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Simulations of the Spread of the Hantavirus Using Fractional Differential Equations

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Abstract In this paper we study a fractional differential equation (FDE) model which describes the spread of Hantavirus infection in a system consisting of the host species and a non-host competitor species. The host species is a mouse species of which a portion is susceptible to infection and the remaining portion is already infected. The main reason we propose this model is due to the condition in real ecosystems where mice compete for resources with other species and the interaction processes among species in the ecosystem become an important agent in controlling the Hantavirus infection. Our results show our FDE model is able to reproduce results which are consistent with a previous study involving ordinary differential equations.

Keywords Fractional Differential Equation; Simulation; Hantavirus infection

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1 Introduction

Since the discovery of Sin Nombre Virus in 1993 as the agent of the severe Hantavirus Cardiopulmonary Syndrome (HCPS) disease in the North American Southwest, several studies have addressed the long-term dynamics of its principal host, the deer mouse (*Peromyscus maniculatus*), and the spread of Hantavirus infection [1–5]. Once infected, the infected mouse will carry the virus without themselves being harmed by it. The infected mouse also does not transmit the disease to offspring since the virus is not vertically transmitted. The most common means of transmission among the mice is generated by pairwise interactions between susceptible and infected mice. Transmission of Hantaviruses to humans most often occurs via inhalation of aerosolized, virus-laden mice excreta [1, 2].

In order to understand the dynamics of the Hantavirus, a mathematical framework has been proposed and analyzed by Abramson et al. [3]. This basic mathematical framework, also known as Abramson-Kenkre model, describes transmission of virus from infected to susceptible mice with a system of (deterministic) nonlinear differential equations. However, basic single species model of Hantavirus dynamics does not consider the effects of predator or other competitor species. In line with this hyphothesis, it has been found that the incidence of the disease decreases with an increasing number of predators [6, 7].

In real ecosystems, mice share the environment with many other animals. In addition, mice may be preyed upon by and compete for resources with other animals. The effect of competitor or predator species, therefore needs to be incorporated into the mathematical model. Peixoto and Abramson [8] proposed a model that takes into account the effect of biodiversity on Hantavirus infection. In their study, they have found that competition reduces, the prevalence of infection. This result is supported by empirical work done with populations of *Z. brevicauda*, the host of Calazabo Hantavirus, in field studies

in Panama [9]. Because of these factors, the modelling of Hantavirus-mice system should include the feedback effect of other species.

Here, we are interested to study the phenomenon of nonhomogeneity in the ecosystems, which occurs when there is a mixing between host and non-host populations. Previously, the equations for basic Hantavirus system proposed by Abramson et al. [3] have limitations due to their unsuitability for a nonhomogeneous setting. Later, Peixoto and Abramson [8] extended the equations developed by Abramson et al. [3] to include the feedback of non-host species. In this paper, we provide an alternative model based on Abramson et al. [3] equations using fractional differential equations to represent the dynamic of interactions among host and non-host populations. In particular, we have two nonlinear ordinary differential equations, and in order to represent the variability of the competitors, we have used $D_t^{1-\alpha} f(t)$ to represent a differential operator of noninteger order. When the power exponent is $\alpha = 1$, this corresponds to the basic Hantavirus model [3] and when $0 < \alpha < 1$ the system is comprised of both host and competitor species. Comparisons between fractional model and biodiversity model proposed by Peixoto and Abramson [8] are also tested on Hantavirus infection system and the results behave as we expected.

The outline of the paper is as follows. The descriptions of the basic system of Hantavirus infection model is given in Section 2. This is followed by an introduction to the biodiversity model in Section 3. Then, an introduction to the fractional differential equations is presented in Section 4. In Section 5, we introduce the fractional form of the Hantavirus infection system. We further state and discuss our findings in Section 6. Finally, we end this paper by some conclusions in Section 7.

2 A Basic System of Hantavirus Infection

A mathematical model originally a system of partial differential equations (PDEs) has been proposed by Abramson and Kenkre [3], with the purpose of providing a theoretical framework for Hantavirus infection. In the model, they assume that the whole population is composed of two classes of mice, susceptible and infected, represented as M_s and M_I. This model incorporates the decay by death of the mice population, the spread of infection through their interaction, the increase by birth and effect of the environment to stabilize the population, and also their movement as a process of diffusion. If movement from one location to another is ignored, the following system of ordinary differential equations is obtained.

$$\frac{dM_s}{dt} = bM - cM_s - \frac{M_s M}{K} - aM_s M_I, \tag{1}$$

$$\frac{dM_I}{dt} = -cM_I - \frac{M_I M}{K} + aM_s M_I. \tag{2}$$

Here, M_s and M_I are the populations of susceptible and infected mice, respectively, and $M(t) = M_s(t) + M_I(t)$ is the total population of mice. Other terms in (1) and (2) are as follows.

