



## Differential equation models for sharp threshold dynamics



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### ABSTRACT

We develop an extension to differential equation models of dynamical systems to allow us to analyze probabilistic threshold dynamics that fundamentally and globally change system behavior. We apply our novel modeling approach to two cases of interest: a model of infectious disease modified for malware where a detection event drastically changes dynamics by introducing a new class in competition with the original infection; and the Lanchester model of armed conflict, where the loss of a key capability drastically changes the effectiveness of one of the sides. We derive and demonstrate a step-by-step, repeatable method for applying our novel modeling approach to an arbitrary system, and we compare the resulting differential equations to simulations of the system's random progression. Our work leads to a simple and easily implemented method for analyzing probabilistic threshold dynamics using differential equations.

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### 1. Introduction

Differential equation models have wide applicability in the study of dynamic systems. They are attractive because they are numerically fast and tractable, transparent in the sense that it is easy to understand how the inputs directly relate to the outputs, and frequently have special cases for which closed-form solutions exist. Our research adapts these models to include systems with stochastic, sharp thresholds. One example of a system with a sharp threshold is a computer network where malicious code is introduced, subject to probabilistic detection and subsequent eradication. In this system, one instant the malicious code is undiscovered, and the following instant it is discovered; discovery defines the sharp threshold and changes system dynamics by allowing a remedy to be applied. For this and many other system, 'half-thresholds', such as "half discovered" are not physically realizable as they do not refer to any realizable state of the system.

A sharp threshold may also be seen in armed conflict where loss of a key capability fundamentally changes the capability of one or both sides. This may be thought of as loss of a key platform or capability. Statements such as "half attrited" do not refer to a realizable state of the system while statements about the probability distribution of a given system surviving are meaningful.

The current method of handling dynamical systems with sharp thresholds is to appeal to simulation of the threshold event by simulating the entire system's random progression. This is useful because it is easily understood, but is expensive, both in terms of computation and time. Often, many simulation repetitions are

required to analyze the average behavior of the system and gain useful insights.

It seems that the threshold process and the differential equation model are irreconcilable, chiefly because the threshold event is not divisible in the sense that its expected state is generally not reachable. Our contribution is to overcome this difficulty in a way that has not been previously shown by applying a mean field approximation to the threshold process. By doing so, we create differential equation models that capture the average performance of systems with probabilistic threshold dynamics.

Our approach is novel in that we incorporate the distribution of the threshold time, which may be dependent on the dynamic system state, to create a representation of the average value of the thresholded process. Our method produces a time-trace of the expected state of the system, as well as an explicitly time-dependent, cumulative distribution of the threshold time.

The advantages to be had are numerous. First, by creating a differential equation model, we are able to verify simulation models by comparing them against derived or numerical results. Second, we may use the fast, cheap, differential equation model to scope complex, expensive simulations. Additionally, as a by-product, the model produces the time-dependent cumulative distribution of the threshold time, which prior to modeling may be expressed in terms of the dynamic system state and therefore may not have explicit time dependence. Finally, after developing the theory, we provide two worked examples, along with a step-by-step tutorial on how to apply this method to any thresholded system with a differential equation model.

The organization of the paper is as follows: In Section 2, we review the applicable literature. In Section 3, we derive our novel methodology by developing a mean-field approximation for spreading malware among a computer network, and extract the

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step-by-step procedure for applying it to other systems. In Section 4, we apply the step-by-step procedure to the Lanchester model of armed conflict. In Section 5, we provide numerical examples comparing the differential equation models to simulations. In Section 5, we also demonstrate that the differential equations from our novel methodology are fundamentally different from differential equations for a non-thresholded system; in other words, no choice of parameters of the non-thresholded differential equations may replicate the behavior of the thresholded differential equations. Finally, in Section 6, we provide some discussion of and directions for future research.

## 2. Literature review

The general theory and application of differential equation models for physical and social phenomena is a common topic that spans several disciplines, including applied mathematics, biology, and operations research. Many good overviews of the topic exist; for a general text, we recommend *Differential Equation Models* by Braun et al. [8]. For an overview of basic analysis and solution techniques, we recommend O’Neil [34]. Mean-field approximations are frequently used in physics; for an in-depth overview, see the second chapter of Freericks [15]. An overview of approximation methods for probabilistic methods is given by Darling [11].

Mean-field models of epidemics have a long history, and are covered in detail in [10] (see also [2,1]). For a short overview, we recommend the recent tutorial by Dimitrov and Meyers [12]. Fitting models to data is addressed by Mollison [30], and stochastic epidemics are reviewed in detail by Andersson and Britton [2]. Specific system behaviors related to our research, such as time of discovery thresholds, are addressed by Metz et al. [29]. The distribution of the number of infected individuals at the moment of first detection is studied by Trapman and Bootsma [37].

