

INTERNATIONAL ATOMIC ENERGY AGENCY  
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SECOND SUMMER COLLEGE IN BIOPHYSICS

30 July - 7 September 1984

- I. DNA conformational statistics, hydrodynamics, gel electrophoresis and DNA bending.
- II. Physical mechanisms of control of prokaryotic gene expression, with application to the lac operon.

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These are preliminary lecture notes, intended only for distribution to participants.  
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Summer College in Biophysics Lectures, D.M. Crothers

- I. DNA conformational statistics, hydrodynamics, gel electrophoresis and DNA bending (3 lectures).
- (a) Polymer statistics and distribution functions.
    - the random flights chain and its analytical solution.
    - stiff chains: the Kuhn segment and the persistence length.
  - (b) Monte Carlo methods.
    - computer generated chains.
    - results for DNA.
  - (c) Ring closure and circular DNA molecules.
    - definitions of twist, writhe and linking number.
    - ligation of DNA into circles and the relationship to DNA stiffness: analytical and Monte Carlo results.
    - distribution functions for twist, writhe and linking number.
  - (d) Hydrodynamic properties.
    - the Oseen tensor and its calculation.
    - rotational diffusion constant for DNA molecules.
    - dimensions from  $\tau_R$ ,  $\tau_T$ : DNA, chromatin fibers.
  - (e) Theories of DNA gel electrophoresis.
    - reptation models.
    - calculated results.
  - (f) Systematically bent DNA molecules.
    - biological origin.
    - detection: gel electrophoresis, hydrodynamics.
    - mapping the bending locus by gel electrophoresis.
    - computer generated chains.
    - methods for quantitative estimations of bending: ring closure, hydrodynamics.
    - influence of DNA-binding drugs.
    - structural models for bending.
- II. Physical mechanisms of control of prokaryotic gene expression, with application to the lac operon (2 lectures).
- (a) Protein-DNA interaction equilibria.
    - methods: filter binding, spectroscopy, gel electrophoresis, footprinting.
    - allosteric effectors.
    - ionic strength effects.
  - (b) Protein-DNA search kinetics.
    - diffusion-limited reactions.
    - sliding.
    - direct transfer.
    - assembly mechanisms.
  - (c) Protein-induced DNA bending.
    - CAP, Eco RI

- (d) Polymerase-promoter complexes.
  - basic model for intermediates in transcription initiation.
  - abortive initiation.
  - physical binding studies.
  - lag kinetics.
  - separation of initiation intermediates by gel electrophoresis.
  - influence of DNA-binding drugs.

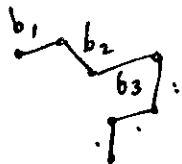
References and notes on the quantitative aspects  
of lectures for the Summer College in Biophysics  
D.M. Crothers

# 1. Polymer statistics and distribution functions

References: (a) elementary treatment - Eisenberg & Crothers, Physical Chemistry with Application to the Life Sciences, Benjamin/Cummings (1979), p 686 ff. (b) Other texts: Tanford, Physical Chemistry of Macromolecules, John Wiley & Sons (1961), chapt 3; Bloomfield, Cotter & Throck, Physical Chemistry of ~~Macromolecules~~ Nucleic Acids, Harper & Row (1974) p 153 ff.

## The random flights problem

represent the chain by vectors corresponding to segments:



simplest case: assume complete flexibility at each segment junction.

