5.2. CRYSTAL-DENSITY MEASUREMENTS

be calculated in advance, and looked for first. The positions of calibration drops and of crystals in these centrifuge tubes can be measured with a hand-held ruler to a resolution of about 0.5 mm.

Particularly for crystals with high values of V_M (*i.e.*, loosely packed) or for crystals of large molecular weight proteins, the apparent crystal density may increase with time: the crystal continues to sink and there is no apparent equilibrium spot. This behaviour is seen in both organic solvent gradients and Ficoll gradients, and the reasons for it are unclear. It may be that, in organic solvent gradients, some of the solvent can dissolve into the crystal; or the crystal may condense from slow dessication. In Ficoll gradients, it may be that sucrose monomers or dimers are present, which diffuse into the crystal over time. A careful study of this behaviour (Bode & Schirmer, 1985) in Ficoll gradients suggested that useful density values can still be obtained for these crystals by fitting the apparent density to an exponential curve:

$$\rho_c(t) = a + b \exp(-\lambda t). \qquad (5.2.6.3)$$

In this expression, parameters a, b and λ must be derived from the fitted curve. The crystals were inserted into the gradient with flame-narrowed Pasteur pipettes. Each crystal was initially surrounded by a small amount of mother liquor, which rapidly diffused into the Ficoll solution. Time zero was assigned as the time when centrifugation first began. It was necessary to observe crystal positions within the first minute, and at two- to five-minute intervals thereafter, to obtain a reasonable time curve for the density function. The experimental goal in the Bode & Schirmer experiment was to obtain a good estimate for the density value at time zero, $\rho_c(0) = a + b$. This was realized in all six of the crystal forms that manifested time-dependent density drift in the study.

5.2.7. How to handle the solvent density

It is necessary to have an accurate estimate of the mean solvent density, ρ_s, in (5.2.4.9). The Ficoll gradient-tube method is particularly convenient for this reason: the gradient can be made without any significant solute other than Ficoll. Since the free-solvent compartment of the crystal is entirely water, $\rho_s = \rho_{bs} = \rho_{fs} = 1.0$ g ml^{-1}. Therefore, in Ficoll density gradients, the crystal density becomes ρ_o, as defined in (5.2.5.2), and the packing number n can be calculated from

$$n = \frac{VN_o}{M} \frac{(\rho_c - 1)}{(1 - \overline{v}_m)}. \qquad (5.2.7.1)$$

Another way to set $\rho_s = 1.0$ g ml^{-1} is to cross-link the crystals with glutaraldehyde (Quiocho & Richards, 1964; Cornick *et al.*, 1973; Matthews, 1985), making the crystals insoluble even in the absence of stabilizing solutes. Once cross-linked, crystals can be transferred to a water solution prior to the density measurement, thereby substituting water for its free solvent. Care must be taken with cross-linking, however. Overnight soaking in 2% glutaraldehyde solutions can substantially increase the crystal density, while destroying its crystalline order (Matthews, 1985). Even 0.5% glutaraldehyde concentrations may change the observed density of some crystals if the exposure is for many hours – which may be necessary to render the crystal completely insoluble. Therefore, the densities observed from cross-linked crystals should be regarded with caution.

If it is necessary to carry out density measurements in an organic solvent gradient, then it is necessary in general to measure the crystal density at more than one free solvent density, since the relative volume fractions of the crystal's components are not known *a priori*. However, if this is a well behaved protein crystal, by setting $\overline{v}_m = 0.74$ ml g^{-1}, $V_M = 2.4$ Å^3 Da^{-1} and $w = 0.25$ g bound water per g protein, one can guess the crystal's volume compartments to be:

$$\varphi_m = 0.51, \qquad \varphi_{fs} = 0.32, \qquad \varphi_{bs} = 0.17,$$

and the mean solvent density to use in (5.2.4.9) would be

$$\rho_s \simeq 0.35 + 0.65\rho_{fs}. \qquad (5.2.7.2)$$

This may give reasonably reliable derivations for n in (5.2.4.9), with just one crystal-density measurement. Over-reliance on parameter estimates, however, can lead to bogus results, and (5.2.7.2) should be used with caution.

References

5.1

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