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Building hydrodynamic bead–shell models for rigid bioparticles of arbitrary shape

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Abstract

The calculation of hydrodynamic and other solution properties of rigid macromolecules, using bead–shell model methodologies, requires the specification of the macromolecular shape in a format that can be interfaced with existing programs for hydrodynamic computations. Here, a procedure is presented for such a structural specification that is applicable to arbitrarily shaped particles. A computer program (MAKEPIXB), in which the user inserts the code needed to determine the structure, produces an structural file that is interpreted by another program (HYDROPIX) which is in charge of the computation of properties. As simple and yet illustrative examples we consider two cases: (1) dimeric structures composed of ellipsoidal subunits; and (2) toroidal structures, presenting simple equations that predict the properties of toroids with varying radial ratios.

Keywords: Rigid macromolecules; Hydrodynamic properties; Bead–shell model; Three-dimensional structure

1. Introduction

Hydrodynamic coefficients and other solution properties of macromolecules are valuable sources of information about macromolecular structure and conformation in solution [1]. For rigid macromolecules, the pioneering work of Bloomfield and coworkers [2,3] described how bead models made up of spherical elements could be used to represent the shape of the macromolecular particle. With an adequate hydrodynamic theory, implemented in computational tools, these models are useful for the prediction of solution properties. Over the years, the theoretical and computational aspects have been developed and improved [4–6]. After the publication of the public-domain computer program HYDRO [7], which performs the hydrodynamic calculation for an arbitrary bead model, the main remaining problem has been the development of procedures for model building. Carrasco and Garcia de la Torre [5] recently concluded that, among the different variations of bead modelling, the most advisable one is the one that after Bloomfield et al., is usually known as shell modelling [2,3]. A procedure has been developed for building shell models, and computing their properties, for rigid macromolecular structures, from

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```
c-----------------------------------------------------------------
C File: maxdims.for
c
C This is for a pair of identical, side-by-side ellipsoids
C with semiaxes 10, 10 and 15. The long axis is along z.
C The ellipsoid centers are on y.
C Spacing is 0.3125=20/32, so that along the shortest dimension of
C the box there are NX=32 pixels
       XMAX=20.
       YMAX=40.
       ZMAX=30.
       SPACING=0.625
c-----------------------------------------------------------------
```

