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Inferring Epidemiological Control Strategies from Complex Network Models of Disease Propagation

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***Abstract*— Severe Acute Respiratory Syndrome (SARS) exhibits several interesting transmission characteristics: spread within specific, but disjoint, geographical regions; and, so-called super-spreader events (SSE). We describe a complex network model which is capable of reproducing these features and apply it to the SARS transmission data from Hong Kong during 2003. We find that the observed data is typical of the models, and that the models are capable of a wide range of behaviours. However, we conclude that transmission within hospitals was a crucial factor for the severity of the SARS outbreak in Hong Kong. Moderately restrictive control practices in the early stages of an outbreak would be sufficient to contain infection and limit contagion.**

***Index terms*— Complex network, disease transmission, SARS.**

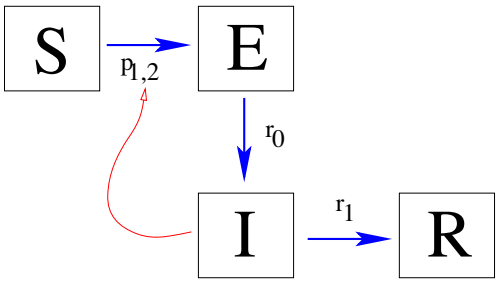

Fig. 1. Transmission sequence. Individuals are initially susceptible (S), and become exposed (E) after contact with an infectious (I) individual with probabilty p_1 or p_2. Exposed individuals become infectious with a fixed rate r_0l, and infectious individuals are removed at rate r_1.

I. Introduction

The first appearance of Severe Acute Respiratory Syndrome (SARS) in Hong Kong was attributed to a mainland doctor visiting the territory in February 2003[1] [1]. Over a period of 100 days, more than 1750 people in Hong Kong had been infected, 300 fatally. Furthermore, outbreaks of the disease occurred in many other countries and territories including: Beijing, Guangdong, Taiwan, Vietnam, Singapore and Canada.

In this paper we present complex small-world (SW) and scale-free (SF) models of disease propagation and apply them to the transmission of SARS in Hong Kong. We argue that these models provides a better fit to the observed data and transmission dynamics than standard methods [2]. We show that both small-world [3] and scale-free [4] models provide a better description of transmission features typical of SARS. In particular, it has widely been reported that cases of SARS tend to cluster around specific geographic location [5] and that so-called Super-Spreader Events (SSE) are common [6]. Both these features are not evident in existing epidemiological models, but are typical of SW and SF models. Moreover, an analytic study of our model allows us to derive precise criteria for control of any outbreak [7]. Details of these methods are also presented in [8].

In the remainder of this section we introduce the general form of our model. In Sec. II we perform an analytic analysis of our model, and in Sec. III we support this with computational examples. In Sec. IV we conclude.

[1]Media reports of an unidentified respiratory disease in Guangdong appeared as early as November or December of the previous year. However, the first confirmed cases were in 2003.

A. The model

We treat individuals in the community as nodes on a grid, the nodes are linked by social and incidental acquitances which may also represent potential pathways for infection. Each node is linked to a small (fixed) number of neighbouring nodes: these represent familial links. Moreover, each node has a (random) number of remote links to nodes in other parts of the network (this corresponds to communal links with social contacts). The number of links to neighbouring nodes is denoted as n_1 and is fixed for all nodes in the network. The number of links to distant nodes follows either an exponential or scale-free distribution and is selected randomly for each node. The expected value is a parameter of the distribution and denoted by μ. Suppose that the rate of infection on neighbouring links is p_1 and the rate of infection on long distant links is p_2. Typically we expect that $p_1 \gg p_2$ and, moreover, that p_2 can more easily be manipulated through social engineering (e.g. quarantine, or school closures).

Each node in the network can be in one of fours states: (1) susceptible to infection, (2) exposed to infection, (3) infectious, or, (4) removed. All nodes are initially susceptible (S): although not infectious, they may be infected. When a node is infected through contact with an infectious individual, they become exposed (E). Exposed individuals carry the virus and will eventually become infectious. An exposed

individual is not, however, infectious (I). Finally, an infectious individual becomes removed (R)through either death or recovery. Removed individuals are no longer either infectious or susceptible to infection. Transition from the exposed to infectious states are at rate r_0, while transition from infectious to removed state is at rate r_1. Figure 1 illustrates the basic transmission sequence.

II. Calculations

As is usual for disease dynamics, the epidemic will eventually be contained if the rate of infection is lower than the rate of removal. Intuitively, provided $(n_1 p_1 + \mu p_2) \gg r_1$ one would expect the disease to become endemic, conversely, if $(n_1 p_1 + \mu p_2) \ll r_1$ the disease will be contained.

