A Computational Model of Mitigating Disease Spread in Spatial Networks

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ABSTRACT

This study examines the problem of disease spreading and containment in spatial networks, where the computational model is capable of detecting disease progression to initiate processes mitigating infection spreads. This paper focuses on disease spread from a central point in a 1 x 1 unit square spatial network, and makes the model respond by trying to selectively decimate the network and thereby contain disease spread. Attention is directed on the kinematics of disease spreading with respect to how damage is controlled by the model. In addition, the authors analyze both the sensitivity of disease progression on various parameter settings and the correlation of parameters of the model. As the result, this study suggests that the radius of containment process is the most critical parameter and its best values with the computational model would be a great help to reduce damages from disease spread of a future pandemic. The study can be applied to controlling other virus spread problems in spatial networks such as disease spread in a geographical network and virus spread in a brain cell network.

Keywords: Computational Epidemiology, Computer Viruses, Disease Progression, Forest Fires, Spatial Networks

INTRODUCTION

Networks are encountered in a wide variety of contexts. For example, computer networks, social networks, circuit networks, networks of neurons, and terrorist networks (Gupta & Kumar, 1998; Kurland & Pelled, 2000; Wetterling, 2001; Newman et al., 2002; Fortunato, 2005; Malarz et al., 2007). In this work we consider the generic problem of damage spreading of in two-dimensional fixed radius random networks. Fixed radius random networks are spatial networks in which the range of connectivity of individual nodes is limited and this network model has been used for
simulation of wireless communication networks and geographical networks.

The control strategies that we design in our model are potentially relevant in diverse contexts that span a range of spatial and temporal scales. These include culling during epidemics in farm animals, fire fighting to wildfires and social bullying in community networks. In biology, mechanisms such as programmed cell death and scar formation are activated to control the spread of pathological processes. Hence, the results presented here could be of relevance in many application areas because we address the problem of how a computational model can detect damage progression and control the spreading of the damage. We show that aggressive defense strategy is not always the best way for the network to control damages, but selectively balanced defense system with best values of parameters is a successful way for controlling spreads with minimum damages.

One of the most critical and intolerable threats for human health could be an unknown influenza pandemic in the near future. Efficient control of potential influenza pandemics would be an important strategy in minimizing their adverse economic and public health impacts. A study shows that stochastic epidemic model can be used to investigate the effectiveness of targeted antiviral prophylaxis, quarantine, and pre-vaccination in containing an emerging influenza strain at the source (Longini et al., 2005). Other studies show that simulations on epidemic models can predict a pattern of reduced and lagged epidemics post vaccination (Ferguson et al., 2005; Kim, 2008, 2009; Pitzer et al., 2009; Kim et al., 2010). Mathematical models also can help determine and quantify critical parameters and thresholds in the relationships of those parameters, even if the relationships are nonlinear and obscure to simple reasoning (Menach, 2006; Smith, 2006; Epstein, 2009).

A contact pattern model on smallpox spread could be used to contain outbreaks by a strategy of targeted vaccination combined with early detection without resorting to mass vaccination of population (Eubank et al., 2004). In addition to avian influenza (H1N5), influenza A (H1N1) virus has spread rapidly across the world (Neumann, Noda et al. 2009; Smith, Vijaykrishna et al. 2009). Several papers analyze the virus spreading patterns and effective vaccination strategies for maximizing the H1N1 containment (Fraser et al., 2009; Munster et al., 2009).

In this paper, we focus on numerical analyses on experimentation results with a computational model of mitigating disease spread in spatial networks. This work is organized as follows. First we focus on describing the model system considered here and the details of our calculations. We present the results of this study next and briefly discuss the properties of fixed-radius random networks considered here. This is followed by details of calculations on the spatial and temporal features of our computational model of the disease spread process and containment process. We analyze both the effect of the disease spreading process and the effect of the containment process with model parameters. We show the spatial features of the model using a real world geological network as a possible application and conclude with summary and future works of the results.

THE SYSTEM MODEL

Many relational and geographical networks have similar properties of fixed-radius random networks. Particularly, communication network models and transportation network models comprise graphs through a set of vertices $V$ embedded randomly in a two-dimensional plane (a geographic map) such that the edges $E$ connecting these vertices exist if the distance between two vertices is less than some maximum range parameter. The set of edges and the resultant network connectivity are emergent properties of the graph that are determined by the locations and communication capability of the vertices.

We will consider the connectivity properties of such random graphs for the purpose of evaluating the ability of the communication network to route messages between pairs of vertices. We will evaluate graphs with fixed vertices, as a model of disease spreading and containment.
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