A Mathematical Model of the Dynamics of *Rickettsia rickettsii* in Tick-Host Interactions

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Abstract

This paper studies the dynamics of the tick population affected by *Rickettsia rickettsii* in order to understand how this disease affects other species. This project modifies the Busenberg-Cooke (BC) model to better account for biological aspects. Mathematical analysis assesses the effect of parameters on the dynamics of the model. One main result is obtained: the populations behavior is found to be chaotic in a region of parameter space that differs from that observed in the BC model. More importantly, the nature of the attractors seems qualitatively different.

1 Introduction

The disease *Rickettsia rickettsii* affects many species of animals, including humans. This is the most important rickettsial disease for humans in the U.S., since there are more than 1000 reported cases per year. The most important vector in the transmission of this disease is the American dog tick (*Dermacentor variabilis*) which is widespread in the Northeastern U.S. If not treated, this disease may be fatal. The original model (proposed by B & C in 1982) and our modified model focus on the population dynamics of ticks, the main vectors of this disease. In addition to RMSF, ticks carry diseases such as Lyme Disease and Heartwater. Organisms that serve as reservoirs of the disease and live in rural areas (generally small mammals such as rodents) are a constant source of infection to ticks, which in turn infect domestic animals like dogs and rats. Domestic animals bring the infected ticks into close contact with humans, who are the terminal hosts of ticks. Dogs, however, are not efficient reservoirs of the disease since they recover after three days.

The life history of the various species of ticks that carry *R. rickettsi* follows the same general pattern. However, there is a difference in the time required for each species to reach maturity. Some may live less than a year, while others have a life span of up to four years. They have three main life stages: larval, nymph, and adult. Larvae and nymphs feed on small mammals, whereas adults feed on large mammals, including humans.

Both models–the model proposed by Busenberg and Cooke (BC model) and our modified model–consider two types of transmission: horizontal and vertical. Horizontal transmission, which depends on the host, occurs between members of the same generation of ticks, whereas vertical transmission is passed from one generation to the next. Both horizontal and vertical transmission are described by their own set of equations: continuous and discrete, respectively. We choose different parameter values for these equations to determine if the population dynamics of ticks will tend to chaos. Our model is not intended to be a detailed description of the relationship between hosts and ticks, but rather an attempt to expand on what has already been modeled by Busenberg and Cooke [1993].

The following sections in this study describe the model equations and numerical results. The model equations section describes the modified model

and the method used to simulate the problem. The part on numerical results shows an analysis of the graphs acquired by implementing the model.

2   Model Equations

We start with six basic assumptions. First, the host groups demography is insignificant and its population size is constant. Second, the probability of transmission from tick to host is equal to that from host to tick, given contact. Third, there is a probability that immigrant ticks are infected or susceptible. The probability of susceptibility, F, is a relatively arbitrary value based loosely on the dynamics from simulations. Fourth, γ includes all possible causes of death in ticks. Fifth, recovered hosts remain susceptible. Sixth, the immigration rate (Λ) is constant in this model.

To study the spread of *R. rickettsii*, it is necesary to understand the groups involved. First the ticks are separated into two classes, susceptible and infected. Second, the infection is spread through hosts, which are also divided into susceptible and infected classes: dI_n/dt, dS_n/dt, dI_h/dt, dS_h/dt are the rates of change in the number of infected and susceptible ticks (n) and hosts (h), respectively, over time. With these criteria, we formulate a model that more accurately describes the relationship between the host and the tick than the one presented by Busenberg and Cooke.

$$
\begin{aligned}
I_h/dt &= LS_h In - \Psi I_h \\
dS_h/dt &= -LS_h I_n + \Psi I_h \\
dI_n/dt &= (1 - F)\Lambda + kS_n I_h - \gamma I_n \\
dS_n/dt &= F\Lambda - kS_n I_h - \gamma S_n \\
k &= pC_n/N_h \\
L &= pC_h/N_n.
\end{aligned}
$$

The susceptible ticks which get infected will move into the infected tick group at a rate of $KS_n I_h$, where K is the horizontal transmission factor. $S_n I_n$ represents a susceptible tick coming into contact with an infected host. This horizontal factor represents the probability per contact per individual, that is, the probability that the infection will be spread from one tick to another tick of the same generation. The term $KS_n I_h$ is added into the same equation for the infected ticks because the newly infected ticks are entering

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the group, while it is subtracted from the equation for the susceptible ticks because it represents the ticks which are leaving the group due to infection.

Ticks that die are also taken into account. The term γS_n is subtracted from the differential equation for susceptible ticks, and γI_n is subtracted from the differential equation for infected ticks.

The immigration of ticks into the tick community is represented by the symbol Λ. The probability that the incoming ticks will be infected is $(1-F)$, so $(1-F)$ is added to the equation for infected ticks. The probability that the incoming ticks are not infected is F, and F is added to the equation for susceptible ticks.