Birth: bM represents birth of mice, all of them born susceptible, at a rate proportional to the total population of mice.

Death: c represents the rate of population decay by death, proportional to the corresponding population. Note that the mice are not affected by Hantavirus infection and the deaths are "natural" deaths.

Competition: $-M_{s,I}M/K$ represent deaths due to competition for shared resources.

K is the capacity of the system to maintain a population of mice. Higher values of K represent higher availability of water, food, shelter and other resources that mice can use to survive [3].

Contagion: aM_sM_I represents the number of susceptible mice that get infected due to an encounter with an infected mouse, at a rate a, that Abramson and Kenkre [3] assumed to be constant.

This ordinary differential equations (ODEs) model is able to reproduce one of the observed features of Hantavirus infection that the infection can completely disappear from the mice population if environmental conditions are unfavourable and to reappear when conditions become favourable [3].

3 Biodiversity Model

In this model, Peixoto and Abramson [8] consider a single non-host population, competing with the host species.

The competitor species does not play a role in transmission of the virus, but it can influence the environment and ecological pressure on the host species in that they compete for shared resources.

Identifying the hosts by the variables M_s (for susceptible mice), M_I (for infected mice), and the non-host by Z, the population dynamics model is [8]

$$\frac{dM_s}{dt} = bM - cM_s - \frac{M_s}{K}(M + qZ) - aM_sM_I, \tag{3}$$

$$\frac{dM_I}{dt} = -cM_I - \frac{M_I}{K}(M + qZ) + aM_sM_I, \tag{4}$$

$$\frac{dZ}{dt} = (\beta - \gamma)Z - \frac{Z}{\kappa}(Z + \epsilon M). \tag{5}$$

The model corresponds to the basic Abramson Kenkre model mentioned in Section 2 when $q = 0$. Here, q refers to the influence of the competitor (non-host or alien) population, K is the carrying capacity in the absence of competitor for the host species, b is the birth rate and c is the death rate. For the alien species, the corresponding parameters are ϵ, κ, β and γ respectively.

The main finding from this model is that the pressure forced by the environment (presence of non-host species) can drive the infection to extinction. Both subpopulations can suffer this pressure but the infected, is more vulnerable and becomes extinct at a finite value of carrying capacity or K [8]. For more complete results, see [8].

4 Introduction to Fractional Differential Equations

This section introduces the fractional differential model with an overview of the concept of fractional derivative and reasons for applying this type of differential equation in the present context.

Given D as a differential operator and n as a positive integer, the n-th derivative of function $y(x)$, given that $y(x)$ exists, can be written as

$$D_x^n(y) = \frac{d^n y}{dx^n}.$$

This concept of integer-order derivative is already well known. The concept of derivatives of non-integer order was developed more than three centuries ago and since then, it has drawn attention from many famous mathematicians such as Euler, Laplace, Riemann, Liouville, Fourier and Abel [10]. In the last few decades, the theory of fractional derivative has attracted a significant attention in various areas such as viscoelasticity [11], signal processing [10], biology [12,13] and other problems in physical sciences. In biological modelling, one of its most prominent uses is in diffusion processes [11, 14].

In diffusion process, the fractional model has been used to describe the anomality of diffusion behaviour upon complex environment [12,13]. The suitability of fractional derivative model for describing the anomalous phenomena has given an opportunity for us to modify the fractional derivative form in order to suit the problem related to infectious disease ecology.

In the context of present model, the fractional derivatives are used to describe non-homogeneous character of the ecosystems, with respect to the presence of competitors. Therefore we need to consider biodiversity or interacting species. Thus, we need to modify equations (1) and (2) by including obstacle parameter densities. In doing this, we need to modify the basic Hantavirus infection model to a fractional form. Before proceeding, we will introduce the fractional derivative model which will be used throughout our discussion in this paper for solving the non-homogeneous ecology problem.

