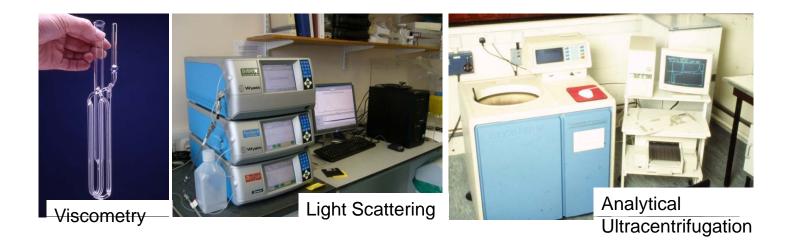
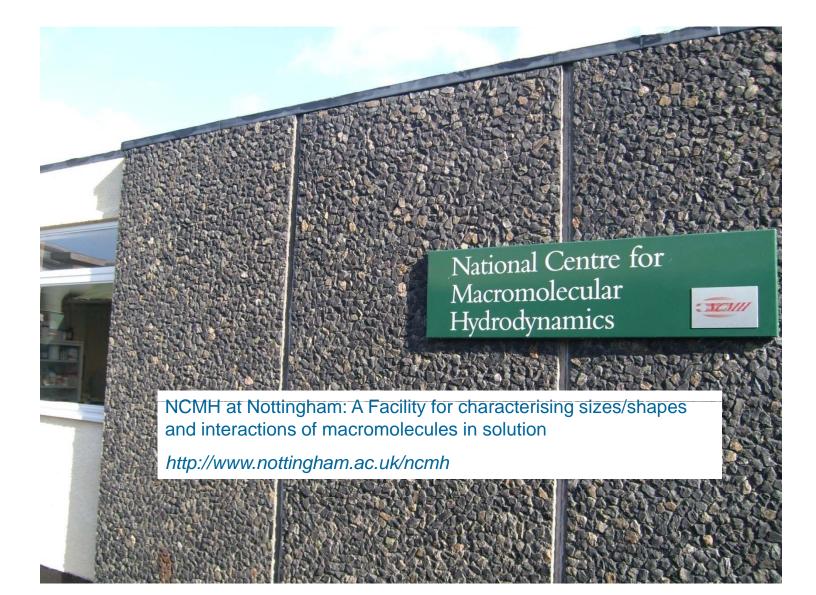
Sizes, shapes and interactions of molecules in solution



Steve Harding, NCMH University of Nottingham



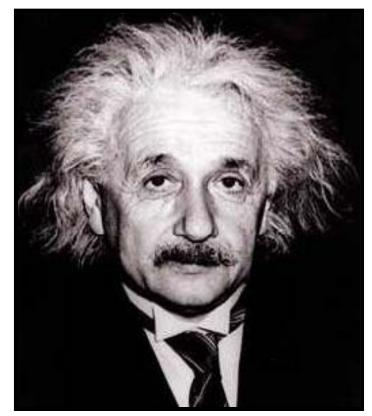
Datum/Zeit	Veranstaltungsort	Thema
Mo, 08.02.2010	Hörsaal Institut für Glaschemie	Albert Einstein and the Viscosity of
10.00-11.30	Fraunhoferstrasse 6	Macromolecules
Mo, 08.02.2010	Hörsaal Haus 1,IAAC,	Light Scattering and SEC-MALLs
12.15-13.45	August-Bebel-Str. 2	
Di, 09.02.2010	Institut für Materialwissenschaft und	Dynamic Light Scattering
12.15-13.45	Werkstofftechnologie, HS 124	
	Löbdergraben 32	
Mi, 10.02.2010	Hörsaal 3	Analytical Ultracentrifugation I
16.15-17.45	Carl-Zeiss-Str. 3	
Do, 11.02.2010	Döbereiner Hörsaal	Analytical Ultracentrifugation II:
14.15-15.45		Interactions





Lecture 1:

Albert Einstein and the Viscosity of Macromolecules





Annalen der Physik Band 19, 1906, 289-306:

3. Eine neue Bestimmung der Moleküldimensionen; von A. Einstein.

Die ältesten Bestimmungen der wahren Größe der Moleküle hat die kinetische Theorie der Gase ermöglicht, während die an Flüssigkeiten beobachteten physikalischen Phänomene bis jetzt zur Bestimmung der Molekülgrößen nicht gedient haben. Es liegt dies ohne Zweifel an den bisher unüberwindlichen Schwierigkeiten, welche der Entwickelung einer ins einzelne gehenden molekularkinetischen Theorie der Flüssigkeiten ent-