```
C-----------------------------------------------------------------
C File: conditions.for
C The ellipsoids are centered at (10,10,15) and (10,30,15);
c so that way they are fully in the all-positive octant, within the box
         D12 = ((X-10.)/10)**2+((Y-10.)/10.)**2+((Z-15.)/15.)**2
         D22 = ((X-10.)/10)**2+((Y-30.)/10.)**2+((Z-15.)/15.)**2
         CONDITION = D12.LE.1.OR.D22.LE.1
C-----------------------------------------------------------------
```

Fig. 1. User-supplied INCLUDE files maxdim.for and conditions.for corresponding to the side-by-side dimer of ellipsoidal monomers, to be used in the compilation of program MAKEPIXB.

atomic co-ordinate files with the Protein Data Bank format [8,9]. Other sources of information on the structure of large macromolecules and macromolecular complexes are electron microscopy techniques, which specify the observed structure in some special formats. In a preceding publication, the construction of bead–shell models from electron microscopy images was described [10].

In the present work, I address the problem of building a bead–shell model for a particle of arbitrary shape in a general way, which does not rely on the specification of the shape by some specific file. The rationale is that the shape of a particle can be ultimately described by a mathematical condition, which states whether or not a point in space belongs to the particle. For instance, for a sphere of radius r, with its centre placed at point (x_c, y_c, z_c) in space the condition that a general point (x, y, z) must satisfy if it belongs to the particle is that $[(x-x_c)/r]^2+[(y-y_c)/r]^2+[(z-z_c)/r]^2<1$. With some complexity, a condition that a point belongs to the particle could be formulated for arbitrary shapes. The computing of solution properties has two main, consecutive phases: model building and hydrodynamic computation. A useful approach could be to separate these phases, making a separate tool for model building based on the mathematical conditions for belonging. In such a tool, the conditions themselves could be a well differentiated part of the computer code, supplied for the user for the structure being considered, which would be assembled with other parts of the code that would form the core of the model building program.

In this work, a computational implementation of this idea is presented. We provide the core of the source code of a computer program (MAKEPIXB) which just requires a few additional lines of code written by the user, specifying the considered structure. When compiled and executed, MAKEPIXB produces a computer file that contains the macromolecular structure in a portable and extremely compact format. This file is the input of another program (HYDROPIX, a variant of HYDRO) which does the shell model hydrodynamic calculations. We describe both internal and prac-

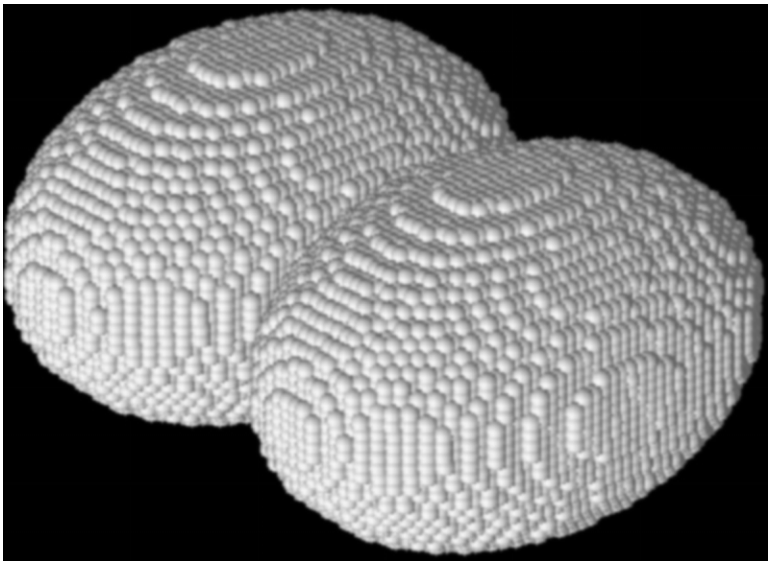

Fig. 2. RASWIN visualisation of the pixbit structure produced by MAKEPIXB for the to the side-by-side dimer. Pixels are viewed as overlapping spheres.

tical aspects of these computational utilities and provide two examples of their utilisation in some problems of biophysical interest.

2. Methods

As introduced above, the calculation of the solution properties is made in two stages, and one computing tool has been devised for each of them. We first describe the MAKEPIXB program, which encodes the structure of the particle in a file with a special format, *pixbit*, that we have designed in this work. Then, we describe how to use the HYDROPIX program to carry out the calculation of the solution properties.

2.1. MAKEPIXB*: construction of the pixbit file*

The *pixbit* file is constructed by a computer program, MAKEPIXB, written in FORTRAN 77 in which the user has to include a few lines of code that specify the three-dimensional size and shape of the particle.

In the first step to build this file, one imagines the particle with a position and such orientation that it is fully included in the $(+,+,+)$ octant of a Cartesian system of co-ordinates, so that the x, y and z co-ordinates of any point in the particle are all positive. Then, one has to figure out three values x_{max}, y_{max} and z_{max}, such that the x, y and z co-ordinates of any point in the particle do not exceed these maximum values. Thus, the particle is enclosed in a box whose diagonally opposite corners are placed at $(0,0,0)$ and (x_{max}, y_{max} and z_{max}). The sides of the box along the three axes are divided in segments of length b, so that the number of segments along each axis are $N_x = x_{max}/b$, $N_y = y_{max}/b$, and $N_z = z_{max}/b$. Thus, the box becomes a grid of cubelets of side b, hereafter called *pixels*. (strictly speaking, *pixels* are the elements of a two-dimensional image, while the proper name for a volume element is *voxel*; anyhow, we shall employ the former denomination because it may be more familiar to readers.) The grid has N_x rows, N_y columns, and N_z slices, and the number of pixels is $N_{pix} = N_x N_y N_z$. In a FORTRAN file with fixed name, maxdims.for, the user provides a few lines specifying the values of x_{max}, y_{max} and z_{max}. In the second stage in model building, one has to find a mathematical relation-

```
34                          Mode PIXBIT
Pair of ellipsoids          Title
twoellipspxb                filename for output files
twoellips.pxb               PIXBIT filename
5                           Number of SIGMAs
0.8                         SIGMAmin
1.6                         SIGMAmax
293.                        Temperature, Kelvin
28400.                      Molecular weigth
0.010                       Solvent viscosity
0.720                       Specific volume of macromolecule
1.01                        Solution density
41                          Values of H
2.E+07                      Hmax (cm^-1)
20                          Intervals for distrib. of distances
0                           Number of Monte Carlo trials for covolume
-1 END OF FILE
```

