Kepler's conjecture confirmed

Neil J. A. Sloane

One of the oldest unsolved problems in mathematics appears to have been settled. On 9 August, Thomas C. Hales announced that he had proved Kepler's assertion of 1611 that no packing of spheres can be denser than a face-centred-cubic lattice.

In face-centred-cubic packing (Fig. 1), seen in the piles of oranges in any grocer's shop, the spheres occupy 0.7405 of the total space available. Ambrose Rogers remarked[1] in 1958 that "many mathematicians believe and every physicist knows" that no denser packing is possible. So why has it taken 387 years for a proof to be found?

There are three reasons. First, technical difficulties come from the fact that the density of a packing is defined as the *limit* of the fraction of space occupied by the balls as the number of balls goes to infinity. This means that (say) a million balls can be thrown away without changing the density.

Second, even if one considers only packings without any obvious gaps, there are still infinitely many different packings that are just as dense as the face-centred-cubic lattice. These are the 'Barlow packings', described in this journal[2] in 1883: put down a layer of spheres arranged in the triangular lattice (the arrangement used when racking billiard balls), place another layer on top, and repeat. There are two ways to place each layer after the second (Fig. 2), giving an uncountable infinity of distinct packing schemes, all with the same density.Third, in the face-centred-cubic lattice, each ball touches 12 others. But there are infinitely many distinct ways to arrange 12 balls around another ball of the same size, because there's a lot of slack — almost room to squeeze in a thirteenth ball.

It is these various kinds of non-uniqueness that make the problem hard. (Paradoxically, the sphere-packing problems in four and eight dimensions may turn out to be easier, because the last two types of non-uniqueness are absent.) So far, no one has found a simple approach to the three-dimensional problem.

The methods that have been tried, and which in Hales's hands finally succeeded, are messy. The basic approach is to reduce a minimization problem involving infinitely many variables to a finite number of subproblems, and until the proof is finished it is never certain that the splitting into subproblems will terminate.

There have been two unsuccessful attacks on the problem in recent years that received widespread attention. Buckminster Fuller claimed to have a proof[3] in 1975, but his arguments amount to a description of the face-centred-cubic packing rather than a proof of its optimality. Then in 1993 Wu-Yi Hsiang published a 100-page paper[4] claiming to give a proof. But there are serious flaws in his arguments too. To quote one review[5]: "If I am asked whether the paper fulfils what it promises in its title, namely a proof of Kepler's conjecture, my answer is: no. I hope that Hsiang will fill in the details, but I feel that the greater part of the work has yet to be done."

Figure 1 **Cannonballs stacked in a face-centred-cubic lattice (Arlington, Virginia, about 1863). There is no denser way to do it.**

Hales has been working on the Kepler conjecture for ten years, having proposed a five-step attack on the problem. Two parts have already been refereed and published[6]. The now completed proof[7] relies heavily on computers, which are used in several different ways. For example, at the heart of the proof are some 100,000 linear programming problems, each involving 100 to 200 variables and 1,000 to 2,000 constraints. Hales has been careful to make all the computer calculations available on his website[7]. Although the final acceptance of his claim must await a careful refereeing of the proof, there is little reason to doubt it. There was never any strong reason to suspect that Kepler's conjecture was false — although it was a little worrisome that there are packings[8] of identical ellipsoids that have densities exceeding 0.75 — but the proof is a considerable achievement.

Far from being the last word, Hales's result is just the beginning. Communication theorists as well as mathematicians are interested in determining the densest sphere packings in dimensions above three. The sampling theorem of information theory[9] says that a signal containing no frequencies above W hertz can be reconstructed from samples taken every $1/(2W)$ seconds. So a signal that lasts for T seconds can be represented by $2WT$ samples. Just as three numbers specify the coordinates of a point in three-dimensional space, so these $2WT$ samples specify a point in $2WT$-dimensional space. The whole waveform is specified by a single point in $2WT$-dimensional space. Similar signals are represented by nearby points, dissimilar signals by well-separated points. So one of the fundamental problems in communication theory is determining the densest packing of balls in high-dimensional spaces.

This geometrical way of representing signals, at the heart of Shannon's mathematical theory of communication[9], underlies the high-speed modems that we now take for granted. One of the most common coding schemes in use today works so well because the signals are represented as points in eight-dimensional space.

Many beautiful packings are known in high dimensions, and have fascinating and unexpected connections with other branches of mathematics[10]. John H. Conway and I have described[11] what we think may be all the best sphere packings in dimensions up to ten, where 'best' means that they have the highest density and contain no obvious flaws such as cavities or cracks.

Let me conclude by mentioning an amazing property of what we conjecture are the densest nine-dimensional packings. In some of these schemes (again there are infinitely many that are equally dense), half the spheres can be moved bodily through arbitrarily large distances without overlapping the other half, only touching them at isolated instants — all without changing

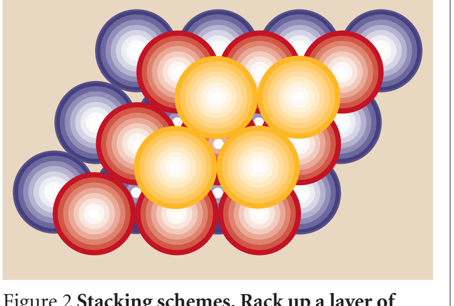

Figure 2 **Stacking schemes. Rack up a layer of billiard balls (purple); place another layer on top of them (red). The third layer can fall in a third position (yellow) as shown, or alternatively can sit above the purple spheres. You also have two choices for every subsequent layer, so there are infinitely many packings as dense as the face-centred-cubic pattern[2] (which corresponds to repeated purple, red, yellow layers).**

the density of the packing.

