

Author's Accepted Manuscript

An Epidemiological Model of Internet Worms with Hierarchical Dispersal and Spatial Clustering of Hosts

David E. Hiebeler, Andrew Audibert, Emma Strubell, Isaac J. Michaud



PII: S0022-5193(17)30033-4
DOI: <http://dx.doi.org/10.1016/j.jtbi.2017.01.035>
Reference: YJTBI8945

To appear in: *Journal of Theoretical Biology*

Received date: 19 August 2016

Revised date: 20 December 2016

Accepted date: 19 January 2017

Cite this article as: David E. Hiebeler, Andrew Audibert, Emma Strubell and Isaac J. Michaud, An Epidemiological Model of Internet Worms with Hierarchical Dispersal and Spatial Clustering of Hosts, *Journal of Theoretical Biology*, <http://dx.doi.org/10.1016/j.jtbi.2017.01.035>

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting galley proof before it is published in its final citable form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

An Epidemiological Model of Internet Worms with Hierarchical Dispersal and Spatial Clustering of Hosts

David E. Hiebeler^{*,a}, Andrew Audibert^{a,b}, Emma Strubell^{c,d}, Isaac J. Michaud^{a,e}

^a*Department of Mathematics and Statistics, University of Maine, Orono, ME 04469*

^b*Bangor High School, Bangor, ME 04401*

^c*School of Computing and Information Science, University of Maine, Orono, ME 04469*

^d*College of Information and Computer Sciences, University of Massachusetts Amherst, Amherst, MA 01003*

^e*Department of Statistics, North Carolina State University, Raleigh, NC 27695*

Abstract

Beginning in 2001, many instances of malicious software known as Internet worms have been using biological strategies such as hierarchical dispersal to seek out and spread to new susceptible hosts more efficiently. We measured the distribution of potentially susceptible hosts in the space of Internet addresses to determine their clustering. We have used the results to construct a full-size simulated Internet with 2^{32} hosts with mean and variance of susceptible hosts chosen to match our measurements at multiple spatial scales. Epidemiological simulations of outbreaks among the roughly 2.8×10^6 susceptible hosts on this full-sized network show that local preference scanning greatly increases the chances for an infected host to locate and infect other susceptible hosts by a factor of as much as several hundred. However, once deploying this strategy, the overall success of a worm is relatively insensitive to the details of its dispersal strategy over a wide range of parameters. In addition, although using localized interactions may allow malicious software to spread more rapidly or to more hosts on average, it can also lead to increased variability in infection levels among replicate simulations. Using such dispersal strategies may therefore be

*Corresponding author

Email address: hiebeler@math.umaine.edu (David E. Hiebeler)

URL: <http://www.math.umaine.edu/~hiebeler> (David E. Hiebeler)

Download English Version:

<https://daneshyari.com/en/article/5760296>

Download Persian Version:

<https://daneshyari.com/article/5760296>

[Daneshyari.com](https://daneshyari.com)