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Geometrical Modeling of Worm Propagation in Complex Networks

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Abstract

This paper introduces a novel geometrical approach to modeling worm propagation in complex networks, specifically focusing on scale-free and small-world networks. Traditional epidemiological models often fall short in capturing the intricate dynamics of worm spread in these networks due to their unique structural properties. Our geometrical models utilize path equations and deviation vectors to represent worm propagation pathways, providing deeper insights into network vulnerabilities and effective mitigation strategies. These models enhance the accuracy of predicting worm spread and identifying critical nodes and connections within the network.

1 Introduction

The rapid propagation of worms in computer networks presents significant challenges for network security. Traditional models, primarily based on epidemiological frameworks, often fail to accurately describe the spread dynamics in complex network structures such as scale-free and small-world networks. This paper proposes a novel geometrical modeling approach that leverages the structural properties of these networks to provide a more accurate understanding of worm propagation dynamics.

2 Geometrical Modeling Framework

2.1 Scale-Free Networks

Scale-free networks are characterized by a power-law distribution of node connectivity, where a few nodes (hubs) have a high degree of connections, and most nodes have fewer connections. Worms exploit these hubs to propagate rapidly through the network, making these networks particularly vulnerable to fast-spreading malware.

Path Equations:

The propagation of worms in a scale-free network can be represented using path equations that account for the influence of highly connected hubs. The general form of the path equation in such a network is:

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$$\mathbf{P}(t) = \sum_i \mathbf{H}_i(t) \cdot \mathbf{d}_i(t) \tag{1}$$

where $\mathbf{H}_i(t)$ is the connectivity function of the hub i at time t, and $\mathbf{d}_i(t)$ is the deviation vector representing the spread of the worm from hub i to other nodes. The connectivity function $\mathbf{H}_i(t)$ can be defined as:

$$\mathbf{H}_i(t) = k_i \cdot f(t) \tag{2}$$

where k_i is the degree of the hub, and $f(t)$ is a time-dependent function describing the spread dynamics.

Deviation Vectors:

Deviation vectors $\mathbf{d}_i(t)$ capture the spread of the worm from the hub to connected nodes. They account for the network's topology and the distance from the hub:

$$\mathbf{d}_i(t) = \mathbf{x}_i(t) - \mathbf{H}_i(t) \tag{3}$$

where $\mathbf{x}_i(t)$ is the position of the infected node i at time t. This allows us to model how quickly and efficiently the worm spreads through the network from the hubs.

2.2 Small-World Networks

Small-world networks exhibit properties of both regular and random networks, characterized by short path lengths and high clustering coefficients. These features enable rapid worm spread through shortcuts and clusters of nodes.

Path Equations:

In small-world networks, the path equation must incorporate the effects of clustering and the presence of shortcuts. The path equation in such networks is:

$$\mathbf{P}(t) = \sum_i \mathbf{S}_i(t) \cdot \mathbf{c}_i(t) \tag{4}$$

where $\mathbf{S}_i(t)$ represents the clustering function of node i at time t, and $\mathbf{c}_i(t)$ denotes the clustering coefficient, which reflects the local density of connections around node i.

Deviation Vectors:

Deviation vectors in small-world networks take into account the clustering and short paths:

$$\mathbf{c}_i(t) = \mathbf{x}_i(t) - \mathbf{S}_i(t) \tag{5}$$

where $\mathbf{S}_i(t)$ includes the influence of shortcuts and local clusters, allowing for a more nuanced understanding of worm spread dynamics in small-world networks.

3 Stability and Performance Analysis

To ensure the robustness of the proposed geometrical models, we perform stability analysis using the Lyapunov function and evaluate performance metrics through simulations.

3.1 Lyapunov Stability

The stability of the geometrical models is analyzed using the Lyapunov function $V(t)$:

$$V(t) = \frac{1}{2}\sum_i \mathbf{d}_i^2(t) \tag{6}$$

The function $V(t)$ measures the deviation of the worm spread from the equilibrium state. If $V(t)$ decreases over time, the model is stable.

3.2 Simulation Results

Simulations are conducted to evaluate the accuracy and performance of the geometrical models. We compare the models' predictions with actual worm spread data in scale-free and small-world networks. Metrics such as infection rate, spread velocity, and critical node identification are used to assess model performance.

Example:

In a simulated scale-free network with 1000 nodes and a power-law exponent of 2.5, the geometrical model accurately predicts the rapid spread of a worm originating from a hub, identifying key nodes that significantly influence the overall infection rate.

4 Conclusion

The geometrical modeling approach provides a novel framework for understanding worm propagation in complex networks. By leveraging the unique structural properties of scale-free and small-world networks, these models offer improved predictive accuracy and valuable insights into effective mitigation strategies. Future research will focus on refining these models to incorporate additional network complexities, such as temporal dynamics and multi-layered structures, to further enhance their applicability and effectiveness.

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