co-workers argue that it can. Excitations created by the incident terahertz radiation involve the transfer of a negatively charged electron from one localized state to another, leaving a positively charged hole behind. These electron–hole pairs interact with each other via long-ranged dipolar interactions, which play a crucial role in the team’s argument. At the same time, there is a finite density of created pairs at small excitation energies owing to unscreened electron–electron interactions. These pairs can coherently hop quantum mechanically from one place to another⁸ and provide just the right decay channels to produce the observed energy dependence of the decay times. It is a delicate balance because the specific forms of the dipolar and electron–electron interactions are crucial for the argument to work and be consistent with the experimental results.

The temperature dependence is also consistent with this theoretical picture. Increasing the temperature destroys the quantum-mechanical coherence of the

hopping and leads to longer decay times, although why this does not reduce the measured decoherence time remains an open question. However, this explanation assumes conditions that are applicable only at doping densities far lower than the critical value at the metal–insulator transition. Why these assumptions should remain valid so close to the transition is unclear.

Unfortunately, other poorly understood aspects of doped semiconductors, such as the behaviour of magnetic excitations across the transition^{9,10}, appear to lie beyond the present scope of the technique. But Mahmood and co-workers have demonstrated the value of terahertz two-dimensional coherent spectroscopy for understanding an important problem in condensed-matter physics. New light sources have only recently made this technique more widely available, and further development may allow it to tackle other challenging problems in doped semiconductors and other strongly correlated systems. □

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Competing interests

The author declares no competing interests.

COMPLEX NETWORKS

Forward thinking on backward tracing

SARS, MERS and now SARS-CoV-2 are unlikely to be the last emerging infections we face during our lifetimes. Tracing contacts both forward and backward through our heterogeneous populations will prove essential to future response strategies.

Johannes Müller and Mirjam Kretzschmar

Urban sprawl and the destruction of natural habitats are steadily increasing the threat of emerging infectious diseases. The first choice for battling an epidemic is, of course, to use an effective vaccine. But the world has suffered a year of lockdown restrictions waiting for the development of effective severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) vaccines — rapid though they may have been. This shows that to be prepared for future pandemics, we need to sharpen our understanding of non-pharmaceutical control measures such as social distancing, screening and isolation, and — last but not least — contact tracing. Writing in *Nature Physics*, Sadamori Kojaku and colleagues¹ report that they have now determined that in heterogeneous populations, contact tracing may be more

effective if it is bidirectional, by identifying your likely infector along with those you may have infected.

Screening or social distancing can be readily modelled at the population level by simple mean-field equations. In contrast, an appropriate model for contact tracing requires keeping track of contacts between individuals explicitly. A natural framework for this is a system of particles interacting on a graph, in which the particles are individuals and the contacts between them are represented by the edges of the graph (Fig. 1). Particles in the system are either susceptible, infected or recovered, and transmission occurs along edges from infected to susceptible particles. Therefore, infection spreads locally, which leads to correlations between the states of neighbouring particles.

Contact tracing introduces an additional local correlation: if an infected individual is diagnosed, it is likely that infected neighbours will also be discovered. In this way, contact tracing can be viewed as a super-infection that spreads along the pathways of infection, racing the disease across the network and complicating analysis by introducing strong spatial correlations. There are further difficulties arising from the fact that transmission and contact tracing are both microscopic, but our interest lies in the spread of infection on a population level — in mesoscopic and macroscopic quantities. It is clear that analysis needs to bridge microscopic and macroscopic scales. A variety of contact-tracing models have been studied², but so far little is known about the probability of eradication of a local outbreak.

Fig. 1 | Contact tracing individuals interacting on a graph. In a simplified model, individuals are represented as either susceptible (black) or infected (red) and the edges between them represent contact without transmission (blue) or directed transmission of the disease (red). Contacts can be either forward traced (green circles), backward traced (blue circle) or both, and this choice can affect the efficacy of the approach.

To address this, Kojaku et al. identified another bias associated with contact tracing, which shows up when contacts are traced backward to the source of an individual's infection. The idea is that the more people an individual infects, the more frequently they will appear as a contact. And this makes backward contact tracing an efficient means of identifying super-spreaders.

In addition, Kojaku et al. proposed a clever approximation to the problem of eradication. Strictly speaking, an infected individual will probably reveal all his or her neighbours as contacts simultaneously, such that any infected neighbours will be removed from the graph at the same time. Kojaku et al. ignored these correlations and instead focused on single edges and decoupled them from the remaining graph. This simplification allowed them to use percolation theory to reveal the phase transition leading to the appearance of a giant component. This in turn offered an estimate for the probability of eradication. The problem of getting a grip on the exact probability for extinction in the full, recursive tracing process is still open, but Kojaku et al. have taken the first step towards an understanding.

These advances in theory are certainly interesting, at least for physicists and mathematicians, but are they relevant

for practice? Kojaku et al. focused on the implications in the context of complex networks, but paid little attention to how the characteristics of the infection might influence the effectiveness of contact tracing, and the relative value of backward tracing. As the authors also acknowledge, in practice, the direction of infection is usually not known, so contact tracing identifies all potentially risky contacts within a certain time period before an index case is diagnosed. Going back further in time, which might be needed for backward tracing infections with longer incubation periods, contact identification may suffer from recall problems. More importantly, the source case may no longer be infectious, and may therefore not test positive once identified.

Whether this is the case or not depends on the epidemiological characteristics of an infection, such as latent period, incubation period, infectious period and the proportion of asymptomatic infections. As we saw in the SARS-CoV-2 pandemic, the secondary cases produced during the presymptomatic phase can play a crucial role in exacerbating the difficulty of performing effective contact tracing. The proportion of transmission occurring before the onset of symptoms is one of the key factors in determining the controllability of an epidemic outbreak³. For SARS-CoV-2, even with perfect

tracing and isolation of contacts without any delays, no more than around 80% of onward transmission of an index case can be prevented⁴.

We are also faced with other practical challenges, such as predicting the public health capacities needed to control an outbreak using contact tracing — a question that depends on the severity of infections. A new aspect of contact tracing is the widespread use of digital tracing devices, such as the coronavirus tracing apps developed and used in several countries. Most likely, the attitude to using the app correlates with the social structure in the population: education, political belief and income all influence the willingness to use such an app, and therefore app users will cluster in the population, while other parts of the population are not well covered by tracing apps.

The combination of simulations and theoretical results in the study by Kojaku et al. is a step to better understand the effects of digital contact tracing in heterogeneous populations. Tracing apps will only be accepted in democratic societies if citizens trust their safety and usefulness, which requires clear and honest communication by public health professionals about the strengths and the weaknesses of digital contact tracing. In that respect, studies like this are invaluable achievements, both intellectually and in terms of their ability to support the policy decisions of public health authorities — and also inform responsible citizens. □

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Competing interests

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