



Spatial correlation as an early warning signal of regime shifts in a multiplex disease-behaviour network

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ABSTRACT

Early warning signals of sudden regime shifts are a widely studied phenomenon for their ability to quantify a system's proximity to a tipping point to a new and contrasting dynamical regime. However, this effect has been little studied in the context of the complex interactions between disease dynamics and vaccinating behaviour. Our objective was to determine whether critical slowing down (CSD) occurs in a multiplex network that captures opinion propagation on one network layer and disease spread on a second network layer. We parameterized a network simulation model to represent a hypothetical self-limiting, acute, vaccine-preventable infection with short-lived natural immunity. We tested five different network types: random, lattice, small-world, scale-free, and an empirically derived network. For the first four network types, the model exhibits a regime shift as perceived vaccine risk moves beyond a tipping point from full vaccine acceptance and disease elimination to full vaccine refusal and disease endemicity. This regime shift is preceded by an increase in the spatial correlation in non-vaccinator opinions beginning well before the bifurcation point, indicating CSD. The early warning signals occur across a wide range of parameter values. However, the more gradual transition exhibited in the empirically-derived network underscores the need for further research before it can be determined whether trends in spatial correlation in real-world social networks represent critical slowing down. The potential upside of having this monitoring ability suggests that this is a worthwhile area for further research.

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1. Introduction

Vaccine-preventable infectious diseases continue to impose significant burdens on populations around the world (Lopez and Mathers, 2013). Access to vaccines remains a significant barrier to providing more widespread protection against infectious diseases. However, a growing obstacle to infection control is vaccine refusal, which can have a large effect on disease prevalence. For instance, the drop in vaccine coverage after Andrew Wakefield's fraudulent 1998 paper about the mumps-measles-rubella vaccine reduced MMR coverage to as low as 61% in some areas of the United Kingdom (Murch, 2003). Lower vaccine coverage caused larger measles outbreaks in the years following the publication of the Wakefield paper (Alazraki, 2011; Jansen et al., 2003). Elimination of polio in Africa was similarly interrupted when a rumor that the vaccine could cause infertility or HIV infection began spreading in 2003, when leaders of three states in north-central Nigeria boycotted the vaccine until it could be tested independently. The

impasse was not resolved until the following year, a time period during which these states accounted for over 50% of polio cases worldwide (Chen, 2004; Jegede, 2007). Vaccine refusal and hesitancy are also common for influenza vaccine, with non-vaccinators citing concern for side effects, lack of perception of infection risk, and doubts about vaccine efficacy as reasons to not become vaccinated (Fiebach and Viscoli, 1991).

Simple differential equation models such as the Kermack-McKendrick SIR (susceptible-infected-recovered) model published in 1927 (originally formulated as an integro-differential equation) (Kermack and McKendrick, 1927), allow us to characterize useful measures such as the expected number of new infections caused by each infection, and are readily fitted to epidemiological data. Classical infection transmission models such as the Kermack-McKendrick model assume that members of the population mix homogeneously. However, in many situations, infection transmission through a network—where individuals are nodes and contacts through which infection may pass are edges—are a more accurate description of infection dynamics (Bansal et al., 2007). Networks tend to be analytically intractable and therefore agent-based models are often used to simulate networks. Agent-based simulations

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on networks allow us to specify complex individual node behavior in a natural way. One of the most ambitious examples of these is the Global-Scale Agent Model, which models the daily behavior and relationships of 6.5 billion people using worldwide GIS data (Parker and Epstein, 2011). However, agent-based network simulations have also been studied in the context of nonlinear interactions between disease dynamics and individual behaviour concerning vaccines and contact avoidance (Fu et al., 2011; Funk et al., 2009; Perisic and Bauch, 2009b; Shaw and Schwartz, 2008; Zhang et al., 2014).

The trajectory that an infection takes as it moves through a population is heavily influenced by the spread of health information between individuals, so more sophisticated models of disease spread often combine disease dynamics and social dynamics. The coupled interactions between individual behaviour and disease dynamics have been modelled under various frameworks and placed under various rubrics including: epidemic games (Wang et al., 2010), coupled behaviour-disease models (Perisic and Bauch, 2009a; 2009b; Wang et al., 2015), socio-epidemiology, economic epidemiology and behavioural modeling (Fenichel et al., 2011). A more recent trend in epidemiological modeling is to abstract these two subsystems into (1) an information transfer network through which information flows between individuals, and (2) a separate physical disease transmission network. A system where each node is part of two or more different networks is called a multiplex network, and is a natural way to implement a coupled disease-behaviour system (Bauch and Galvani, 2013; Wang et al., 2015). For instance, the simultaneous spread of disease and disease awareness over adaptive multiplex networks with scale-free degree distributions has been studied (Granell et al., 2013). Similarly, a three layer network to model the diffusion of infection, awareness, and preventative measures along different contact networks was found to reasonably approximate empirical influenza data (Mao and Yang). Similar approaches consider coupled human and ecological dynamics, which present the opposite problem of species that humans wish to preserve instead of eradicate (Barlow et al., 2014; Henderson et al., 2016; Innes et al., 2013; Sigdel et al., 2017).

