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Complex network models of disease propagation: modelling, predicting and assessing the transmission of SARS

Key Messages

1. Complex network models improve descriptions of disease transmission, and reveal the relationship and contacts between all individuals within a community.
2. These models might have been able to predict the extent of the SARS outbreak. For realistic parameter values (estimated from community demographics), the outbreak was substantial only if transmission within hospitals was not controlled.
3. Super-spreading events can occur as a consequence of human connectivity, and are not necessarily a result of highly infectious individuals.
4. Avian influenza can be described by the scale-free network, which exhibits occasional extremely high connectivity between outbreak sites. This means that merely reducing infectivity cannot effectively control avian influenza. Control can only be achieved by removing places where large numbers of poultry congregate.

Introduction

Traditional (compartmental) models of disease transmission categorise individuals from a population, based on their current pathology. These models trace the proportion of a population based on which state (susceptible, exposed, infected, or resistant to a disease) into which individuals fall. These models provide a population-based description that offers a stabilising response to the presence of an infectious agent. We examined data from two recent Hong Kong outbreaks, namely the current global avian influenza outbreak among birds and the 2003 outbreak of severe acute respiratory syndrome (SARS) among humans. Both cases exhibited large variability in terms of outbreak intensity and hence were not consistent with the standard models of disease transmission. The observed behaviour can be more readily explained using a computational (discrete agent-based) model of transmission on a complex networks. We described a model by which networks consistent with this data may arise in practice, and then provided a mathematical analysis of the epidemic dynamics and spreading behaviour.

Methods

This study was conducted from November 2005 to November 2007. The focus was on the application of computational complex network-based models to describe the SARS outbreak in Hong Kong. Standard models of disease transmission assume that all individuals have an equally small probability of being infected by an infectious person in the community. In contrast, a complex network model actually models the connectivity between individuals and only allows for the possibility of transmission of an infectious agent along those connections. A network consists of a set of nodes, with a set of edges connecting the nodes. Each node in the network corresponds to an individual within the community and a connection is drawn between two nodes (individuals) if there is a non-zero probability of infection. That is, two individuals are connected if they have contact that is sufficiently intimate to allow the disease to pass between them. For example, for a sexually transmitted disease this would require intercourse. For SARS (assuming droplet transmission), this only requires that the two individuals be in physical contact, or close proximity, for some period of time.

It is not feasible to know the full network of connections between individuals in a city of seven million people. Nonetheless, we know a lot about the general structure of that connectivity. Many studies of social phenomena have shown that the connectivity between individuals follows particular patterns. We implemented these patterns in our model. In particular, for human social groups, the individuals typically form a small-world network. That is, one's neighbours on a network typically are neighbours themselves (that is, your friends are usually friends with each other too). However, at the same time each node has some random connections, which violate this pattern. It has been shown that under these conditions the average path between individuals (friend of a friend of a friend and so on) typically consists of a small number of connections. A short chain of mutual acquaintances connects random pairs of individuals. This effect is known as the 'six degrees of separation' and has been observed in diverse social systems: from Hollywood movies, to co-

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authorship of condensed matter physics manuscripts, to internet and email connectivity. The same is also true for social and collegial groupings within a city. We applied this model to the population of Hong Kong and restricted the transmission of a virus to pathways in this network.

Results

Using complex network models (and suitable parameter values chosen from measurable demographic features of the community), computer simulation of SARS transmission matched qualitatively and quantitatively the data observed in Hong Kong. In particular, the clustering of the outbreak in Amoy Gardens and the Prince of Wales Hospital emerged as a natural feature of the model structure. Moreover, the random variability in the degree of connectivity allowed for super-spreader events (localised highly effective transmission) without a need to explicitly include this feature in the model of infectivity. This is a significant improvement on existing models. These complex network models provided a simpler and more effective description of reality, although individual events, such as those cited above, had specific detailed causes. Our models also showed that the degree of infection in the 2003 outbreak in Hong Kong is due primarily to transmission within hospitals. With proper infection control within hospitals, the outbreak would probably have been far less severe.

Nonetheless, given that hospital-based infection did occur (at least initially), our simulations provided an ensemble of predicted outcomes. The actual outcome was typical of that ensemble, but the range of severity was wide. We observed typical outbreaks with fewer than 10 to more than 10 000 casualties.

Discussion

Our simulations for SARS showed a good agreement with reality, but the model itself is not derived from reality. To obtain the actual infection chains between individuals, we studied an outbreak of avian influenza, particularly for animal-to-animal infection, as data pertaining to times and locations of such an outbreak are widely available.

We used these data to construct a network of potential connection pathways to test the hypothesis that this network is complex and pertaining to a small world (consistent with that for SARS in Hong Kong). We found that the network obtained in this way is complex, but not of a small world. The reason for this is a consequence of the global geographical distribution of outbreak sites; geographically distant sites cannot be connected through a short path. Nonetheless, we discovered another important property in this network. We found that the network of avian influenza infection pathways is scale-free. This means that, on average, the number of

secondary infection sites connected to a primary site is very large (it follows a power-law distribution). Although most sites are connected to only a small number of other sites, some sites have a very large number of connections. Moreover, for the parameter values observed, the best guess (on average) that one can make for the number of connections from a given site is infinite (and yet most sites have very few connections). Networks such as this have been theorised by physicists to model disease transmission; we demonstrated evidence of such a network occurring in nature.

The theory presented in the physics community implies that for disease transmission on such a network the disease will continue to exist and be transmitted provided the rate at which infection passes between individuals is greater than zero. This is in sharp contrast to standard epidemiological models where a disease can be eliminated by reducing the infectivity below some finite threshold. For avian influenza this is not possible. The only way in which avian influenza can be eliminated is by changing the structural features of the network of infection pathways. The practical implication of this is that all places where a large number of live poultry are brought together must be eliminated (or at least very strictly controlled). The only other successful control measure is a thorough cull, as implemented in Hong Kong in 1997.

In addition to the data driven analysis described above, we conducted an extensive new mathematical analysis on the transmission of infectious agents on networks. We studied more physically realistic models of disease transmission and examined under which circumstances non-zero thresholds would emerge. The threshold is the critical value of infectivity or transmissibility of a disease. If the rate of infection exceeds this value, then the disease will become endemic, otherwise the disease will be self-terminating. For diseases transmitting on a general class of scale-free networks (including that for avian influenza), it has been shown that the threshold must be zero. Our theoretical work aimed to address the following question: which modifications to this network allow for a non-zero threshold? Such modifications then allow us to plan appropriate control strategies. Our work also examined models for the various control measures that may be implemented, and efforts to economically modify the network topology to allow for easier control of disease transmission.

All the models described in this work, together with the publicly available data are provided as a self-contained software package from the website: <http://small.eie.polyu.edu.hk/jema/>

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