```
                          SUMMARY OF DATA AND RESULTS

                        This file:  twoellipspxb.res
                             Case:  Pair of ellipsoids
                             Mode:  34
                  Structural file:  twoellips.pxb

        Data/results from pixbit :
                          Spacing :  0.625 A
      Nslices ; Nrows ; Ncolumns :  48 64 32
            Number of (+) pixels :  51792
  Approx. volume from PIXBIT file:  1.26E+04 A^3

                Molecular weight:  28400. Da
                     Temperature:  293.0 K
               Solvent viscosity:  0.010 poise
          Partial specific volume:  0.720 cm3/g
                  Solvent density:  1.010 g/cm3
                  Bouyancy factor:  0.273
           Radius of PHM elements:  0.6 A
Translational diffusion coefficient:  1.322E-06 cm2/s
    Stokes (translational) radius:  1.624E-07 cm
                Radius of gyration:  1.391E-07 cm
      Volume (from filling model):  1.376E-20 cm3
 Rotational diffusion coefficient:  3.554E+07 s-1
              Relaxation time (1):  5.537E-09 s
              Relaxation time (2):  5.178E-09 s
              Relaxation time (3):  4.970E-09 s
              Relaxation time (4):  4.069E-09 s
              Relaxation time (5):  4.063E-09 s
Harm. mean relax.(correlation) time:  4.687E-09 s
             Intrinsic viscosity:  9.645E-01 cm3/g
       Sedimentation coefficient:  4.204E+00 svedberg


                Longest distance :  4.217E-07 cm


      Distribution of distances

      Intervals between RMIN and RMAX, centered at R;
      Values of p(R)


    RMIN(cm)    RMAX(cm)     R(cm)    p(R)(cm^(-1))
    0.000E+00   2.109E-08   3.163E-08   8.392E+04
    2.109E-08   4.217E-08   5.272E-08   7.317E+05
    4.217E-08   6.326E-08   7.381E-08   1.721E+06
    6.326E-08   8.435E-08   9.489E-08   2.783E+06
    ..........................................

    Calculation of scattering form factor, P vs h

                      h           P(h)
                     ......................
                    7.50E+06       7.48E-01
                    8.00E+06       7.09E-01
                    8.50E+06       6.70E-01
                     ......................
```

Fig. 3. Input data and output file of program HYDROPIX for the side-by-side dimer of ellipsoidal monomers.

```
c File 'maxdims.for'
c-------------------------------------------------------------------
C This is for a toroid with outer and inner radii ro and ri
c Numerical values:
      ro=100
      ri=30
c Combinations
       rm=(ro+ri)/2.
       rt=(ro-ri)/2
c Maximum dimensions
       xmax=2*ro
       ymax=2*ro
       zmax=2*rt
C Spacing is so that along the longest dimension of
C the box there are NX=192 pixels
       spacing=xmax/float(192)
c-------------------------------------------------------------------



