MODELLING BIOLOGICAL MACROMOLECULES IN SOLUTION:

THE GENERAL TRI-AXIAL ELLIPSOID

by

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A thesis submitted in partial fulfilment
of the regulations governing the Ph.D.
degree at the University of Leicester.

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June, 1980

To Anne

'. . . God, in the beginning form'd Matter in solid, massy, hard, impenetrable, moveable particles . . .'

Newton, Opticks, 1717, Query 31.

Abstract

Hydrodynamic shape functions for modelling biological macromolecules in solution in terms of an ellipsoid of revolution model are reviewed. Several new, hitherto unpublished shape functions whose experimental determination does not require knowledge of the swollen molecular volume in solution, are given. The limitations and inadequacies of this model are explained. The viscosity increment ν for a dilute dispersion of tri-axial ellipsoids of semi-axes $a > b > c$, under dominant Brownian motion is derived and an explicit expression in terms of a, b and c is given. Knowledge of the viscosity increment alone is not sufficient to uniquely determine the axial ratios (a/b, b/c) because (i) in order to determine ν, knowledge of the swollen volume in solution is required and (ii) a particular value for ν has a line solution of possible values for (a/b, b/c). (i) is dealt with by combining ν with the tri-axial frictional ratio function P to give the tri-axial R function and (ii) by combining graphically the R line solution with δ_+ and δ_- swelling independent line solutions. The experimental determination of δ_+ and δ_- requires the resolution of a 2-term electric birefringence decay into its component relaxation times; current data analysis techniques are however not satisfactory for resolving close relaxation times (as for globular proteins) with the current experimental precision. It is however shown by exhaustive computer simulation that using a new R-constrained non-linear least squares iterative analysis this is now possible. It is thus concluded that the general tri-axial ellipsoid as a model for the gross conformation of biological macromolecules in solution can now be employed.

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