Predicting where we walk

Michael Batty

Models that link human behaviour to the way paths are formed provide excellent predictions of path geometry. In principle, such models can be extended to urban areas, and used to help understand how space affects such phenomena as crime, congestion and pollution.

The application of classical physics to human affairs, known as social physics, grew in popularity through the early twentieth century. It reached a peak in the 1950s and 1960s when gravitation and potential theory was widely used to predict traffic flow, migration patterns and the distribution of population. Since then it has lost its appeal but, suddenly, new ideas from physics based on scaling and self-organization once again appear to have wide applicability to the social sciences.

On page 47 of this issue¹, Helbing, Keltsch and Molnár illustrate a simple model of how walkers, crossing an open space, are able to self-organize their walks into paths or trails which have a geometry highly characteristic of how real paths develop. Their model is based on standard notions of defining a potential for walking at any point within the space, moving walkers towards points of highest potential in the direction they are travelling, updating this potential, and then reiterating the process, adding new walkers randomly, until an equilibrium based on a stable structure of paths emerges.

Walking potential at any point is defined with respect to the current location of any walker. Distance between these locations acts as a deterrent while visibility increases potential. Both are weighted by a measure of attraction of the point that has the potential to be part of a trail. This attraction is referred to as the 'comfort of walking'. It is measured from a baseline environment which is 'uncomfortable' for walking but which is made more comfortable as walkers impress their footprints differentially across the space. The baseline environment, which might be a grassy field, say, gradually grows back through time; thus the comfort of walking is a perpetual fight between the number of walkers who visit each point and flatten the grass into more comfortable paths, and the restoration of the initial environment.

This model, which is based on a potential updated by positive feedback incorporating a logistic limit on the comfort of walking, is quite standard in theories of self-organization². In applications to social systems, particularly cities³⁻⁵, it has frequently been used to model the effects of spontaneous growth such as out-of-town centres or malls,

'edge cities' as they are called⁶, or the rapid rehabilitation of inner cities associated with gentrification, for example.

Helbing, Keltsch and Molnár's model extends these applications in two ways. First, the geometry of the system is an emergent property of the model. In most urban applications of social and statistical physics to date, with the possible exception of fractals⁷, the geometrical structure of the system is assumed — it is an input to the model. Here it is a consequence of the model. One of the longest-standing issues in applying quantitative models to human systems has been the inability of those models to link spatial structure to social behaviour. Here at last is an approach to modelling in which spatial structure emerges as a consequence of behaviour. The implications are profound.

The second significant feature of the new approach is its application to routine spatial behaviour at a fine scale. To date, most applications have been to much more aggregate populations organized into social groups and large spatial units. It has long been assumed that such models, especially those involving movement, would only apply to the prediction of aggregate traffic patterns, but these 'active-walker' models, developed elsewhere in physics, are pitched at the level of micro-behaviour. The emphasis here on pedestrian movements is unusual. By concentrating on

relatively simple behaviour where the goals of each walker are unambiguous (to cross the space from some origin to some destination), and by assuming simple, relatively unobstructed spaces, excellent predictions of the paths taken and the volumes of traffic generated can be made. Figures 3 and 4 on pages 48 and 49 mirror our experience of the way paths develop as a compromise between all distinct walking directions.

These models can easily be extended to deal with more complex situations where terrain is uneven, where directions and visibility across and within the space confound the picture, and where classes of walker with different motivations might mix within the space. However, the real challenge is to extend this type of thinking to built rather than natural environments. Most pedestrian movement of significance in cities is along pavements, and within buildings and public squares. Origins and destinations of walkers are diverse, while the motivation for walking within space has to be extended to more casual pursuits such as resting and strolling, where direction is less important.

But by far the most significant issue involves predicting why certain spaces and routes are less favoured than others. Consider the pedestrian movement patterns shown in Fig. 1 for rooms within the Tate Gallery on London's Millbank. Clearly, some rooms in the gallery are hardly visited at all, and it is difficult to see how environmental conditions could be incorporated into Helbing, Keltsch and Molnár's active-walker model which would generate such a configuration of paths. The underlying conditions do not relate to the space itself but to the configuration of rooms that define the space, to the way they draw people towards them, or repel walkers, and to what lies within each room. These are difficult issues to model but they are essential to an understanding of how space affects a variety of phenomena, such as crime, congestion and pollution, which are highly correlat-

Figure 1 Pedestrian paths based on tracking visitors for the first ten minutes after they enter the Tate Gallery, London (August 1995). The challenge is to develop active-walker models of the kind illustrated by Helbing, Keltsch and Molnár¹, as discussed here, which enable such patterns to be predicted. (Figure courtesy of the Space Syntax Laboratory, University College London.)

ed with movement and intensity of use⁸.

One way of proceeding is to measure the underlying structure of movement which such spaces imply and use these 'movements' to condition the environmental baseline. For example, Hillier and Hanson^{9,10} have developed ways in which the syntax or rules that determine the configuration of such space can be detected through the identification of the most significant lines of sight. These 'axial' lines and their relative connectivity to one another are highly correlated with movement¹¹. They suggest an underlying structure to urban space that is determined by the complexity of buildings or rooms which bound the space.