C File 'conditions.for'
C-------------------------------------------------------------------
c Conditions for a toroid
c
       condition = .FALSE.
       IF(z.LE.2*rt) THEN
          delta=SQRT(rt**2-(z-rt)**2)
          rad=SQRT((x-ro)**2+(y-ro)**2)
          IF(rm-delta.LT.rad.and.rad.LT.rm+delta) THEN
            condition = .TRUE.
          ENDIF
       ENDIF
C-------------------------------------------------------------------
```

Fig. 4. User-supplied INCLUDE files maxdim.for and conditions.for for a toroid with inner and outer radii of 100 and 30 Å, respectively.

ship that discerns whether or not a point with co-ordinates (x, y and z) belongs to the particle. A FORTRAN LOGICAL variable will be programmed to specify this condition. The corresponding lines of code will be in another separate, user-supplied FORTRAN file with fixed name, conditions.for. Program MAKEPIXB contains FORTRAN INCLUDE statements that will automatically insert the user-supplied code. Examples of these files, for the applications illustrated in this paper, will be presented below.

The main output of MAKEPIXB is the *pixbit* file whose name is specified by the user (we suggest the use of a .pxb extension). This file will encode the three-dimensional shape of the structure in such a way that the HYDRO software will be able to decode it, transforming the information into a list of the Cartesian co-ordinates that the HYDRO routines need in order to construct a hydrodynamic model.

As an utility to help the user in the visualisation of structure that MAKEPIXB has coded, the program also produces an ASCII file with the Cartesian co-ordinates of the pixels belonging to the particle. The format of this file emulates that of Protein Data Bank (PDB) files, so that it can be visualised with usual PDB viewers, like RASMOL [13].

2.2. Internals of the pixbit file

The following information is not needed for the practical use of MAKEPIXB in the generation of .pxb files to be used by the HYDRO software. However, it is pertinent to describe how our *pixbit* is constructed. The program scans the N_{pix} pixels in the cubic grid, assigning to them a binary digit

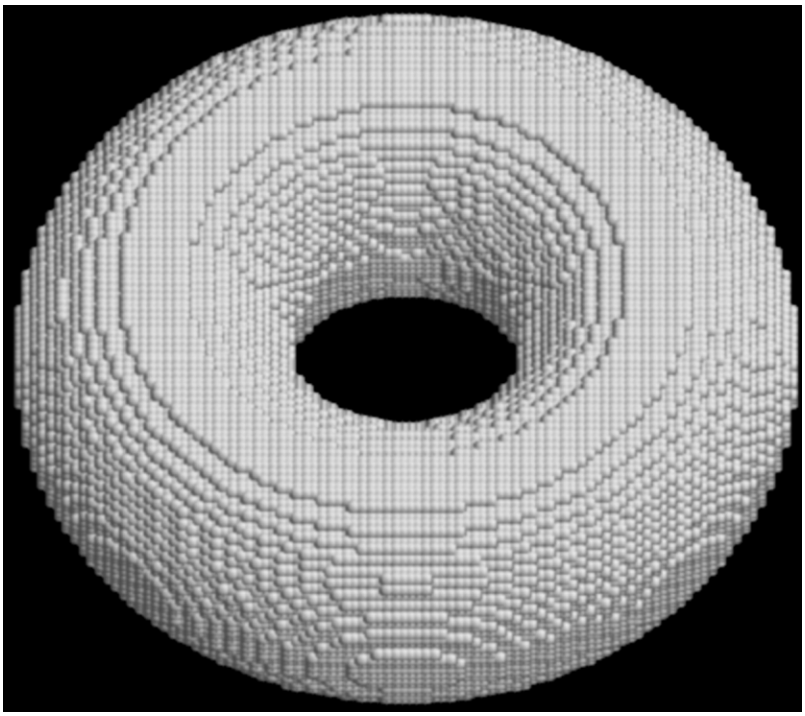

Fig. 5. Raswin visualisation of the pixbit structure produced by MAKEPIXB for the toroid specified by the data in Fig. 4.

(a *bit*), being one when the pixel belongs to the particle, and zero elsewhere. The axis which is scanned first is *x*, then *y* and finally, *z*. In order words, the scanning order of the pixel indices is (1,1,1), (2,1,1),... (N_x,1,1), (1,2,1), (2,2,1),... (N_x,2,1),..., (N_x, N_y, 1), (1,1,2),..., etc.,...,(N_x N_y N_z). Every eight consecutive *bits* (values, 0s or 1s) are grouped in an eight-bit *byte* that is coded in FORTRAN as an INTEGER*1 variable, INT, that takes the value

INT4 = BIT(1)*2**7 + BIT(2)*2**6 + ... + BIT(8)

where BIT (1), BIT (2),... BIT (8) are the eight consecutive bits.

The .pxb file contains first the FORTRAN REAL*4 values of N_x N_y N_z and *b*. Then, a list of the INT4 values follows and is written in FORTRAN binary format. The number of bytes in the resulting .pxb file will be $1+N_x\ N_y\ N_z\ /8$. We note that the *pixbit* format is extremely compact: a fairly compact macromolecule with a molecular weight of approximately 10 kDa gives a *pixbit* file occupying, typically, less than 50 kb.

2.3. HYDROPIX: *reading the pixbit file and calculation of properties*

The programs that read the .pxb file, firstly get N_x N_y N_z and *b* from the header. Then, the values of INT4 are read consecutively; each of them is decoded to get the pixel value, 0 or 1. For bits valued 1, the Cartesian co-ordinates are computed from the pixel indices deduced from the writing order mentioned above. This finally, results in a list of the Cartesian co-ordinates of all the pixels belonging to the particle.