Question: how do polymer dimensions

depend on polymer contour length ( $L$ )?

$$L = \sum b_i$$

For example, end-to-end vector  $\vec{L}$

$$\vec{L} = \sum \vec{b}_i$$

$$L^2 = \vec{L} \cdot \vec{L} = \left( \sum \vec{b}_i \right) \cdot \left( \sum \vec{b}_j \right)$$

$$\langle L^2 \rangle = \sum_i \sum_j b_i b_j \langle \cos \theta_{ij} \rangle$$

(average over all configurations)

Exercise: Show that if the joints are completely flexible,

$$\langle L^2 \rangle = N b^2$$

(assuming all  $b_i$  the same length;  $N$  = number of segments) [Hint:  $\langle \cos \theta_{ij} \rangle_{i \neq j} = 0$  when joints are flexible]

### Distribution functions

- a) radial distribution:  $W(L, N) dL =$   
probability that the two ends are a distance between  $L$  and  $L+dL$  apart. Averages are readily calculated if  $W$  is known; for example

$$\langle L^2 \rangle = \int_0^{\infty} L^2 W(L, N) dL$$

So the problem is to calculate the distribution function

- b) The other distribution function is the volume distribution:  $W'(L, N) dV =$  probability that chain ends are located within volume  $dV$  at a distance  $L$  from origin.

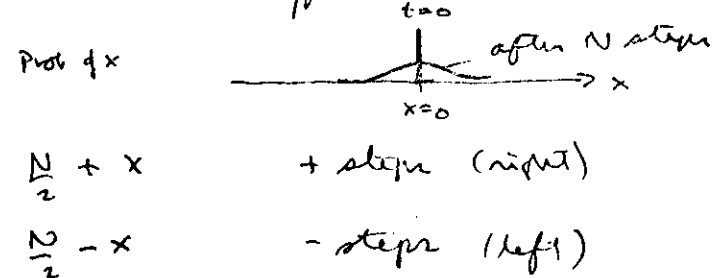
Note that  $W(L) dL$  can be rewritten as

$$W(L) dL = \underbrace{\frac{W(L)}{4\pi L^2}}_{W'(L)} \underbrace{4\pi L^2 dL}_{\text{volume } dV \text{ of a spherical shell}}$$

Hence  $W'(L) = \frac{W(L)}{4\pi L^2}$  for a spherically symmetric distribution

The random walk problem: this is a classic problem in statistical mechanics, which is not too difficult to work out for a one-dimensional system:

Let there be equal probability of moving left or right (+ or -) on a line, for a total of  $N$  steps. On average there will be  $N/2$  steps of each kind, so the distribution will remain centered at the origin. However, not every case will yield  $N/2$  + or - steps; an excess of one over the other leads to a broadening of the distribution ("diffusion") over time:



The probability of  $x$  depends on the number of ways  $\Omega$  that a given value of  $x$  can be achieved. For example ( $N=4$ )

++++	$x=2$	$\Omega=1$
-+++ , +-++ , ++-+ , +++-	$x=1$	$\Omega=4$
---+ , --+- , -+-- , +---	$x=0$	$\Omega=6$
+-+- , -+-+ , -++- , -+--	$x=-1$	$\Omega=4$
----	$x=-2$	$\Omega=1$

in general, for  $N$  steps

$$\Omega = \frac{N!}{\left(\frac{N}{2} + x\right)! \left(\frac{N}{2} - x\right)!} \quad (1)$$

$$[\ln N! = \text{constant} + N \ln N - N]$$

$$\text{Then } \ln \Omega = \text{const}' - \frac{2x^2}{N} \quad (2)$$

$$\text{and } P(x) \propto \exp\left(-\frac{2x^2}{N}\right)$$

Exercise: Use the approximation for  $N!$  above, and the expansion of the logarithm  $\ln(1+y) = y - y^2/2 + \dots$  to obtain eq. (2) from eq. (1)

Therefore  $P$  is a Gaussian function of the displacement  $x$  from the origin.