In fact, with this model we can analytically compute the probability of an outbreak being self-terminating. For a single infectious node, assuming a SF distribution, the probability of no further infections on *a given day* is given by

$$\begin{aligned} P_{\rm no1} &= \sum_{m=0}^{\infty} \left[(1-p_1)^{n_1} (1-p_2)^m P(n_2^{(i)} = m) \right] \\ &= (1-p_1)^{n_1} (1 - e^{-\frac{1}{\mu}}) \sum_{m=0}^{\infty} \left[e^{-\frac{1}{\mu}} (1-p_2) \right]^m \\ &= \frac{(1-p_1)^{n_1} (e^{\frac{1}{\mu}} - 1)}{e^{\frac{1}{\mu}} - 1 + p_2} \end{aligned} \quad (1)$$

Where $n_2^{(i)}$ is the actual number of links to non-neighbouring nodes. Hence the probability of *no further infections* from this node can be closely approximated by the infinite geometric series using the average $P_{\rm no1}$ computed in Eqn. (1)

$$\begin{aligned} &P_{\rm none} \\ &\approx P_{\rm no1} r_1 + P_{\rm no1}^2 (1-r_1) r_1 + P_{\rm no1}^3 (1-r_1)^2 r_1 + \dots \\ &= \frac{P_{\rm no1} r_1}{1 - P_{\rm no1}(1-r_1)} \end{aligned} \quad (2)$$

provided $|P_{\rm no1}(1-r_1)| < 1$. Upon substitution of equation (1) into (2) we find that

$$P_{\rm none} = \frac{r_1 (1-p_1)^{n_1}}{1 - (1-r_1)(1-p_1)^{n_1} + p_2 / \left[e^{\frac{1}{\mu}} - 1 \right]} \quad (3)$$

Equation (3) is the probability of no infections from a given individual and is therefore a weak lower bound on the probability of no general outbreak.

Let us now denote the probability of no further infections occurring given that there are k infectious nodes by

$$\begin{aligned} P^k &= P_{\rm none}^k \\ &= \text{Prob(no further infection } | k \text{ infectious nodes)} \end{aligned}$$

where for notational convenience we will drop the subscript on $P_{\rm none}$. Treating infections as discrete events we have that $(1 - P^k)$ is the probability of at least one further infection from k infectious nodes. The probability that the epidemic will terminate is given by

$$\begin{aligned} P_{\rm safe} &= P + (1-P)\left[P^2 + (1-P^2)\left[P^3 + \dots \right.\right. \\ &\quad \left.\left. (1-P^3)\left[P^4 + (1-P^4)[\dots] \right] \right] \right] \\ &= \sum_{m=0}^{\infty} P^{m+1} \prod_{n=1}^{m} (1-P^n) \end{aligned} \quad (4)$$

where $P = P_{\rm none}$ is given by equation (3). By expanding equation (4) and comparing to the Pentagonal Number Theorem, we find that equation (4) can be rewritten as an infinite sum

$$\begin{aligned} &\sum_{m=0}^{\infty} P^{m+1} \prod_{n=1}^{m} (1-P^n) = \\ &\quad P + P^2 - P^5 - P^7 + P^{12} + P^{15} - P^{22} + \dots \\ &= \sum_{m=1}^{\infty} (-1)^{m+1} \left[P^{\frac{1}{2}m(3m-1)} + P^{\frac{1}{2}m(3m+1)} \right] \end{aligned} \quad (5)$$

where the sequence of indices $0, 1, 2, 5, 7, 12, 15, 22, 26, 35 \dots$ are the Generalised Pentagonal Numbers. Equation (5) may also be re-written in terms of the Dedekind eta function, but for the purposes of this discussion it is unnecessary to do so. Nonetheless, for $0 \le P < 1$ this sequence converges fairly rapidly as the order of the exponent increases.

Following [10] we can define

$$\begin{aligned} g_1(x) &= (1 - p_1 + p_1 x)^{n_1} \sum_{m=0}^{\infty} \frac{1}{C} e^{-\frac{m}{\mu}} (1 - p_2 + p_2 x)^m \\ &= \frac{(1 - p_1 + p_1 x)^{n_1} (1 - e^{-\frac{1}{\mu}}) \mu}{1 - e^{-\frac{1}{\mu}} (1 - p_2 + p_2 x)}, \end{aligned} \quad (6)$$

the probability generating function for the number of secondary cases produced by a single infectious case in a day. Then the probability generating function for the overall number of secondary infections from a single primary case is

$$\begin{aligned} g(x) &= \sum_{j=1}^{\infty} g_1(x)^j r_1 (1-r_1)^{j-1} \\ &= \frac{r_1 g_1(x)}{1 - (1-r_1) g_1(x)}. \end{aligned} \quad (7)$$

One can then obtain the probability of no general outbreak (i.e. the probability of the disease not becoming endemic) as the smallest solution $x \in [0, 1]$ of $g(x) = x$.