Annalen der Physik Band 34, 1911, 591-592:

11. Berichtigung zu meiner Arbeit: ,,Eine neue Bestimmung der Moleküldimensionen^(*1); von A. Einstein.

Vor einigen Wochen teilte mir Hr. Bacelin, der auf Veranlassung von Hrn. Perrin eine Experimentaluntersuchung über die Viskosität von Suspensionen ausführte, brieflich mit, daß der Viskositätskoeffizient von Suspensionen nach seinen Resultaten erheblich größer sei, als der in § 2 meiner Arbeit entwickelten Formel entspricht. Ich ersuchte deshalb Hrn. Hopf, meine Rechnungen nachzuprüfen, und er fand in der Tat einen Rechenfehler, der das Resultat erheblich fälscht. Diesen Fehler will ich im folgenden berichtigen.

Auf p. 296 der genannten Abhandlung stehen Ausdrücke für die Spannungskomponenten X_{u} und X_{z} , die durch einen

Viscometry

Intrinsic Viscosity of Macromolecular Solutions

Viscosity of biomolecules

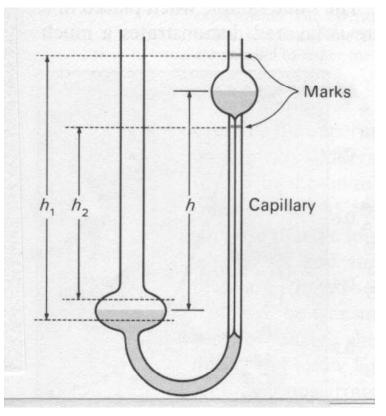
Why viscometry?

Simple, straightforward technique for assaying

- Solution conformation of biomolecules & volume/ solvent association
- 2. Molecular weight of biomolecules
- 3. Flexibility ""

Types of Viscometer:

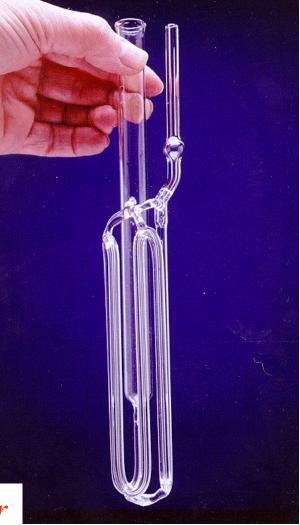
- 1. "U-tube" (Ostwald or Ubbelohde)
- 2. "Cone & Plate" (Couette)



Ostwald Viscometer

Types of Viscometer:

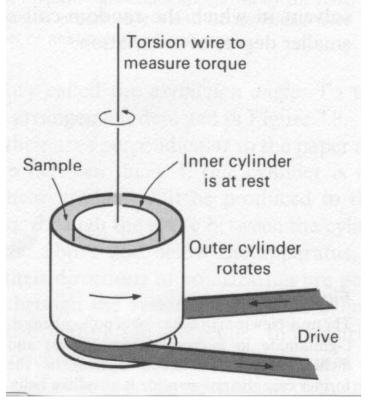
- 1. "U-tube" (Ostwald or Ubbelohde)
- 2. "Cone & Plate" (Couette)



Extended Ostwald Viscometer

Types of Viscometer:

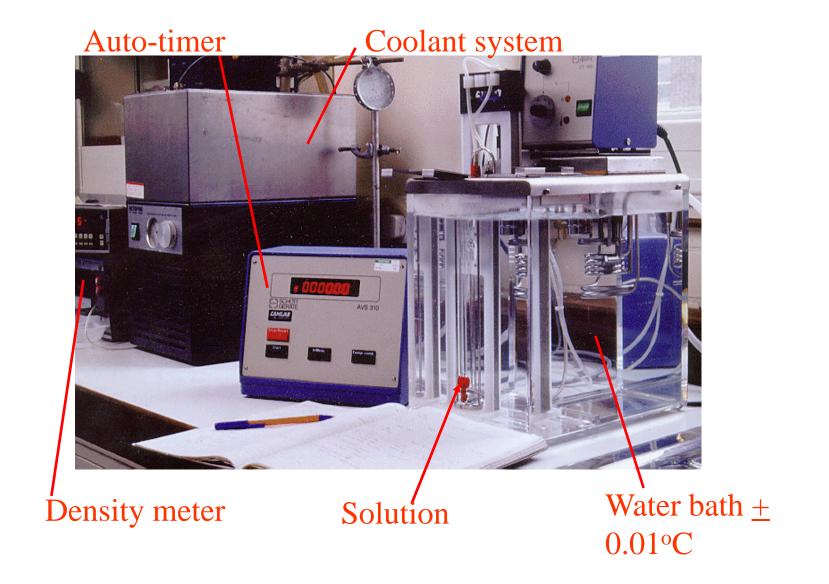
- 1. "U-tube" (Ostwald or Ubbelohde)
- 2. "Cone & Plate" (Couette)