For a 3-dimensional chain (see Tanford)

$$W(L, N) dL = 4\pi \left(\frac{3}{2\pi N b^2}\right)^{3/2} \exp\left(-\frac{3L^2}{2N b^2}\right) L^2 dL$$

again, this is a Gaussian distribution function

The volume distribution function is

$$w'(L, N) = W(L, N) / (4\pi L^2)$$

Average dimensions

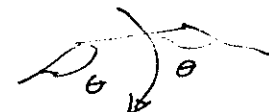
$$\begin{aligned} \langle L^2 \rangle &= \int_0^\infty W(L, N) L^2 dL \\ &= \left(\frac{3}{2\pi N b^2}\right)^{3/2} \int_0^\infty L^4 \exp\left(-\frac{3L^2}{2N b^2}\right) dL \end{aligned}$$

$$= N b^2 \quad ; \quad \langle L^2 \rangle^{1/2} = b \sqrt{N}$$

note that the average chain dimension rises with  $\sqrt{N}$

Exercise: Show that  $W(L)$  is maximum (the most probable value of  $L$ ) when  $L = \sqrt{\frac{2N b^2}{3}}$

Next level of complication: fixed valence angle



rotate dihedral angle

In this case (Tanford, pg 156)

$$\langle L^2 \rangle = Nb^2 \frac{(1 + \cos \theta)}{(1 - \cos \theta)}$$

In general, for a high polymer

$$\frac{\langle L^2 \rangle}{Nb^2} = C_{\infty} \rightarrow \text{Re "Flory characteristic ratio"}$$

for example, for single stranded polynucleotide,  $C_{\infty} = 17$

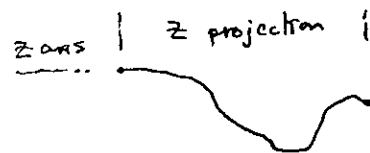
$$C_{\infty} = \frac{1 + \cos \theta}{1 - \cos \theta} ; \text{ for a stiff polymer } \theta \rightarrow 0, C_{\infty} \rightarrow \infty$$

Re "Kuhn statistical segment": model the stiff chain as a collection of  $N_e$  rod-like segments (of length  $b_e$ ), connected by totally flexible joints. Conditions:

$$\begin{aligned} N_e b_e &= Nb \quad (\text{contour length fixed}) \\ N_e b_e^2 &= \langle L^2 \rangle \quad (\text{equivalent random chain}) \end{aligned}$$

Exercise: show that the Kuhn statistical segment length  $b_e = C_{\infty} b$

Persistence length and the "wormlike chain"



$$\langle Z \rangle = \left\langle \sum_{i=1}^N z_i \right\rangle$$

Sum of projection of all bonds on the initial chain direction

$$\langle Z \rangle = b + b \langle \cos \theta_{1,2} \rangle + b \langle \cos \theta_{1,3} \rangle + \dots$$

constant bond angles  $\theta$

$$\langle \cos \theta_{i,i+k} \rangle = (\cos \theta)^k$$

$$\therefore \langle Z \rangle = b \sum_{i=0}^{N-1} \cos^i \theta = \frac{b(1 - \cos^N \theta)}{1 - \cos \theta}$$

$$\lim_{N \rightarrow \infty} \langle Z \rangle = \frac{b}{1 - \cos \theta} = a \quad \text{persistence length}$$

Relationship between  $a$  and  $b_e$ :

$$\langle L^2 \rangle = Nb^2 \frac{(1 + \cos \theta)}{(1 - \cos \theta)} ; \text{ stiff chain } \theta \rightarrow 0$$

$$1 + \cos \theta \approx 2 ; 1 - \cos \theta = b/a$$

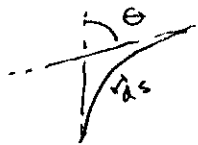
$$\therefore \langle L^2 \rangle = Nb^2 \left( \frac{2}{b/a} \right) = \frac{2Nb^2 a}{b} = 2La$$

Compare with  $L b_e = \langle L^2 \rangle$  to conclude that

$$\underline{\underline{2a = b_e}}$$

Exercise: Use  $500 \text{ \AA} = 50 \text{ nm}$  for the persistence length of DNA, and calculate the average (rms) end-to-end distance in a bacterial DNA molecule containing  $1.5 \times 10^6 \text{ bp}$ . Use the Kuhn model, and assume the long chain limit. (Hint:  $b_e = 100 \text{ nm}$ ;  $N_e = L / b_e = (1.5 \times 10^6 \times 0.34 \text{ nm}) / 100 \text{ nm}$ .) Compare the results with the size of a typical bacterium  $\sim 1 \mu\text{m} = 10^3 \text{ nm}$ .