But until someone extends Hales's result to higher dimensions, we have no proof that any packing in a dimension greater than three is optimal. □

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Evolutionary biology

Origin of the spider's head

Michalis Averof

Comparing the structure of the head between different classes of arthropod has been controversial and often frustrating, yet it can tell us about the origins and relatedness of these different classes. The heads of crustaceans, myriapods and insects contain a characteristic set of at least five segments, which are thought to be homologous among these groups. But the morphology of chelicerates — which include spiders, scorpions, mites and horseshoe crabs — gives no good clues about the relationship of their segments to the head segments of other arthropods. Now, however, studies based on the expression of developmental genes by Damen *et al.*[1] and Telford and Thomas[2], published in *Proceedings of the National Academy of Sciences*, provide convincing evidence for previously unexpected homologies.

Chelicerates do not have a body region that could be obviously characterized as a head. Their bodies are subdivided into two portions — the prosoma (front) and the opisthosoma (back). The prosoma contains segments that bear the chelicerae (spider's fangs), pedipalps and four pairs of walking legs. It carries the main feeding, sensory and locomotor apparatus and, in a functional sense, acts as a head and thorax combined (Fig. 1). But from its morphology, we have so far been unable to find clear evidence for the relationship between this region and the segments of other arthropods.

Damen *et al.*[1] and Telford and Thomas[2] now provide evidence that comes not from the morphology itself, but from the genes that generate that morphology. They studied the Hox (homeotic) genes, which are known to specify the identity of the different types of segment within the body of insects[3]. These genes are particularly attractive for distant evolutionary comparisons of segment specialization[3–5] because their function seems to be widely conserved (in animals as diverse as arthropods, vertebrates and nematodes), and their activity is faithfully reflected by restricted expression in particular regions of the body. Different classes of arthropod have almost identical sets of Hox genes[3,5], but these are expressed differently in animals that have distinct patterns of segmental specialization[4–6]. Similarities in the expression of these genes have been used as evidence for a common origin (homology) of the corresponding specialized types of segment[4].

Damen *et al.* and Telford and Thomas report the identification and expression of Hox genes in two different members of the Chelicerata, a spider[1] and a mite[2]. The results from the two species are congruent and point to the same conclusion — that expression of Hox genes in the prosoma of chelicerates is similar to the expression of homologous genes in the head segments of other arthropods. This suggests that the entire prosoma of chelicerates may correspond to a head (Fig. 2). Indeed, the similarities are so striking that the authors do not hesitate to suggest specific one-to-one homologies between segments of the prosoma and the head segments of other arthropods.

Most convincing are those of the most anterior parts of the body, between the cheliceral segment and the first antennal (deutocerebral) segment, and between the pedipalpal and the second antennal or intercalary (tritocerebral) segment. In more

Figure 1 **The prosoma of a horseshoe crab (ventral view). The mouth is surrounded by legs bearing prominent endites (arrowheads), a characteristic associated with feeding. Damen *et al.*[1] and Telford and Thomas[2] propose that the prosoma corresponds, in evolutionary terms, to the head of other arthropods such as crustaceans and insects.**

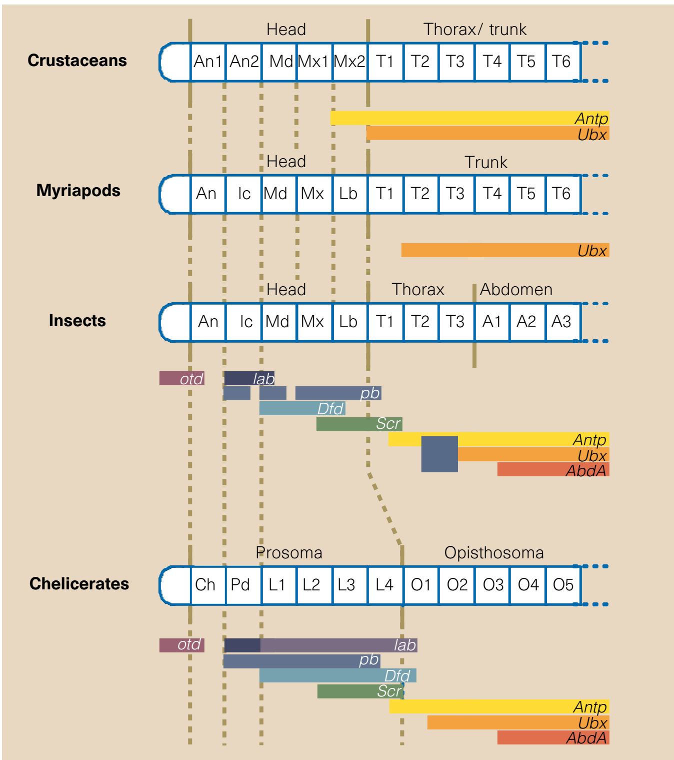

Figure 2 **Expression of Hox genes and inferred relationships among anterior body segments in different arthropods. Arthropods express almost identical sets of Hox genes in different regional domains (colour coded for homologous genes)[1–6,9]. Although there are some variations within arthropod classes, the expression domains shown are those thought to be typical or ancestral for each class. The homologies between insect, crustacean and myriapod segments are based on morphological evidence.**