Unfortunately, equation (7) cannot be readily used for further analysis. Similarly, although equation (4) can be easily computed, it is not in a form which is immediately amenable for further analysis. However, since $P_{\rm safe} \ge P_{\rm none}$ it is clear that $\mu \left[1 - (1-p_2) e^{-\frac{1}{\mu}} \right] \gg 1$ will make $P_{\rm safe} \approx 0$. Hence, either $\mu \gg 1$ or $p_2 \approx 1$ will lead to widespread infection (as expected). Differentiating (4) with respect to $(1-p_1)^{n_1}$ we can easily verify that $P_{\rm safe}$ is a monotonic function of both p_1 and n_1. One can therefore observe that $P_{\rm safe} \approx 0$ if $p_1 \approx 1$ or $n_1 \gg 1$.

The most unrealistic restriction on equation (4) and also equations (6-7) is that we assume that no infected nodes have

common neighbours: and therefore that all of the neighbours are susceptible. In reality some of the potential neighbours may already be infected. In fact, this is an essential feature of the "clumpy" growth of infections. It is therefore important to obtain a measure of the number of neighbours of an infected node which have been infected.

This is equivalent to estimating the ratio of local and non-local infections in an epidemic. We can achieve this as follows, suppose that there is no non-local infections (i.e. $p_2 = 0$) and that infections grow in a single (roughly spherical) "clump". Then, if the clump consists of $I(t)$ individuals (see Eqn 10, below) then the radius of this clump will be $\sqrt{\frac{I(t)}{\pi}}$ and the number of susceptible individuals is $2\sqrt{I(t)\pi}$. Now, further suppose that all nodes in the clump are infectious (i.e. $r_1 = 0$) then the mean number of links per infected individual is $2\sqrt{\frac{\pi}{I(t)}}$. Even with $r_1 > 0$, as the clump grows there are, on average, fewer potential infection paths.

One can consider the network of infected individuals as consisting of a number of "clumps". One clump for each non-local infection (i.e. each clump is seeded by a non-local transmission, all other transmissions *within* that clump are local). Provided $p_2 > 0$, this implies that as the clump gets bigger the probability of any given infection being a long range infection will increase. Conversely, as the number of clumps increases the proportion of local infection (relative to nonlocal infection) will increase. Moreover, one can estimate the number of clumps K. Observe that

$$\begin{aligned} K &= \frac{\mu p_2}{(N_s-\mu)p_1 + \mu p_2} \times I \qquad (8)\\ &= \frac{\mu p_2(n_1 k p_1 + \mu p_2)}{n_1 p_2(n_1 k^2 p_1 + \mu p_2) + \mu p_2(n_1 k p_1 + \mu p_2)} \times I \end{aligned}$$

where I is the total number of infections.

Let us now estimate the expected number of connections from an infected node. Let N_S denote the expected number of susceptible nodes linked to a random node. If this node is the result of a non-local infection then we suppose $N_S = n_1 + \mu$, however, if this is the result of a short range infection then this number should be lower (certainly no more than $\mu + n_1 - 1$). Now,

$$\begin{aligned} \text{Prob(long range infection } | \text{ infection)} &= \frac{\mu p_2}{n_1 k p_1 + \mu p_2}\\ \text{Prob(short range infection } | \text{ infection)} &= \frac{n_1 k p_1}{n_1 k p_1 + \mu p_2} \end{aligned}$$

where k is the proportion of local links that support possible infection and $0 < k \leq \frac{n_1-1}{n_1}$. Hence,

$$\begin{aligned} N_S &= (n_1+\mu)\frac{\mu p_2}{n_1 k p_1 + \mu p_2} + (n_1 k + \mu)\frac{n_1 k p_1}{n_1 k p_1 + \mu p_2}\\ &= n_1 \frac{n_1 k^2 p_1 + \mu p_2}{n_1 k p_1 + \mu p_2} + \mu \qquad (9) \end{aligned}$$

Hence, if infection grows in a single clump then $k \approx \frac{1}{2}$. Moreover, $k < \frac{1}{2}$ only if nodes remain infected when they are on the interior of such "clump" (i.e. when r_1 is very low).

