Physics 850: Soft Condensed Matter Physics, Fall04

A.D. Dinsmore

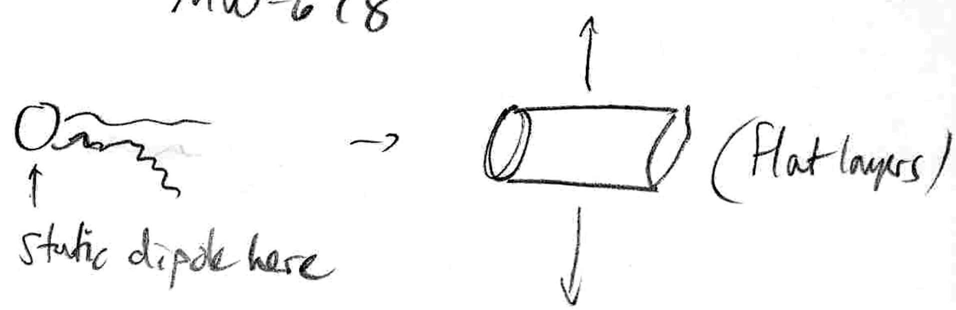
Lecture 12 – The shape of a meniscus; capillary forces

Lipids

2-tailed surfactants

e.g. Dimyristoyl phosphatidylcholine (DMPC)

MW=678



Fun facts about membranes

Lipid bilayer membranes (made in lab)

- 4nm thick
- stable (resist puncture, self healing)
- somewhat permeable to water, not to ions
- Fluid — no long-range order. Lipids move in-plane $D \sim 1 \mu m^2/s$ (if lipid is fluid)
  rotation on axis (fast) 
  flip-flop < 1/month 

Biological (eg cell) membranes

- many lipids (~6 species)
  + cholestrol (~1:1, to prevent crystallization)

- 25-75 wt % protein. $N_{protein} \simeq \frac{1}{50} N_{lipid}$
- proteins make pores to enhance permeability of select ions & enhance flip-flop
- attached to elastic (protein) network

From Alberts *et al*, Molecular Biology of the Cell

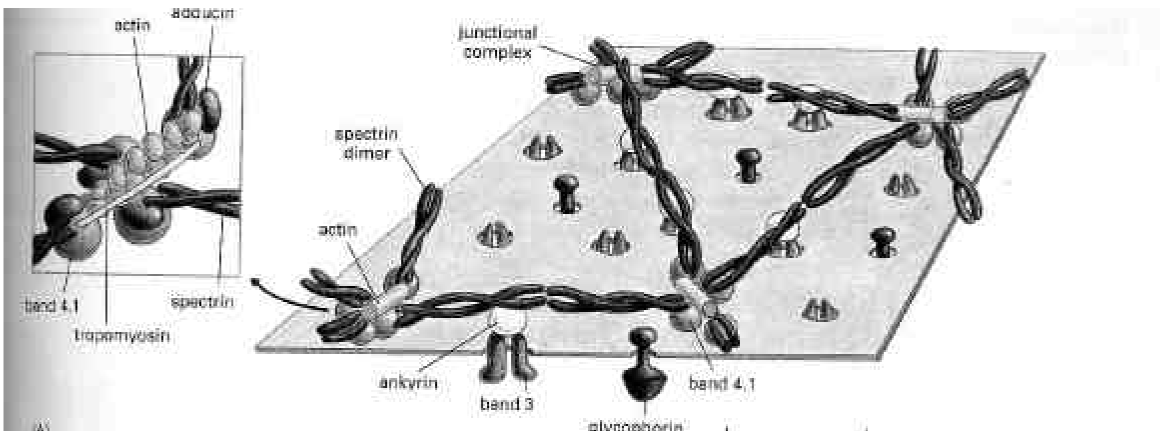
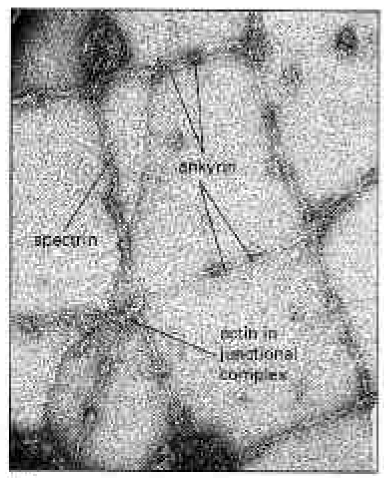


