Global vaccination strategies in Modular Networks

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Global vaccination strategies in Modular Networks

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Abstract.   We study the effect of vaccinating networks with different growing strategies, using various techniques that require the complete knowledge of the network. The goal is to restrain the epidemic before it spreads throughout the network and target the few key nodes that will help contain it. Our target networks are chosen to have relatively large modularity index and various immunization techniques are applied to them.

1. Introduction

The spread of epidemics can be considered to occur on networks that describe contacts between individuals. The process of epidemic spreading throughout large networks is being researched widely the last years. The spreading dynamics are closely related to the structure of networks. For this reason network epidemiology has become one of the most vibrant subdisciplines of complex network studies [1],[2] and [3].

The form of epidemic spreading can also be acknowledged as information flow in a network. If we consider the virus spreading in an epidemic, we can safely say that an information will spread the same way. In this case, we want the opposite results than the virus spreading. The fortunate news are that with successful vaccination techniques, we can control the information flow, by immunizing or not certain nodes that are points of strategic importance in the network's topology.

Disease propagation has also been studied in scale-free networks [4], [5] and the problem of vaccination strategies has been specifically addressed [6]. Many times, it is not possible to vaccinate the whole population, due to high price of the vaccine. Some vaccines have severe side effects and for this reason one may also want to keep the number of vaccinated individuals low.

In this paper, in search of a better vaccination technique, we study two different approaches in selecting the group of nodes to be immunized. These techniques require the full knowledge of the network and their characteristics that define them. The networks that we use for this study, are of medium scale (approximately 2000 nodes) and are created with specific models throughout the bibliography of complex networks.

2. Network Models and Parameters

As indicated earlier in the paper, the main parameter, taken into consideration to select the networks in which we will experiment, is the modularity factor. This factor indicates the degree in which the network can be divided into modules or communities. It is simply the probability

that a link begins at a node i, a_i, multiplied by the fraction of links that end at a node in i, a_i. So the expected number of intra-community links is just $a_i a_i$. On the other hand we know that the real fraction of links exclusively within a partition is e_{ii}. So, we can compare the two directly and sum over all the partitions in the graph. Modularity fluctuates between the values of zero and one with one being the completely modular network. The equation for the modularity index is $Q = \sum(e_{ii} - a_i{}^2)$. The range following this pattern, four models of growing networks are chosen, as to satisfy that parameter. These four models are of different parameters, but the common parameter for all of them is the number of nodes they are containing, which is 2000 (medium-scale).

The first model for growing network which examine, introducing as basic content the fact that new nodes are attached to the network through one existing node and then explore the network through the links of the visited nodes [**?**]. At each time step, a new node is introduced into the preexisting network. This new new node, chooses at random, a node in then network. The new node follows the path of neighbors, starting from the random chosen node. As it passes through the node trail, it decides if it will connect or not. In our network that probability is p=0.2. This network is directed.

The second network based on Volkan Sevin and Per Arne Rikvold model [8]. In this model we use the preferential-attachment scheme which is primarily used in the Barabasi Albert model [9]. The model, has a user-defined number of initial nodes. These nodes have only outgoing links, in a way that they provide incoming links to the nodes that join at each time step. The new node attaches to an existing node with probability $\Pi(k_i) = k_i - 1$ where k_i, is the number of outgoing links at i. This model creates directed networks.

The next network is based on a modified BA model [9] in which all the edges connected to the new nodes are made locally to the creator and its nearest neighbors [10]. This means that, once again, at each time step a new node is introduced in the network. This node chooses among the preexisting nodes of the network, with the logic of preferential-attachment. After it has chosen a node, it uses the same PA scheme to choose the next, but only among the first node's neighbors. This model is used primarily for the generation of networks that simulate various natural food webs in certain ecosystems. In the network used in this paper, the new node makes two new connections with existing nodes. In contrary with the previous networks, this network is undirected, and the epidemic is spread differently.

