mately linearly with radius before flattening off at a value that remains constant as far out as it can be followed. The 'rotation curve' of Disk 2, shown in the figure, is very different. Near its centre the line-of-sight velocity changes by 800 km s<sup>-1</sup> in 5 arcseconds (about 2.4 kiloparsec). In fact this change may be even steeper than the figure suggests, as Bland-Hawthorne *et al.* could not have spatially resolved a more abrupt change. In any event, if one assumes that material at the peaks of the rotation curve is on circular orbits, one can estimate the mass within 2.5 arcseconds required to hold it on such orbits; nothing less than  $4.5 \times 10^{10} M_{\odot}$  will do.

This is, by any standards, a lot of mass in a small space, but what makes it more remarkable is how little light is coming from the same region. This region does not include the galaxy's double-humped nucleus, and even after making generous allowance for absorption of its luminosity by dust, with this mass estimate it contains more than six times as much mass per unit luminosity as a normal stellar population. Thus the straightforward interpretation of the rotation curve in the figure suggests that near the centre of Disk 2 NGC6240 is twice as dark as the famous core of Messier 87. If this darkness is caused by adding a black hole to a normal stellar population, the hole must weigh more than  $3 \times$  $10^{10} M_{\odot}$ , much more than any conceivable black hole in Messier 87.

The key question is: can one safely interpret the peaks in the rotation curve as the local speed of a circular orbit? One striking feature of the figure is the extremely rapid decline in the rotation velocity just outside the peak. This decline is faster than the form,  $v \propto 1/r^{1/2}$ , characteristic of rotation about a point mass. Such a steep fall-off in velocity is most naturally explained in terms of a stellar bar across the middle of the galaxy; the shapes of orbits in a barred gravitational field can change rapidly from elongated to round, and this gives rise to steep gradients in lineof-sight velocities when the system is viewed from certain angles5. Furthermore, numerical simulations of mergers<sup>6</sup> show that the old stellar components of merging galaxies tend to develop strong bars whose gravitational fields deprive gas of its angular momentum. The gas then plunges to the system's centre on highly elongated orbits. Could the observations of Bland-Hawthorne et al. be neatly explained by such a model without invoking a massive black hole? In any event, the search for these objects must go on. 

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MODEL MEMBRANES

## **Playing a molecular accordion**

## Michael Cates

BIOLOGICAL membranes, such as cell walls, are composed mainly of lipid bilayer. In red blood cells, the stability and shape of the membrane is partly controlled by coupling to an adjacent network of polymer molecules (the cytoskeleton), attached to the membrane by anchor groups. The physical

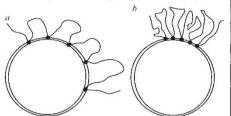


FIG. 1 Adsorbed state of polymer and lipid bilayer. *a*, Good solvent; *b*, poor solvent.

properties of purified model membranes, which can be made to form small spherical shells called liposomes, have been studied extensively<sup>1</sup>. Now, Ringsdorf *et al.*<sup>2</sup> have studied the adsorption of a synthetic polymer (with suitable anchor groups) onto liposomes, and have shown that a reversible folding of the attached polymer can occur under changes in temperature; they call their system a "molecular accordion" (Fig. 1). The authors draw a parallel between this effect and the reversible changes of shape that occur in the cytoskeleton of red blood cells during cell motion.

The system the authors studied consists of a high-molecular-weight, water-soluble polymer, poly-N-isopropylacrylamide (PNIPAM), to which aromatic side groups (the anchor groups) are attached every 200 monomers or so along the chain. The authors added this to a solution of unilamellar liposomes. The state of adsorption and folding of the chain was monitored by a fluorescence technique, which provides data on what fraction of the anchor groups are close to another such group. The fraction is high when the polymer is dissolved in water (without added liposome) since in this case the polymer forms a micellar structure (Fig. 2) in which the anchor moieties are clustered together to avoid unfavourable contact with water. On addition of liposomes (made of dimyristoyllecithin, DMPC), the fluorescence signal decreases dramatically, indicating that anchor groups are well separated - as with the adsorbed-layer structure of Fig. 1a.

The molecular-accordion effect is then brought about by increasing the temperature of the system. At around 32 °C, PNIPAM has a lower critical solution temperature: water is a good solvent for the polymer below this temperature, and an isolated coil of pure PNIPAM (without any anchor groups) will form an expanded structure to maximize its contact with the solvent. At higher temperatures, however, such contacts are unfavourable and the coil collapses. This coil-globule

transition is ubiquitous in simple polymers (although in many systems the dependence on temperature is reversed). A similar transition is often seen in proteins, although the chemical heterogeneity of the chain means that the effect is a more complex one. Ringsdorf et al. exploit the phenomenon by raising the temperature of the combined polymerliposome system (Fig. 1a). The collapse of the chain causes the anchor groups to move inwards, increasing the number of anchoranchor contacts and enhancing the fluorescence signal (Fig. 1b). The whole process is reversible, so that the adsorbed polymer can be expanded and contracted repeatedly by cycling the temperature - like playing an accordion.

This is certainly a neat experiment, which illustrates an elegant if straightforward piece of physics. But what is its significance for biology? The new results of Ringsdorf *et al.* follow earlier work in which it was shown that the equilibrium shape of a liposome can be strongly altered by adding adsorbed polymer<sup>3,4</sup>. Despite this, there is no evidence in the PNIPAM/DMPC system that the liposomes actually 'dance to the accordion' by undergoing sympathetic changes in shape (the anchor groups could simply slide together within the bilayer, which acts as a two-dimensional liquid). The authors sug-



FIG. 2 Micellar state of a free chain containing anchor groups.

gest that this might be achieved by choosing larger, more flexible liposomes and by crosslinking the adsorbed polymer into a network. In any case, the numerous shape changes of red blood cells suggest an exquisite dependence of the cytoskeletal protein network on physiological conditions; it would be surprising if such subtlety were related to so gross a conformational change as a coilglobule transition. We do not yet know whether the molecular accordion and the red blood cell cytoskeleton are really playing the same tune.

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