Similarly, susceptible hosts are transferred into the infected host group at the rate of LS_hI_n, where S_hI_h represents a susceptible host coming into contact with an infected tick, and L is the horizontal transmission factor. The recovery rate for the host is ΨI_h, which is added to the equation for susceptible hosts and subtracted from the equation for infected hosts. Since the host is immortal from the perspective of the tick, the number of hosts, $N_h = I_h + S_h$, is a constant.

Vertical transmission is represented by the difference equations:

$$
\begin{aligned}
I_N(N) &= \frac{1-p}{M_2 - M_1} \int_{M_1+N-1}^{M_2+N-1} b_1(t) I_{N-1}(t) \left[1 - I_{N-1}(t) - S_{N-1}(t)\right] dt \\
S_N(N) &= \frac{1}{M_2 - M_1} \int_{M_1+N-1}^{M_2+N-1} \left[b_s(t) S_{N-1}(t) + p b_I(t) I_{N-1}(t)\right] \\
&\quad \times \left[1 - I_{N-1}(t) - S_{N-1}(t)\right] dt \\
\text{for } n &= 2,3,\cdots \text{ and } I_1(1) = I_0, S_1(1) = S_0
\end{aligned}
$$

Since the differential set of equations only deals with the horizontal transmission and not with the vertical transmission of the disease, the values of infected and susceptible ticks in a generation, $I_n(n)$ and $S_n(n)$, respectively, depend on the number of both groups from the previous generation. The life span of a tick is between 2 to 3 years. In the model we normalize this period to one unit of time, that is, each generation lives one unit of time. Ticks take a certain length of time to mature, after which they are able to lay eggs; m_1 and m_2 are the lower and upper boundaries, respectively, of the time interval in which a female tick can lay eggs. The interval $m_1 - m_2$ is called the maturation window. Vertical transmission occurs when the female

tick passes the infection to her offspring. Therefore, to measure the vertical transmission would mean to take the integral from m_1 to m_2. Thus, we have the integral taken from $m_1 + n - 1$ to $m_2 + n - 1$, where $n - 1$ is the end of the previous generation.

In the difference equation for the infected tick population $(1 - p)/(m_2 - m_1)$ represents the probability that the new generation is infected. The term $b_t(t)I_{n-1}(t)$ represents the number of infected born from previous infected generations. The second term, $[1 - I_{n-1}(t) - S_{n-1}(t)]$ is the logistic control on the oviposition, or the laying of the eggs.

In the difference equation for the susceptible ticks, the first term inside the integral, $[b_s(t)S_{n-1}(t) + pb_I(t)I_{n-1}(t)]$, represents the births for the susceptible ticks of the previous generation and the probability of susceptible births from the previous infected generation.

The second term inside the integral is the logistic control on the oviposition. The term outside the integral shows that there is no change in the spread of the infected from the previous generation during the maturation window.

In this model, the maturation window has been modified. It is assumed that all female adult ticks lay their eggs simultaneously, that is, $m_1 \to m_2 = m$. By applying the fundamental theorem of calculus to the difference equations, this new set of difference equations is obtained:

$$
\begin{aligned}
I_N(N) &= [(1 - p)b_I(M + N - 1)I_{N-1}(M + N - 1] \\
&\quad [1 - I_{N-1}(M + N - 1) - S_{N-1}(M + N - 1)] \\
S_N(N) &= [b_s(M + N - 1)S_{M+N-1} + pb_I(M + N - 1)I_{N-1}(M + N - 1)] \\
&\quad [1 - I_{N-1}(M + N - 1) - S_{N-1}(M + N - 1)] .
\end{aligned}
$$

Using the difference and differential sets of equations, two *Matlab* programs were developed and run on SunSparc4 and SunSparc5 for various values of m, b_I, and b_S. The first program, "driver" (see Appendix 1) depends on the second, "difchaos" (see Appendix 2). We assign arbitrary initial conditions to the four differential equations. Then we solve them for I_h, I_n, S_h, S_n. We graph these solutions over a time interval. At the end of this simulation, we obtain values for these variables, taking into consideration only I_n and S_n because they refer to the tick population. We ignore the variables S_h and I_h because they deal with the hosts, and relative to the lifespan of the ticks,

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the hosts have a much longer life span and can be assumed to live forever. The ODEs are solved for the time interval n and $n + m$, where $n + m$ will provide the population size at time $n + m$, when female ticks lay eggs. These are plugged into the difference equations to obtain the population sizes of I_n, S_n, I_h, S_h at the beginning of the next generation. The ODEs are solved between n and $n + 1$ and the values at n+1 are plotted. Then the process is repeated for the new initial values obtained from the difference equations.