The final network is based in the creation of triangles [11]. The newly introduced node, chooses at random among the preexisting edges of the network and it then connects to both ends of this edge. The control parameter q decides if the old edge between the two preexisting end-nodes, stays or not. This model operates in such a way as to create network with embedded small-world property. In the network examined in this paper, the control parameter q has the value of 0.5, which means that approximately half of the edges in question, are erased. This network is also undirected.

3. Vaccination Techniques
Describing the vaccination techniques in this section, first we will analyze the way the infection spreads over the networks. The epidemic model we choose for this occasion is the SIR model. The specific model of epidemic spreading operates with basic principle that there are three pools which contain all the nodes of the network. At the beginning of the spreading all the nodes (except from the vaccinated ones) are in the "Susceptible" pool. As the spreading progresses, the nodes are transferred with probability $p_i = 0.5$ to the "Infected" pool. Then with probability $p_c = 0.1$ are transferred to the Recovered pool. The key component of the SIR model is the fact that, as soon as a node has recovered from the infection, it can no longer carry it again. This is why the three states of the model are Susceptible Infected Recovered. The vaccinated nodes are considered to be in the Recovered state as soon as the infection starts to spread.
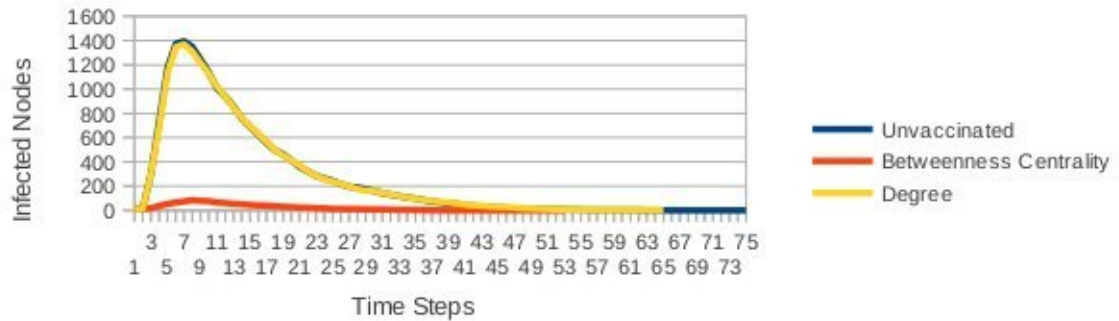
Figure 1. The epidemic spreading of the first network.

The first vaccination technique that we use in this paper, is the most commonly used in the papers that study immunization in complex networks. The nodes that are selected to be immunized before the spread of the epidemic are the ones with the highest degree of the network. For this vaccination, we target the highest 1% of the total population.

The other vaccination technique which yielded the most promising results is the vaccination based on the betweenness centrality factor of the network nodes. This metric indicates the number of shortest paths passing through a node. The value fluctuates between zero and one (0-1) with the values closer to one showing higher number of shortest paths passing through the specific node. The equation of the betweenness centrality factor is

$$C_B(v) = \sum_{s \neq v \neq t \in V} \frac{\sigma_{st}(v)}{\sigma_{st}}$$

For the purpose of this experiment we locate the 1% of the total nodes that have the higher value of betweenness centrality factor.

4. Results and Discussion

The results of the vaccination and epidemic spreading will be presented in the following graphs. These graphs show the number of infected nodes per time step. For reference purposes, we give in each graph, the values of the epidemic spreading without vaccination. As we expect, in all occasions, the number of infected nodes, as well as the speed of the spreading are higher than the vaccinated ones.

The first network that we examine has a modularity factor of 0.753 which is considered to be fairly modular. This network is created from the model of Alexei Vazquez paper [7]. The chart below **Figure 1** shows the progression of the infection in the three occasions.

