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Scale-free network of a dengue epidemic

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Abstract

In this work we show that the dengue epidemic in the city of Singapore organized itself into a scale-free network of transmission as the 2000–2005 outbreaks progressed. This scale-free network of cluster comprised geographical breeding places for the aedes mosquitoes, acting as super-spreaders nodes in a network of transmission. The geographical organization of the network was analysed by the corresponding distribution of weekly number of new cases. Therefore, our hypothesis is that the distribution of dengue cases reflects the geographical organization of a transmission network, which evolved towards a power law as the epidemic intensity progressed until 2005.

Keywords: Power-law; Scale-free network; Dengue; Singapore

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1. Introduction

In the study of epidemic networks, it is interesting to inspect the effect of their complex features on the dynamics of epidemic and disease spreading. The characterization and understanding of epidemic dynamics on these networks can find immediate applications to a large number of problems, in particular epidemiology [1]. Recent papers [2–7] have demonstrated that for small-world networks, there is a critical threshold, below which an infection with a spreading rate dies out. Moreover, in finite size scale-free networks the epidemic threshold in the transmission rate is much lower than in corresponding random networks [8].

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In this paper we address the recent dengue epidemic in Singapore by a graph theory approach and show that as the outbreak progressed, transmission tends to form a scale-free network of cluster comprising various geographical breeding places for the aedes mosquitoes, acting as super-spreaders of the infection. The geographical organization of the network was also analysed it corresponds to the distribution of weekly number of new cases. Therefore, the hypothesis we are going to test is that the distribution of dengue weekly cases reflects the geographical organization of a transmission network, comprised by cluster of cases, which evolved towards a power law as the epidemic intensity progressed until 2005.

1.1. Dengue in Singapore

In Singapore, dengue is endemic with year-round transmission [9]. The disease was first recognized as a public health problem in the 1960s when a nationwide *Aedes* control programme was implemented [10]. The programme basically integrated larval source reduction by the use of chemical larvicides with measures inspired by public health education that consisted in instructing people to avoid the occurrence of accumulated water in home recipients. The programme was backed by law enforcement with heavy fines imposed on people who failed to comply with those measures [9]. This programme resulted in a marked decline in dengue incidence, which coincided with a drop on the overall *Aedes* house index from over 25% to the present 1–2%. Despite the low *Aedes* house index, however, outbreaks recurred from 1989 onwards with a discernible seasonal increase in the second half of each year [9].

A total of 13,817 dengue cases have been reported in 2005 [11], peaking at 697 cases in the last week of September. This year of 2005 exceeded all previous records of annual dengue incidence.

In terms of circulating virus strain, DEN-1 predominates even though DEN-3 has become more prevalent in the last months of the study period. Among cases, the male-to-female ratio was 1.4:1 with adults aged 15–44 years representing 65% of all reported cases. The highest age-specific incidence was in the 15–24 years age group while the lowest was in those under 5 years [12].

In addition, there has been an expansion in the geographical distribution of dengue outbreaks recently, from traditional landed areas in the eastern and southeastern sectors of the island to new areas in the western and northern sectors where high-rise public housing estates are located. Dwellers of those high-rise public housing estates represented 75% of reported dengue cases in 2004 and 2005 [12].

2. Methods

2.1. The dynamical model

In order to calculate the intensity of transmission of dengue in Singapore, we applied the dynamical model for dengue described in [13,14].

2.2. Graph analysis

The graphs relative to the year 2005 was constructed considering the weekly number of new cases, distributed into bins calculated according to the method of Sturges [15], that is, the number, N, of intervals is given by

$$N = 1 + 3.322\log(n),$$

where n is the number of weeks in the year (52). This equation was used in order to standardize the binning. The log–log of the distribution provides a visualization of the network organization. The graph for cluster size distribution was defined according to the method described in [16].

2.3. The force of infection

The force of infection, i.e. the per capita number of new infections per time unit [17,18], $\lambda(t)$, is defined for vector-borne infection as

$$\lambda(t) = ab \int_0^t \frac{S_M(s)}{N_H(s)} \mathrm{d}s \int_0^t \frac{I_M(s)}{N_M(s)} \mathrm{d}s, \tag{1}$$

where a is the mosquitoes' daily biting rate, b is the proportion of infected bites that are actually infective to humans, S_{M} and I_{M} are the number of susceptible and infected mosquitoes, respectively, and N_{H} and N_{M} are the total number of humans and mosquitoes, respectively.