3 Numerical Results

Using the computer simulations, we obtained several graphs which illustrate the chaotic behavior of our model. In Figures 1 and 2 we plot I_n versus S_n for $n = 101 : 1000$ (i.e., generation numbers n ranging between 101 and 1000) with the constant parameter values $b_S = bS = 3.6$, $b_I = bI = 4.0$, $p = 0.01$, $L = 0.5$, $\Psi = \Psi = 0.5$, $\Lambda = \Lambda = 0.4$, $\gamma = G = 0.3$, $K = 0.4$, $F = 0.35$ and initial conditions: $I(1) = 0.3$, $S(1) = 0.6$. As m was varied ($m = 0.02$ for Fig. 1, and $m = 0.5$ for Fig. 2), we observed that the shape of the attractor also changed. This result indicates that m plays an important role in determining the dynamics of the systems.

In Figures 3 and 4, we tried to identify the transient and true attractors for $m = 0.05$, $bS = 4.0$, $bI = 3.6$ (all other constant parameter values were kept). In Figure 3 we plotted I_n versus S_n for $n = 101 : 1000$. As expected, we found points that more or less seemed evenly distributed. In Figure 4, we plotted I_n versus S_n for $n = 101 : 100,000$. We obtained a more or less evenly distributed region of points which intuitively indicated the existence of only one true attractor.

In Figures 5 and 6 we illustrated the dynamic behavior by plotting the last hundred points for infected and susceptible tick populations out of Fig. 3 and Fig. 4 versus time; at m for each generation n, we obtain points with respect to time which describe the size of the infected and susceptible populations of the next generation. These points are connected so as to provide a better visual idea of the chaotic behavior of the system.

4 Conclusion

Based on the characteristics of chaos given by Kaplan and Glass (*Understanding Nonlinear Dynamics* 1995), we conclude by saying that our model seems to have chaotic behavior. It is important to note that our modified model has an attractor that seems to differ from that in the BC model. From a biological point of view because there is no pattern to follow in order to reach specific conclusions. More mathematical analysis is needed to see the biological implications of the systems behavior. Due to time constraints, this was not possible.

Suggestions for Future Study

In order to form a better model, revising the model is suggested so that a broader maturation window can be included in it. More simulations would enhance the hypothesis and help characterize chaos in a more precise way. Another way to describe the boundaries of chaos more clearly is to find the bifurcation diagram for this model. Unfortunately, the end of the summer also brought dissolution of our research group.

Acknowledgments

References

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Fivaz, B. T. Petney, and I. Horak, *Tick Vector Biology: Medical and Veterinary Aspects*, Springer-Verlag, New York, 1992.

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Figure 1

This is the graph for the infected ticks versus susceptible ticks for 1000 generations. The maturation window is 0.02, the birthrate of susceptible ticks is 3.6, and the infected birthrate is 4.0.

Figure 2

In this graph, all parameters were kep the same from the previous figure except that the maturation window is 0.5, which is of greater value. This graph also shows the simulation over 1000 generations.

Figure 3

In this figure, the value for the maturation window is 0.05, but the infected and susceptible birthrates have been switched. This graph also shows the simulation over 1000 generations.

Figure 4

This graph shows the simulation of infected versus susceptible ticks. The maturation window is 0.05, the infected birthrate is 3.6 and the susceptible birthrate is 4.0.

Figure 5

Last 100 generations of population of infected ticks with respect to the generations, graphing only every 15th generation of Fig. 3.

