			Centr	ifugatio	n		
1. Princ	iples of	Centrif	ugation	/ theory a	nd key eq	uations	
		$F_{\rm s}$ =	<i>= m</i> ω ²	$r = \frac{M}{N}$	$\omega^2 r$		
	where	$\omega = a$	ngular v	elocity (ra	dians / sec)	
		$\mathbf{r} = \mathbf{r}\mathbf{a}$	adius of	particle fro	om axis of	rotation	
	note:	ω (1/sec)) = rpm	$x (2\pi rad)$	/ rev) x (1	min / 60 se	ec)
RCF (Re	el. Centi	rifugal Fo	orce) = =	$\frac{Fc}{Fg} = 1.119 x 10$	$\frac{\mathrm{m}\omega^{2}\mathrm{r}}{\mathrm{ma}} = \frac{(2}{2})^{-5} (\mathrm{rpm})^{2} \mathrm{r}$	2π rpm/60) ² 980 cm/ se	$\frac{2}{c^2}$ x r
			for r	= 9.0 cm			
	rpm	1000	5000	10,000	20,000	40,000	
	RCF	100	2500	10,000	40,000	160,000	

Substance	⊽ (mL/g)			
Proteins	0.73	(0.70-0.75)		
Polysaccharides	0.61	(0.59-0.65)		
RNA	0.53	(0.47-0.55)		
DNA	0.58	(0.55-0.59)		













Analytical Ultracentrifuge: The sorts of questions for which answers are sought

- (1) Is the sample homogeneous? Is it pure?
- (2) If there is a single component, what is the molecular weight?
- (3) If more than one type present, can the molecular weight distribution of the sample be obtained?
- (4) Can an estimate be obtained of the size and shape of the particles? Are the molecules compact and spherical (globular) or long and thin (rod-like)?
- (5) Can the macromolecules be distinguished on the basis of density?
- (6) Can interactions between solute molecules be detected? Aggregation between molecules changes molecular weight, changes in molecular weight as a function of the concentrations of the components can illuminate the type of reaction (e.g., reversible or nonreversible?), the stoichiometry, and the strength of binding.
- (7) Can changes in conformation or shape of the particles be measured?

Molecular Weight Determination

Light scattering / Centrifugation / Osmometry / X-ray diffraction

Electrophoresis and chromatographic methods are popular for rapid estimation of molecular weights of proteins and nucleic acids. However, such methods, though rapid and sensitive, have no rigorous theoretical base; they are empirical techniques that require calibration and assumptions that may be invalid.

The analytical ultracentrifuge enables the direct measurement of molecular weights of solutes in the native state and as they exist in solution, without calibrations or assumptions concerning shape. The method is applicable to molecules with molecular weights ranging from several hundreds (sucrose) up to many millions (virus particles).

Sedimentation equilibrium methods require only small sample sizes (20-120 μL) and low concentrations (0.01-1 g/L).

Conformational Changes

X-ray diffraction and NMR techniques are currently the only techniques available that are capable of providing structural details at atomic resolution.

Nevertheless, the overall size and shape of a macromolecule or complex in solution can be obtained through measurement of the rate of movement of the particles through the solution. Sedimentation velocity experiments in the analytical ultracentrifuge provide *sedimentation and diffusion coefficients* that contain information concerning the size and shape of macromolecules and the interactions between them. Sedimentation coefficients are particularly useful for monitoring *changes* in conformation in proteins.









































Figure 16. Sedimentation equilibrium distribution of two different solutes. Data were simulated for two species: (o) $M_r = 40,000$; (Δ) $M_r = 80,000$. The angular velocity was 15,000 rpm, and a partial specific volume of 0.73 was assigned to both species. The distribution of total solute concentration in the cell is also shown (\bullet).



Sedimentation Equilibrium
$$\int_{c_0}^{c} \frac{1}{C} dC = \frac{M \, \omega^2 (1 - \overline{\nu} \rho)}{RT} \int_{r_0}^{r_b} r \, dr$$
After Integration: $C = C_0 \exp^{\frac{M \omega^2 (1 - \overline{\nu} \rho)}{RT} (r^2 - r_0^2)} + Baseline$ The equilibrium gradient is dependent on rotor speed, temperature, an on the molecular weight and buoyancy of the solute. This equation can be fitted by nonlinear least squares.