For the hydrodynamic calculation, a material (non-point like) representation of the pixels is required. Each pixel is replaced by a sphere of radius *a*, whose precise size is unimportant; it just must be of the same order as the spacing *b*. Choosing $a=b$ each sphere overlaps with all its neighbours and so there are no voids in the model.

We have designed a new program, named HYDROPIX (a new member of the HYDRO suite of programs), that reads the .pxb file in the way described above, and defines the hydrodynamic

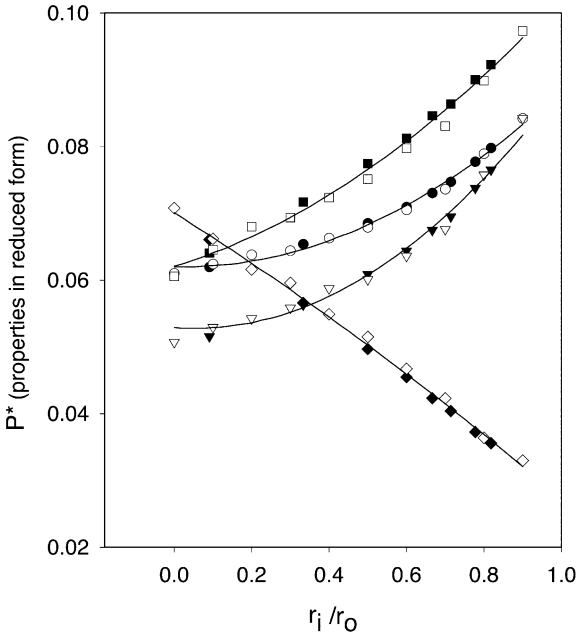

Fig. 6. Values of the reduced properties (see text for definitions) vs. the inner-to-outer ratio of radii. Circles: translational diffusion. Triangles: parallel rotational diffusion. Squares: perpendicular rotational diffusion. Diamonds: intrinsic viscosity. Filled symbols: Allison [21]. Open symbols: this work.

model of particle as the set of overlapping spheres, one for each pixel. This is considered as the *primary hydrodynamic model*, similarly to how the juxtaposition of overlapping spheres, each representing an (hydrated) atom is considered as the primary hydrodynamic model in the atomic-level modelling of proteins or nucleic acids in HYDROPRO [8] and HYDRONMR [9]. The procedure followed in HYDROPIX for the calculation of the hydrodynamic properties comprises the same steps as in those programs: the primary model is replaced by a filling model made of beads with radius σ, which is in turn, emptied to obtain a shell model on which the HYDRO calculation is performed, with results for varying σ extrapolated to the shell model limit of $\sigma=0$. This is the same procedure as the one used in the shell-model calculations for the atomic structures of proteins by HYDROPRO [8], or for electron microscopy images by HYDROMIC [10]. Optionally, as in other modes of HYDRO, the calculation of scattering form factor (angular dependence of scattered intensity), distribution of intramolecular distances, and of molecular covolume can be carried out [11,12]. We recall that the calculation of these properties (particularly the covolume) may be time-consuming.

3. Examples

3.1. Dimers of ellipsoidal monomers

As a simple example of this procedure, consider the following case. The biological macromolecule being modelled is a dimeric protein consisting of two subunits that are approximately ellipsoidal. The analysis of the solution properties of the isolated subunits has yielded an equivalent revolution ellipsoid that is prolate, with semi-axes of, for instance, 15, 10 and 10 Å, and an axial ratio $p=1.50$. The purpose of the calculation is to ascertain whether in the dimer subunits are in arranged side-by-side or end-to-end. Let us consider in detail the side-by-side arrangement. We imagine that the ellipsoids have their long axes along z, and they are in touch along the y direction, as shown in Fig. 1. The maximum dimensions of such a particle would be $x_{max}=20$ Å (twice the short semi-axis), $y_{max}=40$ Å (four times the short semi-axis), and $z_{max}=30$ Å (twice the long semi-axis). The spacing is taken as $b=0.625$ Å. This value could be smaller or larger, resulting in more or less pixels, respectively, in the grid. An important condition is that b must be an integer divisor of x_{max}, y_{max} and z_{max}. In summary, at this stage we have determined the values of x_{max}, y_{max}, z_{max} and b, which will be supplied in file maxdims.for presented in Fig. 1.

A point with co-ordinates (x, y, z) belongs to an ellipsoid centred at (x_c, y_c, z_c), with semi-axes a, a and b, along directions (x, y and z), if and only if: $[(x-x_c)/a]^2+[(y-y_c)/a]^2+[(z-z_c)/b]^2<1$. The points at which the ellipsoids are centred at (10, 10, 15) and (10, 30, 15), in Ångstroms. A point belongs to the particle if it belongs to one of the two ellipsoids. Thus, the condition is easily programmed in the file conditions.for, as illustrated in Fig. 1. This file, along with the file maxdims.for will be present at the time of the FORTRAN compilation of MAKEPIXB, that will produce an executable, that when execut-

