

Hierarchies defined through human mobility

Elsa Arcaute

An analysis of worldwide data finds that human mobility has a hierarchical structure. A proposed model that accounts for such hierarchies reproduces differences in mobility behaviour across genders and levels of urbanization. **See p.402**

Our intuition suggests that humans travel across characteristic spatial scales, such as neighbourhoods, cities and countries. However, analyses of large data sets indicate that human mobility has no intrinsic scales^{1–3}. On page 402, Alessandretti *et al.*⁴ combine worldwide data with modelling to solve this conundrum.

Rural areas, settlements and cities evolve to sustain the lives of their inhabitants. For example, footpaths sometimes transition into roads or even railways to facilitate the different interactions between individuals, communities and other social groups. At the individual level, each person travels to connect with others and exchange friendship, knowledge or goods, to be part of rituals and to access urban functions such as education, economic opportunities and leisure.

Each of us is unique, and we might be convinced that our lives are more exciting than are those of our neighbours – but maybe not as exciting as those of musicians, who are regularly out rehearsing, holding gigs in different parts of the city and touring all over the country or even the world. However, if our daily movements left traces, as ants leave pheromone trails, would these have a perceptible pattern? And would this pattern hold if we were living in a different city or country?

These questions can be answered properly only by analysing global mobility patterns. Widespread geographical tracking of the use of smartphones, credit cards and other technologies has allowed academics to tap into these data sets and conclude that human travel cannot be characterized by spatial scales^{1–3}. Such results have made their way into leading scientific journals. However, they seem to contradict not only our intuition but also what is accepted in the field of geography – that the mobility of individuals depends on context and is constrained by cost.

We plan our trips and perceive the associated space in a hierarchical way. This viewpoint is reflected in the selection of a specific mode of transport according to where we want to go.

For example, we might ask which metro line will take us north of the city, whether there are direct trains to a particular city or which airline will take us to a particular country.

The paper by Alessandretti and colleagues provides a solution to this mobility riddle. It presents a model that agrees with our hierarchical perception of space – that individuals have different scales of mobility depending on context. The authors analysed GPS location data for hundreds of thousands of people worldwide at a high temporal and spatial resolution, and they inferred the hierarchical structure of each individual's mobility. They confirmed that the perceived structure is not an artefact of our brains, nor of the imposition of administrative delimitations, but corresponds to the way we move in space.

Alessandretti *et al.* used these global traces to identify typical spatial scales, which are referred to as containers in the paper (Fig. 1a). The authors discovered that container size has a probability distribution known as a log-normal distribution (Fig. 1b), corroborating recent results on the distribution of settlement sizes⁵. They found that a log-normal distribution provides a better statistical fit than does a scale-free (power-law) distribution, in opposition to the scale-free mobility behaviour reported in the literature^{1–3}. The authors reconciled these results by obtaining a power-law distribution from the aggregation of all containers (Fig. 1c).

A further achievement of the paper relates to the use of the model to produce simulated traces of human mobility, and how these traces reproduce differences in mobility behaviour associated with gender and level of urbanization. Alessandretti *et al.* found that, although the mobility of women is more complex than is that of men, it is also spatially smaller. Moreover, they confirmed that people living in rural areas have much larger containers than those of individuals in urban areas.

The origin of the observed hierarchical structure has puzzled academics for more than a century. Many theories and models^{6–8} have been developed in an attempt to capture patterns resulting from the co-evolution of the physical form⁹ and the function of cities. However, these attempts have encountered various challenges emerging from the fact that infrastructure changes slowly, whereas land use and demographics change quickly.

