Information Management and SARS : Applying a Network Analysis Framework in Outbreak Control

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Abstract

In this paper a network analysis framework is used to examine data visualization, collection and the use of information systems in outbreak management, with particular reference to the recent SARS outbreak.

Keywords:
Medical informatics; Network Analysis; SARS; Epidemiology; Outbreaks

Introduction

Back to Basics

SARS is the first severe and readily communicable new disease to emerge this century. [1] As a disease without treatment or vaccine, health authorities have had to rely upon a basic set of control measures: epidemiological tools, isolation and quarantine.

Especially in the acute phase, the response to SARS has been hampered by a long list of unknowns: no clear-cut clinical diagnosis, no laboratory test, and no idea of mode of transmission or clinical course – amongst others. [2]

In the face of these constraints, the decisive factor in improving the response to a threat of this nature is information. It is critical to improve the information infrastructure supporting the use of this limited set of control measures, whether it is in terms of data collection, visualization, collaboration or co-ordination.

To this end, we would like to propose the use of a network analysis framework to guide the use of information tools as well as information systems design in the management of outbreaks of novel diseases such as SARS.

The Network is the Disease

Data Visualization

Conventional Approach

Contact mapping is a basic visualization tool used to target isolation and quarantine measures. In constructing a contact map, the current paradigm is the concentric circle approach. (Figures 1a, 2) This approach is centered upon the diseased individual (ie the index case). Relations between individuals on the map are depicted in terms of how they lead back to the index case. Interconnections amongst contacts are usually not part of the map. [3] In an epidemic, investigation of multiple cases generates multiple contact maps, each depicting its own cluster of infection. (Figure 1b)

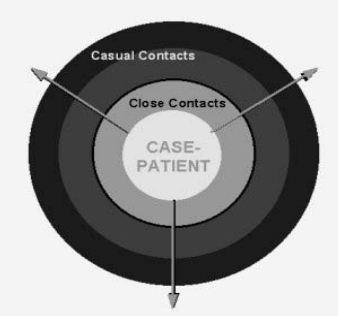

Figure 1a- Concentric Circle Approach

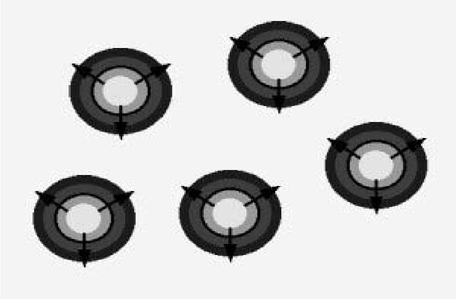

Figure 1b – Multiple Outbreak Clusters

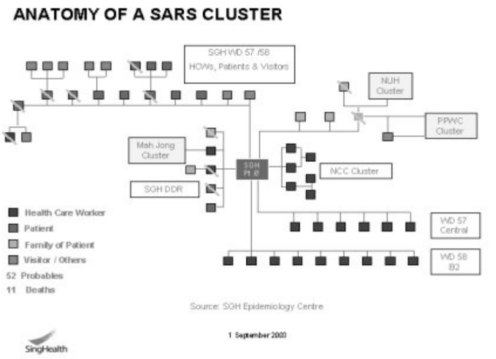

Figure 2 – SARS outbreak cluster
Source: Singapore General Hospital (SGH) Epidemiology Center

Problems with Conventional Approach

In the context of SARS, the concentric circle approach poses several problems.

Firstly, assigning disease status is not a straightforward matter.

The SARS case definitions include both clinical features and contact/travel history. [4] However, atypical clinical presentations may occur, especially in individuals with co-morbidities. Based on the Singapore experience, these individuals pose the greatest risk [5]. Patients presenting with overt symptoms suggestive of SARS are unlikely to to be the source of an outbreak. [6] In addition, contact or travel histories are not always reliable, the patient not being able in some cases to appreciate the significance of a contact.

For probable SARS in particular, positive laboratory findings (ie. PCR, seroconversion) are part of the case definition. But this is confounded by the fact that seroconversion and consistent virus/RNA excretion occur late in the course of the disease (how this correlates with infectivity is unclear). [7]

Secondly, the underlying assumptions that casual contacts and interconnections amongst contacts are not important [3] are not necessarily true, as will be discussed in detail subsequently.

Applying Network Analysis to Data Visualization

In contrast, network analysis is centered upon *relations* between individual elements, rather than their attributes or characteristics, as a means of explaining behaviors and outcomes. [8] As applied to data visualization, a network map of an outbreak appears more complex than conventional contact maps. (Figure 3) This is to be expected, as it is constructed on top of a larger data set. Ideally, including case-patients as well as their social contacts (who may be of indeterminate disease status). In addition, interconnections between contacts are depicted, not merely the relations that lead back to the index case. These interconnections may be seen to connect different clusters of infection, in effect creating a larger, integrative map.

