Constructing a stingy scaffolding for foam

The iridescent bubbles that crowd together to form a quivering foam arrange themselves to fill space in the most efficient way possible. Separated by thin liquid films, these tightly packed gas bubbles settle into patterns that minimize their combined surface area.

Inspired by studies of foams, physicists have now provided a new answer to the longstanding mathematical question of what space-filling arrangement of bubbles (or cells) of equal size has the minimum surface area. The pattern discovered by Denis L. Weaire and Robert Phelan of Trinity College in Dublin, Ireland, improves on a structure first proposed more than 100 years ago by Lord Kelvin.

"We weren't out to challenge Lord Kelvin," Weaire insists. But while investigating how the amount of liquid present in the films separating bubbles affects a foam's arrangement, they came across a pattern that looked like it had a smaller surface area than Lord Kelvin's structure.

"To our great astonishment, it worked," Weaire says. The researchers describe their findings in the February PHILOSOPHICAL MAGAZINE LETTERS.

Mathematicians (and possibly honeybees) have long known that dividing a two-dimensional surface into a honeycomb of hexagons of equal area — rather than squares, triangles, or other shapes — requires the least amount of fencing. In the three-dimensional case, however, no one knows the most efficient way of filling space with cells of equal volume.

In 1887, Lord Kelvin proposed an arrangement based on a polyhedron obtained by slicing off the six vertices of an octahedron (which has eight triangular faces) at a certain distance from each vertex. The resulting three-dimensional shape has 14 faces.

By slightly curving the faces and edges to make the polyhedrons a little more spherical, then packing these curved polyhedrons together into a space-filling pattern, Lord Kelvin achieved what he suggested was the best way to package space into equal volumes, using the smallest possible surface area. But with no mathematical proof that this was so, researchers tried to better Lord Kelvin's result, with no success until now.

Weaire and Phelan based their arrangement of polyhedral cells on a chemical structure known as a clathrate. In the particular example they chose, cages of bonded silicon atoms totally enclose sodium atoms — in the ratio of 46 silicon atoms to 8 sodium atoms — to create a three-dimensional, repeating pattern. The researchers used the sodium locations as the centers of the polyhedrons in their array.

The resulting structure requires two different types of polyhedrons (see illustration). The 14-sided polyhedron has 12 pentagonal and 2 hexagonal faces. The other polyhedron has 12 faces, each a somewhat distorted pentagon. Units consisting of six 14-sided polyhedrons and two 12-sided polyhedrons can be stacked in three dimensions to fill space.

To equalize the volumes of these polyhedral cells and minimize the array's surface area, Weaire and Phelan used a special "surface evolver" computer program, which slightly curved the faces and edges. The program also enabled them to calculate that their arrangement beats Lord Kelvin's structure by about 0.3 percent.

The result represents "a remarkably large margin of superiority in this context," Weaire and Phelan comment.

One clue that this arrangement would work was the number of pentagons it contained. The angles at which the surface films of bubbles in foams cluster are often close to the angles of a pentagon, and researchers had tried in the past to find patterns that included as many pentagons as possible.

"As soon as I saw all those pentagons, I knew that [Weaire and Phelan] had a winner," says Kenneth A. Brakke of the University of Minnesota's Geometry Center in Minneapolis, who had developed
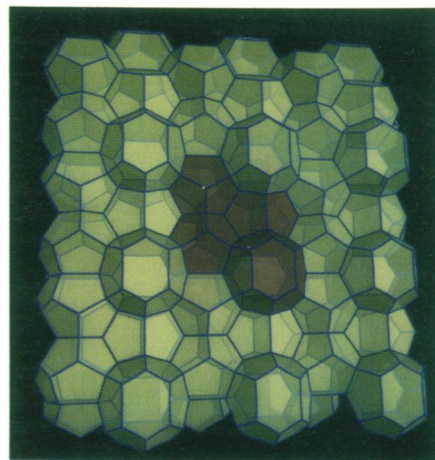
Efficiently filling space with arrays of 14-sided and 12-sided polyhedrons.

the surface evolver software.

Weaire and Phelan had a second, more complicated candidate structure, but new results show that it fails. Weaire now suspects that no one is likely to do better. "If somebody can find a very clever structure that does it, good luck to them," Weaire says. "But I don't think it will happen."

Weaire and Phelan have also made real foams that appear to incorporate the new structure. "We have photographs of something that looks remarkably like what [the computer] shows," Weaire remarks.　　　　　　　— *I. Peterson*
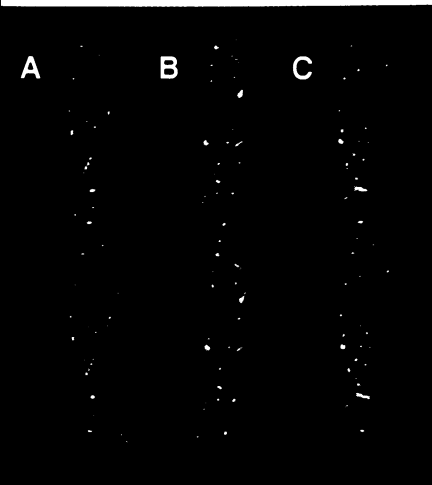
Muscle molecules: A textbook picture

Those breathtaking jumps and twirls of Olympic skaters boil down to the microscopic twitches of muscle proteins. Over the past few years, sophisticated techniques have revealed motion's molecular mechanisms: Thick myosin and thin actin filaments move across each other during contractions (SN: 11/13/93, p.316).

These three-dimensional images of thin filaments now show that actin does have "off" (a,c) and "on" (b) states, as predicted by a theory developed 20 years ago. According to that model, a slender protein strand called tropomyosin switches contraction on and off, says William Lehman, a muscle biophysicist at Boston University School of Medicine. Textbooks often present that model, which was based on X-ray diffraction data.

For this new work, Lehman first isolated thin filaments from horseshoe crabs and demonstrated that their muscle proteins worked like vertebrate muscle proteins by combining the two kinds of proteins into functional hybrids.

Then Roger Craig from the University of Massachusetts Medical School in Worcester examined hundreds of thin filaments with an electron microscope and selected 10 in solutions devoid of calcium (a,c) and 6 in calcium-rich solutions (b) for analysis. With Peter Vibert of Brandeis University in Waltham, Mass., Lehman analyzed diffraction patterns obtained from the electron microscope and used a computer to reconstruct the filaments' structures.

In the March 3 NATURE, they describe how tropomyosin works. It winds around actin's helical core and shifts by about 25° when exposed to calcium (b). It changes its point of contact along actin and interacts with troponin, a molecular complex that includes a calcium docking site. This enables myosin to bind with actin and slide over it.