### Persistence length and DNA bending



$\theta$  is the angle between vectors tangent to the chain

The free energy of bending is related to the curvature by

$$dG = \frac{\alpha}{2} \left( \frac{d\theta}{ds} \right)^2 ds \quad ; \quad \alpha = \text{bending force constant}$$

Take  $\theta$  linear in  $s$

$$\theta = cs \quad ; \quad d\theta/ds = c$$

$$dG = \frac{\alpha}{2} c^2 ds$$

Integrate

$$\begin{aligned} \Delta G &= \frac{\alpha}{2} c^2 L \\ &= \frac{\alpha}{2} (\theta^2 / L^2) L \\ &= \frac{\alpha}{2} \theta^2 L \end{aligned}$$

Compare this result with average thermal bending (see Bloomfield et al) to conclude that

$$\boxed{a = \frac{\alpha}{kT}}$$

Therefore the free energy of bending is (per unit

$$\Delta G = \frac{\alpha kT \theta^2}{2L}$$

Exercise: Calculate the bending energy of two turns of DNA in 146 bp in a nucleosome. ( $a = 50 \text{ nm}$ ,  $\theta = 4\pi$ ,  $T = 298$  K,  $L = 146 \times 0.34 = 49.6 \text{ nm}$ ) (Answer =  $\Delta G = 79.6 \times kT \approx 197 \text{ kJ/mol} = \frac{47.1}{4.184} \text{ kcal/mol}$ )

[For the most recent (and elegant) theory of the wormlike coil, see Shimada & Yamakawa, *Macromolecules* 1984, 17, 689-698]



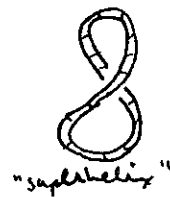
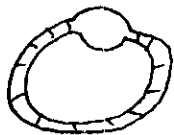
## 2. Topological properties of closed circular DNA molecules

Both strands covalently closed, strands are linked around each other



$$Lk = 4$$

Superhelical structures result when there is a deficit (or, less commonly, an excess) of turns needed to make an ideal double helix, i.e.



"superhelix"

Note that superhelical stress increases the tendency toward local helix melting

Twist, writhe and linking number

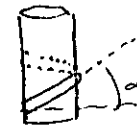
Lk Linking number, an integer, gives the number of times one strand is linked through the other

(References: Crick, PNAS 73, 2639 (1976);  
Dauer, Crick & White, Science 187, 100 (1975))

Lk is broken into two parts mathematically  
Twist is the part of the linking which results from rotation of the vector joining the two strands about the local helix axis.

Writhe is everything else, and can be calculated from the Gauss integral over the curve described by the local helix axis (see below).

Twist of a ribbon wound flat on a cylinder



$Tw = N \sin \alpha$  (in turns)  
 $\alpha =$  pitch angle  
 $N =$  # of turns

Note that the writhe of the curve also depends on pitch angle

Gauss integral (see Brauer, J. Mol. Biol. 163, 613 (1973))

$$Wr = \frac{1}{4\pi} \iint \left( \frac{\partial \vec{e}_{12}}{\partial s_1} \times \frac{\partial \vec{e}_{12}}{\partial s_2} \right) \cdot \vec{e}_{12} ds_1 ds_2$$