ed, will originate a *pixbit* file (named, for instance, twoellips.pxb). As mentioned above, a PDB-like format is also produced that, when visualised with a molecular viewer (RASMOL) produces the image in Fig. 2.

Fig. 3a displays the input file used for the HYDROPIX calculation. In addition to some elementary physical data concerning the solvent and solute, it contains the name of the *pixbit* file to be processed, and the range of values of σ to be used in the shell-model extrapolation. In this example, the calculations of scattering form factor and distribution of distances are carried out, and that of covolume is discarded. Fig. 3b presents the output file resulting from this calculation.

This example also illustrates how MAKEPIXB and HYDROPIX can be employed to analyse solution properties of oligomeric structures, when the constituting subunits are not spherical. For instance, neurophysin is a dimer whose subunits, which have been separately characterised, are prolate with an axial ratio of approximately four [14–16]. The dimer-to-monomer ratios of translational diffusion and intrinsic viscosity are $D_t(2)/D_t(1)=0.92$ and $[\eta](2)/[\eta](1)=0.84$, and the question is how the subunits are arranged in the dimer? Almost 20 years ago, López Martínez and García de la Torre [17] presented a compilation of calculated results for oligomer/monomer ratios of properties of oligomeric subunit structures, with prolate ellipsoidal monomers of varying axial ratio. The calculations employed modelling and computational methods that are now somewhat obsolete. The present, more advanced methodology allows more precise estimations for oligomeric proteins. The axial ratio of the monomers can be first determined on the basis of ellipsoidal model [16,18], and then MAKEPIXB and HYDROPIX can be employed to search possible structures of the oligomer. For the example of neurophysin, several arrangements of the two ellipsoids can be tried with our programs, and it is found that while structures in which the subunits are joined end-to-end give values of the ratios very different from experimental data, a side-by-side arrangement predicts rather well the experimental results.

3.2. Toroidal particles

Particles having a toroidal, doughnut-shaped appearance are sometimes found in molecular biology. For instance, under the action of some multivalent cations, including some polyamines, DNA in low ionic strength solutions collapses to a peculiar, doughnut-like shape [19,20]. Contrary to the related geometrical shape of the cylinder, the hydrodynamics of toroids has been scarcely studied. After some earlier papers (see ref. [21], and references cited therein), Allison [22] has revisited this problem using the hydrodynamic methodology of boundary element representation, which is related to, but formally different from bead modelling. In the present work, we considered that the toroid provides an interesting and useful example of the HYDROPIX calculation.

The geometry of a toroid can be easily specified in the HYDROPIX method as follows. Suppose a system of Cartesian axes (x', y', z') centred at the centre of the toroid, z' being the axis of revolution symmetry. The only two dimensions that specify the size and shape of the toroid are the inner and outer radii, r_i and r_o. The value of r_i may range from zero (no central hole) to near r_o (for a very thin toroid). The cross-sectional radius of the toroidal tube is $r_t=(r_o-r_i)/2$ and the mean radius is $r_m=(r_o+r_i)/2$. The values of z' are confined in the range $(-r_t,\ +r_t)$, and those x' and y' are in $(-r_o,\ +r_o)$. The intersection of the toroid with horizontal planes, with constant z' are rings with inner and outer radii $r_m-(r_t^2-z'^2)^{1/2}$ and $r_m+(r_t^2-z'^2)^{1/2}$. In order to fit the toroid in the positive octant, the axis are translated (without rotation) to point with co-ordinates (r_o, r_o, r_t). Thus the conditions satisfied by points in the ellipsoid (in the final system of co-ordinates) are, for co-ordinate z:

$$0<z<2r_t \tag{1}$$

and for x and y:

$$r_m-(r_t^2-z'^2)^{1/2}<(x'+y')^{1/2} <r_m+(r_t^2-z'^2)^{1/2} \tag{2}$$

or, more specifically,

$$r_m-\left(r_t^2-(z-r_t)^2\right)^{1/2}<\left((x-r_o)^2+(y-r_o)^2\right)^{1/2}<r_m+\left(r_t^2-(z-r_t)^2\right)^{1/2}. \quad (3)$$

Fig. 4 shows an example of the INCLUDE files needed to specify a toroidal geometry, and Fig. 5 displays the resulting model. Using MAKEPIXB, including these files, the solution properties have been calculated for several geometries, employing HYDROPIX. The main results are: the translational diffusion coefficient, D_t, the intrinsic viscosity, $[\eta]$, and the rotational diffusion coefficients for rotation around the main, symmetry axis, $D_r^{(\mathrm{axis})}$, and that for rotation around a perpendicular axis in the equatorial plane, $D_r^{(\mathrm{perp})}$. The results can be presented as universal, reduced quantities that do not depend on the individual dimensions of the particle, but rather depend on ratios of dimensions. These are: for translational diffusion, $\eta_o D_t r_o/(k_B T)$, where η_0 is the viscosity of the solvent, k_B is the Boltzmann constant and T is the absolute (Kelvin) temperature; for rotational diffusion, $\eta_o D_r r_o^3/(k_B T)$, and for the intrinsic viscosity, $0.01[\eta]M/(N_A r_o^3)$, where M is the molecular weight of the particle, and the numerical factor 0.01 has been introduced so that the values of this quantity are of the same order of magnitude as that of the translational and rotational ones. As the independent variable, it is convenient to choose the ratio of the inner to the outer radius, $x=r_i/r_o$ which goes from $x=0$ for the toroid with a vanishing hole to $x=1$ for a very thin toroid. The results are displayed in Fig. 6, where we include also the numerical values reported by Allison [22]. It is clear that our bead–shell calculation and the boundary–element calculation of this author are in good agreement.

The form in which the hydrodynamic properties are made dimensionless is such that they vary slightly between the two limits of x, and this makes it possible to find interpolating expressions. We have found second-degree polynomials that describe well this slight dependence. The coefficients were found by linear least-squares fitting, in which we included both our results and those from Allison [22]. The interpolating polynomials, valid for $x=0$–0.9 (beyond 0.9 the toroid is too thin), are:

$$\eta_o D_t r_o/(k_B T)=0.0620-0.00143x+0.0278x^2 \quad (4)$$

$$\eta_o D_r^{(\mathrm{axis})} r_o^3/(k_B T)=0.0529-0.00444x+0.0404x^2 \quad (5)$$

$$\eta_o D_r^{(\mathrm{perp})} r_o^3/(k_B T)=0.0621+0.0176x+0.0227x^2 \quad (6)$$

$$0.01[\eta]M/(N_A r_o^3)=0.0701-0.0365x-0.00629x^2. \quad (7)$$

For a toroid with given values of r_i and r_0, in a solvent of viscosity η_0 at the absolute temperature T, the diffusion coefficients can be readily calculated from Eqs. (4)–(7). Because of its symmetry of revolution, the toroid has three rotational relaxation times given by $\tau_a=1/(6D_r^{(\mathrm{perp})})$, $\tau_b=1/(5D_r^{(\mathrm{perp})}+D_r^{(\mathrm{axis})})$, and $\tau_c=1/(2D_r^{(\mathrm{perp})}+4D_r^{(\mathrm{axis})})$. If the property that is being used to monitor rotational diffusion presents also axial symmetry, only the first time, τ_a, will be observed. Finally, the intrinsic viscosity can be evaluated from Eq. (7), if the molecular mass of the particle is known. It is hoped that Eqs. (4)–(7) will be helpful to analyse experimental data for possible toroidal particles

4. Computer programs

