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## Mathematical model on malicious attacks in a mobile wireless network with clustering



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### ABSTRACT

A mathematical model has been formulated for the analysis of a wireless epidemic on a clustered heterogeneous network. The model introduces mobility into the epidemic framework assuming that the component nodes have a tendency to be attached with a frequently visited home cluster. This underlines the inherent regularity in the mobility pattern of mobile nodes in a wireless network. The analysis focuses primarily on features that arise because of the mobility considerations compared in the larger scenario formed by the epidemic aspects. A result on the invariance of the home cluster populations with respect to time provides an important view-point of the long-term behavior of the system. The analysis also focuses on obtaining a basic threshold condition that guides the epidemic behavior of the system. Analytical as well as numerical results have also been obtained to establish the asymptotic behavior of the connected components of the network, and that of the whole network when the underlying graph turns out to be irreducible. Applications to proximity based attacks and to scenarios with high cluster density have also been outlined.

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### 1. Introduction

The fundamental inherent characteristics of wireless networks are often found to be advantageous as far as the perpetrators of malicious attacks on such networks are concerned. The traditional wireless networks including the cellular networks, the WiFi LANs and also Bluetooth networks, can be identified in terms of two basic characteristics, which strongly influence their security [1]. Firstly, occurrence of communication over a wireless channel makes it prone to attacks including eavesdropping, jamming or overusing. The second important characteristic is that of node mobility, and the limited resources available with these mobile portable devices. The evolution of wireless network technology has resulted in a transition from centralized

network architecture towards distributed and then to self-organized networks. Newer types of networks like Wireless Mesh Networks (WMN), Mobile ad hoc networks (MANET), Vehicular ad hoc networks (VANET) and Wireless Sensor Networks (WSN) have become common. For such networks, multi-hopping has become an essential characteristic where neighboring nodes cooperate for an efficient data transmission at the expense of lesser resources. Other features include greater programmability of wireless devices, increased use in financial and commercial transactions, selection of heterogeneous networks based on ease or availability of networks, emergence of communication between embedded devices like sensors and vehicles, and miniaturization of devices leading to further reduction in available energy resources, transmission capabilities and often computational power. Such features have not just made the threat scenario more critical but its analysis has also become more challenging.

The need to understand and analyze network attacks and their spread has often been addressed using the efficient

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tool provided by the principles of epidemiology. The seminal ideas in this field can be traced to the work of Cohen where he highlighted several undecidable detection problems. The problems included those about virus detection based on behavior or appearance, evolution stages of known viruses, and also about triggering mechanisms and their evolution [2]. White is credited for further outlining and analyzing a number of open problems in computer virus research [3]. These problems later provided the basis for several investigations, including White's and Kephart's work concerning directed graph based epidemic models for virus spread [4]. This is considered to be the beginning of the use of such methods for the analysis of virus spread in traditional computer network. Kleinberg is probably the first to identify the imminent threat of a wireless epidemic arising from the developments and large scale adoption of wireless communication technologies [5]. He highlighted several important features and also the major possibilities as well as challenges in using such an approach in the wireless domain. An important observation was that progress of attacks utilizing short range wireless communication technologies like Bluetooth closely tracked patterns of human mobility. The design of such wireless worms is supposed to infect mobile devices like cell phones. The progress occurs through scanning of other devices within short distances. Another important contribution was made by Gonzalez et al. where they tried to understand and individual human mobility patterns [6]. They analyzed the trajectories of 100,000 mobile phone users by tracking their positions over a period of 6 months. They observed that in spite of the large diversity in the trajectories of human travel history, an individual human trajectory shows a high degree of temporal as well as spatial regularity. An important outcome of their work was that they established a significant probability for an individual to return to a few locations that were highly frequented. This was a branching from the traditional view-point of random trajectories used very commonly in most mobility models like the random walk models.