2.4. The density of infected nodes

From the force of infection it is possible to calculate the density of infected nodes of the network by the Barabási–Albert's [5] model as described by Pastor–Satorras and Vespignani [19]. These authors proposed that the relative density $\rho_\kappa(t)$ of infected nodes with given connectivity κ, that is, the probability that a node with κ links is infected, has a dynamics given by

$$\frac{\partial \rho_\kappa(t)}{\partial t} = -\rho_\kappa(t) + \lambda\kappa[1 - \rho_\kappa(t)]\Theta(\lambda), \tag{2}$$

where λ is the force of infection and $(\Theta\lambda)$ is the probability that any given link points to an infected node. The solution of this equation is [19]

$$\rho \cong 2\exp\left[-\frac{1}{m\lambda}\right], \tag{3}$$

where m is the number of links.

3. Results

Fig. 1 shows the estimation of the average force of infection, calculated from model described in [13,14]. The result of the network analysis can be seen in Figs. 2 and 3. Fig. 2 shows the time distribution of cases. Fig. 3 shows the geographical network of cluster of cases. Here a cluster is defined as an area that comprises any two confirmed dengue cases occurring not more than 150 m from each other, and the onset dates of the two confirmed dengue cases are within 14 days from each other [20]. The figure shows the observed clusters of active infections during the peak of the epidemic in September 2005, with the distribution of cluster sizes represented as a log–log plot. We see that clustering of cases indeed approximates the expected distribution of connectivity for a scale-free network, where each cluster represent a node and the contact between clusters through infected mosquitoes represent the edges of the transmission network.

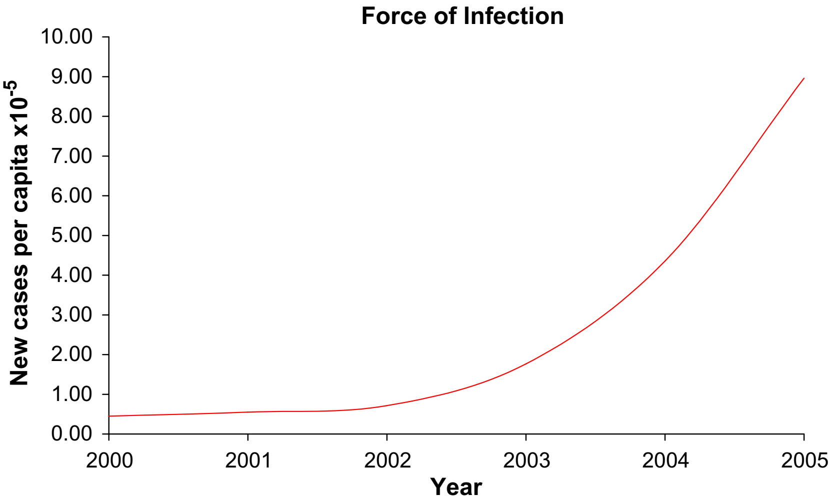

Fig. 1. The force of infection calculated according with Eq. (1).

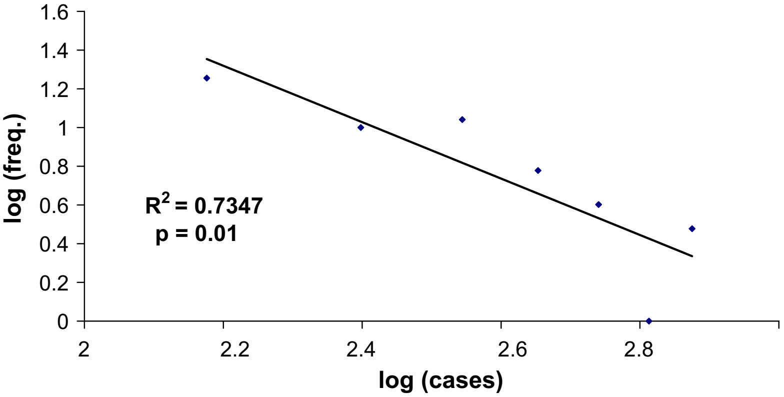

Fig. 2. Log–log distribution of weekly dengue cases in Singapore, 2005, with $\gamma = 2.46$.