Consider the fractional differential equation of the form

$$\begin{aligned} \frac{dy(t)}{dt} &= D_t^{1-\alpha} f(y(t)) + g(y(t)),\ t \in [0, T], \\ y(0) &= y_0,\ y_0 \in \mathbf{R}^m, \end{aligned} \tag{6}$$

where $0 < \alpha < 1$. There are FDEs in which both the temporal derivative and spatial derivative operators are fractional, but in this chapter, we consider only those whose fractional derivative operators are with respect to time. $D_t^{1-\alpha} f$ denotes the Riemann-Liouville fractional derivative [10] of the function f, defined by

$$D_t^{1-\alpha} f(t) = \frac{1}{\Gamma(\alpha)} \frac{d}{dt} \int_0^t \frac{f(s)}{(t-s)^{1-\alpha}} ds. \tag{7}$$

$\Gamma(\alpha)$ is the Gamma function defined by

$$\Gamma(\alpha) = \int_0^\infty e^{-t} t^{\alpha-1} dt.$$

The Caputo fractional derivative is given by

$$\widehat{D}_t^{1-\alpha} f(t) = \frac{1}{\Gamma(\alpha)} \int_0^t \frac{f'(s)}{(t-s)^{1-\alpha}} ds. \tag{8}$$

If $f(t)$ is continuous and $f'(t)$ is integrable in the interval $[0,T]$, then for every $0 < \alpha < 1$ the Riemann-Liouville and the Caputo fractional derivatives satisfy the following relation [10]

$$D_t^{1-\alpha} f(t) = \widehat{D}_t^{1-\alpha} f(t) + \frac{t^{\alpha-1}}{\Gamma(\alpha)} f(0), \qquad t > 0. \tag{9}$$

A number of authors, for example Diethelm et al. [15,16], Ford et al. [17], consider the numerical solution of so-called Caputo FDEs that take the form $\widehat{D}_t^{\alpha} y(t) = f(y(t))$, but we prefer the form (6), as it is more naturally allied to problems discussed in this paper. This form also appears in solving problems in systems biology arising from the anomalous diffusion and chemical kinetics of molecular species in a crowded environment [12,13].

To solve problem (6), we use Implicit Fractional Trapezoidal method written as

$$y_{n+1} = y_n + \frac{h}{2}(D_t^{1-\alpha}(f(y_n) + f(y_{n+1}))) + \frac{h}{2}(g(y_n) + g(y_{n+1})), \tag{10}$$

where h refers to the time stepsize.

In order to implement such method, we need numerical approximations to the fractional derivative operator. Here, we use the approximation by Diethelm et al. [18] when approximating the Caputo fractional derivative operator

$$D_t^{1-\alpha} f(y_n) \approx \frac{h^{\alpha-1}}{\Gamma(1+\alpha)} \sum_{j=0}^{n} c_{jn} f(y_j), \tag{11}$$

where $h = T/n$ is the integration stepsize, $t_j = jh,\ j = 0, 1, 2, \cdots, n,\ y_n$ is an approximation to exact solution $y(t_n)$.

$$c_{jn} = \begin{cases} \alpha n^{\alpha-1} - n^{\alpha} + (n-1)^{\alpha}, & if\ j = 0, \\ (n-j+1)^{\alpha} - 2(n-j)^{\alpha} + (n-j-1)^{\alpha}, & if\ j = 1, 2, \ldots, n-1, \\ 1, & if\ j = n. \end{cases} \tag{12}$$

5 Fractional Abramson-Kenkre Model

This section we present the fractional order derivative analog of the system (1-2) presented in section 2. Note that the effect of diffusion is not included in the model.

The resulting model can be written as

$$\frac{dM_s}{dt} = D_t^{1-\alpha}\Big(bM - cM_s - \frac{M_s M}{K} - aM_s M_I\Big), \tag{13}$$

$$\frac{dM_I}{dt} = D_t^{1-\alpha}\Big(-cM_s - \frac{M_I M}{K} + aM_s M_I\Big). \tag{14}$$

The parameter α characterizes the density of competitor species in the system. Notice that when the power exponent is $\alpha = 1$, this corresponds to equations (1) and (2), and varies the competitor's populations when $0 < \alpha < 1$. As α moves away from 1, the density of competitor or alien species will increase in the populations.

In the next section, we present the simulation results based on equations (13), (14) and we also compare with biodiversity equations; (3), (4), (5) introduced in section 3.