Figure 6

The last 100 generations of the population of susceptible ticks with respect to the generations, graphing only every 15th generation of Fig. 3.
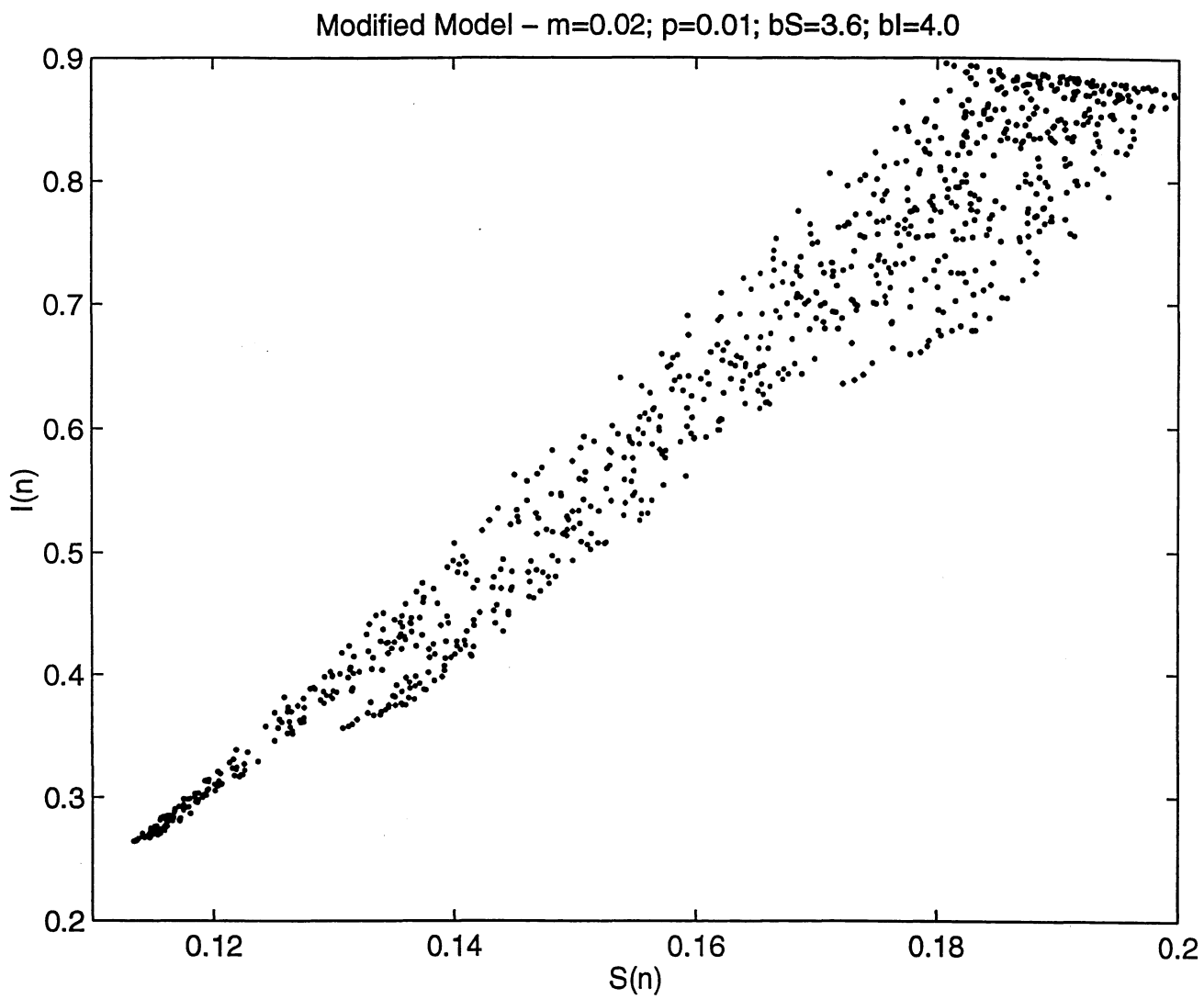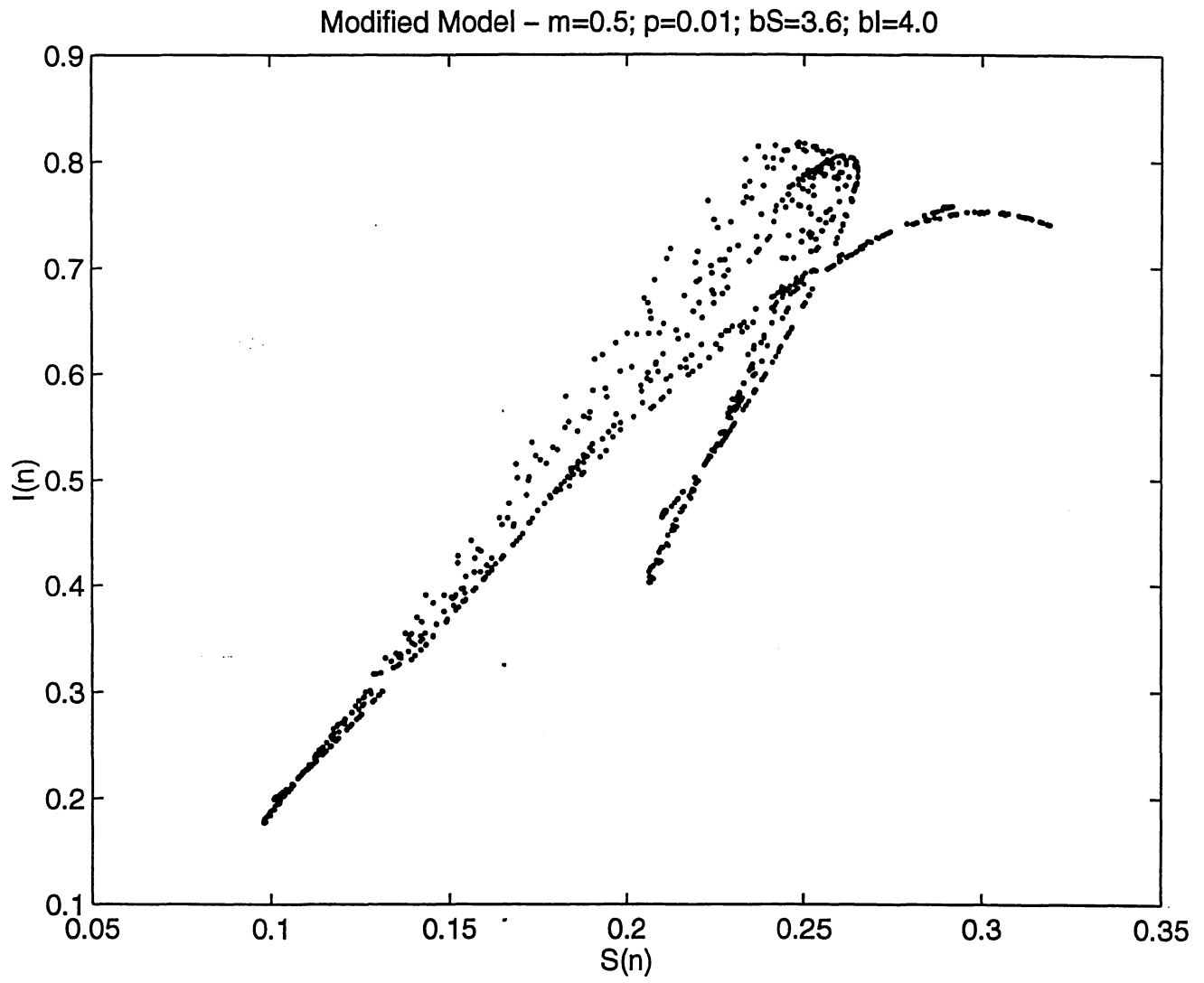
Modified Model – m=0.02; p=0.01; bS=3.6; bI=4.0