Figure 10–26 **The spectrin-based cytoskeleton on the cytoplasmic side of the human red blood cell membrane.** The structure is shown schematically in (A) and in an electron micrograph in (B). The arrangement shown in (A) has been deduced mainly from studies on the interactions of purified proteins *in vitro*. Spectrin dimers associate head-to-head to form tetramers that are linked together into a netlike meshwork by junctional complexes composed of short actin filaments (containing 13 actin monomers), tropomyosin, which probably determines the length of the actin filaments, band 4.1, and adducin (enlarged in the box on the *left*). The cytoskeleton is linked to the membrane by the indirect binding of spectrin tetramers to some band 3 proteins via ankyrin molecules, as well as by the binding of band 4.1 proteins to both band 3 and glycophorin (not shown). The electron micrograph in (B) shows the cytoskeleton on the cytoplasmic side of a red blood cell membrane after fixation and negative staining. The spectrin meshwork has been purposely stretched out to allow the details of its structure to be seen; in the normal cell the meshwork shown would occupy only about one-tenth of this area. (B, courtesy of T. Byers and D. Branton, *Proc. Natl. Acad. Sci. USA* 82:6153–6157, 1985.)



(B)

. . . Lipid membranes . . .

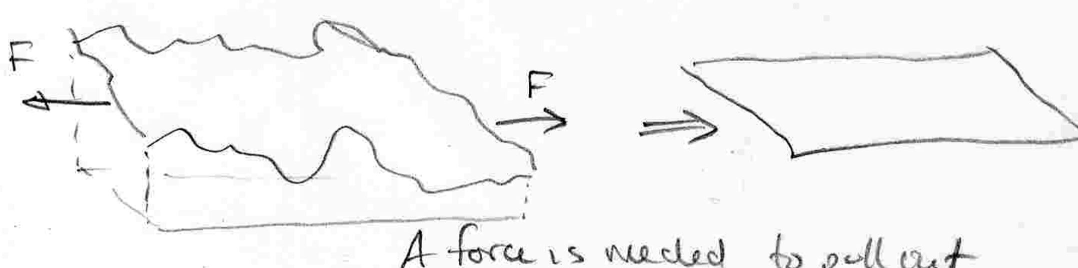
Surface tension = 0 !

Self assembled surface – lipids
adjust to minimize F

$$\text{so } \left.\frac{\partial F}{\partial A}\right|_N = 0 = \sigma$$

(A free-floating membrane has $A \neq 0$ even though it can change A)

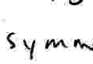
<u>**But**</u> there is an <u>apparent</u> σ
from entropy:



A force is needed to pull out wrinkles & increase <u>projected</u> area. True area = constant.

A model for membranes :

$$F = \int dA \left\{ \frac{A}{R_1} + \frac{B}{R_2} + \frac{C}{R_1{}^2} + \frac{D}{R_2{}^2} + \frac{E}{R_1{}^3} + \cdots + \frac{F}{R_1{}^4} + \cdots + \frac{G}{R_1 R_2} \right.$$

- in-plane isotropy $\rightarrow$ $A = B$, $C = D$
- up-down symmetry $\rightarrow A = B = E = 0$ ( and  cost the same energy)
  - and coefficents of $\frac{1}{R^3}$, $\frac{1}{R^5}$, etc $= 0$
  - $G \neq 0$ because $\frac{1}{R_1 R_2}$ is the same for the two cases sketched
- dimensional analysis :

$C \rightarrow$ [energy]

$G \rightarrow$ [energy]

$F \rightarrow$ [energy $\cdot$ length^2] — F is a material constant, so this length must be characteristic of the material, i.e of order Å – nm, and $\ll R_1$ or R_2

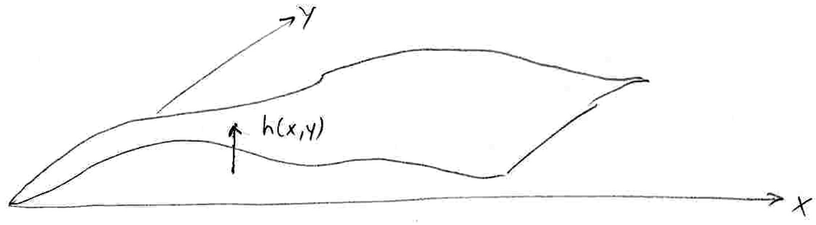
↑ assumed to be $\approx$ energy scale in C, G.