Although there have been no studies applying network analysis to SARS data, a study conducted on a Tuberculosis outbreak by the Division of Tuberculosis Elimination, CDC [3] arrived at several applicable conclusions:

Firstly, inclusion of named contacts in addition to case-patients resulted in a more comprehensive map of the outbreak. Cases initially appearing to be isolated were linked back to the network through mutual contacts. Given the difficulties in assigning disease status in SARS, it may be prudent to expand data sets beyond case-patients in a similar fashion, to include as large a set of named contacts as possible. Social contacts that may not fit case-definitions initially could eventually emerge as links between outbreak clusters.

Related to this was the second finding – that disease status need not correlate with "network status". In practical terms, an uninfected individual located within the network core would be more valuable to interview compared to an infected individual at the fringe of the network. Using the conventional concentric circle approach one would instead gradually work "inside-out", interviewing infected individuals in a centrifugal manner.

Although network analysis can provide a holistic approach to infection mapping, the major limitation is the complexity of network maps. This often necessitates the use of computer applications rather than manual methods.

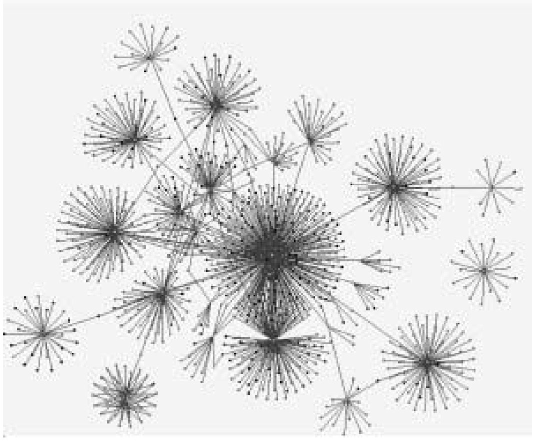

Figure 3 – Example: Network Map of Outbreak

It's a Small World

Beyond data visualization, the next step is to use network analysis to explain network behavior. Network structure is closely related to network growth. Models of disease spread based on various network topologies [9]-[13], demonstrate that network structure affects the speed and extent of disease transmission.

At the two ends of the spectrum, the connection topology of a network may be either completely ordered or completely random. Many biological and social networks (including infection networks) lie in between these extremes. Watts and Strogatz [14] have attempted to simulate these intermediate network topologies by taking an ordered network and introducing increasing amounts of randomness into it. The results of this "random re-rewiring" have been termed "small-world" networks. (Figure 4)

What is evident in "small-world" networks is that the introduction of just a few *long-range random* connections replacing the local connections of a ordered network greatly decreases the characteristic path length through the network, - in effect a "shortcut". At the same time, clustering (the "cliquishness" of the network) changes very little.

As applied to infection networks, diseases are predicted to spread far more quickly in a "small world". Also, it appears that only a small number of shortcuts are necessary to make the world small. [ibid]

In the context of SARS, international travel has been a key "shortcut". The disease has spread along routes of international travel with outbreaks concentrated in transportation hubs. In Taiwan for example, 83% of probable case-patients reported travel to mainland China and Hong Kong in the 10 days before illness onset. [15]

Of particular interest is the role of the Metropole hotel in Hong Kong. On the 21st of February, an infected doctor from Guangdong checked into a room on the 9th floor of the Metropole. Guests from this floor were responsible for carrying SARS associated coronavirus to the hospital systems of Singapore, Canada, Hong Kong and Vietnam – resulting in the earliest and most severe outbreaks. [16][17]

In effect, the random contacts that occurred upgraded the status of SARS from regional to global outbreak.

Random long-range connections are equally important in the local setting. Prompt measures in placing 2500 individuals under home quarantine when a vendor at one of the largest markets in Singapore was identified as a case-patient, were in part tacit recognition of the fact that that could have been the local equivalent of the Metropole hotel.

It follows that in order to effectively bring about network disruption, control measures need to target potential shortcuts for disease transmission. The advantage of using of network visualization techniques as opposed to the conventional concentric circle approach is in helping to identify these shortcuts.

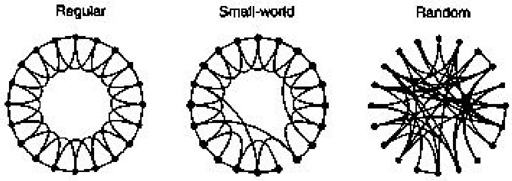

Figure 4

Data Collection

One of the inherent difficulties in mapping infection networks is data collection. In this respect an infection network resembles other opaque or covert social networks, - for example criminal, terrorist networks. [18][19]. Data has to be collected indirectly and is often incomplete. In addition, these networks are dynamic, not static. Every piece of information has a time/date and every relationship a distribution over time. [19].

Despite these difficulties it is important to work towards as complete a data set as possible. The more transparent the network, the greater the opportunity for pre-emptive action.