Figure 1

Modified Model – m=0.5; p=0.01; bS=3.6; bI=4.0

Figure 2

Modified Model – m=0.05; p=0.01; bS=4.0; bI=3.6

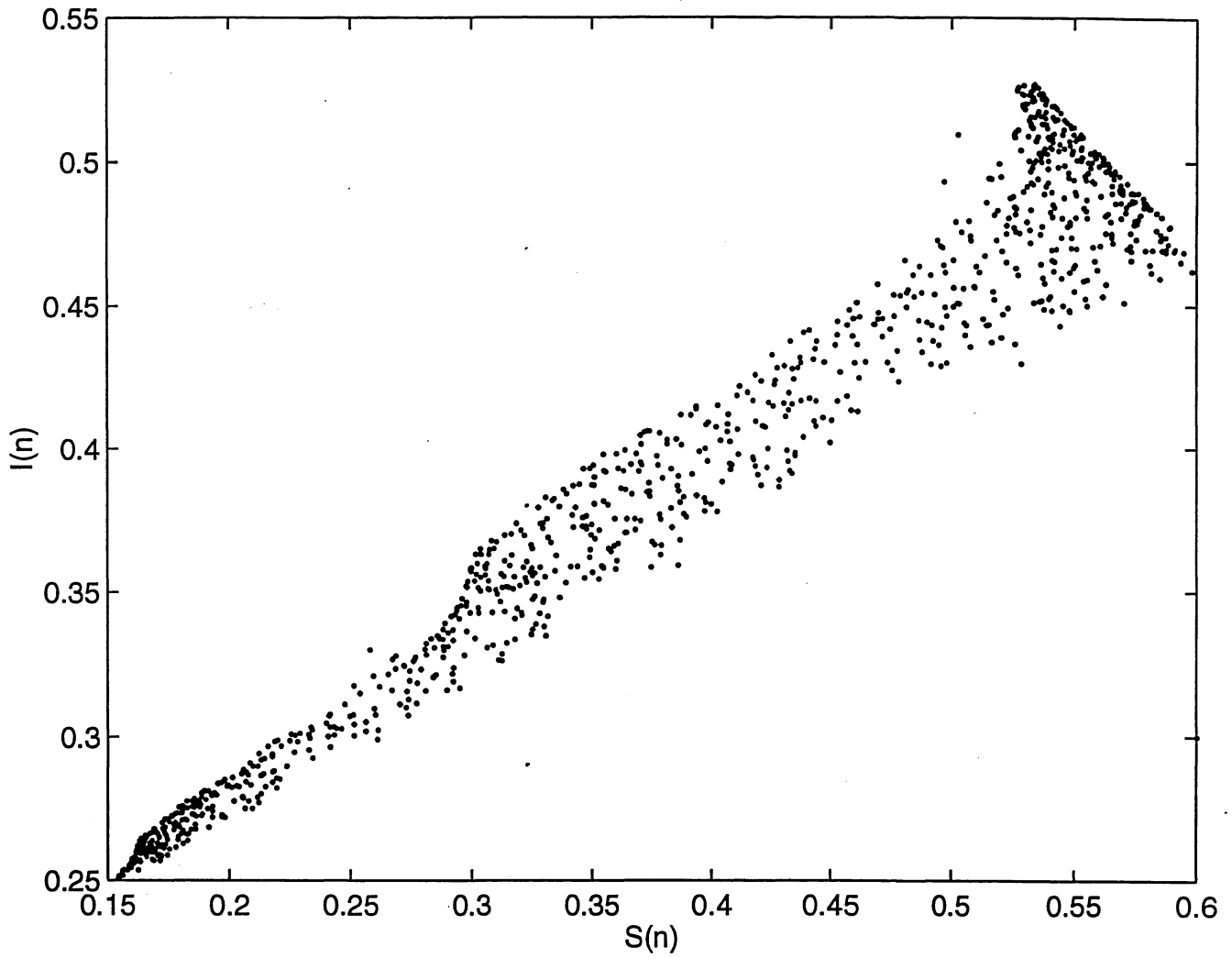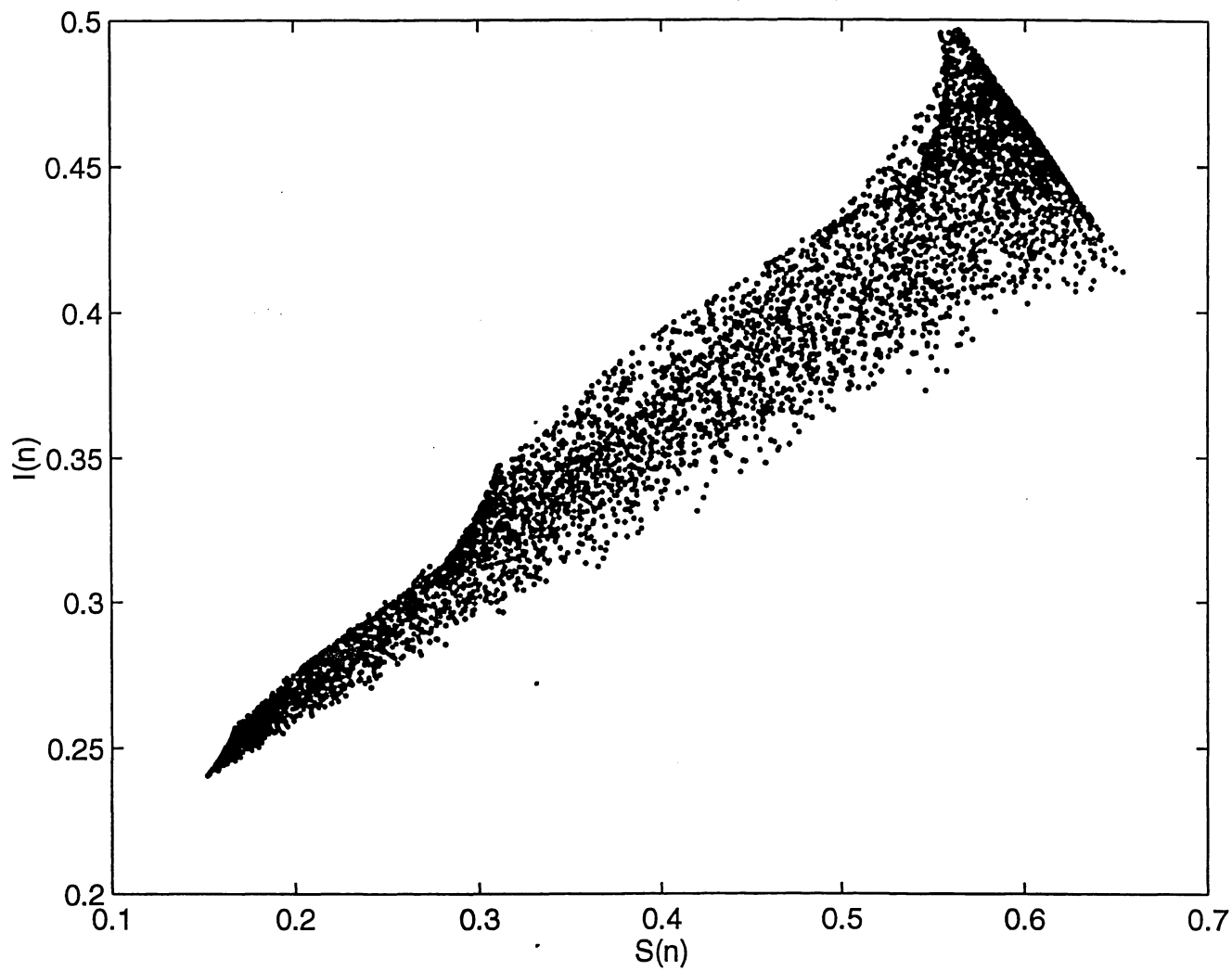Figure 3

