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A biologically inspired immunization strategy for network epidemiology

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HIGHLIGHTS

- We study an efficient, bio-inspired immunization strategy for network epidemiology.
- Inspiration stems from a single-celled, ameba-like organism, *Physarum polycephalum*.
- Our strategy goes beyond the node degree in selecting targets for immunization.
- The strategy performs considerably better than several well-known competitors.

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ABSTRACT

Well-known immunization strategies, based on degree centrality, betweenness centrality, or closeness centrality, either neglect the structural significance of a node or require global information about the network. We propose a biologically inspired immunization strategy that circumvents both of these problems by considering the number of links of a focal node and the way the neighbors are connected among themselves. The strategy thus measures the dependence of the neighbors on the focal node, identifying the ability of this node to spread the disease. Nodes with the highest ability in the network are the first to be immunized. To test the performance of our method, we conduct numerical simulations on several computer-generated and empirical networks, using the susceptible-infected-recovered (SIR) model. The results show that the proposed strategy largely outperforms the existing well-known strategies.

1. Introduction

Infectious agents, in the broadest sense, can spread in a 'population' of humans, animals, and nowadays technological devices. In the case of an outbreak, the goal is to minimize the damage to the 'population' without violating the constraints of a limited budget. Achieving this goal in 'populations' other than the primitive, well-mixed ones is the main reason why the problems of (i) epidemics spreading in complex networks (Pastor-Satorras and Vespignani, 2001; Saumell-Mendiola et al., 2012; Zhou et al., 2012; Wang and Xiao, 2012; Buono et al., 2014) and (ii) the corresponding immunization strategies (Balthrop et al., 2004; Bauch and Earn, 2004; Schneider et al., 2011; Hébert-Dufresne et al., 2013) attracted considerable attention in the literature. Such a trend is further spurred by the outcomes of ineffectively controlled epidemics—exemplified by the severe acute respiratory syndrome (SARS) and the swine flu (Schneider et al., 2011)—which rapidly spread all over the world due to globalization and better means of transport (Colizza et al., 2007; Perra et al., 2012). An immediate concern, therefore, is the development of the effective countermeasures against epidemics, wherein immunization science plays an important, if not critical, role.

Multiple immunization strategies have been considered for complex networks. *Uniform* or *random* immunization (Pastor-Satorras and Vespignani, 2002) selects any node in the network with

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equal probability at each time step, which results in a strategy suitable for homogeneous networks, but ignores the fact that in highly heterogeneous networks eradicating an infective agent cannot be guaranteed regardless of the fraction of immunized nodes. *Targeted* immunization (Mirzasoleiman et al., 2012; Schneider et al., 2012) seeks to overcome this problem by selecting the nodes with the highest ability to spread the disease. Such ability is often measured in terms of degree centrality, defined as the number of ties a node has, or betweenness centrality, which indicates how often a node is located along the shortest route between two other nodes. A strategy based on degree centrality is highly effective, yet it neglects the structural significance of a node because the most connected nodes are not necessarily the ones that facilitate disease propagation from one dense cluster to another (Hébert-Dufresne et al., 2013). Betweenness centrality can be used to overcome such a shortcoming, but suffers from a considerable computational cost (Hébert-Dufresne et al., 2013). In general, targeted immunization requires global knowledge of network properties, which is impractical. Motivated by such an impracticality, so-called *acquaintance* immunization (Cohen et al., 2003; Gallos et al., 2007) was developed, whereby immunized nodes comprise only a small fraction of random neighbors of randomly selected nodes. Furthermore, a number of alternative and/or more specialized strategies have also been discussed (Fu et al., 2008; Lü et al., 2011; Gong et al., 2013; Wang et al., 2014; Yan et al., 2014). Owing to their immediate practical and economic implications, additional studies involving novel immunization strategies are still of considerable importance.

Herein we propose an efficient biologically inspired immunization strategy for network epidemiology. The term *biologically inspired* is used in the sense that we draw inspiration from a single-celled, ameba-like organism *Physarum polycephalum*, capable of transporting signals and nutrients through a dendritic (i.e. tree-like) network of tubular structures called pseudopodia (Nakagaki et al., 2000). *Physarum* is particularly interesting because of the ability to perform cellular computations of a sort, which lead to the solution of, for example, the shortest path problem. This and similar observations served as a basis for constructing a mathematical model of an adaptive transport network driven by Poiseuille flow that exhibits computational abilities much like *Physarum* itself (Tero et al., 2007). Subsequently, a *Physarum*-type algorithm has been used for solving the Steiner Minimum Tree problem (Tero et al., 2008, 2010), for optimizing network design (Tero et al., 2010; Watanabe et al., 2011; Liu et al., 2015; Song et al., 2014), and for a variety of other applications (Zhang et al., 2012, 2013; Gao et al., 2013; Adamatzky, 2014; Adamatzky and Schubert, 2014).