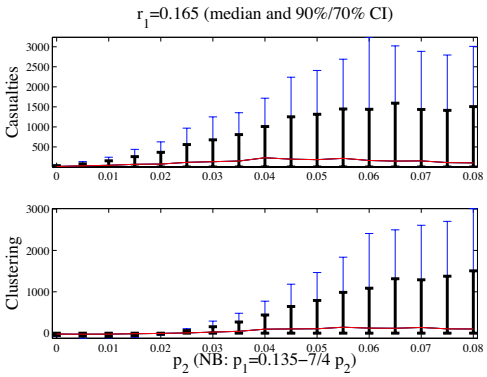

Fig. 2. Unconstrained growth of the infectious population. The upper panels show the number of individuals infected after 50 days, the lower plot show the number of distinct clusters detected after the same time.

Therefore, $\frac{1}{2} \leq k \leq \frac{n_1-1}{n_1}$. The value of k will both depend on the various model parameters, and vary with time.

Finally, we consider the rate of transmission. Let $P(t)$, $I(t)$, and $R(t)$ be the number of prone, infected and removed individuals at time t (in days). The probabilities r_0 and r_1 can therefore be considered as the rates at which prone nodes become infectious and infectious nodes become removed (respectively). Similarly $(n_1 p_1 k + \mu p_2)S(t)I(t)$ is the expected number of new infections. Suppose that $S(t) \gg R(t) + I(t) + P(t)\ \forall t$. Then

$$\begin{aligned} R(t+1) &= R(t) + r_1 I(t)\\ I(t+1) &= I(t) - r_1 I(t) + r_0 P(t) \qquad (10)\\ P(t+1) &= P(t) - r_0 P(t) + n_k I(t) \end{aligned}$$

where $n_k = (n_1 p_1 k + \mu p_2)$ is the expected number of links for each infectious node. Assuming that the population is seeded with a single infectious individual, the solution of equation (10) is given by

$$\begin{aligned} \begin{bmatrix} R(t)\\ I(t)\\ P(t) \end{bmatrix} &= \begin{bmatrix} 1 & r_1 & 0\\ 0 & (1-r_1) & r_0\\ 0 & n_k & (1-r_0) \end{bmatrix}^t \begin{bmatrix} 0\\ 1\\ 0 \end{bmatrix}\\ &= PD^tP^{-1}[0\ 1\ 0]^T \qquad (11) \end{aligned}$$

where $P = [v_1\ v_2\ v_3]$ is the matrix of eigenvectors and

$$D^t = \begin{bmatrix} \lambda_1^t & 0 & 0\\ 0 & \lambda_2^t & 0\\ 0 & 0 & \lambda_3^t \end{bmatrix}$$

is formed from the corresponding eigenvalues, given by

$$\begin{aligned} \lambda_1 &= 1\\ \lambda_{2,3} &= 1 - \frac{r_0+r_1}{2} \pm \sqrt{\frac{1}{4}(r_0-r_1)^2 + n_k r_0}. \end{aligned}$$

It then follows that the system has a marginally stable focus (i.e. the epidemic will terminate) if $|\lambda_{2,3}| < 1$ i.e.

$$\begin{aligned} n_k &< r_1 \qquad (12)\\ n_k r_0 &< (2-r_0)(2-r_1) \qquad (13) \end{aligned}$$

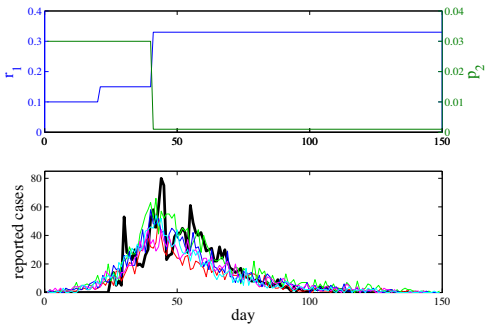

Fig. 3. The top panel shows the change in parameters r_1 and p_2 with time (all other parameters are constant: $p_1 = 0.08$, $n_1 = 4$ and $\mu = 7$). The complex network is SW, but not SF. The bottom plot shows five model simulations and the true SARS data for Hong Kong.

The second condition (13) is only violated if $n_k > 1$ which would also violate condition (12). Therefore the epidemic is controllable provided $n_k = n_1 p_1 k + \mu p_2 < r_1$. The right hand side of this inequality is the rate of infection and the left hand side is the rate of removal, as expected. In fact, this result is exactly analogous to the equivalent result for the continuous SIR model [11]. Moreover,

$$\max_{i=1,2,3} |\lambda_i| = 1 - \frac{r_0 + r_1}{2} - \sqrt{\frac{1}{4}(r_0 - r_1)^2 + n_k r_0} \qquad (14)$$

Computationally [4], we can see that as r_0 or n_k increases then the rate of growth of the epidemic also increases. Conversely, as r_1 increases the rate of growth decreases. This is as one would expect as increasing r_1 will decrease the number of infectious individuals while increasing either r_0 and n_k increase this quantity.