- $\Rightarrow$ higher order terms (in $\frac{1}{R}$) will be much smaller.
- now, $H \equiv \frac{1}{2}\left(\frac{1}{R_1} + \frac{1}{R_2}\right)$ "mean curvature"

$G \equiv \frac{1}{R_1 R_2}$ "Gaussian curvature"

$$F = \int dA \left(2K\left(H(\vec{r}) - H_0\right)^2 + \bar{K}\, G(\vec{r}) \right)$$

↑ "spontaneous curvature" thrown in here.



$h(x,y)$ = height of membrane above the point (x,y) measured in a flat plane

Mean curvature

"Monge representation"

If the membrane is nearly flat $\left(\frac{\partial h}{\partial x} \ll 1\right)$,

then $$H = \frac{1}{2}\left(\frac{\partial^2 h}{\partial x^2} + \frac{\partial^2 h}{\partial y^2}\right) = \frac{1}{2}\nabla^2 h(x,y)$$

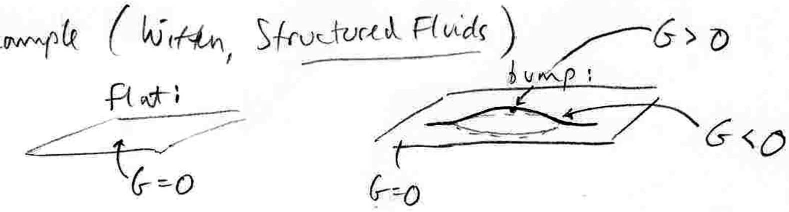
Gaussian curvature:

Gauss-Bonnet theorem

$$\int_{\text{surface}} G(\vec{r})\, dA = \text{constant, independent of shape}$$

for any continuous deformation

example (Witten, Structured Fluids)



So membrane undulations cannot change the $\bar{K}$ term in F.

How flat is a membrane? How large does it have to be in order to appear highly crumpled (Ans: astronomically large!)

(ie how much does $\underbrace{\nabla h}_{\text{slope}}$ vary?)

$$\langle |\nabla h(\vec{r})|^2\rangle = \langle \left| \frac{1}{L_0^2}\sum_q \frac{\partial}{\partial r} e^{iqr}\hat{h}(q)\right|^2\rangle$$

$$= \langle \left| \frac{1}{L_0^2}\sum_q iq\, \hat{h}(q)\right|^2\rangle$$

$$= \langle \frac{1}{L_0^4}\sum_q q^2 |\hat{h}(q)|^2\rangle$$

$\sum_q = L_0^2\int \underbrace{2\pi q\,dq}_{\text{units}=\frac{1}{\text{length}^2}}$

$$= \frac{1}{L_0^2}\int \underbrace{2\pi q\, dq}_{d\vec{q} \text{ in 2D cylindrical}}\; q^2\, \frac{k_BT}{K}\,\frac{L_0^2}{q^4}$$

$$= \frac{k_BT}{K}\cdot 2\pi \int_{\frac{1}{L_0}}^{\frac{1}{a}} \frac{dq}{q}$$

a = lipid size

$$\langle |\nabla h(r)|^2\rangle = \frac{k_BT}{K}\, 2\pi\, \ln\left(\frac{L_0}{a}\right)$$