In this paper we build on these fundamental ideas and try to analyze the impact of node mobility and also that of cluster formation in wireless network epidemics. Clustering is a phenomenon arising inherently as a culmination of constrained energy resources and multi-hop data transmission. An epidemic model is proposed that takes into consideration the impact of the mobility of nodes between their home clusters, i.e. the cluster to which a node is usually attached, and a foreign cluster which may be visited by a mobile node. The limited inter-cluster communication models the limited transmission range and also the cooperation between neighboring nodes, and it effectively presents a restriction on the spread of an attack. The model differs from most epidemiology based approaches in its consideration of an essentially heterogeneous underlying framework, together with the inclusion of a mobility paradigm into the epidemic structure. The analysis of the impact of mobility and related features like density of population or the intensity of interactions in a cluster provide us with dimensions that are interesting and meaningful in the context of wireless networks. In Section 2, the model is mathematically formulated. In Section 3, the basic behavior of the system is highlighted in the form of a number of preliminary results, while Section 4 discusses some of the interesting results that show the effect of the

inclusion of mobility into the epidemic framework. Finally, Section 5 concludes the paper.

## 2. Mathematical model

Inclusion of the concept of mobility requires that two separate frameworks be defined, one for the epidemic process and the other for the mobility process. Before obtaining a mathematical representation of the two processes, we first briefly highlight the basic assumptions on which the model will be formulated. The number of clusters is pre-defined and is taken to be a fixed finite positive integer. This assumption is based on the fact that we are starting from a stable state, as far as cluster formation is concerned. The nodes at this stage are expected to have been already associated with a unique *home cluster*. The nodes belonging to a specific home cluster may move out of that cluster due to mobility, but their general tendency is to stay in that cluster. Mobile nodes may travel to other clusters which will be called *foreign clusters*. These concepts can be seen as an abstraction of the concepts of *home link* and *foreign link*, which were used in RFC 3775, while introducing the operating principles of Mobile IPv6 [7]. The rates of inclusion of new nodes and that of removal of non-functional nodes are assumed to be equal so that the total population remains constant. The inclusion of new nodes in a cluster is assumed only because of the nodes for which the cluster is a home cluster. A node may stop functioning, both inside its own cluster or while in transit in a foreign cluster. The distance between clusters is not considered explicitly, but the outgoing and incoming mobility rates provide an implicit consideration. The epidemic process in each cluster assumes that the population in each cluster is categorized into three compartments, viz. *susceptible* and *infected* and *recovered*, and nodes are assumed to have only temporary immunity. The disinfection mechanism is assumed to be uniform across all the clusters. This is represented by taking an equal rate for the infected nodes to recover and also to again become susceptible in each of the clusters. It is also assumed that a cluster may not be accessible from one or more of the other clusters, or that it is totally isolated.

The total number of clusters is taken as  $n$ . The parameter  $\mu$  represents the rate at which new nodes are added to the network as well as that by which existing nodes become non-functional. The parameter  $\alpha_i$  represents the per capita rate of outward mobility per unit time from a home cluster. The fraction of these outgoing nodes that go to cluster  $j$  from cluster  $i$  is taken as  $q_{ji}$  where  $q_{ji} \geq 0$ ,  $q_{ii} = 0$  and  $\sum_{j=1}^n q_{ji} = 1$ . The per capita rate at which nodes of cluster  $i$  return from a foreign cluster  $j$  is given by  $m_{ij}$  where  $m_{ij} \geq 0$  and  $m_{ii} = 0$ . The parameter  $\beta_{ijk}$  represents the proportion of sufficient contacts between a susceptible node from cluster  $i$  and an infected node from cluster  $j$  in cluster  $k$ , that results in infection. The parameter  $p_k$  gives the average number of such contacts per unit time in cluster  $k$ . The rate at which the infected nodes again become susceptible is given by  $\xi$ . Based on the assumptions mentioned earlier, and the transfer diagram shown in Fig. 1, we first frame the mobility model and then the epidemic model for our system.

If the number of nodes of home cluster  $i$  present in any cluster  $j$  at time  $t$  be denoted by  $N_{ij}(t)$  then the number of

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