$s_1 =$  point on the line

$\vec{e}$  is the normalized connection vector

between points 1 and 2

$$\vec{e}_{ij} = \frac{\vec{r}_j - \vec{r}_i}{|\vec{r}_j - \vec{r}_i|}$$

Approximate the curve by a series of discrete points (ie, bp)

$$W_r = \frac{1}{4\pi} \sum_{i \neq j} \frac{L^2}{|\vec{r}_i - \vec{r}_j|^2} ((\vec{t}_i \times \vec{e}_{ij}) \cdot \vec{t}_j)$$

$\vec{t}_i$  is the normalized chain tangent vector:

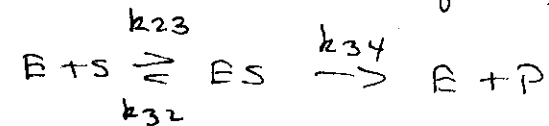
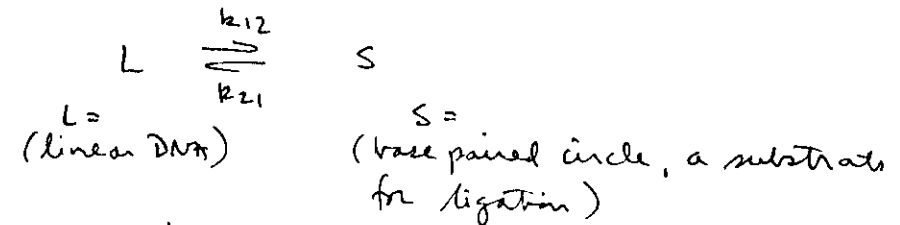
$$\vec{t}_i = \frac{\vec{r}_{i+1} - \vec{r}_{i-1}}{|\vec{r}_{i+1} - \vec{r}_{i-1}|}$$

(The Gauss integral can be applied to curves which are not closed, but the results are strongly dependent on end effects: ie,  $\vec{t}_1$ )

### 3. Measuring DNA bending and torsional stiffness by ligation into circles

References: Shore et al, PNAS 78, 4833 (1981)  
Shore & Baldwin, J. Mol. Biol. 170, 957 and 983 (1983).  
Hornitz & Wang, J. Mol. Biol. 173, 75 (1984).

#### Enzymatic ligation



Because the  $L \rightleftharpoons S$  equilibrium is fast, the rate of the ligation reaction is directly proportional to the equilibrium concentration of cyclized molecules,  $S$ .

So by kinetic analysis yields first order rate constant for ligation into circles:

$$k_1 = \frac{k_{34} [E_0] K_c (1-f_a)}{(K_m + [S])}$$

where  $k_1$  is defined by

$$\frac{d[D]}{dt} = -k_1 [D]$$

$$[D] = [L] + [S] = \text{total DNA concentration}$$

$$K_m = \frac{k_{32} + k_{34}}{k_{23}} ; f_a = \frac{[S]}{[D]}$$

Exercise Derive the equation for  $k_1$  above, using the steady state assumption

The second order rate constant is

$$k_2 = \frac{k_{34} [E_0] K_c (1-f_a)^2}{(K_m + [S])}$$

where

$$\frac{d[D]}{dt} = -k_2 [D]^2$$

$K_c$  = equilibrium constant for bimolecular joining of ends A and B.

The Shinkovoy-Jacobson j-factor is the ratio of the equilibrium constant for cyclization to the eq. constant for bimolecular joining  
 $j = K_c / K_a$

The j-factor can also be thought of as the ratio of the molar concentration of one DNA end around the other, considering also the probability that the two ends are properly oriented for forming a double helix, to the molar concentration of one end around the other (1M) in the bimolecular joining reaction.