To this end a number of strategies may be used. [18] The first approach is to utilize multiple sources of data. For example, at Singapore Health Services Pte Ltd (Singhealth), one of Singapore's two healthcare clusters, the SARS taskforce was able to combine data from varied sources : Singhealth's existing information architecture – a SAP enterprise resource planning (ERP) system (containing admissions, billing data), it's electronic medical record system (Sunrise Clinical Manager), as well as non-electronic data from contact lists, staff rosters and case sheets. [20]

Secondly, diverse agencies need to integrate their disparate data sets into a larger emergent map. This relies upon the network connecting the relevant agencies. In other words, "the good guys have to build a better (information and knowledge sharing) network than the bad guys". [21]

Network vs Network

Infection Network vs Health Systems Network

As mentioned previously, one of the key features of the SARS outbreak is that health authorities have had at their disposal only the basic control measures of isolation and quarantine. In implementing these measures, timely relevant information can make a crucial difference.

How do we improve the efficiency of information and knowledge sharing networks so as to facilitate speedy decision-making? Again, network analysis can provide a useful framework for addressing this problem.

Rewiring the Network

Applying the small world network model, one can see that shortcuts can drastically reduce mean path length in an infection network. How do we apply these principles with regards to the outbreak control network? Or in other words how do we provide shortcuts for information to reach key decision makers within the shortest number of steps?

In this respect, outbreak alert and surveillance networks can play an important role in helping decision makers at national or global level (ie WHO) gather epidemic intelligence. Such systems are already in place for other diseases such as influenza: Developed by the WHO in conjunction with the Institut National de la Santé et de la Recherche Médicale (INSERM), Flunet is one example of a global electronic disease surveillance system. It allows approved users to remotely submit data in electronic form, with the results, – realtime epidemiological and virological information freely accessible via the Internet. [22][23]

There are also automated systems for disease surveillance. The Global Public Health Intelligence Network (GPHIN) application developed by Health Canada and used by WHO since 1997 is such a system. It is a web-based search engine that systematically scans 950 international news feeds and electronic discussion groups for rumors and unconfirmed reports of infectious disease events. [1][24] GPHIN was able to provide some of the earliest warnings of a mid-November 2002 outbreak of atypical pneumonia in China, – which has since been recognized as the first known SARS outbreak. [1] In a conventional outbreak alert system, an alert would be sounded only after local case reports had been collated at a national level and a formal report submitted to the WHO.

Early warnings systems can also be deployed on a regional or national level in the form of syndromic surveillance systems. The term applies to "surveillance using health-related data that precede diagnosis and signal a sufficient probability of a case or an outbreak to warrant further public health response". [25] In other words, health authorities can be alerted *before* the clinician formulates a diagnosis and submits a case report. Much of the recent work in this area has been undertaken by military agencies, with the goal of enhancing the response to bioterrorism threats. [26] Commercially, software systems of this nature are available. For example, the Redbat software system, which scans symptom data in hospital emergency room databases and is able to sort the data into syndrome categories for direct submission to health departments. [27]

At the local level, clinicians and other frontline staff routinely received directives and guidelines from regional and national health authorities. But there is a lag time for documents to filter down the hierarchy. To a large extent one of the roles of the Internet in the SARS outbreak has been to shortcut the traditional information routes, allowing frontline staff to access up-to-the-minute information directly from the WHO, CDC, and other health agencies world-wide. Furthermore, various parties (clinicians, paramedical staff, travelers, public health officials) have enjoyed the benefit of information tailored according to their specific needs.

A prime example of the importance of the global knowledge and information sharing network in an outbreak is the sequence of events that averted the spread of SARS in Germany : A Singaporean physician who had treated SARS cases in Singapore (linked to the Metropole Hotel in Hong Kong) had boarded a return flight from a conference in New York, stopping over in Frankfurt, Germany. Prior to departure he had mentioned to a colleague via telephone that he had symptoms suggestive of SARS. Subsequently the colleague notified Singaporean health authorities who alerted the WHO via urgent telecommunication. The WHO was then able to locate the flight and with the co-operation of local authorities in Frankfurt remove the physican and his traveling companions from the flight for hospitalization and isolation. [1] If the data had been slow in reaching the relevant decision makers it is conceivable that Germany could have been added to the list of SARS-afflicted countries.

Conclusion

The central premise of this paper is that relevant, timely information is the foundation of outbreak management. This is especially so in dealing with novel pathogens, where the list of unknowns is long and the set of control measures small.

We have used a network analysis framework to examine some aspects of the underlying information infrastructure supporting an outbreak response, with particular reference to the recent SARS global epidemic. Network analysis can provide a more holistic picture of infection networks than conventional means of data visualization. It can also be used to explain network behavior. For example, network growth. The "small world" network model, as applied to SARS, helps explain how international travel and casual contacts have played a role in rapid global spread of the disease. In the response to SARS, a global knowledge and information sharing network, formed via formal or ad-hoc ties, has made unprecedented use of electronic modes of communication such as the internet to "shortcut" the flow of information to key decision makers, allowing appropriate pre-emptive measures to be taken.

Future directions should therefore involve the strengthening of early warnings systems, exploring new approaches such as syndromic surveillance, as well as committing resources to the further development of collaborative technologies and platforms. These efforts should be undertaken in advance of future outbreak threats: including SARS, other novel diseases, as well as the accidental or deliberate release of biological agents.

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