MAKEPIXB and HYDROPIX will be freely available, along with our other computer programs, from our web site http://leonardo.fcu.um.es/macromol.

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References

[1] K.E. van Holde, W. Johnson, P. Ho, Principles of Physical Biochemistry, Prentice Hall, Upper Saddle River, NJ, USA, 1998.

[2] V.A. Bloomfield, W.O. Dalton, K.E. van Holde, Frictional coefficients of multisubunit structures. I. Theory, Biopolymers 5 (1967) 135–148.
[3] V.A. Bloomfield, D.P. Filson, Shell model calculations of translational and rotational frictional coefficients, J. Polym. Sci. C 25 (1968) 73–83.
[4] J. Garcia de la Torre, V.A. Bloomfleld, Hydrodynamic properties of complex, rigid, biological macromolecules. Theory and applications, Quart. Rev. Biophys. 14 (1981) 81–139.
[5] B. Carrasco, J. Garcia de la Torre, Hydrodynamic properties of rigid particles. Comparison of different modelling and computational procedures, Biophys. J. 76 (1999) 3044–3057.
[6] O. Byron, Hydrodynamic bead modelling of biological macromolecules, Methods Enzymol. 321 (2000) 278–304.
[7] J. Garcia de la Torre, S. Navarro, M.C. Lopez Martínez, F.G. Diaz, J.J. Lopez Cascales, HYDRO: a computer software for the prediction of hydrodynamic properties of macromolecules, Biophys. J. 67 (1994) 530–531.
[8] J. Garcia de la Torre, M.L. Huertas, B. Carrasco, Calculation of hydrodynamic properties of globular proteins from their atomic-level structures, Biophys. J. 78 (2000) 719–730.
[9] J. Garcia de la Torre, M.L. Huertas, B. Carrasco, HYDRONMR: prediction of NMR relaxation of globular proteins from atomic-level structures and hydrodynamic calculations, J. Magn. Reson. 147 (2000) 138–146.
[10] J. García de la Torre, O. Llorca, J.L. Carrascosa, J.M. Valpuesta, HYDROMIC: prediction of hydrodynamic properties of rigid macromolecular structures obtained from electron microscopy images, Eur. Biophys. J. 30 (2001) 457–462.
[11] J. García de la Torre, B. Carrasco, S.E. Harding, solpro: theory and computer program for the prediction of solution properties of rigid macromolecules and bioparticles, Eur. Biophys. J. 25 (1997) 361–372.
[12] J. García de la Torre, S.E. Harding, B. Carrasco, Calculation of NMR relaxation, covolume and scattering-related properties of bead models using the SOLPRO computer program, Eur. Biophys. J. 28 (1999) 119–132.
[13] R. Sayle, A. Bissell, A program for fast realistic rendering of molecular structures with shadows. Proceedings of the Tenth Eurographics UK '92 Conference, University of Edinburgh, Scotland, 1992.
[14] P. Nicolas, M. Batelier, M. Rholam, P. Cohen, Bovine neurophysin dimerization and neurohypophyseal hormone binding, Biochemistry 19 (1980) 3565–3573.
[15] M. Rholam, P. Nicholas, Side-by-side dimerization of neurophysin: sedimentation velocity, viscometry, and fluorescence polarization, Biochemistry 20 (1981) 5837–5843.
[16] S.E. Harding, A. Rowe, Modelling biological macromolecules in solution. 1. The ellipsoid of revolution, Int. J. Biol. Macromol. 4 (1982) 160–162.
[17] M.C. López Martínez, J. García de la Torre, Transport properties of rigid, symmetrical oligomeric structures composed of prolate ellipsoidal subunits, Biophys. Chem. 18 (1983) 269–279.
[18] S.E. Harding, H. Colfen, Inversion formulae for ellipsoid of revolution macromolecular shape functions, Anal. Biochem. 228 (1995) 131–142.
[19] L.C. Goluse, J.A. Schellman, Compact form of DNA induced by spermidine, Nature 259 (1976) 333–337.
[20] V.A. Bloomfield, D.M. Crothers, I. Tinoco, Nucleic Acids. Structures, Properties and Functions, Chapter 14, University Science Books, Sausalito, California, 2000.
[21] S.L. Goren, M.E. O'Neill, Stokes flow past toroidal particles, J. Fluid Mech. 101 (1980) 97–110.
[22] S.A. Allison, Low Reynolds number transport properties of axisymmetric particles employing stick and slip boundary conditions, Macromolecules 32 (1999) 5304–5312.