III. Computations

Subject to the choice of parameters in the previous sections we now simulate the expected dynamics and compare this to the theoretical bounds of Sec. II. The parameters, selected according to a rationale described in [3], are based on physical observation of the system. We set the expected number of short and long range connections to be 4 and 7, respectively. The rate r_0=0.1 and $r_1 = 0.165$, based on the presumed incubation period (for r_0) and the rate of hospitalisation (assuming no nosocomial transmission). The infection parameters p_1 and p_2 are restricted so that $n_1 p_1 + n_2 p_2 = 0.54$: giving an average of 2.7 secondary infections from each primary.

According to Sec. II, restricting the infectious period to 5 or fewer days does not yield a growth rate large enough to be consistent with the observed data. In Fig. 2 we test that assertion numerically and find that only with $r_1 \geq 0.165$ do we obtain results for which the true data is not statistically highly atypical. Moreover, this result is robust to moderate changes of the other relevant parameters [4]. In other words, the removal rate is greater than the observed rate at which patients are hospitalised. Nosocomial transmission is a significant factor.

As a form of qualitative comparison, we also provide simulations of the Hong Kong epidemic and from multiple simulations estimate the likelihood of various outcomes based on the model. We initiate the model with a single infected individual and a relatively low removal rate r_1. We use a SW rather than SF network. Figure 3 depicts our results.

We can see from Figure 3 that many of the features of the true data are reproduced well in the simulations. However, two important aspects of the simulations are not sufficiently similar to the data. Firstly, the initial spreading of the disease is exponential rather than the single SSE observed in the real data. Secondly, the magnitude of the SSEs in the simulations is somewhat smaller than the largest SSEs in the data. Both these problems can be overcome by replacing the SW with a SF network. The SF network generates occasional extreme events, sufficient to generate simulations with a bursty appearance similar to the true data.

IV. Conclusion

The model we have introduced provides a good fit to the observed data. Both qualitative and quantitative features of the data are evident in the model. In particular, the model exhibits both SSEs and localised clusters of infection as was observed in Hong Kong. However, we found that the model can only reliably produce infection of the magnitude observed in the real data if significant infection occurs within hospitals. Effective infection control in hospitals results in a substantially reduced spread. Without nosocomial transmission the effect of a relatively slow moving virus such as SARS is severely limited.

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References

[1] World Health Organisation, "Consensus document on the epidemiology of SARS," World Health Organisation, Tech. Rep., 17 October 2003, http://www.who.int/csr/sars/en/ WHOconsensus.pdf.

[2] M. Small, P. Shi, and C. K. Tse, "Plausible models for propagation of the SARS virus," *IEICE Transactions on Fundamentals of Electronics, Communications and Computer Sciences*, vol. E87-A, pp. 2379–2386, 2004.

[3] M. Small and C. K. Tse, "Small world and scale free model for transmission of SARS," *International Journal of Bifurcation and Chaos*, vol. 15, pp. 1745–1755, 2005.

[4] ——, "Clustering model for transmission of the SARS virus: Application to epidmic control and risk assesment," *Physica A*, vol. 351, pp. 499–511, 2005.

[5] S. Riley *et al.*, "Transmission dynamics of the etiological agent of SARS in Hong Kong: impact of public health interventions," *Science*, vol. 300, pp. 1961–1966, 2003.

[6] M. Lipsitch *et al.*, "Transmission dynamics and control of sever acute respiratory syndrome," *Science*, vol. 300, pp. 1966–1970, 2003.

[7] M. Small and C. K. Tse, "Small world network model for transmission of the SARS virus," 2004, submitted.

[8] M. Small, *Applied Nonlinear Time Series Analysis: Applications in Physics, Physiology and Finance*, ser. Nonlinear Science Series A. Singapore: World Scientific, 2005, vol. 52.
[9] N. Sloane, "On-line encyclopedia of integer sequences," Online, 2005, http://www.research.att.com/∼njas/sequences/Seis.html.
[10] O. Diekmann and J. Heesterbeek, *Mathematical Epidemiology of Infectious Diseases*. Chichester: John Wiley & Son, 2000.
[11] J. Murray, *Mathematical Biology*, 2nd ed., ser. Biomathematics Texts. Springer, 1993, vol. 19.