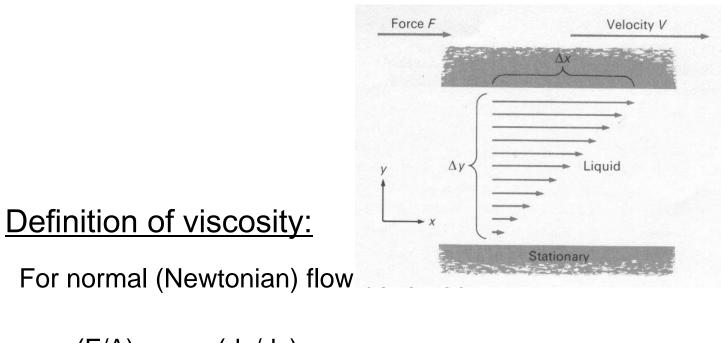


Couette-type Viscometer

Anton-Paar AMVn Rolling Ball viscometer







$$\tau = (F/A) = \eta . (dv/dy)$$

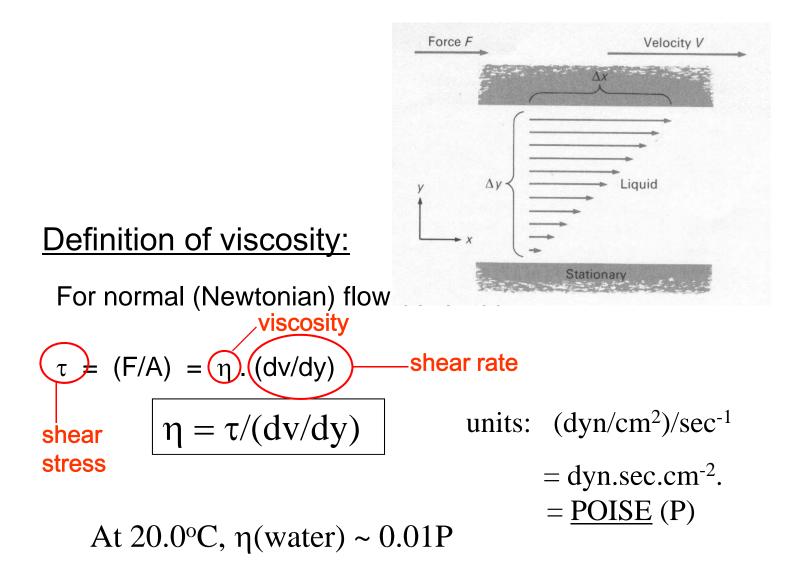
$$\eta = \tau/(dv/dy)$$

units: $(dyn/cm^2)/sec^{-1}$

$$= dyn.sec.cm^{-2}.$$

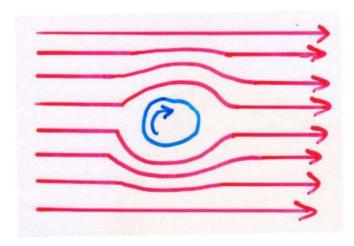
$$= \underline{POISE} (P)$$

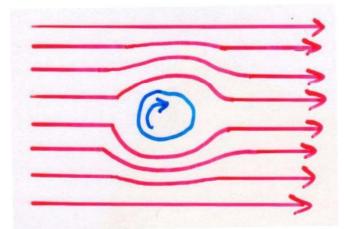
At 20.0°C, η (water) ~ 0.01P



Viscosity of biomolecular solutions:

A dissolved macromolecule will <u>INCREASE</u> the viscosity of a solution because it disrupts the <u>streamlines</u> of the flow:





We define the <u>relative viscosity</u> η_r as the ratio of the viscosity of the <u>solution</u> containing the macromolecule, η , to that of the pure solvent in the absence of macromolecule, η_o :

 $\eta_r = \eta/\eta_o$ <u>no units</u>

For a U-tube viscometer, $\eta_r = (t/t_o)$. (ρ/ρ_o)

Reduced viscosity

The <u>relative viscosity</u> depends (at a given temp.) on the concentration of macromolecule, the shape of the macromolecule & the volume it occupies.