We can estimate the concentration term from the Kuhn model for DNA, and the Gaussian distribution function. (The estimate of the j factor which ignores the angular orientation of the two ends is called  $J_0$ .)

$$J_0 = \frac{W'(N, L=0)}{N_A}$$

For a 4362 bp DNA (pBR322);  $b_e = 100 \text{ nm}$

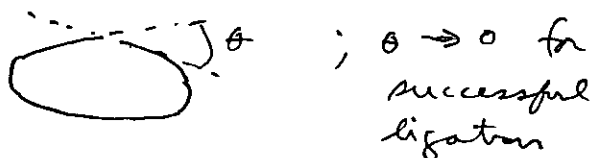
$$N_e = \frac{L}{b_e} = \frac{4362 \times 0.34}{100} = 14.8$$

$$W' = \left( \frac{3}{2\pi N_e b_e^2} \right) \exp\left( \frac{-3L^2}{2N_e b_e^2} \right)$$

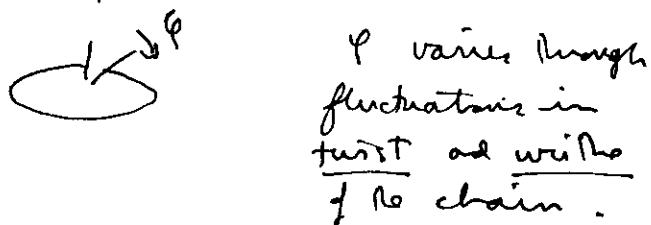
$$J_0 = \frac{1000 \text{ cm}^3}{L} \left( \frac{3}{2\pi \times 14.8 \times (10^{-8} \text{ cm})^2} \right)^{3/2} \frac{1}{6.023 \times 10^{23} \text{ mol}^{-1}}$$

$$= 9.7 \times 10^{-9} \text{ M}^{-1} \text{ (experimental } J \approx 8 \times 10^{-9} \text{ M}^{-1})$$

For shorter chains, the angular factors become increasingly important:  $J_1$  includes tangent angle dependence



$J$  includes in addition the torsional match between the glycosidic bond vectors in the chain



Let  $\alpha$  = total linking number in a hypothetical molecule containing a flexible joint, allowing  $\phi$  to vary continuously. Let  $\alpha_0$  = average value of the twist in the hypothetical molecule.

$$P(\alpha) = \frac{\exp[-K(\alpha - \alpha_0)^2/RT]}{\int_{-\infty}^{\infty} \exp[-K(\alpha - \alpha_0)^2/RT] d\alpha}$$

(note that in  $\alpha$  ligated molecules,  $\alpha$  must be an integer)  
 $P(\alpha)$  can also be expressed in terms of the variance of the distribution,  $\langle(\Delta\alpha)^2\rangle$

$$\langle(\Delta\alpha)^2\rangle = RT/2K$$

$$P(\alpha) = \frac{\exp[-(\alpha - \alpha_0)^2/(2\langle(\Delta\alpha)^2\rangle)]}{\int_{-\infty}^{\infty} \exp[-(\alpha - \alpha_0)^2/(2\langle(\Delta\alpha)^2\rangle)] d\alpha}$$

Fluctuations in  $T_w$  and  $W_r$  (in the hypothetical molecule containing a flexible joint) are uncoupled, so

$$\langle(\Delta\alpha)^2\rangle = \langle(\Delta T_w)^2\rangle + \langle(\Delta W_r)^2\rangle$$

By classical mechanics

$$\langle(\Delta T_w)^2\rangle = \frac{L k_B T}{4\pi^2 C} ; C = \text{torsional rigidity}$$

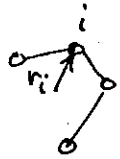
The experiment gives  $\langle(\Delta\alpha)^2\rangle$ , theory gives  $\langle(\Delta W_r)^2\rangle$  difference gives  $\langle(\Delta T_w)^2\rangle$  and hence  $C$ .

#### 4. Hydrodynamic properties of DNA molecules

(Illustrated for rotational motion)

Reference: Hagerman & Zimm, Biopolymers 20, 1481 (1981)

Consider the chain to be rigid during rotational motion



The beads  $i$  are the hydrodynamic elements  
 $\sigma$  = the radius of the sphere.