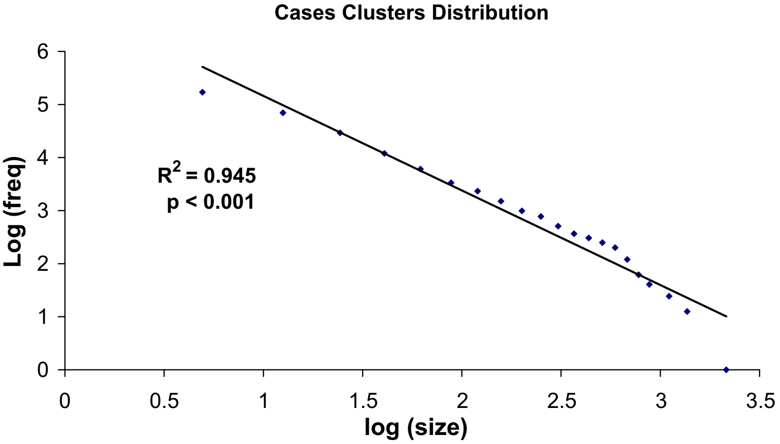

Fig. 3. Log–log distribution of cluster sizes of dengue cases in 2005, with $\gamma = 2.78$.

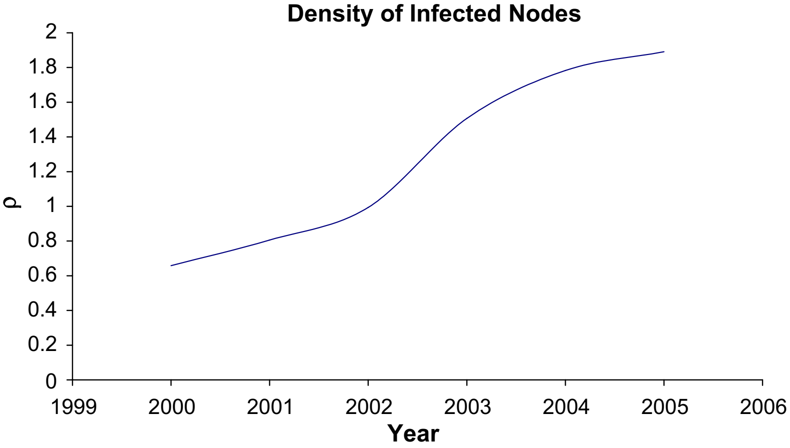

Fig. 4. Density of infected nodes in dengue transmission network, calculated according to Eq. (3).

Fig. 4 shows the time variation in the density of infected nodes, ρ. Note that yearly ρ increases with time as the network organizes itself in clusters representing infected nodes.

As the density of infected nodes increases with time, we think that dengue transmission organized itself into scale-free network with time, peaking in 2005 the most severe year, as far as outbreak intensity is concerned.

4. Discussion

The recent upsurge in the number of articles dealing with epidemic spread in scale-free network testifies the importance of this area.

In the particular area of vector-borne infections, the seminal work by Bailey [21] in malaria has already demonstrated that in this kind of indirectly transmitted infection the epidemic threshold was much lower than in directly transmitted diseases, a result obtained in the recent analysis from Pastor-Satorras and Vespignani [19].

In this latter field, a network analysis by Schneerberger et al. [22] has demonstrated that in case of a scale-free network of transmission with a coefficient less than 3, because the variance or second moment of the transmission network tends to infinity, the basic reproduction number will always be greater than 1 regardless of the value of the transmission probability or the duration of infection. This implies that a small number of super spreading nodes is enough to maintain the infection circulating in this population.

The result of such network analysis of vector-borne and sexually transmitted infections has an impact on the design of control strategies difficult to super estimate. The main implication is that any control strategy should be target to the super spreading hubs of the network (for an example of target chemotherapy against macroparasites see [23]).

In this work we show that the dengue epidemic in Singapore organized itself into a scale-free network of transmission as the outbreak progressed.

There has been an expansion in the geographical distribution of dengue outbreaks in Singapore, from traditional landed areas in the eastern and south-eastern sectors of the island to new areas in the western and northern sectors where public housing estates are located. Dwellers of those public housing estates represented 75% of reported dengue cases in 2004 and 2005. Therefore, the 2004–2005 outbreak had a spatial organization that differed from the interepidemic period anterior to the recent epidemic. The implication of our results, however, is that a more detailed analysis of the epidemiological characteristics of the larger clusters of infection is required, in terms of the sites and housing type of the cases involved; such an analysis is outside the scope of this present paper.

