(Fig. 1). Attempts to understand how this system works focused first on trying to find a protein that binds to the SECIS region, on the assumption that such a protein might work in a similar way to the bacterial SelB protein. Nevertheless, despite numerous false alarms, the mammalian counterpart(s) of the bacterial SelB remained elusive. These 'scarlet pimpernel' properties can be explained by the discovery that, in mammals, the functions of SelB are divided into two proteins.

One protein, called SBP2 (SECIS-binding protein 2), binds the SECIS element[5]. The binding specificity[5] of this protein depends on a key feature of the SECIS — a quartet of non-Watson–Crick base pairs[6]. But this protein does not have the task of binding to the selenocysteine-carrying tRNA, and it does not have the sequence features that would be expected of a protein that brings tRNAs to the ribosome. The discovery of the mammalian protein that does this — called eEFsec[1,2] — was helped by the finding[7] of a specialized elongation factor in *Methanococcus jannaschii*, a microorganism from the Archaea. This elongation factor from *M. jannaschii* does not bind to the SECIS element, but does bind to the selenocysteine tRNA.

Tujebajeva *et al.*[1] and Fagegaltier *et al.*[2] have now discovered the mammalian counterpart of this archaeal protein, by searching through sequence databases using the amino-acid sequence of the archaeal protein as a starting point. Like its archaeal counterpart, the mammalian protein does not bind the SECIS element but does interact directly with both tRNAs bearing selenocysteine[1,2] and SBP2 (ref. 1). So the SECIS element — through a two-protein complex containing SBP2 and eEFsec — can recruit selenocysteine-carrying tRNAs (Fig. 1).

But this protein complex, when bound to the stem-loop structure, is a long way from the UGA codon. How does the distant complex find the waiting ribosome and deliver selenocysteine? This is especially perplexing in the case of a protein called SelP, whose mRNA has between 10 and 17 UGA codons depending on the species[8,9], each coding for selenocysteine. For such cases, one could imagine a processive model based on the known proximity of the two ends of an mRNA strand. In this model the SECIS element would deliver the SBP2 complex to a ribosome that is just starting translation. When the ribosome reaches the first UGA codon, the required selenocysteine is already with the ribosome, ready to be inserted into the growing protein. Afterwards, the ribosome-bound tRNA might be able to pick up a second tRNA-bound selenocysteine, and so on. But, if operative, this or other processivity models must have sophisticated aspects that are not yet apparent[10].

The obvious model, by analogy with the situation in *E. coli*, is that the protein complex, bound to the tRNA and to the SECIS element, reaches back and delivers the tRNA (plus selenocysteine) directly to the ribosome[11] (Fig. 1). But how the loaded SECIS finds the waiting ribosome remains a mystery. With the new proteins[1,2,5] now identified, one hopes that answers to these questions will not be long in coming. Help will no doubt come from studies of the supramacromolecular translation complexes[12] that may coordinate interactions central to the decoding of genetic text.

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Statistical physics

Following the crowd

David J. Low

When we are at a major sporting event or travelling on public transport, our safety and comfort depend crucially on our fellow crowd members and on the design and operation of the facility we are in. So it is unnerving to realize that the modelling currently used to design and operate these venues has more in common with the design of water-pipe networks than anything with a human dimension. On page 487 of this issue[1], Helbing, Farkas and Vicsek present a dramatically different and potentially far more realistic modelling approach.

The movement of large numbers of people is important in many situations, such as the evacuation of a building in an emergency. In large crowds there is a risk of injury, and even loss of life, owing to the enormous forces that can be exerted on a single individual by the surrounding throng. The pressures that build up can bend steel barriers or push down brick walls. The consequences of crushing, trampling and panic in crowds are well known[2,3], and a proper understanding of how groups of people move is vital if we are to minimize risks in these situations.