$\vec{\omega}$  = angular velocity of the chain about its center of frictional resistance (CFR) (which is at rest)

$\vec{V}_i$  = relative velocity of the  $i$ th bead with respect to the local fluid.

$\vec{r}_i$  = position of  $i$ th bead relative to the CFR

$\vec{v}_i$  = velocity of ~~bead~~ the fluid at  $r_i$  due to motion of  $N-1$  beads, but with  $i$  absent

$$(1) \quad \vec{V}_i = \vec{\omega} \times \vec{r}_i - \vec{v}_i$$

motion relative to fluid      linear velocity      fluid motion due to other beads

Basic hydrodynamic equation:

$$(2) \quad \vec{v}_i = \sum_j \vec{T}_{ij} \cdot \vec{F}_j \quad (j \neq i)$$

velocity perturbation at bead  $i$

Oseen Tensor      force on bead  $j$

$$(\vec{F}_j = \rho \vec{V}_j \cdot \hat{z}, \quad \rho = \text{frictional coef} = 6\pi\eta_0\sigma)$$

where the Oseen Tensor is given by

$$\vec{T}_{ij} = (8\pi\eta_0 \vec{R}_{ij})^{-1} \left[ \left( \vec{I} + \frac{\vec{R}_{ij} \vec{R}_{ij}}{R_{ij}^2} \right) - \frac{2\sigma}{R_{ij}} \left( \frac{\vec{I}}{3} + \frac{\vec{R}_{ij} \vec{R}_{ij}}{R_{ij}^2} \right) \right]$$

$R_{ij}$  = scalar distance between  $i$  &  $j$

$$\vec{R}_{ij} \vec{R}_{ij} =$$

One does not, in general, know the CFR

$$\vec{r}_{i,0} = \vec{r}_i + \vec{R}_0$$

positions with respect to arbitrary origin

CFR relative to arbitrary origin

$$\vec{\omega} \times \vec{r}_{i,0} = \vec{\omega} \times \vec{r}_i + \vec{\omega} \times \vec{R}_0$$

From eq (1), we get

$$(3) \quad \vec{V}_i = -\vec{\omega} \times \vec{R}_0 + \vec{\omega} \times \vec{r}_{i,0} - \vec{v}_i$$

Frictional force exerted on the fluid by each bead

$$\vec{F}_i = \rho \vec{V}_i$$

or, with eq (3)

$$(4) \quad \vec{F}_i = \rho (\vec{u} + \vec{\omega} \times \vec{r}_{i,0} - \vec{v}_i)$$

$-\vec{\omega} \times \vec{R}_0$  = velocity of arbitrary origin  
 = 0 + ...

Here are  $3N+3$  unknowns:  $N$   $3N$  components of  $\vec{F}_{i,\alpha}$  ( $\alpha = x, y, z$ )  
+  $N$  components of  $\vec{u}$ .

- The  $\vec{r}_{i,0}$  are known (fixed molecular shape)
- $\vec{V}_i$  are known from eq. (3)
- $\vec{v}_i$  are known from eq. (2)

Eq. (4) gives  $3N$  equations, plus 3 equations from the fact that there is no net force on the chain:  $\sum_i \vec{F}_{i,\alpha} = 0$  ( $\alpha = x, y, z$ )

The torque is given by

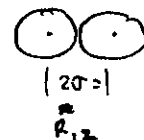
$$\vec{T} = \underline{\underline{J}} \cdot \vec{\omega}, \quad \underline{\underline{J}} = \text{friction tensor for rotation}$$

$$\vec{T} = \underline{\underline{J}} \cdot \vec{\omega} = \sum_i \vec{r}_i \times \vec{F}_i = \sum_i \vec{r}_{i,0} \times \vec{F}_i$$

Diagonalize  $\underline{\underline{J}}$  to get  $N$  3 principal rotational diffusion coef.

$$\underline{\underline{J}} = \frac{kT}{D_p}, \quad p = x, y, z$$

Exercise Write out the hydrodynamic equations explicitly for a system of spheres:



Where is the C.F.R.? What are the rotational frictional coeffs? What is  $\underline{\underline{J}}$  if you neglect hydrodynamic coupling.

