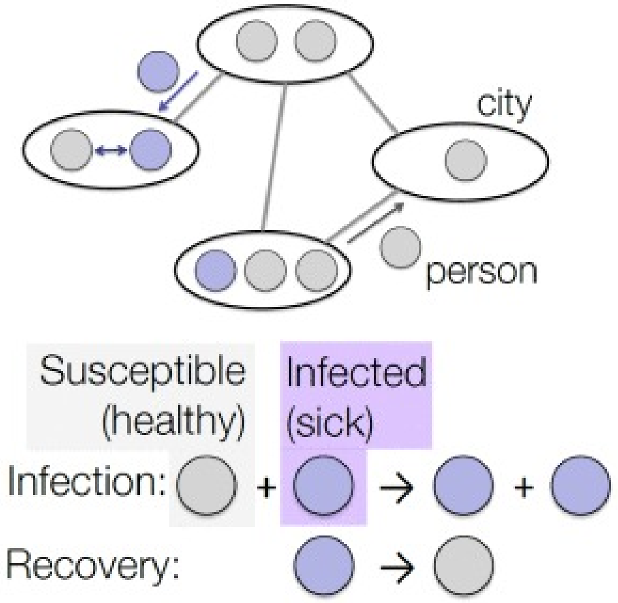
Improving the mathematical estimation of the epidemic threshold on networks

Infectious diseases spreading via person-to-person contacts, such as plague, flu, and Ebora, have threatened humanity since the beginning of the recorded history. Societies have long been using the power of sciences to understand and mitigate the impacts of the diseases. For example, biologists have uncovered the characteristics of pathogen viruses. Physiologists have explored the infection process happening in our body. Aside from them, mathematics can also play an important role in our fight against the viruses, although a less obvious one.



One possible way to use mathematics to think of disease spreading is as follows. First, we construct a network of subpopulations (e.g., schools, cities, or countries) and weighted links between them, representing flows of human mobility. Second, we consider the mobility and interactions of a large number of individuals on the corresponding network. To make the problem simple, we often assume that all the individuals are statistically identical and that each of them takes either of two states: Healthy or Infected. Interactions between individuals can mediate the infection and only occurs inside each subpopulation. These simplifications allow us to describe the dynamics by means of mathematical equations, which can then be solved in order to improve our understanding of the spreading.

What type of quantity can we compute? A key quantity is the epidemic threshold, the critical value of the infection strength. If the infection strength of a pathogen is below the threshold, the expected number of infection cases is negligible compared to the total population. By contrast, if it is above the threshold, the infection could go viral up to the size comparable with the entire population. In general, the epidemic threshold depends on the network topology and on the rules of human mobility and their interactions.

It is generally difficult to obtain the exact expression for the epidemic threshold, despite the simplification of the processes. A way to circumvent this problem is to proceed by means of computer simulations. However, only an analytical expression can help us identify without ambiguity the factors affecting the epidemic threshold. Previous studies have made the problem even simpler by imposing an approximation about the network topology, and have analytically derived an estimate of the epidemic threshold. Since the approximation sounds unrealistic, alternative approaches, applicable for general networks, are needed.

In a paper published recently, we have proved, without relying on the same approximation, that their expression is an upper bound for the exact value of the epidemic threshold. In addition, we have extended the proof to derive an improved estimation of the epidemic threshold. What does our improved estimation tell us? It shows that not only the presence of hubs (entities having large number of connections) is important, but also how they are connected with each others. If we observe more connections between hubs, the estimated threshold gets smaller. It is intuitive that such strong connectivity between hubs makes infection spread easier. More than that, this network property may change whether there IS a spreading or not, which is the meaning of the change in the epidemic threshold.

Although our results are still based on simplified models, this first step with sound mathematical analysis provides the ground for the study of more realistic processes. Ultimately, cooperation with biological and physiological researchers would lead to better prediction and intervention strategies for future disease spreading.

Publication

Sufficient conditions of endemic threshold on metapopulation networks.
Takaguchi T, Lambiotte R
J Theor Biol. 2015 Sep 7