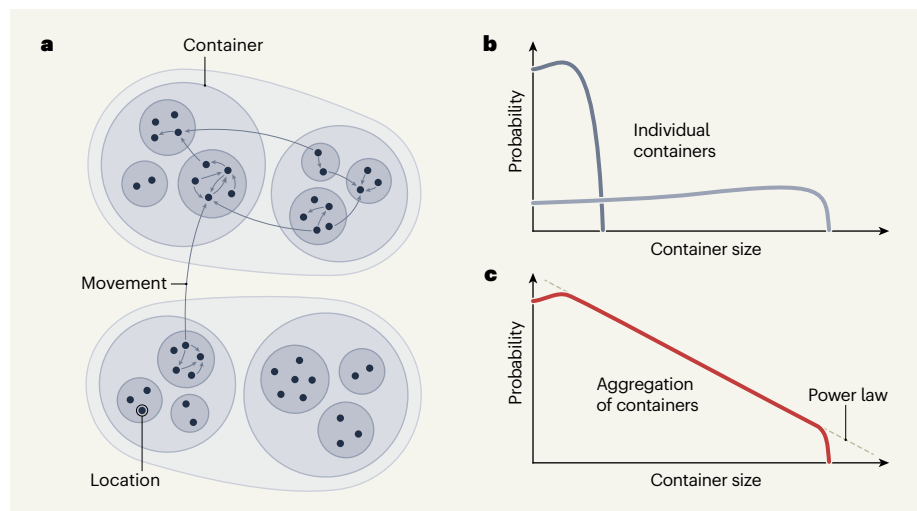


Figure 1 | A model of human mobility. **a**, Alessandretti *et al.*⁴ present a model that can reproduce key properties of human mobility. In the model, observed spatial scales of human movement – such as the scales of neighbourhoods, cities and countries – are represented by different-sized containers. In this schematic, a person moves between particular locations in small containers, which are inside medium-sized containers, which are inside large containers. **b**, The authors applied their model to global mobility data. This plot illustrates, for two individual containers, the probability of it having a particular size, on a log–log scale. Such probability distributions are known as log-normal distributions. **c**, When all the containers are aggregated, rather than being considered individually, the container size instead follows a distribution called a power law. The generation of these two different distributions from the same data set reconciles two different perspectives on human mobility.

Urban systems have been shaped by mobility and the need to satisfy different human interactions modulated by the speed of transportation¹⁰. For centuries, we have left traces of mobility through our road networks¹¹, encoding the hierarchical structure of urban systems at multiple scales. An open question is whether Alessandretti and colleagues' research can be extended to explain why such patterns emerge worldwide and why cities have their particular morphologies. Is the observed organization of urban spaces the result of centuries of mobility? And could the authors' work help us predict the future of our cities, now that we can tap into the traces of the movements that shape them?

Elsa Arcaute is at the Centre for Advanced Spatial Analysis, University College London,

London W1T 4TJ, UK.
e-mail: e.arcaute@ucl.ac.uk

1. Brockmann, D., Hufnagel, L. & Geisel, T. *Nature* **439**, 462–465 (2006).
2. González, M. C., Hidalgo, C. A. & Barabási, A.-L. *Nature* **453**, 779–782 (2008).
3. Song, C., Koren, T., Wang, P. & Barabási, A.-L. *Nature Phys.* **6**, 818–823 (2010).
4. Alessandretti, L., Aslak, U. & Lehmann, S. *Nature* **587**, 402–407 (2020).
5. Corral, Á., Udina, F. & Arcaute, E. *Phys. Rev. E* **101**, 042312 (2020).
6. Christaller, W. *Central Places in Southern Germany* (Prentice-Hall, 1966).
7. Alonso, W. *Location and Land Use: Toward a General Theory of Land Rent* (Harvard Univ. Press, 1964).
8. Wilson, A. G. *Entropy in Urban and Regional Modelling* (Pion, 1970).
9. Batty, M. & Longley, P. *Fractal Cities: A Geometry of Form and Function* (Academic, 1994).
10. Pumain, D. *Espace Géogr.* **26**, 119–134 (1997).
11. Arcaute, E. *et al. R. Soc. Open Sci.* **3**, 150691 (2016).