This network is not created using preferential-attachment and this is the main reason that the basic characteristic of the network is the existence of triangles. This is why the network is very susceptible to the epidemic spreading, due to the great number of alternative routes that exist. As it is shown in **Figure 1**, the vaccination with respect to the betweeness centrality has
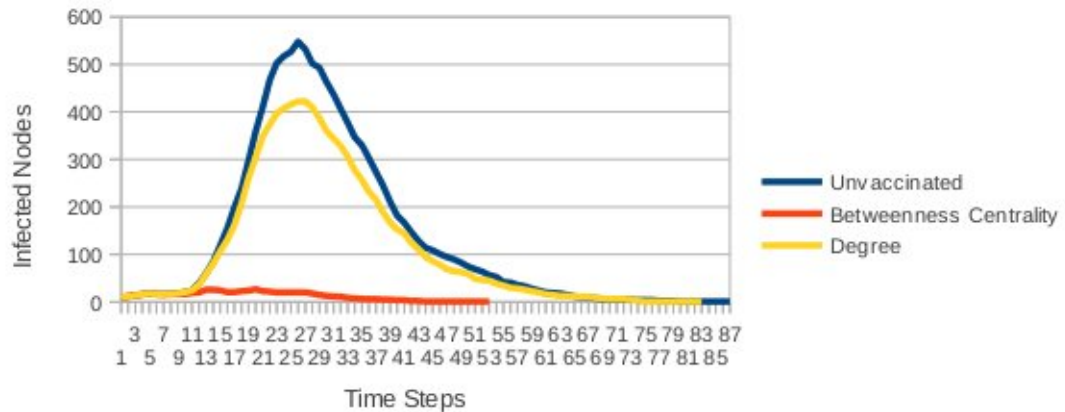
Figure 2. The epidemic spreading of the second network.

the best performance. This result makes sense because the network is fairly modular, but the scale of it is an important outcome.

The second network has a modularity factor of 0.939 for which we can safely say that is very modular. It is generated with the model introduced in the paper of Volkan Sevim and Per Arne Rikvold [8].It is fairly obvious in **Figure 2** that this network shows great resilience against epidemic spreading. The technique in which this network is generated, since it is a food-web based model, has minimal number of connections per node, and the existence of hubs is close to zero. The unvaccinated spreading reaches up to 25% of the population being simultaneously infected (approximately 550 nodes peaking at the time step 26). This proves the resilience of the network, even if there is no immunization. If we proceed to the next line of the chart which shows the vaccination with the degree, we will see even more resilience, but the difference is not very significant, due to the structure of the network as described above. The final line in the chart, shows the epidemic spreading with the vaccination of some nodes using the betweenness centrality value of the nodes. The results here are even more impressive than the previous network, because the modularity factor of the network is even higher than the previous one.

The third network has a modularity factor of 0.93 and it is also considered very modular. It is generated as a variation of the Barabasi Albert model [9], used to give small world networks [10]. This network was firstly introduced in the paper of XU Xin-Ping, LIU Feng and Li Wei [10] and the network we examine here, is created in relation to the model described in that paper. Results as shown in **Figure 3**.Even though this network is also very modular, it allows the spreading to reach higher levels than the previous network. This is because the structure of the network is very different than the previous one but quite similar to the first one. This network has many triangles which allow to the epidemic to spread more easily throughout the network. The fact that the vaccination technique using the degree of the nodes behaves better than the first network, which also has triangular structure, is caused by the use of the preferential-attachment in the model. Again due to high modularity and the network structure the vaccination technique using betweenness centrality value performs significantly better than the other two.

