylindrically averaged Patterson function removes the strong vectors related to axially invariant (or cylindrically symmetric) parts of the map, and can aid interpretation (Namba *et al.*, 1980; Stubbs, 1987). It is also important when calculating cylindrically averaged Patterson functions to use data only at a resolution that is appropriate to the size and spacings of features one is looking for (Stubbs, 1987).

Cylindrically averaged Patterson functions were used in early applications of fibre diffraction analysis (Franklin & Gosling, 1953; Franklin & Klug, 1955). The intermolecular peaks that usually dominate in a cylindrically averaged Patterson function can help to define the locations of multiple molecules in the unit cell.

references