The syntax based on such lines might be used to condition the environmental variables in the active-walker model, which in turn determine the potential for walking at different points within the space. Further developments for more structured kinds of vehicular traffic at the micro-spatial scale suggest themselves. Traffic prediction along streets is difficult and the macro-models rarely hold up. Active-walker models might be used to embed such macro-predictions into a local geometric context, picking up data on environmental conditions which have no meaning at more macro levels where conventional traffic models operate.

There is a wealth of possible applications and extensions of such models, not only to human but to animal populations, and to social as well as physical spaces. These models naturally extend to problems where the goal is to optimize, to design 'best' paths, as is characteristic of many planning problems where the task is to design high-quality urban environments. □

Michael Batty is at the Centre for Advanced Spatial Analysis, University College London, 1-19 Torrington Place, London WC1E 6BT, UK.
e-mail: m.batty@ucl.ac.uk

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Membrane fusion

Bridging the gap by AAA ATPases

Tony Rowe and William E. Balch

Membrane fusion is central to a number of tightly regulated events, including vesicle transport, the maintenance of subcellular compartments, and the disassembly and reassembly of organelles during cell division. Targeting and fusion of transport vesicles¹ requires many membrane-bound and cytosolic factors, and much attention has been paid to the ATPase, *N*-ethylmaleimide-sensitive factor (NSF) and its functional partners — the soluble NSF attachment proteins (SNAPs), and SNAP receptors (SNAREs).

NSF belongs to a growing family of proteins known as the AAA-type ATPases, which are implicated in a diverse array of activities including intracellular membrane dynamics². All of the AAA-type proteins contain one or two copies of a 200-amino-acid ATPase module that is essential for ATP binding and hydrolysis. One member of this family — the product of the yeast cell-cycle gene *CDC48* — is involved in the fusion of endoplasmic reticulum and nuclear membranes³. The rat homologue of *Cdc48p* is p97, and this protein is involved in the reassembly of Golgi cisternae after cell division^{4,5}.

Although much is known about the binding partners for the NSF, the factors that

interact with the other AAA-type ATPases are unknown. But on page 75 of this issue, Kondo *et al.*⁶ report that they have identified an accessory factor, called p47, which is required for p97-dependent membrane fusion *in vitro*. They find that p47 forms a stable cytosolic complex with p97, at a stoichiometry of one trimer of p47 per hexamer of p97. Furthermore, the active cytosolic component that is required for membrane assembly is the p97/p47 complex, rather than p97 alone as was previously suggested³⁻⁵.

When examined by electron microscopy, the p97/p47 complex shows a barrel-shaped structure containing a central channel that is ringed by the p47 trimer. This structural organization is very similar to NSF and other members of the AAA-type ATPase family, including molecular chaperones, indicating that they may share similar modes of action. Although the sequence of p47 is unrelated to the SNAPs, it is homologous to yeast Shp1p, which is a protein of unknown function that is required for normal cell growth. So Shp1p is probably the cytosolic binding partner for *Cdc48p*.

With the discovery of p47 by Kondo *et al.*, the molecular details of p97-dependent fusion can now be addressed. For instance,

what is the role of p47? Is it an 'adaptor' protein that mediates the binding of p97 to a membrane-bound receptor(s) — in the same way as SNAPs recruit NSF? And at what step of the membrane targeting/fusion pathway does the p97/p47 complex act? This question is relevant to the debate over the mechanism of NSF action⁷: whereas the original proposal of the SNARE hypothesis was that NSF could promote fusion following membrane docking, recent results indicate that NSF is needed at a pre-docking (or 'priming') step^{7,8}. So NSF, p97 and related AAA-type ATPases may coordinate the protein-protein interactions that mediate membrane priming and targeting⁷, and analysis of the p97/p47-mediated pathway could help to resolve this issue.

Another potentially common feature of membrane-recognition events that involve AAA-type ATPases is the Rab family of GTPases. These proteins are required for many NSF-dependent steps, leading to the homotypic assembly of organelles (that is, fusion of 'like' membranes)^{9,10}, and heterotypic fusion (vesicular transport between different compartments)¹. So are these Rab proteins necessary for the function, in membrane dynamics, of other AAA-type ATPases such as p97? Consistent with this possibility, a Rab GTPase is required for the homotypic assembly of mammalian endo-

Figure 1 Members of the AAA-type family of ATPases are involved in the membrane dynamics of subcellular compartments. Many of them, such as *N*-ethylmaleimide-sensitive factor (NSF) and yeast *Cdc48p*, have accessory factors. The accessory factor for the rat homologue of *Cdc48p*, p97, has now been found by Kondo *et al.*⁶. p97 forms a complex with this accessory factor (p47), and the p97/p47 complex forms the active cytosolic component for membrane assembly. AAA-type ATPases are required for homotypic events (that is, between 'like' membranes) involved in the assembly and maintenance of different compartments (X and Y), and vesicular trafficking between these compartments. The membrane-recognition events that are controlled by these proteins and their accessory factors may involve an evolutionarily conserved mechanism.