The traditional approach to predicting the motion of large crowds of pedestrians models the crowd as if it were a continuous homogeneous mass that behaves like a fluid flowing along corridors. The predicted flow rate indicates how quickly the crowd will move. However, this traditional approach assumes that the crowd is made up of identi-
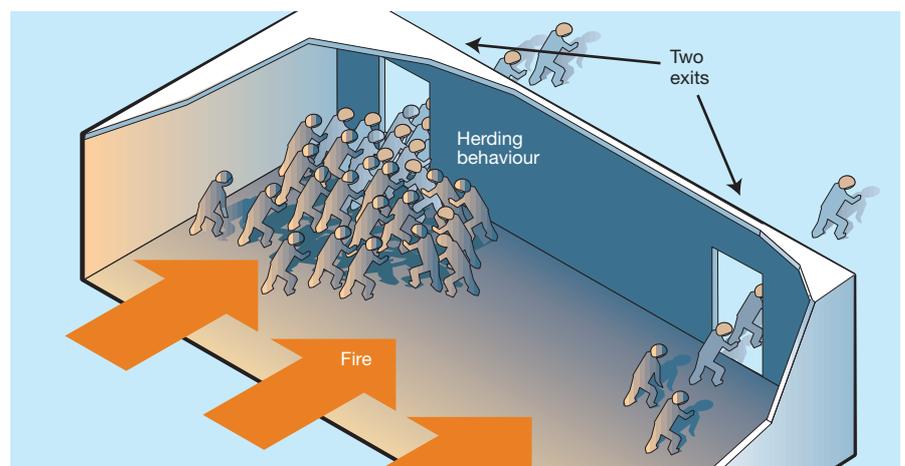

Figure 1 **How crowd behaviour affects escape from a smoke-filled room. Previous simulations of pedestrian behaviour in crowds have used a model based on fluid flow through pipes, but these ignored the actions of individuals. According to the individual-centred model of Helbing *et al.*[1], the evacuation of pedestrians from a smoke-filled room with two exits can lead to herding behaviour and clogging at one of the exits. By contrast, a traditional fluid-flow model would predict the efficient use of both exits. A more individual-centred approach is required to reproduce the behaviour of real crowds.**

cal, unthinking elements. A fluid particle cannot experience fear or pain, cannot have a preferred direction of motion, cannot make decisions, and cannot stumble or fall. The diverse behaviour of individual crowd members can drastically change the way in which the crowd as a whole behaves. Injuries to crowd members are related less to average pressure within the crowd than to point pressures at individual localities, and an injured pedestrian can fall and become an obstacle to the movement of others.

The new approach requires a recognition that the crowd is made up of individuals who possess the ability to think and react to events around them. One of the most dramatic cases in which human behaviour influences events is in a panic situation. Helbing *et al.* address this particular problem with a computer model of pedestrian behaviour that includes realistic reactions to crushing, panic and reduced visibility. They also simulate the tendency of people to do what others do and 'follow the crowd', but also allow for individuals to adopt personal strategies. Helbing *et al.* demonstrate that, because of their increased speed, panicking individuals will block up an exit that they could pass through safely at normal walking speed. They also show that a widening in a corridor actually slows down the movement of pedestrians, rather than allowing them to move faster, as one would assume. This surprising result is explained by those pedestrians who might have tried to move away from or overtake each other having to squeeze back into the mainstream flow at the end of the widening.

Modelling a crowd composed of discrete individuals rather than a continuous fluid clearly brings added complications. Helbing *et al.* model 'non-fluid' crowd properties, such as the 'faster-is-slower' phenomenon in which people in a rush end up going slower. They also investigate the best evacuation strategy for people in a smoke-filled room (Fig. 1). Such information can then be used to work out low-risk designs for the width of corridors, the number and position of doors, and the size of areas where people may gather. But these types of study can also provide us with a wider range of possible solutions to crowd problems. The crowd composed of individual people can respond to information directed towards them, to help them choose the most appropriate direction to take or the most appropriate exit to use.