### Results on DNA

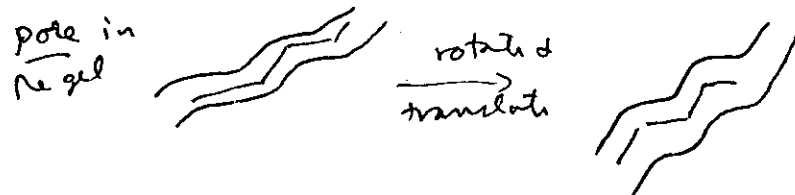
see Hagerman, Biopolymers 20, 1503 (1981)  
Eliass & Eden, Macromolecules 1981, 14, 410-41  
Mandelkern et al. J. Mol. Biol. 152, 153-161 (1981)

Dimensions of chromatin fibers from hydrodynamics  
see Lee et al., Biochemistry

# 5. Theories of gel electrophoresis

see Lerman & Frisch, Biopolymers 21, 995  
 Lumbain & Zimm, " 21, 2315

Lerman & Frisch start with the reptation model of  
 de Gennes (J. Chem. Phys. 55, 572 (1971));  
 " Scaling concepts in Polymer Physics, Cornell Press  
 (1979).



Scaling of diffusion constant (de Gennes)

$$D \propto \langle L^2 \rangle / N^3$$

$$f \left( \frac{dx}{dt} \right) = F \quad ; \quad f = \text{frict coef} = \frac{kT}{D}$$

velocity                      force                      other of the vasa

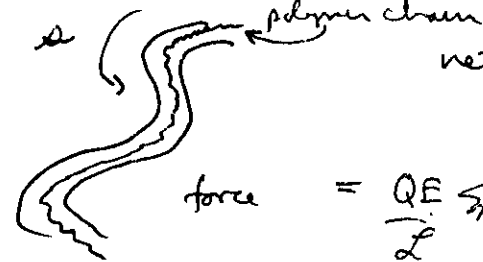
$$\frac{dx}{dt} = \frac{DF}{kT} \quad ; \quad F \propto EN \quad ; \quad E = \text{field}$$

$$\frac{dx}{dt} \propto \frac{E \langle L^2 \rangle}{N^2} \quad ; \quad \langle L^2 \rangle \propto N^\nu$$

$$\frac{dx}{dt} \propto EN^{\nu-2}$$

Gaussian chain,  $\nu = 1$   
 then  $\frac{dx}{dt} \propto N^{-1}$  ; [experiment:  
 (approximately true)  $\mu \propto \log(N_0/N_1)$

Lumbain & Zimm



$Q = \text{charge}$   
 $f = \text{frict coef.}$

$$\text{net force} = \frac{Q}{L} \int \vec{E} \cdot d\vec{s}$$

$$\text{force} = \frac{QE}{L} \int \vec{i} \cdot d\vec{s} = \frac{QE h_x}{L}$$

$\vec{i}$  is a unit vector along the field.  
 $h_x = \text{component of polymer's end-to-end vector along the field.}$

lower forces

$$f \frac{dx}{dt} = \frac{QE h_x}{L}$$

$$\frac{dx}{dt} = \frac{dx}{dt} \frac{h_x}{L}$$

$$\frac{dx}{dt} / E = \frac{\langle h_x^2 \rangle Q}{L^2 f}$$

(Q/f) independent of L

$$\therefore \mu \propto \frac{\langle h_x^2 \rangle}{L^2}$$

Gaussian chain,  $\mu \propto L^{-1}$