If we are going to use viscosity to infer on the shape and volume of the macromolecule we need to eliminate the concentration contribution.

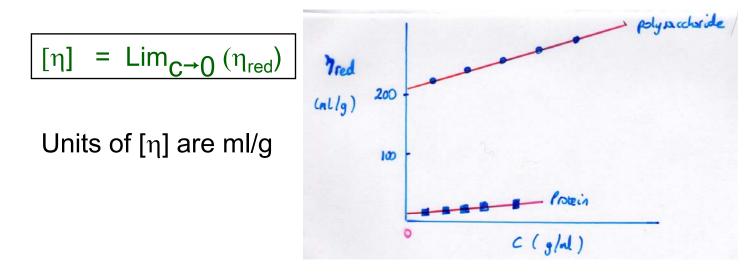
The first step is to define the reduced viscosity

 η_{red} = $(\eta_r - 1)/c$

If c is in g/ml, units of η_{red} are ml/g

<u>The Intrinsic Viscosity [η]</u>

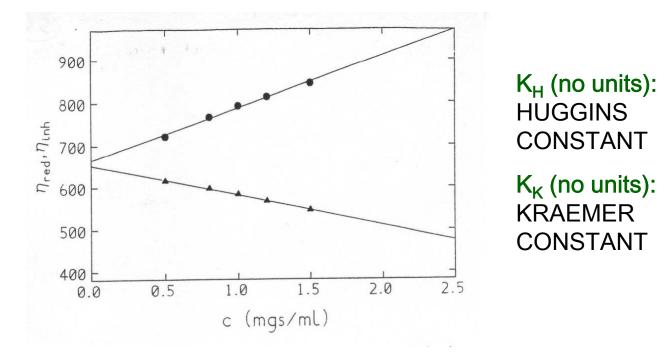
The next step is to eliminate <u>non-ideality</u> effects deriving from exclusion volume, backflow and charge effects. By analogy with osmotic pressure, we measure η_{red} at a series of concentrations and extrapolate to zero concentration:



Form of the Concentration Extrapolation

2 main forms

Huggins equation: $\eta_{red} = [\eta] (1 + K_H[\eta]c)$ Kraemer equation: $(\ln \eta_r)/c = [\eta] (1 - K_K[\eta]c)$



A variant of the Huggins equation is:

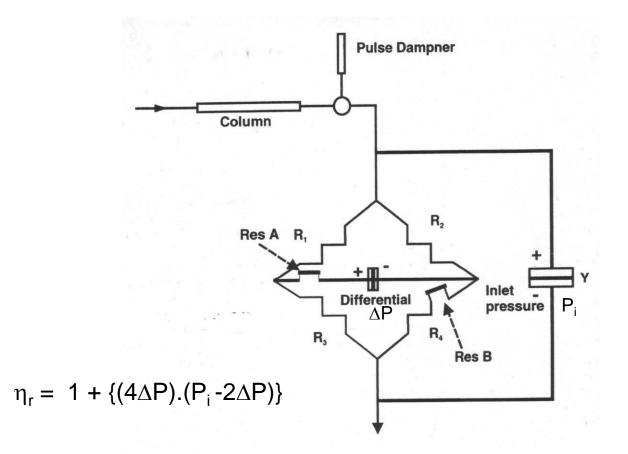
 $η_{red} = [η] (1 + k_η.c) k_η: ml/g$

and another important relation is the <u>SOLOMON-</u> <u>CIUTA</u> relation, essentially a combination of the Huggins and Kraemer lines:

[η] ~ (1/c) . [2 (η_r – 1) – 2 ln(η_r)] ^{1/2}

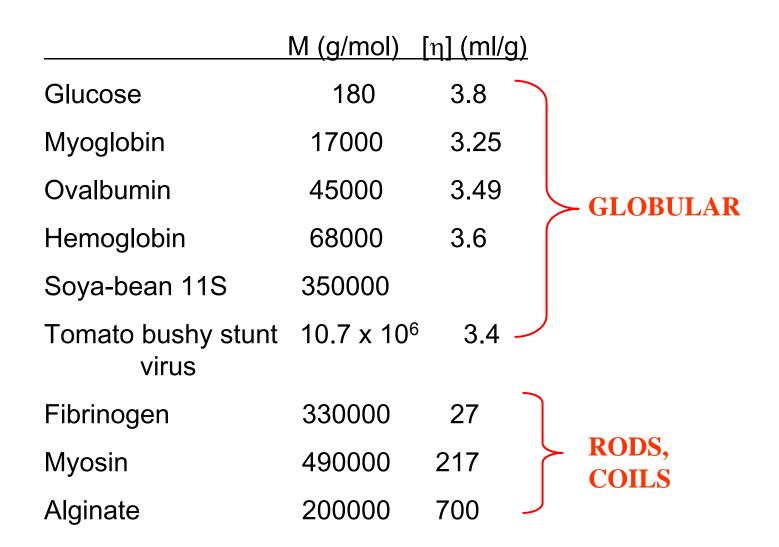
The Solomon-Ciuta equation permits the approximate evaluation of $[\eta]$ without a concentration extrapolation.

Differential Pressure Viscometer:



Intrinsic Viscosity and its relation to macromolecular properties

[η] so found depends on the shape, flexibility and degree of (timeaveraged) water-binding, and for <u>non-</u> <u>spherical</u> particles the molecular weight:



Intrinsic Viscosity and Protein Shape and Hydration

 $[\eta] = v \cdot v_s \tag{1}$

v: Simha-Saito function (function of shape & flexibility)

- v_s : swollen specific volume, ml/g (function of H₂O interaction)
- v: Einstein value of 2.5 for rigid spheres >2.5 for other shapes
- v_s: volume of "hydrated" or "swollen" macromolecule per unit anhydrous mass
 - = $v + (\delta/\rho_0) = v \cdot S_w$
- δ : "hydration" (g H₂O/g protein)
- v: partial specific volume (anhydrous volume per unit anhydrous mass)

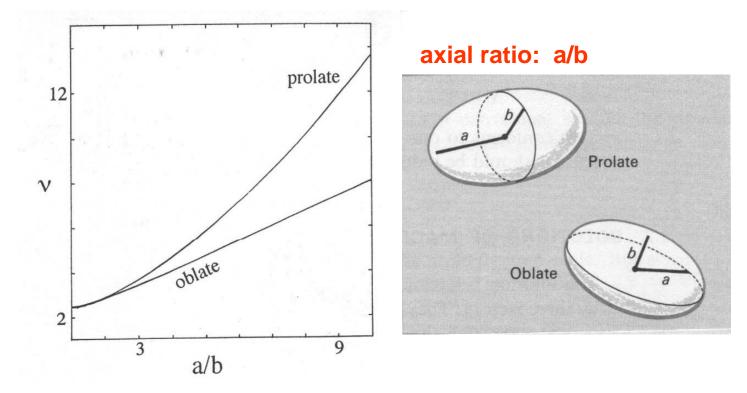
So, 3 forms of Eqn. (1):

 $\begin{bmatrix} [\eta] = v \cdot v_{s} \\ or \\ [\eta] = v \cdot \{\overline{v} + (\delta/\rho_{o})\} \\ or \\ [\eta] = v \cdot \overline{v} \cdot \overline{S}_{w} \end{bmatrix}$

For proteins, $\overline{v} \sim 0.73 \text{ml/g}$, $v_s \sim 1 \text{ml/g}$, $S_w \sim 1.4$, {For polysacchs, $\overline{v} \sim 0.6 \text{ml/g}$, $v_s >>1 \text{ml/g}$, $S_w >>1$ }

