



Peer-to-Peer Networks for Modeling Malware Propagation

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Abstract— A key emerging and popular communication paradigm, primarily employed for information dissemination, is peer-to-peer (P2P) networking. In this paper, we model the spread of malware in decentralized, Gnutella type of peer-to-peer networks. Our study reveals that the existing bound on the spectral radius governing the possibility of an epidemic outbreak needs to be revised in the context of a P2P network. We formulate an analytical model that emulates the mechanics of a decentralized Gnutella type of peer network and study the spread of malware on such networks. We show analytically, that a framework which does not incorporate the behavioral characteristics of peers ends up over estimating the epidemic threshold metric, R_0 . This in turn results in false positives, an undesirable feature. We also characterize the conditions under which the network may reach a malware free equilibrium and validate our theoretical results with numerical simulations.

1. INTRODUCTION

Peer to peer networks provide a paradigm shift from the traditional client server model of most networking applications by allowing all users to act as both clients and servers. The primary use of such networks so far, has been to swap media les within a local network or over the Internet These networks have grown in their popularity in the recent past and the fraction of network trap c originating from these networks has consistently increased .The growing popularity and high penetration of P2P clients such as KaZaa, Gnutella and BitTorrent have provided virus writers with a potent means of compromising hosts on a large scale.

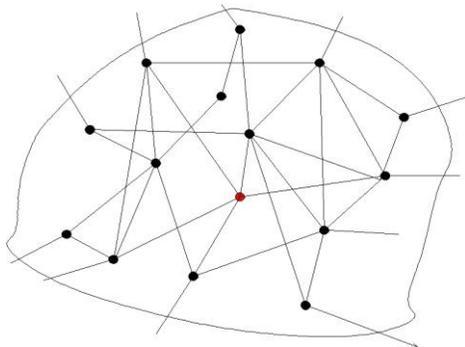


Fig. 1. Infection radius when $T T L = 2$.

The use of P2P networks as a vehicle to spread malware enjoys some important advantages over worms that spread by scanning for vulnerable hosts. This is primarily due to the methodology employed by the peers to search for content. For instance, in decentralized P2P architectures such as Gnutella, where search is done by coding the network, a peer forwards the query to its immediate neighbors and the process is repeated until a specified threshold $T T L$ is reached. Here $T T L$ is the threshold representing the number of overlay links that a search query travels. A sample scenario of the above description is depicted in Fig. (1), wherein the malicious host, labeled I, can potentially infect all peers that are within a distance of $T T L = 2$ hops from it. A relevant example here is the M andragore worm [that affected Gnutella users. Having infected a host in the network, the worm cloaks itself for other Gnutella users, leading them also to believe that it is actually an MP3 music le or an image le. Every time a Gnutella user searches for media les in the infected computer, the virus always appears as an answer to the request. The design of the search technique has the following implications: rst, the worms can spread much faster, since they do not have to probe for susceptible hosts and second, the rate of failed connections is less. Thus, rapid proliferation of malware can pose a serious security threat to the functioning of

P2P networks.

Understanding the factors affecting the malware spread can help facilitate network designs that are resilient to such attacks, thereby ensuring proper protection of the networking infrastructure. In this paper, we address this issue and develop an analytic framework for modeling the spread of malware in a peer-to-peer environment while accounting for the architectural, topological and user related factors.

Having motivated our work, we proceed to explore various facets of the problem. The rest of the paper is organized as follows: Section II differentiates the work presented in this paper from existing literature; in Section III, we lay the grounds for our modeling work and present the analytic framework in Section IV. We analyze the model in detail and Section V and present the numerical results validating our theory in Section VI. Finally, Section VII presents the concluding remarks.

2. RELATIONSHIP TO PRIOR WORK

In this section, we provide a brief overview of modeling literature in P2P networks, not necessarily in the realm of malware spread, and differentiate the current work from existing ones. Though the initial thrust in P2P research was measurement oriented, recent works, have proposed analytical models for the temporal evolution of information in the network. A branching process approximation characterizing the file transfer was presented, a stochastic uid model for BitTorrent-like networks is formulated and the steady state properties of the system are analyzed. A limitation of the above works is that they are specialized to Bit-torrent like networks and the framework cannot be extended to analyze P2P networks such as Gnutella or KaZaa. Although, the authors do not model the offline/online transition, their framework is more representative of a Bit-torrent network than existing ones. Again, the model's applicability is limited and cannot be extended to a Gnutella like network.

The issue of worms in peer-to-peer networks is addressed in wherein the authors perform a simulation study of the dangers posed by P2P worms and proceed to outline possible mitigation mechanisms. Modeling studies addressing malware spread in P2P networks appear wherein the authors formulate a deterministic model having its basis in the field of epidemiology. In formulating the equations for the various classes of peers, the authors assume that a vulnerable peer can be infected by any of the infected ones in the network. This assumption is certainly not true since the likely candidates for infected peers are limited to those present $T T L$ hops away from it and not the entire P2P network. Incorporating this detail in the model is imperative since it gurus in the expression for the *basic reproduction*

number, a metric that determines the presence/absence of an epidemic. Another important omission is the incorporation of user behavior in the analytic framework. Typically, users in a P2P network, alternate between two states: the on state, where they are connected to other peers and partake in network activities such as query forwarding/response, query initiation etc. and the off state wherein they are disconnected from the network. Peers going off act as an inherent deterrent to the density of infected hosts and can help check the rapid proliferation of the virus. This is so because a susceptible peer going off implies one lesser candidate choice for infection and an infected peer going off naturally lessens the intensity of malware spread.