The nonlinear coupling between disease and social processes creates feedback loops between infection prevention mechanisms and disease spread. Nonlinear feedback in other complex systems such as from solid state physics and theoretical socio-ecology has often been shown to yield critical transitions (Guo et al., 2015; Sigdel et al., 2017; Xia and Liu, 2013). A critical transition is defined as an abrupt shift from an existing dynamical regime to a strongly contrasting (and sometimes unfavourable) dynamical regime as some external parameter is pushed past a bifurcation point (Bauch et al., 2016; Scheffer et al., 2009a). Fortunately, critical transitions (and other regime shifts associated with a bifurcation where the dominant eigenvalue of the Jacobian matrix around the equilibrium approaches zero) often exhibit characteristic early warning signals beforehand that allow these shifts to be predicted (Bauch et al., 2016; Boettiger et al., 2013; Dakos et al., 2010). Critical slowing-down (CSD) based indicators were one of the first early warning signals to be studied. CSD occurs because the speed with which a system responds to perturbations slows as it approaches bifurcations where the magnitude of the dominant eigenvalue of the Jacobian approaches zero at the bifurcation point. Since nearly all systems in the real world are subject to perturbations, the lag-1 autocorrelation of a time series can be used as a relatively universal (or at least potentially common) indicator of CSD. Lag-1 autocorrelation appears to be a robust statistic and has been shown to be present in predicting catastrophic bifurcations in complex real world systems such as the global climate (Scheffer et al., 2009b), human nervous systems (Elger and Lehnertz, 1998), and stock markets (Lebaron, 1992).

The discrete fourier transform (DFT) of a network is another example of a CSD-based early warning signal. Under some assumptions, the Weiner-Kinchin Theorem shows that we can use the discrete Fourier transform (DFT) to measure spatial correlation in system state, and this has been shown to work in some ecological applications (Carpenter and Brock, 2010; Cline et al., 2014). Lag-1 spatial correlation can in some cases provide a better early warning signal than time-domain methods, because “a spatial pattern contains much more information than does a single point in a time series, in principle allowing shorter lead times” before the critical transition occurs (Dakos et al., 2010; Guttal and Jayaprakash, 2009). This observation has been corroborated in three ecological dynamical systems (Dakos et al., 2010).

Early warning signals of regime shifts in coupled behaviour-disease networks have received relatively little attention in the literature on modelling interactions between disease dynamics and human behaviour. This appears to be a significant knowledge gap because early warning signals for vaccine scares could help public health anticipate widespread vaccine refusal and prepare for outbreak response in advance, as well as build efforts to improve trust between the public and the health authorities. In this paper we use an agent-based model on a two-layer multiplex network to simulate the coupled disease dynamics of a vaccine-preventable infection and social dynamics of vaccination in a population. We show that spatial correlation can be used as an early warning signal for regime shifts in this system on most (but not all) network topologies. In the next section we discuss the model structure and methods of analysis, followed by a section on results and finally a discussion section.

2. Methods

2.1. Simulation

Our agent-based model simulated a population of 10,000 individuals (nodes), where every node belongs to two different connectivity networks: a transmission network and a social network. In the transmission network, each node is connected to other nodes from which they can contract infection. Two nodes are linked in the social network if they can be influenced by one another's opinions on vaccination. These networks were simulated as fixed graphs upon which stochastic processes occurred, with a variety of degree distributions and average path lengths.

We modelled a hypothetical acute, self-limiting infection with rapidly waning natural immunity. Each node on the physical layer is in one of four possible states: susceptible (S), infected (I), recovered (R), or vaccinated (V). Each node on the social layer also has an opinion on the vaccine: they are either a non-vaccinator (η), or a vaccinator (ν). We will denote the biological state of a node v by $B(v)$, and the opinion of a node v by $\Theta(v)$. The transmission network is a graph denoted by $T(V, E_T)$, and the social network is a graph denoted by $O(V, E_O)$. We assume that they share the same set of vertices V although this assumption could be relaxed in future work. The set of nodes in the neighbourhood of v is $adj_T(v)$ or $adj_O(v)$ for the transmission and the social network respectively.

The algorithm used to simulate the social and transmission processes used discrete timesteps. At each time step, for each $v \in V$:

- If $B(v) = I$, then for all $u \in adj_T(v)$ such that $B(u) = S$ and $\Theta(u) \neq \nu$, set $B(u) = I$ with probability p (infection event)
- If $B(v) = I$, let $B(v) = R$ with probability r (natural recovery event)
- If $B(v) = R$, set $B(v) = S$ with probability γ (loss of immunity event)
- If $B(v) = S$, set $B(v) = I$ with probability $\sigma \ll 1$ (case importation event)

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