The fourth and final network has a modularity factor of 0.931 which makes this network very modular as well. The model from which this network was created is an attempt to create
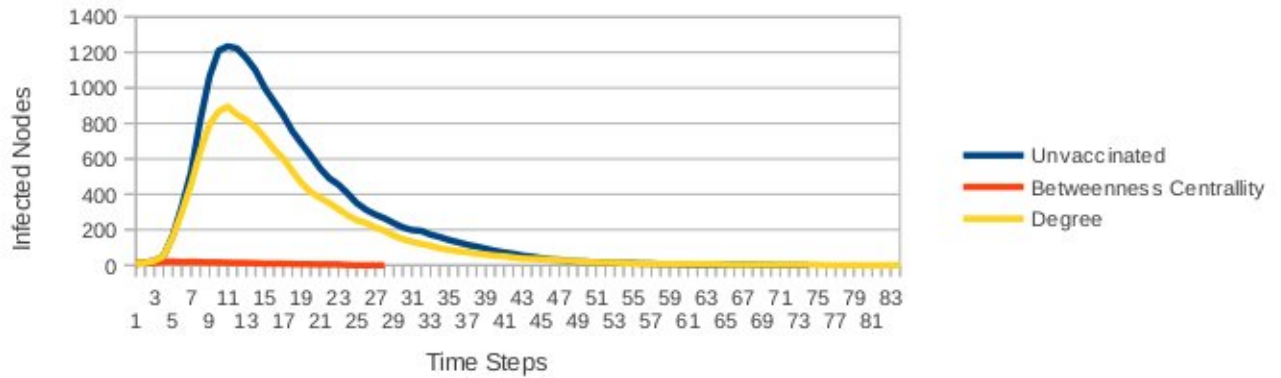
Figure 3. The epidemic spreading of the third network.

small-world networks [11]. The results in **Figure 4** show an interesting outcome.This network's behavior in epidemic spreading is quite similar to the previous networks. Yet we observe an important differentiation. The spreading in the procedure with vaccination based on the degree is significantly delayed than the other two. This means that the spreading has a small fluctuation in the beginning before it reaches its high peak (approximately at the time steps 77) in comparison with the other two techniques which have their peak earlier in the procedure.For the purpose of this experiment we locate the 1% of the total nodes that have the higher value of betweenness centrality factor.
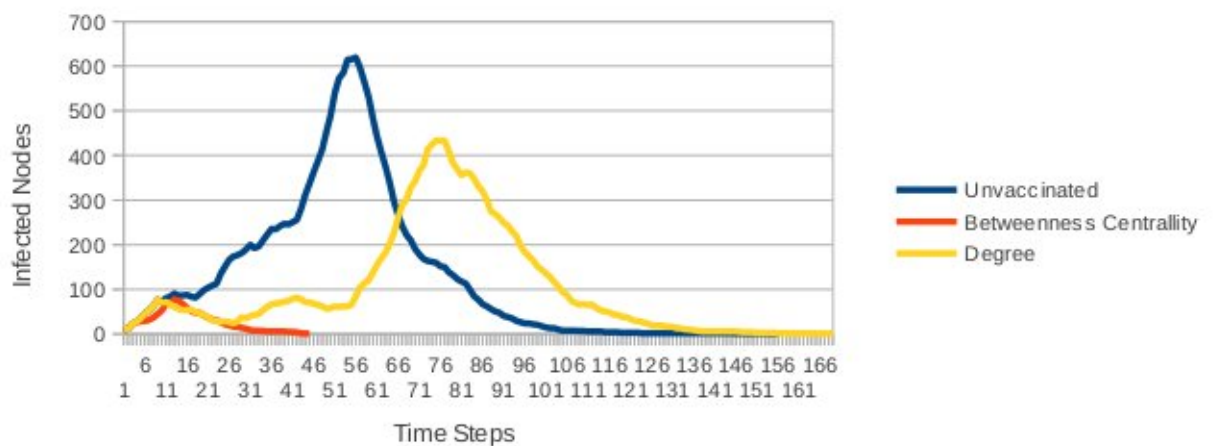

Figure 4. The epidemic spreading of the fourth network.

5. Conclusions

Summarizing this paper's results, it is safe to say that networks with high modularity index are more susceptible to the vaccination technique using the betweenness centrality of the nodes. Yet we observe that the networks that have triangles in their basic structure are more resilient in the epidemic spreading even without vaccination. This is a safe conclusion when we the knowledge of the networks are in global scale.

Acknowledgment

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