The paper is organized as follows. In Section 2 we describe how to construct a *Physarum* model and modify it into a strategy for immunizing complex networks. Model properties and performance are examined in Section 3. In particular, we emphasize (i) the difference in functioning between the proposed strategy and other, well-known counterparts, (ii) the gain in performance by accounting for the structural importance of nodes, and (iii) the ability to capture the key attributes of a whole network based solely on the successive use of local information. Finally, in Section 4 we summarize the take-home message and discuss the potential drawbacks, as well as the future developments.

2. Methods

The proposed, biologically inspired strategy (denoted simply AS, where A stands for ameba) is constructed in three steps. First, we describe the *Physarum* model for the shortest path selection. We then modify the model by adding a noise factor to select the paths alternative to the shortest one along which the disease can still spread, albeit with a lower probability. Second, the original *Physarum* (single-source, single-sink) model is further modified to become a single-source, multi-sink model to consider the spread of the disease to multiple targets simultaneously. With these modifications, the model measures the dependence of each node in the network on the focal node. The third and final step in the construction of AS is motivated by the fact that applying the modified *Physarum* model to a large network is impractical due to a possible lack of information on the network structure or the high computational expense. Accordingly, for each focal node, a subnetwork consisting of the focal node itself and its R-step neighbors is separated from whole network, whereupon the model is applied to this R-local subnetwork. To test the performance of AS, we conduct numerical simulations on several computer-generated and empirical networks.

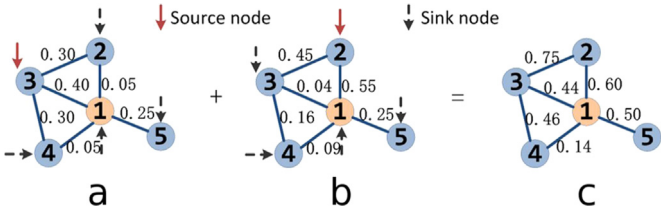

Fig. 1. Internal functioning of AS. Node 1 marked with wax-yellow color is the focal node, whereas the other nodes are its first-level neighbors. Panels a and b show the results of two model iterations in which nodes 3 and 2 are selected as the source nodes, respectively. These results are summed to produce the so-called flow matrix in panel c. Upon running all possible iterations (see the accompanying text), the *AS*-score for the focal node is obtained by summing the elements of the flow matrix across all edges.

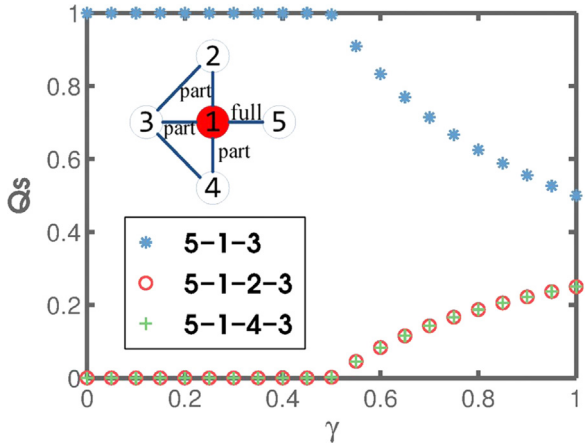

Fig. 2. The role of the noise factor and irrational path selection. The distribution of flows, Qs, along the different paths from node 5 to node 3 (in the inset) is shown as a function of the noise factor, γ. If $\gamma > 0.5$, in addition to shortest path 5-1-3, some flow is equally distributed between the two remaining paths, 5-1-2-3 and 5-1-4-3, meaning that the relative importance of disease spreading pathways is correctly distinguished.

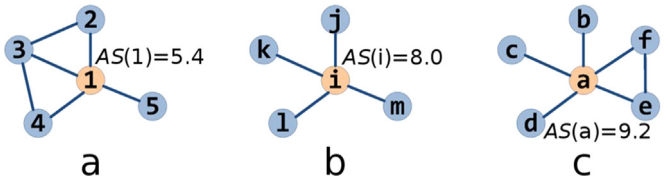

Fig. 3. The advantage of AS over the other comparable strategies. Schematic network representations in which the node marked with wax-yellow color is the focal node, whereas the other nodes are its first-level neighbors. DCS fails to distinguish between the focal nodes in panels a and b. BCS fails to do the same for the focal nodes in panels b and c. AS, by contrast, does not suffer from the same problems as illustrated by displayed *AS*-scores.