Microbiology

Identifying gut microbes that affect human health

Sigal Leviatan & Eran Segal

When determining whether gut microbes affect human health, it is hard to distinguish between a causal and a correlative relationship. Analysis of microbial links to human traits and habits correlated with disease offers a step forward. **See p.448**

The resident microorganisms in the human body, termed the microbiota, represent diverse communities of microbial species comprising a complex ecology of tens of trillions of mainly bacterial cells¹. Our gut microbiota, the largest and most diverse of these communities, is in constant interaction with our body's cells and systems (such as the immune system)², and it both shapes, and is being shaped by, our health status. The particular composition and diversity of the gut microbiota are associated with many health conditions³. However, it is usually not known whether such associations are just correlative or a consequence of the health condition, or whether they might cause, or contribute to, the illness. Addressing this problem is highly challenging because of the many physiological and lifestyle differences that can exist between individuals who are healthy and those who have the illness of interest. Such confounders – the variables that correlate with both microbiota and health status – might underlie the many discrepancies observed between the outcomes of different studies linking the composition of the gut microbiota and human health⁴.

On page 448, Vujkovic-Cvijin *et al.*⁵ tackle

this problem. First, they consider physiological and lifestyle differences between people with and without a particular disease, and identify differences that might themselves be associated with the composition of the gut microbiota. Such differences can cause variation in the composition of gut microbes between healthy individuals and those who

“Failing to match individuals on their level of alcohol consumption could result in a misleading conclusion.”

have the disease. Without knowing about these differences, it would be easy to misclassify a correlative and confounding association between lifestyle and the microbiota as being an informative causal association between disease and microbiota composition.

Next, the authors attempted to deal with such confounders by taking the approach of one-to-one matching⁶ of individuals who had a particular condition with healthy individuals who were similar to them with regard to such potential confounders (Fig. 1). An example

might be matching with an individual of the same age, gender and body mass index (a value used in assessing a person's weight that takes height into consideration). This type of matching procedure is often used in observational studies in which individuals cannot be assigned randomly to two groups and subjected to the two different scenarios being compared⁷.

Vujkovic-Cvijin *et al.* report that gender, age, bowel-movement quality (categorized as stools that are solid, normal or loose), body mass index and level of alcohol consumption are among the strongest potential confounders that could hinder efforts to identify true associations between disease and gut-microbiota composition. This is because these characteristics are strongly associated both with microbiota composition and with disease status. When examining the differences between individuals with a condition such as type 2 diabetes and people who do not have this condition (but who might have other diseases), there seem to be many statistically significant associations between disease status and the abundances of different gut bacteria. By contrast, if individuals who have or do not have the disease are matched using some of the confounder criteria mentioned, many of these associations cease to be statistically significant. This implies that some gut-microbiota changes previously attributed to certain diseases might instead stem from other underlying causes related to these confounders.

For example, alcohol consumption causes gut-microbiota changes, and individuals who have certain diseases consume less alcohol than average (perhaps because of the drugs that they take). Therefore, failing to match individuals on their level of alcohol consumption could result in a misleading conclusion that microbiota changes associated with the disease are attributable to the disease itself, rather than to a below-average alcohol intake.

A potential problem with Vujkovic-Cvijin and colleagues' approach is that some of the suggested confounders might be associated with disease symptoms, rather than being lifestyle choices; people in these confounding categories could in that case already be sick but undiagnosed, or on the path to being ill. In such cases, matching with healthy individuals might actually introduce bias⁸. For example, matching people on their level of alcohol intake makes no sense when studying alcoholic liver disease. Moreover, even if potential confounders are not linked to the defining symptoms of the disease in question, or are not uniquely matched to symptoms of the disease, it should still be a cause for concern if matching for the confounder would mean that the resulting matched group is not representative of healthy individuals. For instance, matching people who have lung cancer with individuals who don't have it, after the same number of