This hypothesis of a geographical organization of the transmission network is supported by the fact that in October 2005, in the peak of the epidemic, the local authorities decided to carry out a campaign aimed to search and destroy breeding places of aedes mosquitoes, which was based on targeting the clusters of transmission (super-spreading nodes), together with other control efforts [10]. These control strategies significantly reduced the number of weekly cases from almost 800 to less than 40 in a few weeks.

References

[1] R. Albert, A.-L. Barabási, Statistical mechanics of complex networks, Reviews of Modern Physics 74 (2002) 47–97.

[2] S.N. Dorogovtsev, J.F.F. Mendes, Evolution of networks, Advances in Physics 51 (2002) 1079–1187.

[3] M.E.J. Newman, The structure and function of complex networks, SIAM Reviews 45 (2003) 167–256.

[4] D.J. Watts, S.H. Strogatz, Collective dynamics of complex networks, Nature 393 (1998) 440–442.

[5] A.-L. Barabási, R. Albert, Emergence of scaling in random networks, Science 286 (1999) 509–512.

[6] A.-L. Barabási, R. Albert, H. Jeong, Mean-field theory for scale-free random networks, Physica A 272 (1999) 173–187.

[7] N.T.J. Bailey, The Mathematical Theory of Infectious Diseases, second ed., Griffin, London, 1975.

[8] I.Z. Kiss, D.M. Green, R.R. Kao, Infectious disease control using contact tracing in random and scale-free networks, Journal of the Royal Society Interface 3 (2006) 55–62.

[9] K.T. Goh, Changing epidemiology of dengue in Singapore, Lancet 1995, October 21, 346 (8982) (1995) 1098.

[10] NEA – National Environmental Agency, Ministry of Environment and Water Resources of Singapore. (2005). NEAs key operation strategies in dengue control. September 2005.

[11] WID – Weekly Infectious Diseases Bulletin. vol. 1, 52 (2005). <http://www.moh.gov.sg/cmaweb/attachments/publication/2005_week_52.pdf>.

[12] MOH – Ministry of Health of Singapore . Final Report of the Expert Panel on Dengue. (2005) <http://www.moh.gov.sg/cmaweb/attachments/topic/3625c5ae51QU/Final_Report-dengue_7_Oct_05.pdf>.

[13] F.A.B. Coutinho, M.N. Burattini, L.F. Lopez, E. Massad, An approximate threshold condition for non-autonomous system: an application to a vector-borne infection, Mathematical and Computers in Simulation 70 (2005) 149–158.

[14] F.A.B. Coutinho, M.N. Burattini, L.F. Lopez, E. Massad, Threshold conditions for a non-autonomous epidemic system describing the population dynamics of dengue, Bulletin of Mathematical Biology 68 (2006) 2263–2282.

[15] E. Massad, R.X. Menezes, P.S.P. Silveira, N.R.S. Ortega (Eds.), Quantitative Methods in Medicine, Manole Editions Press, São Paulo, 2004.

[16] M. Pascual, M. Roy, F. Guichard, G. Flieri, Cluster size distributions: signatures of self-organization in spatial ecologies, Philosophical Transactions of the Royal Society B: Biological Sciences 357 (2002) 657–666.

[17] R.M. Anderson, R.M. May, Infectious Diseases in Humans: Dynamics and control, Oxford University Press, Oxford, 1991.

[18] R.S. Azevedo Neto, A.S.B.S. Silveira, D.J. Nokes, H.M. Yang, S.D. Passos, M.R.A. Cardoso, E. Massad, Rubella seroepidemiology in a non-immunized population of São Paulo State, Brazil, Epidemiology and Infection 113 (1994) 161–173.

[19] R. Pastor-Satorras, A. Vespignani, Epidemic spreading in scale-free networks, Physical Review Letters 86 (2001) 3200–3203.

[20] MOH – Ministry of Health of Singapore. Epidemiological News Bulletin, January–March 32 (2006) 1–15. <http://www.moh.gov.sg/corp/publications/enb>.

[21] N.T. Bailey, The Biomathematics of Malaria, Charles Griffin & Company Ltd., London, 1982.

[22] A. Schneeberger, C.H. Mercer, S.A.J. Gregson, N.M. Fergunson, C.A. Nyamakupa, R.M. Anderson, A.M. Johnson, G.P. Garnett, Scale-free networks and sexually transmitted diseases, Sexually Transmitted Diseases 31 (2004) 380–387.

[23] R.M. Anderson, The population dynamics and control of hookworm and roundworm infections, in: R.M. Anderson (Ed.), The Population Dynamics of Infectious Diseases: Theory and Applications, Chapman and Hall, 1982.