In the past, one of the main barriers to adopting this approach was the enormous number of calculations that are required to solve separate equations of motion for each crowd member. Modern computing power has dramatically changed that situation. Indeed, individual-centred approaches are now widely used in the modelling of road traffic networks[4,5], which also used to be dominated by fluid-flow models. Similar individual-centred traffic models[6] have produced excellent results and have led to effective new traffic management strategies. There has been extremely strong financial motivation to produce such improved traffic models. Traffic management strategies and road-building projects cost enormous sums of money, as do the delays caused by road congestion, and improved traffic modelling techniques can produce considerable savings. But the potential benefit of improved pedestrian models is even more valuable — a reduction in personal injury.

The model presented by Helbing *et al.* is just one of many possible models. To decide whether a particular model is an accurate description of real life, or to determine which model is the 'best' for the situation under consideration, requires real data to compare with each model's predictions. But such data are scarce or non-existent and may be extremely difficult to collect. With any type of mathematical modelling we always have to be careful to distinguish between 'real life' and our attempt to model it. Failing to recognize this difference can have serious consequences. But provided we are aware of when it is appropriate to use a particular model, it can provide valuable information to guide the planning process, for construction and for dealing with emergencies. Perhaps perfect safety is unattainable, but improved models of crowd dynamics can help to increase our safety in crowded situations. ∎

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Genomics

Use your neighbour's genes

Don Cowan

On page 508 of this issue, Ruepp and colleagues[1] describe the complete genome sequence of the acid- and heat-loving microorganism *Thermoplasma acidophilum*. This hardy organism, which lacks a cell wall, grows best on organic substrates at pH 2 and 59 °C. It was first isolated, in the late 1960s, from a self-heating ore pile[2]; such ore piles generate heat through internal microbial activity.

Microbial physiologists and structural biologists have long been fascinated by the ability of this microorganism to grow at high temperatures and low pH without the structural protection of a conventional cell wall. *T. acidophilum* is also interesting from an evolutionary perspective. Its cellular morphology seems primitive, and it contains complexes involved in protein folding, degradation and turnover that look like simple versions of related structures in eukaryotic cells (loosely, those cells with a nucleus — the type of cell that makes up higher organisms such as you and me). These facts intrigue evolutionary biologists, who have speculated that *T. acidophilum* is an ancestor of the eukaryotic cell.

Initially, *T. acidophilum* was classified as a thermophilic mycoplasm — a heat-loving example of a group of primitive, gliding bacteria, which lack cell walls[2]. But following analysis of its lipid composition and ribosomal RNA sequences, it was reassigned to the new 'third domain of life' — the Archaea[3] (Fig. 1). *T. acidophilum* is the ninth member of the Archaea for which the genome has been completely sequenced[4–10]. All except one of these microorganisms are heat-loving. Why is there this focus on the ther-
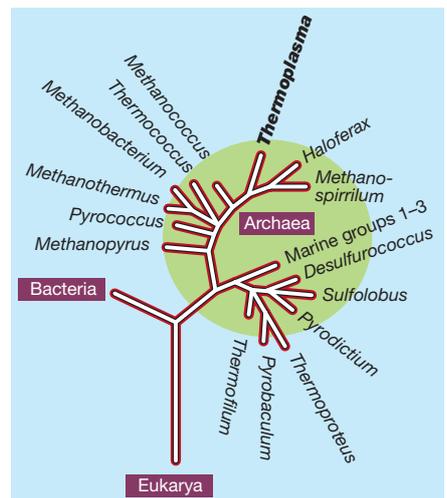

Figure 1 **The three domains of life, showing how** ***Thermoplasma acidophilum*** **— the latest archaeon whose genome has been sequenced[1] — fits into the evolutionary scheme of things. On the basis of its primitive morphology and the presence of what seem to be several primitive cellular structures,** ***T. acidophilum*** **was once thought to be an ancestor of eukaryotic cells. But details of its genome sequence[1] make this unlikely. This phylogenetic tree is based on 16S ribosomal RNA sequences (modified from ref. 12).**