

**MODELLING BIOLOGICAL MACROMOLECULES IN SOLUTION:  
THE GENERAL TRI-AXIAL ELLIPSOID**

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## CHAPTER 5

### Concluding Remarks

In this study an extensive review of all the possible shape functions available for modelling a biological macromolecule in solution in terms of an ellipsoid model with the restriction of two equal axes has been given, thus updating the classical reviews of Edsall (1953) and Tanford (1961). It was concluded that the most suitable shape parameter (particularly for axial ratios less than 20:1) was the R parameter which can be determined from the ratio of the sedimentation regression coefficient,  $k_s$  to the intrinsic viscosity,  $[\eta]$ . A word of warning should perhaps be given out here in that the  $k_s$  value found from fitting sedimentation coefficient versus concentration data either to the general equation (60) or to the approximate linear equation (58), is the value based on particle migration relative to the solvent, whereas the  $[\eta]$  values are normally measured to solution density (Tanford, 1955). The value of  $k_s$  must therefore be corrected to solution density, and this can be achieved simply by subtracting the value of the partial specific volume,  $\bar{v}$  (Rowe, 1977) since this latter can be equated to the reciprocal density of the solute, an assumption reasonably accurate for proteins and possibly for nucleic acids (Pearce et al, 1975). It is also now possible to estimate a value for  $k_s$  direct from a knowledge of the sedimentation coefficient, the molecular weight and  $\bar{v}$  (Appendix VI).

Despite the availability of the R function for determining the 'equivalent hydrodynamic ellipsoid of revolution' for a structure in solution to a reasonable precision (and also the  $\Pi$  function for prolate ellipsoids - Appendix III), it was clear from a perusal of the crystallographic dimensions given in Table 3 and a comparison of model dependent with model independent estimates for  $\bar{v}_s/\bar{v}$  in Table 2, that for many macromolecules the assumption of two equal axes on the ellipsoid model is a poor

approximation to the real structure in solution. This stimulated my attempts to develop the necessary theoretical and data analysis techniques so that the restriction of two equal axes could be dispensed with and the subsequent research has shown that the more general tri-axial ellipsoid can now, in principle at least, be successfully employed for modelling biological macromolecules in solution.

The first step was to derive an explicit expression for the viscosity increment  $\eta$  for a dilute suspension of general tri-axial ellipsoids in overwhelming Brownian motion, based on a model first given by Simha (1940) and improved by Saito (1951) for ellipsoids of revolution. Although the assumption of the particles rotating on average with the same local angular velocity of the fluid has only been rigorously proved so far for ellipsoids of revolution (Brenner, 1972a), it was assumed that this would be a very close approximation for tri-axial ellipsoids, particularly for low axial ratios ( $<3.0$ , i.e. the globular particle range). After the derivation of equation (88) a numerical procedure (involving complicated numerical matrix inversions), but based on a full statistical analysis of the angular motion was made available by Rallison (1978). It was explained in section 2.8. how the difference in the results predicted by equation (88) and Rallisons approach was negligible ( $<.01\%$ ) for the globular particle range mentioned above, and for some particles of higher asymmetry discrepancies of not more than 1% arose. Rallison has also given a numerical procedure for calculating the normal stress coefficients in terms of axial ratio; normal stress effects are however second order in the shear rate, thus in order to measure these coefficients it is necessary to use high shear rates. However, the assumption of overwhelming Brownian motion with respect to the shear rate ceases to be valid, and hence, unfortunately, the normal stress coefficients cannot be applied.

It was described how the problem of the line solution (i.e. how a given value for  $\nu$  does not uniquely fix a value for the axial ratios ( $a/b$ ,  $b/c$ )) could be dealt with by combining it graphically with translational frictional or rotational relaxation line solutions. I was able to give the R function for tri-axial ellipsoids and also many other tri-axial functions whose experimental determination did not require a knowledge of the swollen molecular volume in solution. After a careful consideration of all these line solutions with regard to giving suitable intersections, experimental measurability, insensitivity to experimental error and sensitivity to axial ratio, it was decided that the best approach for determining a unique solution would be to combine the R line solution graphically with the  $\delta_+$  and  $\delta_-$  line solutions, the latter to be determined from the two electric birefringence decay constants and the intrinsic viscosity.

Unfortunately, this still requires having to resolve the two decay constants or relaxation times from a two-term exponential birefringence decay for a homogeneous solution of asymmetric particles. This problem is notoriously difficult, as reported by Jost & O'Konski (1978) and O'Connor, Ware & Andre (1979), particularly for close relaxation times (as applies to globular proteins). The currently best available methods evident from these studies, viz. the non-linear least squares iterative method and possibly the Fourier Transform solution of the Laplace Integral equation method of Gardner et al (1959) were tested by exhaustive computer simulation to see how much error on the data points each could tolerate before failing to resolve the decay constants within reasonable limits. The Fourier method failed, even for data of machine accuracy (14 figures). The non-linear least squares method was found to be unstable due to the problem

of subsidiary minima located in the iteration procedure, even for data of two orders of magnitude more precise than that currently available from the best instrumentation.