"Flat" over region of size L_0 such that $\langle|\nabla h|^2\rangle < 1$

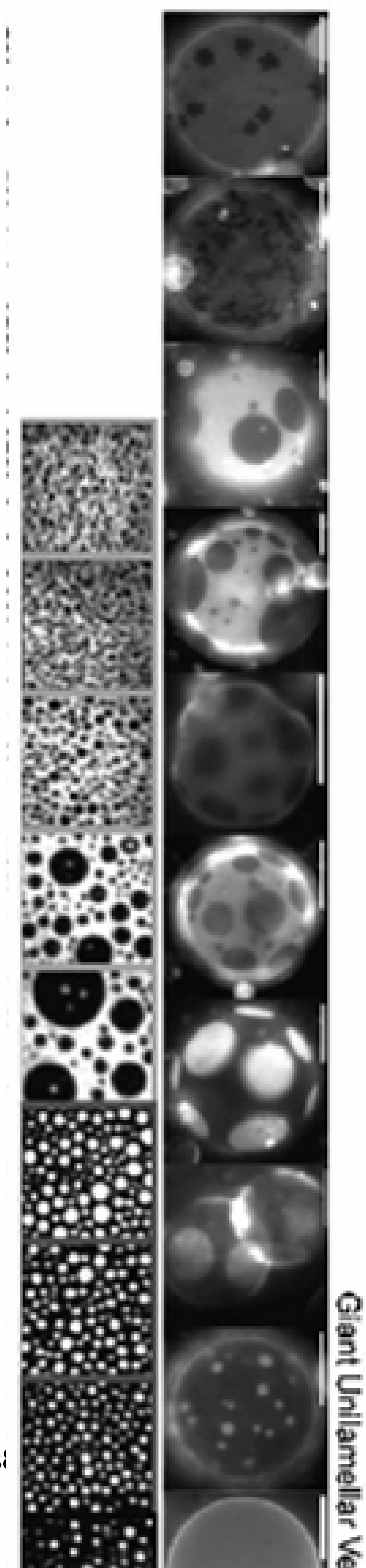
? (I think that a missing factor of $(2\pi)^2$) this is correct

ie $\frac{k_BT}{K}\, 2\pi \ln\frac{L_0}{a} = 1 \rightarrow L_0 \simeq a\cdot e^{\frac{2\pi K}{k_BT}}$

$a = 1\text{nm},\quad K = 15\, k_BT \Rightarrow L_0 \cong 10^{30}\,\text{m}$

Lipid Membranes with multiple components: Phase separation of lipids.

Organization in Lipid Membranes Containing Cholesterol,
Veatch and Keller, PRL 89, 268101 ('02)



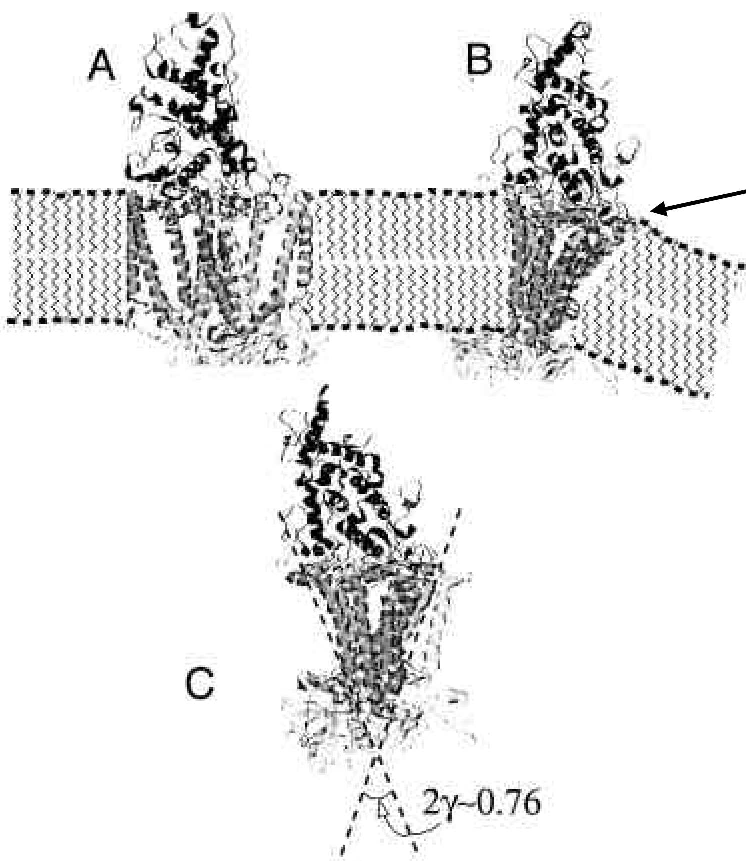
Fluorescence images.

Two types of lipids mixed in equal amounts. (di(18:1)PC and di(16:0)PC. Texas Red dye added for contrast.

increasing cholestrol

Forces among intra-membrane proteins
"**Curvature-Mediated Interactions between Membrane Proteins**," Kim, Neu and Oster, Biophys J. **75**, 2274 ('98).
"**Statistical Theromdynamics of Membrane Bending-Mediated Protein-Protein Attractions**," Chou, Kim and Oster, Biophys. J. **80**, 1075 ('01).

(In their model, proteins create bend in membrane; attractions are analogous to capillary forces at oil-water interface)



Photoreaction center of *Rhodopseudomonas viridis*. Configuration in the membrane is inferred from x-ray crystal structure.