What is the hydrodynamic radius (R_H)?

Chapter: Dynamic Light Scattering
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The measured data in a dynamic light scattering (DLS) experiment is the correlation curve. Embodied within the correlation curve is all of the information regarding the diffusion of particles within the sample being measured. The diffusion coefficient (D) is calculated by fitting the correlation curve to an exponential function, with D being proportional to the lifetime of the exponential decay (see Figure 1). The hydrodynamic radius (R_H) is then calculated from the diffusion coefficient using the Stokes-Einstein equation, where k is the Boltzmann constant, T is the temperature, η is the medium viscosity, and $f = 6\pi\eta R_H$ is the frictional coefficient for a hard sphere in a viscous medium.

$$D = \frac{kT}{f} = \frac{kT}{6\pi\eta R_H}$$

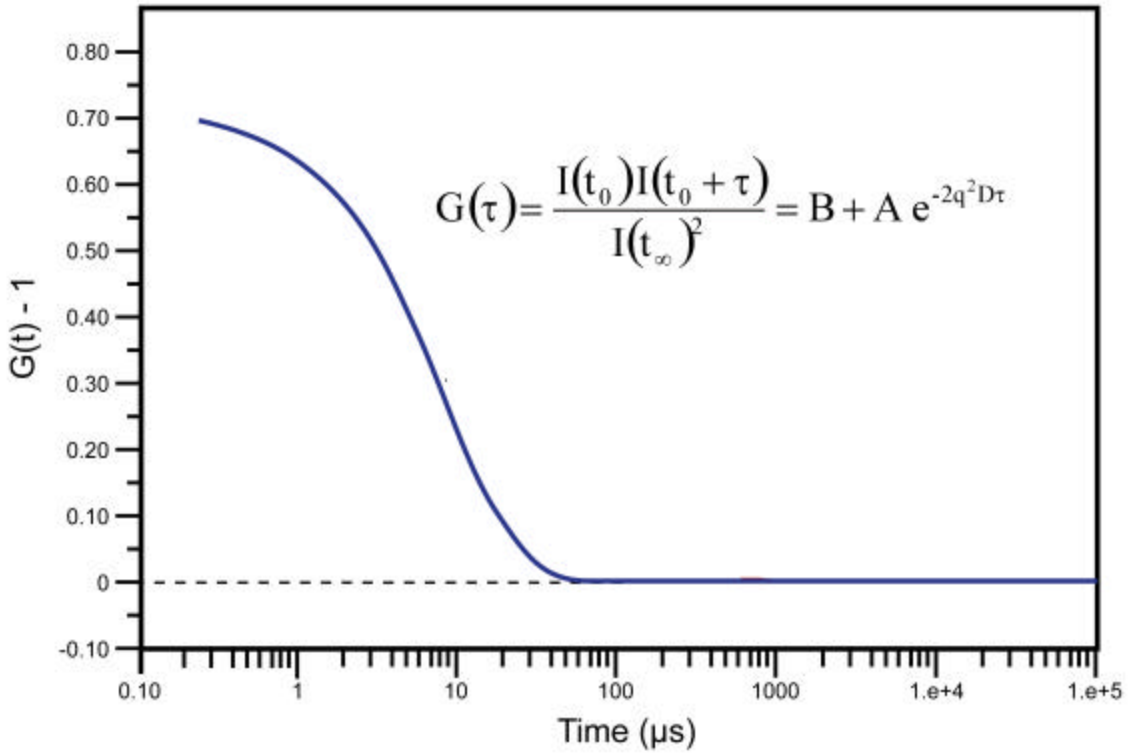

Figure 1: Representative correlation function measured during a dynamic light scattering experiment.

By definition then, the DLS measured radius is the radius of a hypothetical hard sphere that diffuses with the same speed as the particle under examination. This definition is somewhat problematic with regard to visualization however, since hypothetical hard spheres are non-existent. In practice, macromolecules in solution are non-spherical, dynamic (tumbling), and solvated. As such, the radius calculated from the diffusional properties of the particle is indicative of the *apparent* size of the dynamic hydrated/solvated particle. Hence the terminology, 'hydrodynamic' radius.

A comparison of the hydrodynamic radius to other types of radii can be shown using lysozyme as an example (see Figure 2). From the crystallographic structure, lysozyme can be described as a 26 x 45 Å ellipsoid with an axial ratio of 1.73. The molecular weight of the protein is 14.7 kDa, with a partial specific volume or inverse density of 0.73 mL/g. The radius of gyration (R_g) is defined by the expression given below, where m_i is the mass of the i^{th} atom in the particle and r_i is the distance from the center of mass to the i^{th} particle. R_M is the equivalent radius of a sphere with the same mass and particle specific volume as lysozyme, and R_R is the radius established by rotating the protein about the geometric center.

$$R_g^2 = \frac{\sum m_i r_i^2}{\sum m_i}$$

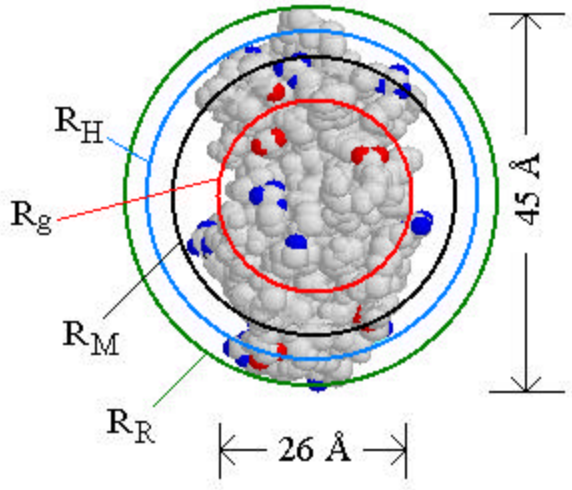

Figure 2: Comparison of hydrodynamic radius (R_H) to other radii for lysozyme.

It is instructive to note here, that R_M is the hypothetical radius for a hard sphere with the same mass and density as lysozyme. One might expect then, to see a closer correlation of R_M with R_H. Remember however, that R_H is the *hydro-dynamic* radius, which includes both solvent (hydro) and shape (dynamic) effects.

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