Modified Model – m=0.05; bI=3.6; bS=4

Figure 4
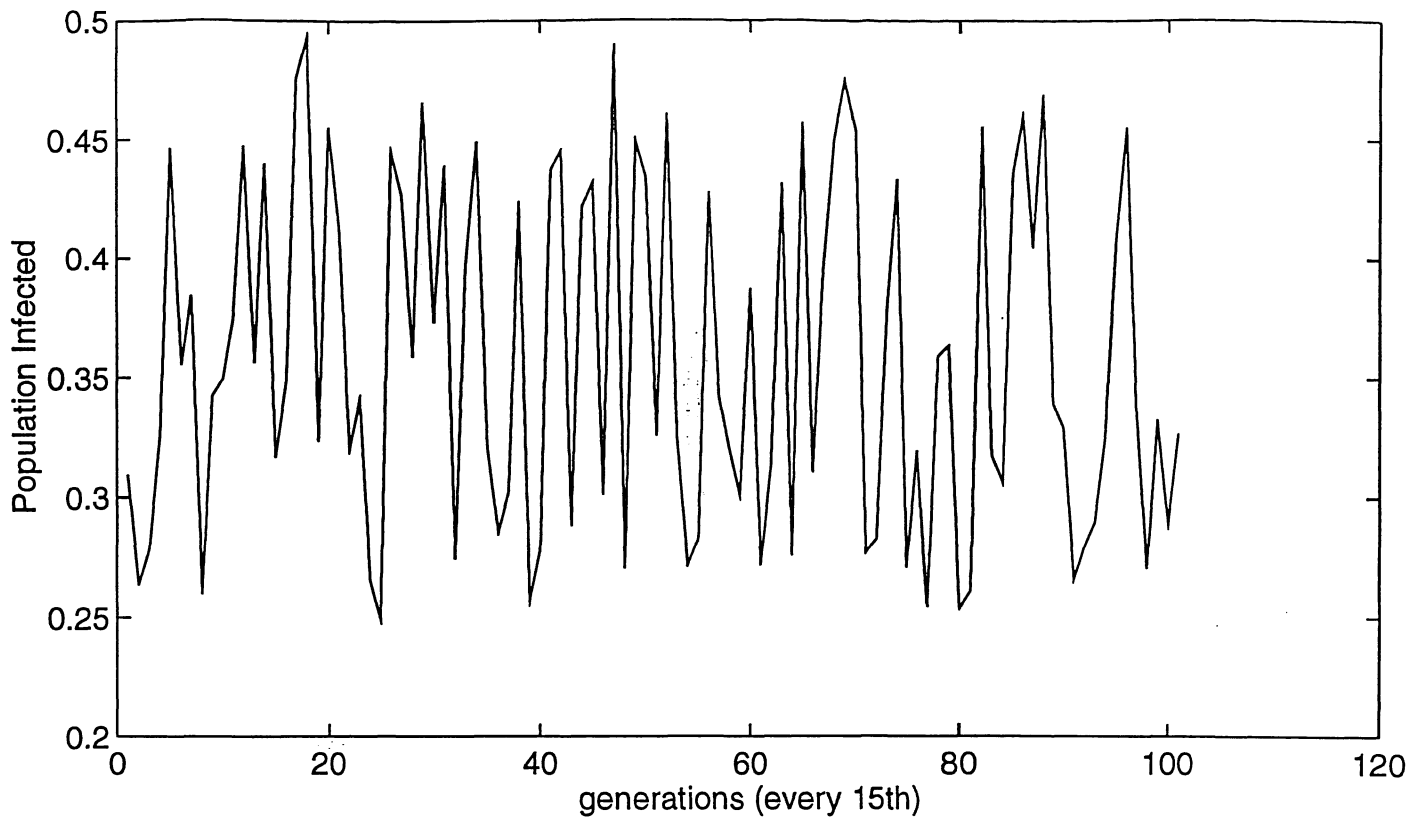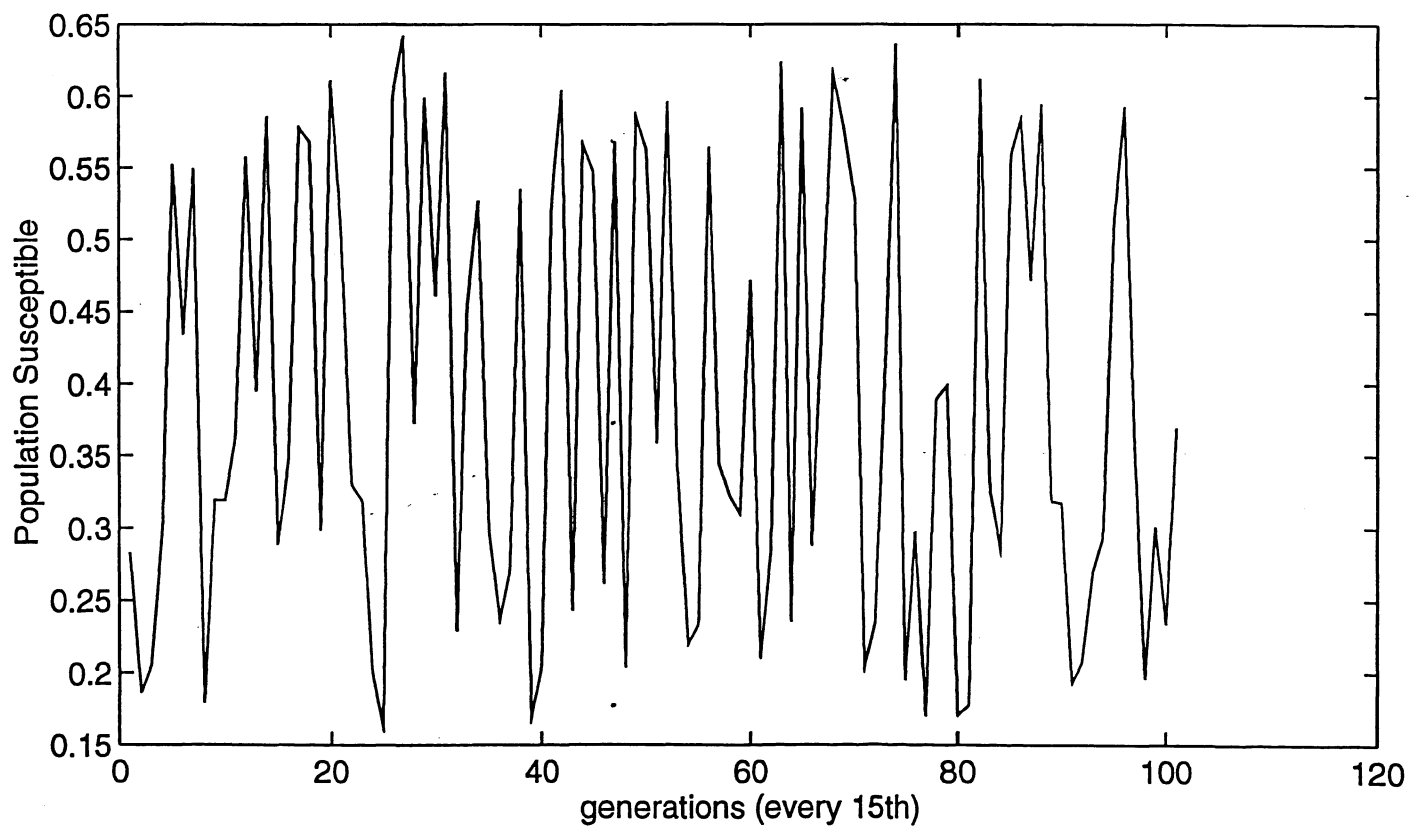
Figure 5