The idea of applying the R function line solution as a constraint in the least squares analysis was then applied to the three simulated decays thus effectively reducing the problem from one of four independent variables (the two pre-exponential factors and the two decay constants) to one of three (two pre-exponential factors and one axial ratio,  $a/b$ ). The algorithm was then shown to be very successful for synthetic data corresponding to that available from current experimental precision. The problem of the concentration dependence of the decay constants (or equivalently the relaxation times) was then mentioned, and the necessity for extrapolating the values for the axial ratios determined at various concentrations to infinite dilution. The need for extrapolating axial ratios is somewhat conceptually difficult to envisage at first sight, since one would more naturally extrapolate the decay constants and then calculate the axial ratios from them. In the algorithm however, I have included the R value as the constraint - the R function line solution of possible values of ( $a/b$ ,  $b/c$ ) is the value applicable at infinite dilution, thus the decay constants in the algorithm are constrained to lie on the 'infinite dilution' curve; hence none of these values are the true values for the decay constants at each particular solute concentration. Any extrapolation procedure is therefore empirical, whether it be for the decay constants or for the values of the axial ratio  $a/b$ .

Investigation of the theoretical reasons for the concentration dependence of the decay constants provides however both an interesting and important field for further work. It has been described (section 1.7.1. &

Appendix IV) how several important results have arisen from consideration of the concentration dependence of the 'translational' (i.e. viscosity, sedimentation and diffusion) transport coefficients: for example, in producing the R function and making available an estimate of the swollen volume of a macromolecule in solution independent of any model assumed for the macromolecule. The analysis of the concentration dependence of the decay constants is however much more complicated: Rowe's (1977) theory for the translational coefficients was derived assuming only hydrodynamic (i.e. volume flux) concentration effects, viz. solutions of high ionic strength ( $>0.1M$ ) and such that electric charge effects (solute-solute interactions) were not present. The situation is apparently the reverse when we come to consider the decay constants: since we are dealing with a rotary macromolecular property, there should be no solute volume flux effects on average giving rise to the hydrodynamic concentration effects considered by Rowe. On the other hand, the current practical restriction of low ionic strengths for the electric birefringence probably results in some solute-solute electric charge effects; the double layer thickness of charge around a macromolecule in solution is inversely proportional to the square root of the ionic strength (Guoy, 1910, Chapman, 1913). For example, for a macromolecule suspended in a  $0.1M$  NaCl buffer the thickness of the double layer is  $\sim 1nm$ , whereas in a  $0.001M$  NaCl buffer, the thickness is as high as  $10nm$  (Shaw, 1970). There is therefore a greater likelihood of interference between the relaxations of individual macromolecules, the degree of which one would expect to increase with concentration.

In section 1.6. the techniques of light and low-angle x-ray scattering were discussed as an alternative to the hydrodynamic techniques, and stated how Martin (1964) had given formulae relating the radius of gyration to

axial ratio for ellipsoids of revolution. Mendelson and Hartt (1980) have applied results from low angle x-ray scattering in terms of a general triaxial ellipsoid model to the regulatory light chains of scallop myosin, and determined axial dimensions of  $16\text{nm} \times 4.16\text{nm} \times 1.26\text{nm}$ . We also mentioned however that the major disadvantage of the scattering approach was that it is necessary to assume the macromolecule to be of uniform electron density; this can lead to errors of the order of 3%, notwithstanding other errors in measurement as the simple calculation given in Appendix VII for a hypothetical spherical macromolecule with a cavity (based on the electron microscopy and x-ray diffraction results for apoferritin - Harrison, 1959) shows.

It is hoped however that the results of the research described here have now made it possible to determine the gross conformation of biological macromolecules in solution in terms of a general ellipsoid - independent of any assumptions concerning the internal homogeneity of the macromolecules - by combining the results of viscosity, sedimentation and electric (or acoustic) birefringence. There are some macromolecules however that apparently will never be modelled by an ellipsoid, even tri-axial. Bovine serum albumin (BSA) is a typical example; McCammon et al (1975) have attempted to account for a value for  $\beta$  below the theoretical minimum of  $2.112 \times 10^6$  (and above the theoretical maximum for  $R$  of 1.6 - see Table 2) by assuming its structure to be porous with respect to the solvent, but found the discrepancy was still far too large. With the availability of the tri-axial ellipsoid model and a comparison with model independent estimates for the swollen molecular volume, a classification of proteins into those which do and those which do not behave as hydrodynamic tri-axial ellipsoids in solution can now be made.

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