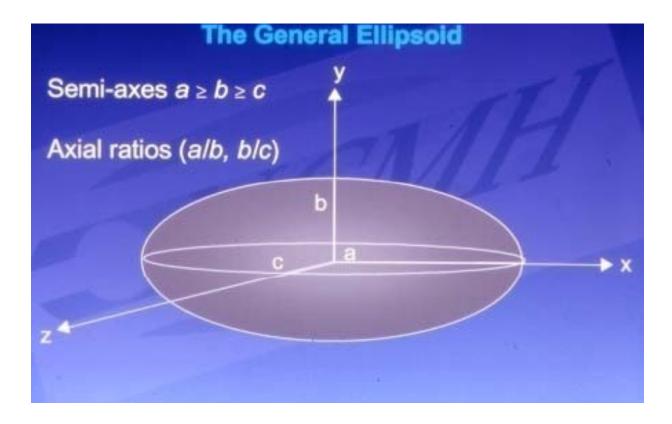
Getting a shape from the viscosity v parameter

SIMPLE ELLIPSOIDS OF REVOLUTION:

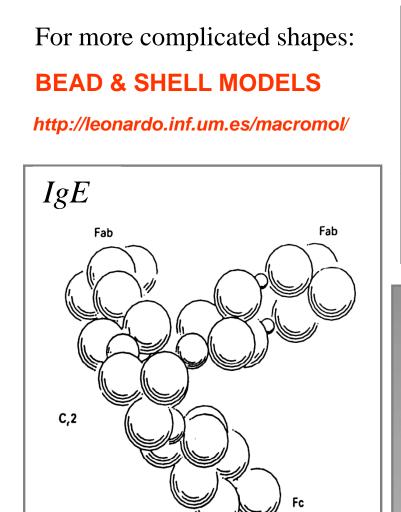


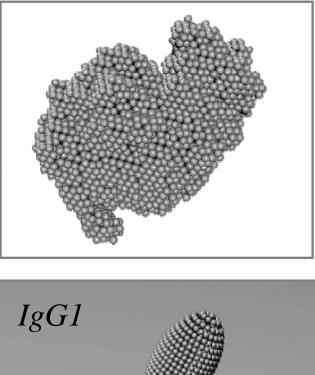
Computer program ELLIPS1 downloadable from www.nottingham.ac.uk/ncmh

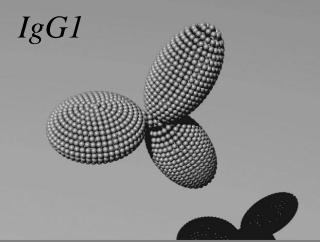
Getting a shape from the viscosity v parameter



Computer program ELLIPS2 downloadable from www.nottingham.ac.uk/ncmh

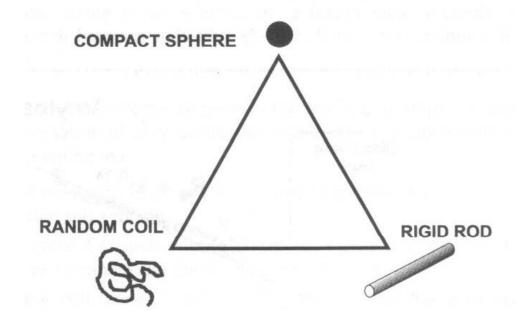






GENERAL CONFORMATIONS

The three extremes of macromolecular conformation (<u>COMPACT SPHERE</u>, RIGID ROD, <u>RANDOM COIL</u>) are conveniently represented at the corners of a triangle, known as the <u>HAUG TRIANGLE</u>:



Each extreme has its own characteristic dependence of $[\eta]$ on M.

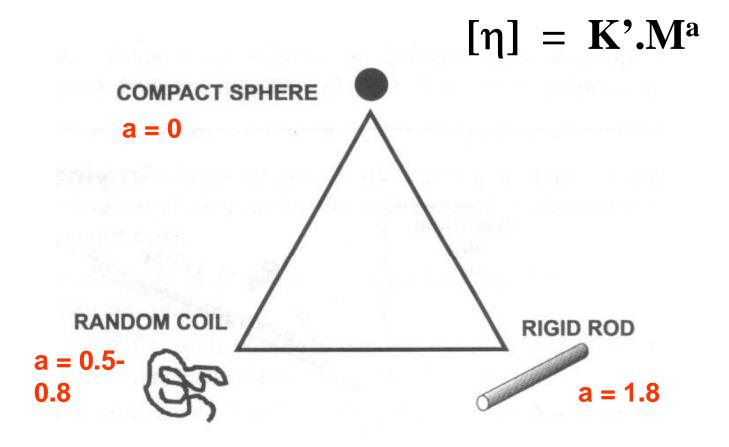
Mark-Houwink-Kuhn-Sakurada equation

 $[\eta] = K'.M^a$

Analagous power law relations exist for sedimentation, diffusion and R_g (classical light scattering)

