

CT 1.1.3

Controls of nosocomial infection based on observed social networks of a community hospital

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Introduction

Nosocomial infection, namely, disease spreading inside healthcare facilities such as hospitals, is a prominent public health issue. Some antibiotics resistant such as methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant enterococci (VRE) are characteristic to healthcare facilities rather than to general populations. Healthcare facilities are also often the source of global outbreaks, as is the case in past outbreaks of influenza and severe acute respiratory syndrome.

Although network analysis has been successful in comprehending and controlling global epidemics (e.g. Colizza *et al* 2006), our knowledge about how social networks of healthcare facilities affect nosocomial infection is not sufficient (but see Meyers *et al* 2003). Actually, how diseases propagate in healthcare facilities may be very different from how they do in urban community setting or in the whole world due to different network architecture. We construct a social network of a hospital in Tokyo based on observations and simulate stochastic susceptible-infected-recovered (SIR) dynamics to explore effective containment strategies (intervention and vaccination protocols).

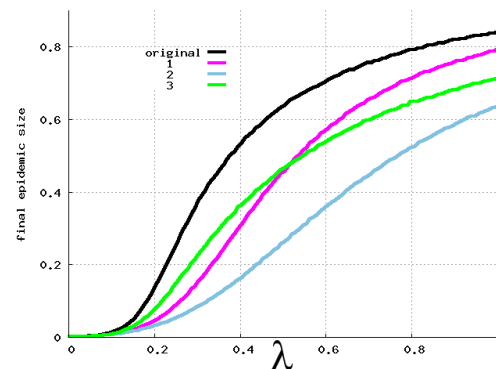
Results

We observed social networks of the hospital based on medical records at two time points (Ueno and Masuda 2008). Because the numerical results are qualitatively the same for the two networks, we state the results for one of them. The network has 605 individuals (388 patients, 94 nurses, 123 medical doctors) and 3046 edges. The network has a hierarchical and modular structure stemming from dense substructure in the hospital, such as departments, wards, rooms, and teams of medical doctors. These structures serve as network communities. In other words, nodes are densely connected within a substructure, whereas they are only loosely connected globally. The network does not have a scale-free-like degree distribution. Therefore, the social network of the hospital is qualitatively different from other social networks underlying disease transmission (e.g. Liljeros *et al* 2001).

Healthcare workers, particularly medical doctors, are main vectors of diseases, which is quantified by large values of the various centrality measures owned by healthcare workers. This is because patients are constraint to a single room, and nurses are constrained to a single ward, whereas medical doctors visit different wards in which they have their patients. In accordance, intervention methods that lessen visits of medical doctors to multiple wards (interventions 1 and 2 in Fig.1) are more effective in reducing the final epidemic size than intervention methods that directly protect patients, such as introduction of single rooms to isolate the patients (intervention 3 in Fig.1). As for vaccination, vaccinating doctors with priority rather than patients or

nurses is more effective in reducing the epidemic size. Note that the doctor-oriented vaccination is effective even to reduce the epidemic size of the patients.

Fig.1. Final epidemic size for different intervention strategies. The infection rate of the SIR model is denoted by λ . We set the recovery (or death) rate of the SIR dynamics equal to unity for normalization. original: the original observed network, 1: intervention 1 in which the teams of medical doctors are manually reallocated to different patients so that the visits of doctors to different wards are minimized. 2: intervention 2 in which teams of the medical doctors are resolved so that doctors examine patients alone when possible. 3: intervention 3 in which all the patients are isolated in single rooms so that disease transmission among patients is prohibited.



Discussion

We have shown that doctor-oriented intervention and vaccination strategies are effective in reducing the final epidemic size than the patient-oriented ones. This is true even to protect patients, who have large case fatality in contrast to healthcare workers. A remaining theoretical issue is to thoroughly understand how SIR and other disease spreading dynamics behave on networks with network communities and hierarchical structure. On a practical side, important future problems include application of our framework to specific nosocomial pathogens such as MRSA and VRE, and examination of how disease transmission dynamics and dynamics of social networks interact, which requires observation of the hospital social networks at more time points.

References

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