The application of infectious disease models to computer infections has been recommended by Jason [20], an independent group of scientists advising the United States government. A related and noteworthy reference is the case study of the Code Red worm by Moore et al. [31]. Epidemics on networks, and particularly the  $S-I-R$  model is studied by Draief et al. [13], and the implications of several theoretical network topologies are examined. The spread of malware on wireless networks is considered by Hu et al. [19]. This paper examines the performance of malware—and the steps taken to prevent it—on representative topologies for seven urban areas in the United States.

The work most closely related to our application in malware infections is [38]. Their model closely matches the dynamics of ours in that machines may be in two competing states—infected or patched—and the system operator wishes to maximize the number of patched machines. Our work differs from theirs because, in our model, the detection event occurs as a function of the infection process.

Two recent books by Newman [33,32] describe the formulation and analysis of network models and include cases of epidemics spread on networks as well as the general theory of mean-field approximations. For the specific application of computer infection, our work is different in that we consider both epidemic detection and spread simultaneously in a single, integrated set of differential equations that track the whole progression of the epidemic. Epidemics on networks are also considered in Keeling and Eames [22], where the force of infection changes as a function of time. This work [22] bears some similarity to the Lanchester example we use in this manuscript—in which an equation parameter changes after a certain random threshold event—however, the methods we develop address general changes in dynamics, beyond parameter changes. In Section 3.4, we describe a general,

step-by-step method in which system dynamics can change arbitrarily as a function of a threshold event. For example, we could study a system where one set of machines,  $I$ , infect another set of machines,  $S$ , then based on some random event that itself depends on the numbers of  $I$  and  $S$  machines the dynamics switch and now  $S$  machines infect  $I$  machines. This extreme example illustrates the broad applicability and potential of our methodology, in that it can handle whole-sale changes of the entire system, where the timing of the change itself is dependent on the system state.

Mean-field models have been applied in epidemic models of network infections by Lelarge and Bolot [27], and a development of their applicability to general infectious disease models is given in [24], who justify the use of the mean-field approximation for sufficiently large, non-homogeneous networks. Aparicio and Pascual [4] describe the mean-field approach and demonstrate specific cases where it diverges from more sophisticated methods. Essentially, mean field, also called “compartmental” or “mass action” models assume homogeneous mixing. In large networks this may be unsatisfactory because it ignores the dynamic that individuals tend to interact more with those who are close to them than those who are far away. This dynamic is further complicated by considering epidemics on information systems, where the network topology may have little correlation with physical topology. Keeling [21] develops a correction to the basic  $S-I-R$  model by replacing the stationary infectivity parameter,  $\beta$  with a non-stationary  $\beta(t)$ , which captures the effect of faster transmission in the beginning stages of infection and slower transmission at the end of the epidemic. Keeling and Eames [22] also addresses the applicability of mean-field models to network epidemic transmission. Though, the focus of this work is a general procedure of creating mean-field models as opposed to the specific application of mean-field models to networks.

Infections with multiple stages are considered by Gani [16]. Their approach partitions the infective population into two sub-populations; a susceptible individual becomes fully part of the infective class after having contact with both the first-stage and second-stage of the infection.

Multiple Stages are also developed by Chowell [9]. These approaches increase the partitioning of the model or generalize the distribution time in each partition but do treat the threshold as global. Finkelstein [14] also studies epidemics with multiple stages. They share our approach of making the first stage of their model the unencumbered, or basic  $S-I-R$  model. The second stage they consider measures the cost associated with the epidemic. These two stages are analyzed iteratively to determine the amount of prophylactic vaccination that minimizes the epidemics’ impact from a cost perspective. Aggressive prophylactic measures, such as vaccination in biological epidemics are considered by House and Keeling [18]. The problem of determining the correct amount of preventative measure is similar to our problem of patch dissemination in a malware context.

Another perspective on multiple stage epidemics is provided by Klepac and Caswell [25]. Here, feedback exists between the infective process and the ‘demographic’ process—which consists of immigration and birth. Their approach includes processes that work on different time scales operating in the same model; their overall development measures density-dependent disease transmission. Conversely, our development focuses on the global, uniform change in dynamics created by discovery of malware, or loss of a critical combat enabler. Our threshold may be explicitly dependent on time or implicitly dependent on the other state variables. Furthermore, we extend our model approach beyond epidemics to general dynamic systems, using the Lanchester model of aimed fire as an example. It is possible that for specific scenarios, Kelpac and Caswell’s model produces similar results.

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