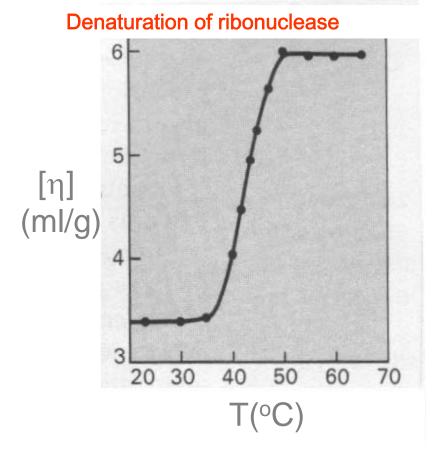
 $s_{20,w}^{o} = K''.M^{b};$ $D_{20,w}^{o} = K'''.M^{-\varepsilon};$ $R_{g} = K'''.M^{c};$

By determining a (or b, ε or c) for a <u>homologous</u> series of a biomolecule, we can pinpoint the conformation type

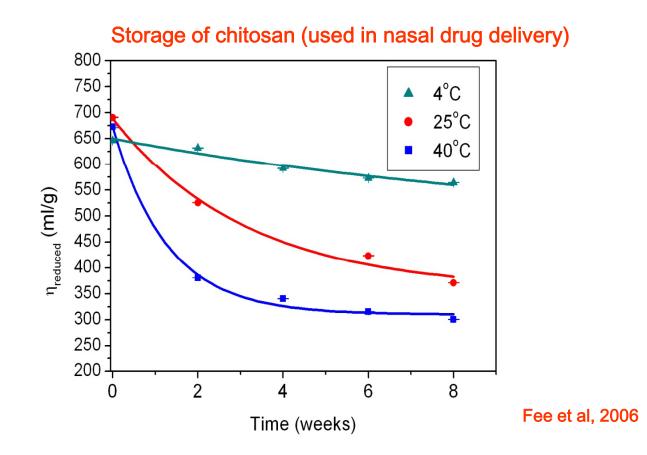


Globular proteins, a~0.0, polysaccharide, a ~ 0.5 – 1.3

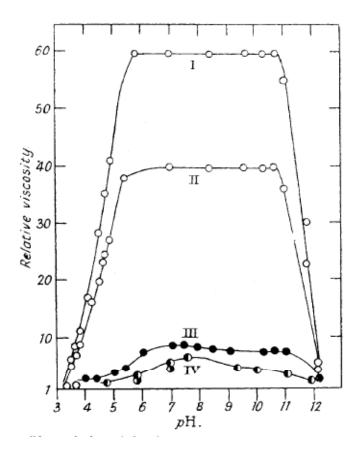
The intrinsic viscosity is ideal for monitoring conformation change:



The intrinsic viscosity is also ideal for monitoring stability:



Demonstration of H-bonding in DNA



Creeth, J.M., Gulland J.M. & Jordan, D.O. (1947) J. Chem. Soc. 1141-1145

The variation of the viscosity of solutions of various specimens of deoxypentose nucleic acid.

Tetrasodium salt of deoxypentose nucleic acid of calf thymus, O:

I (applied pressure 3000 dynes/cm.²), II (applied pres-sure 7000 dynes/cm.²).

Tetrasodium salt of deoxypentose nucleic acid after alkal-ine treatment, III, •; after acid treatment, IV, •. Tetrasodium salt of deoxypentose nucleic acid of calf thymus supplied by Professor Caspersson, IV, •.

J.Michael Creeth, 1924-2010



Follow up reference sources:

Serydyuk, I.N., Zaccai, N.R. and Zaccai, J. (2006) *Methods in Molecular Biophysics*, Cambridge, Chapter D9

Harding, S.E. (1997) "The intrinsic viscosity of biological macromolecules. Progress in measurement, interpretation and application to structure in dilute solution" *Prog. Biophys. Mol. Biol* 68, 207-262.
http://www.nottingham.ac.uk/ncmh/harding_pdfs/Paper192.pdf

Tombs, M.P. and Harding, S.E. (1997) *An Introduction to Polysaccharide Biotechnology*, Taylor & Francis, ISBN 0-78074-405169