6 Results and Discussion

In this section, we numerically solve the governing equations to study the effects of decreasing the value of α, i.e. increasing the number of alien species. For the basic system of Abramson and Kenkre the critical value of K above which the infection will persist is given [3] by $K_c = b/(a(b-c))$. In the presence of alien population this critical value can be generalized [8] to $K_c^A = K_c + (q/(b-c))Z$. Furthermore, Peixoto and Abramson [8] have shown that the minimum initial alien population to inhibit infection is given by $Z(0) = (K(aM_s(0) - c) - M(0))/q$.

We choose $a = 0.1,\ b = 1,\ c = 0.5$ as this was used by Abramson and Kenkre in their study [3]. The initial values for the host population were $M_s(0) = 40$ and $M_I(0) = 10$ to indicate a mice population where the situation is infected [9].

Figure 1 shows the results of the simulation based on equations (13) and (14) using the values mentioned above. When $\alpha = 1$, equations (13), (14) will correspond to equations in (1) and (2), i.e. there is no alien species in the ecosystem (basic Abramson Kenkre system). There is an increase in the infection reaching a peak of $M_I = 20$ at two months. It then falls but there is a persistence in the infection with $M_I = 10$ from 10 months onwards.

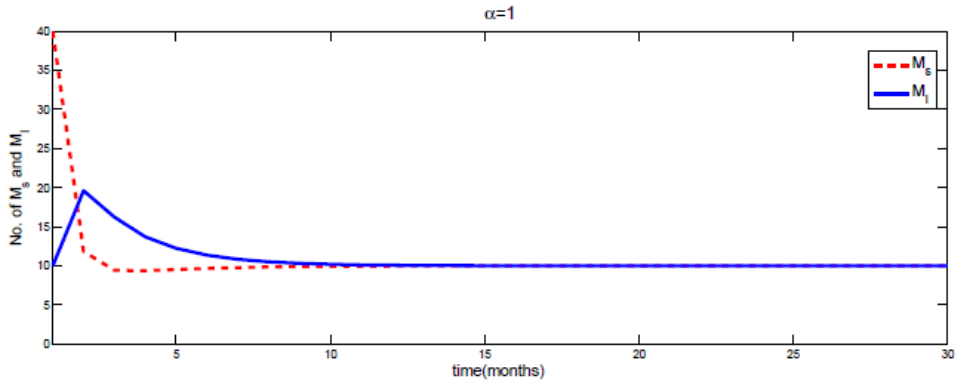

Figure 1: Simulation results for fractional Abramson Kenkre model with $\alpha = 1$.

Figure 2 shows the simulation results across a range of α ($\alpha = 0.6, 0.3, 0.25$), that is we simulate the results when the number of alien species increases. In Figure 2, the results indicate that for $\alpha = 0.6$ the number of infected mice decreases with $M_I = 8.7$ after 30 months. However after 30 months the number of infected mice is still greater than the number of susceptible mice.

For $\alpha = 0.3$ and $\alpha = 0.25$, it can be seen that the infection decreases even more rapidly with M_I reaching 5.3 and 4.4 respectively after 30 months. For both cases, after 30 months the number of susceptible mice is greater than the number of infected mice in the ecosystem. This indicates that there is some correlation between α values and rate of infection upon the ecosystem in which α acts as reference to the density of alien species. When α is nearly zero, then there is more ecological pressure on the host, and this eventually affects the dynamics of infection.

Table 1 shows the results as we vary the α parameters based on equations (13) and (14).