In the current work, we formulate a comprehensive model for malware spread in Gnutella type P2P networks that addresses the above shortcomings. We develop the model in two stages: first, we quantify the average number of peers within $T T L$ hops from any given peer and in the second stage incorporate the neighborhood information into the final model for malware spread. While determining the average number of peers that are within k hops away is not feasible for arbitrary networks, the fact that the degree distribution of peers in Gnutella follows a power law distribution [7], makes the task realizable for such networks. In the next section, we report our simulation result that questions the validity of the bound on the spectral radius of the P2P adjacency matrix that is widely accepted to hold true in the presence/absence of a large scale infection. This finding, further substantiates the need to incorporate the limited view of a peer in a P2P network into the analytic model.

3. VIRUS PROPAGATION IN P2P GRAPHS

Hypercube have often been chosen as a graph model for P2P networks and the authors derive a limiting condition on the spectral radius of the adjacency graph, for a virus/worm to be prevalent in the network. For instance, in the authors, when deriving the threshold for P2P like graphs, do not consider the fact that once a peer is infected, any susceptible peer within a $T T L$ hop radius becomes a likely candidate for a virus attack.

In order to arrive at the threshold estimate for the virus spread, one needs to look at the spectral radius of the *modified adjacency matrix*, M . Specifically, this is a graph constructed from the original adjacency matrix, wherein an edge exists between two peers as long as there are within $T T L$ hops from each other.

4. P2P MODEL

In this section, we present our analytic framework for modeling the spread of information, in our case in the form of malware, in peer-to-peer networks. While the framework we develop is robust and is applicable across

varied architectures such as Bit-torrent networks, we confine ourselves to the analysis of Gnutella like networks. We first describe the search process and the likelihood of file transfer and then present the model for the spread of files based on a compartmental model.

A. Search Mechanism

The transfer of information in a P2P network is initiated with a search request for it. There exist several search mechanisms, popular among which are coding and the random walk. In this section, we derive an expression for the search neighborhood, z_{av} , under the assumption that the search mechanism employed is flooding, as is the case in Gnutella networks. In this scenario, a peer searching for a file forwards a query to all its neighbors. A peer receiving such a request first responds affirmatively if in possession of the file and then checks the hop count of the query. If this value is greater than zero, it forwards the query outwards to its neighbors, else, the query is discarded.

B. Compartmental Model

We formulate our model for the P2P network as a compartmental model, with the peers divided into compartments, each our formulation is based on the principle of mass action, wherein the behavior of each class is approximated by the mean number in the class at that instant of time. By employing the mean field approach to characterize each compartment, we make the following assumptions about the system:

5. MODEL ANALYSIS

In this section, we analyze the model presented in the previous section, in total and specific illustrative cases, and obtain the necessary conditions for the global stability of the malware free equilibrium.

Malware Free Equilibrium

We now proceed with the derivation of the *basic reproduction number*, R_0 , a metric that governs the global stability of the malware free equilibrium (henceforth termed VFE). Here, R_0 quantizes the number of vulnerable peers whose security is compromised by an infected host during its lifetime. It is an established result in epidemiology, that $R_0 < 1$ ensures that the epidemic dies out fast and does not attain an endemic state. Stability information of the VFE is important since this guarantees that the system continues to be malware free even if newly infected peers are introduced.

We follow the methodology presented in [1], where “next generation matrices” have been proposed to derive the basic reproduction number. In this method, the transition of individuals (cell phones in our case) between the states are written in the form of two vectors F and V which describe the in-own of new infected individuals and all other own in the system, respectively. These vectors are then differentiated with respect to the state variables,

evaluated at the disease (malware) free equilibrium, and only the part corresponding to the infected classes are then kept to form the matrices F and V .

6. RESULTS

In this section, we demonstrate the essence of our analysis presented thus far through numerical simulations. We first present our numerical results for the simple SIR epidemic described in the latter part of the previous section. The reason behind this is that the qualitative behavior of the model in is similar to that presented in [2]. Further, since the sampled model has a closed form expression for R_0 , it is easy to see its dependence on various model parameters and this relationship can be extended to the more detailed model. The experiments were carried out using parameters emulating a 20000 node. The initial number of infective was set at 50. We see that R_0 is directly proportional to t_{on} . The essence of this equation is that, nodes staying on-line for long periods as compared to their off-line durations result in a higher intensity of malware presence in the network. Numerical simulations concurred with the above observation. A similar trend was observed for the detailed model. The curve at the bottom corresponds to $t_{on} = 0:1$ and the intensity of the epidemic increases monotonically with an increase in

7. CONCLUSION

In the current work, we motivated the need to understand the dynamics of malware spread, especially in the context of inter-acting heterogeneous environments such as peer-to-peer networks. The need for an analytic framework incorporating user characteristics (e.g. off-line to on-line transitional behavior) and communication patterns (e.g. the average neighborhood size) was put forth by quantifying their influence on the basic reproduction ratio. It was proved analytically that a model that does not incorporate the above features runs the risk of grossly overestimating R_0 and thereby falsely reporting the presence of an epidemic. Further, our simulations show that the bound on the spectral radius for the spread of malware needs to take into account, the underlying communication pattern, especially in a P2P kind of setting so as arrive at an accurate estimate. The model was also extended to characterize the dynamics of malware spread in networks of smart cell phones.

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