Figure 6

Computer Programs

The following section contains the computer programs in *Matlab* used to generate the simulations.

```matlab
function y =driver(RR)

%parameter values will change at each simulation
bi=3.6; bs=4.0; p=0.01;

%initial time and number of ticks and dogs
i=1;
its=15;             %we save only every "its"th point
m=.5;               %maturation point,  time when ticks start laying eggs
x0=[.2 .8 .3 .6]';          %initial values Id, Sd, In, and Sn for generation 1

%initializes a matrix of zeroes where the solutions y will be saved
y=zeros(round((RR-100)/its),2);

%finds the solutions for every generation, from 1 to RR
for n=1:RR

%finds solutions to the ODE system from the beginning of the generation
%up to time n+m
[t2,x2]=ode45('difchaos',n,n+m,x0);

%finds the last component of the ODE solution x2
d2=length(x2(:,1));

x0=x2(d2,:)';

%finds solutions to the ODE system from the beginning of the generation
%up to time n+1
[t1,x1]=ode45('difchaos',n+m,n+1,x0);

%finds the last component of the ODE solution x1
d1=length(x1(:,1));


%x(3,d) = # infected ticks at end of the generation
%x(4,d) = # susceptible ticks at end of the generation

%set of difference equations
In=(1-p)*bi*x2(d2,3)*(1-x2(d2,3)-x2(d2,4));
Sn=(bs*x2(d2,4)+p*bi*x2(d2,3))*(1-x2(d2,3)-x2(d2,4));

%new initial points for the next generation
x0=[x1(d1,1) x1(d1,2) In Sn]';

%saves only every "its"th point
if ( (rem(n,its) == 0) & (n > 100) )

        y(i,1:2)=[x1(d1,4) x1(d1,3)];
        i=i+1;
end;

end;
```

```matlab
function xdot = difchaos(t,x)

L=.5;
Psi=.5;
Lam=0.4;
G=0.3;
K=.4;
F=0.35;

% x(1)=Id(t), x(2)=Sd(t), x(3)=In(t), x(4)=Sn(t)


%system of ODE's
xdot(1) = L*x(2).*x(3) - Psi*x(1);
xdot(2) = -L*x(2).*x(3) + Psi*x(1);
xdot(3) = K*x(4).*x(1) - G*x(3) + (1-F)*Lam;
xdot(4) = -K*x(4).*x(1) - G*x(4) + F*Lam;
```