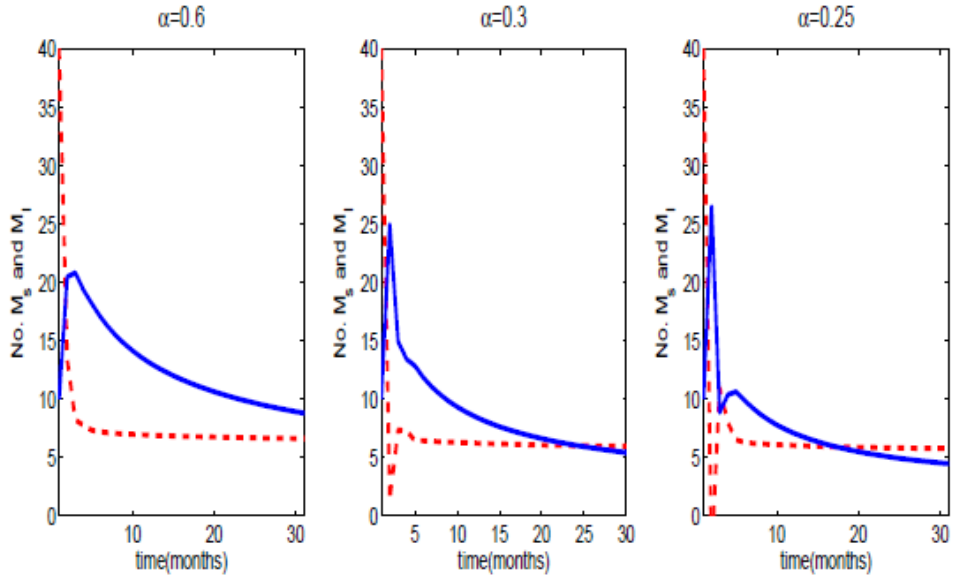

Figure 2: Simulation Results for Fractional Abramson Kenkre Model with $\alpha = 0.6, 0.3, 0.25$.

The values given in the table represent the survival number of populations as we conduct the test for 100 months.

From Table 1, it can be seen that even though the value of carrying capacity, K, is high, the competitive pressure among host and a high number of non-host species, can result in a drastic reduction in the number of infected mice (and also reduce the number of susceptible mice). This result is also consistent with the biodiversity model proposed by Peixoto and Abramson [8].

Figure 3 illustrates the effect α to the infected and susceptible mice population densities. The dashed line represents the infected mice population able to survive and the solid line represents the susceptible mice population. It shows here, as $\alpha < 0.5$, there is a drop in the number of survivors for infected and susceptible mice. The infected mice population densities drops below the susceptible mice population densities, thus emphasize the effect of α values in controlling the infection.

7 Conclusions

In this paper, we have introduced a fractional ordinary differential equation model to represent an ecosystem with non-host competitor species and host mice species which are associated with Hantavirus infection. The model has been investigated using Fractional Implicit Trapezoidal method. We used fractional model of a host-Hantavirus system to incorporate the diversity of an ecosystem, where the ecosystem can comprise host and non-host competitor populations. Here, the model assumes a constant competitor rather than a dynamically evolving competitor. The competition among host and an increasing non-host population (represented by a decreasing α) can significantly affect the propagation of Han-

Table 1: Survivors (or Population Densities) at $t = 100$ Months for Fractional Model $(M_s(0) = 40, M_I(0) = 10, K = 40, K > K_c^A)$

α	Susceptible	Infected
1	10.0052	9.998
0.9	10.002	10.0098
0.8	8.8928	10.0935
0.75	8.5026	10.1861
0.7	8.0665	9.7618
0.6	7.2618	7.0663
0.5	6.5468	6.3167
0.45	6.291	5.3981
0.4	6.0845	4.6132
0.3	5.79	3.5451
0.2	5.5609	3.0192
0.15	3.4494	1.4731

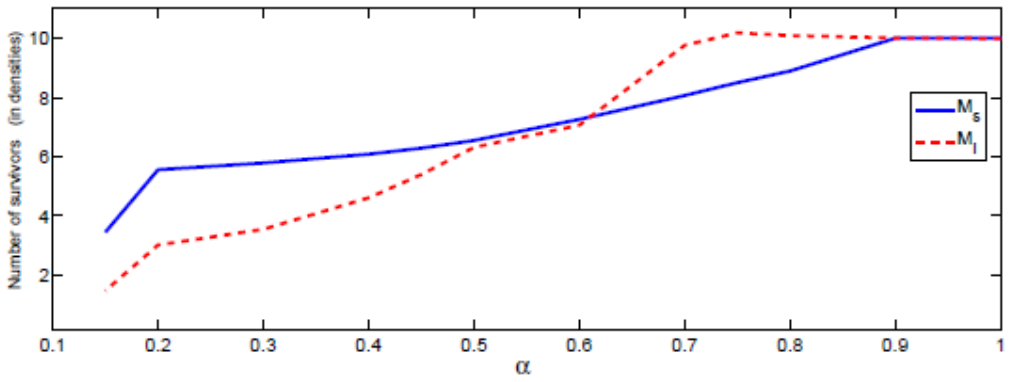

Figure 3: Survivors of Susceptible (Solid Line) and Infected (Dashed Line) Mice Populations Versus α.

tavirus infection. Our result is consistent with that of Peixoto and Abramson [8]. However, there are other aspects that need to be explored regarding the stability of the fractional Abramson Kenkre model. Given their recent arrival to the modeling of population dynamics numerical methods remain primitive (lack of efficiency), we present a new technique based on fractional differential equation which is a novel approach to model transmission dynamics of Hantavirus.

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