Stochastic Simulations of a Spatial SIR Model

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ABSTRACT. In this paper we consider a stochastic spatial SIR (Susceptible-Infectious-Recovered) model. We assume that the population is distributed in separate cells. The disease is transmitted within the cell by direct contact, and from cell to cell through an external object (vector or vehicle) capable of carrying the disease. We simulate this model in a 10×10 grid of cells, and investigate the effects of the relative rates of transmission within and between cells on the predictability and progression of the disease. Results of simulation indicate that as the rate of intercellular transmission increases relative to intracellular transmission, the mean number becoming effected within each cell increases but so does the spatial variability. We also found that the time for the epidemic to run its course reaches a maximum average value at intermediate relative rates as does the spatial variability.

1. Introduction

The common mathematical models for diseases are the SIS (Susceptible-Infectious-Recovered) models, developed by Kermack and McKendrick (see discussion in [2], [5] and [6]). In the case when infective individuals recover and again become susceptible to the disease, the model used is the SIS. In the case when infective individuals recover and attain permanent immunity, we use an SIR model. The classical models do not consider how the population is distributed in space, only the number of individuals in each class.

In this paper we describe a spatially discrete model, and simulate this model in a 10×10 grid of cells. The effects of the relative rates of transmission within and between cells on the predictability and progression of the disease are investigated.

2. The Spatial Model

The classical SIS and SIR models do not take into account how the individuals are distributed in space. However, spatial models have been studied. For instance, D. G. Kendall (see discussion in [1] and [2]) formulated the following model: assuming that the individuals are continuously distributed on a region of the plane with density σ individuals per unit area, $S(x,y,t)$, $I(x,y,t)$, and $R(x,y,t)$ being the density of susceptible, infectious and recovered individuals, respectively, at point (x,y) and at time t, we have the equations

$$\begin{aligned}
\frac{\partial S(x,y,t)}{\partial t} &= -\beta S(x,y,t)\,\overline{I}(x,y,t) \\
\frac{\partial I(x,y,t)}{\partial t} &= \beta S(x,y,t)\,\overline{I}(x,y,t) - \gamma I(x,y,t) \\
\frac{\partial R(x,y,t)}{\partial t} &= \gamma I(x,y,t)
\end{aligned}$$

where β is the infection rate, γ is the recovery rate, and $\overline{(I)}$ is a spatially weighted average of I given by

$$\overline{(I)}(x,y,t) = \int\int W\left[(x'-x),(y'-y)\right] I(x',y',t)\,dx'dy',$$

W being an appropriate nonnegative weighting coefficient satisfying

$$\int\int W\left[(x'-x),(y'-y)\right]\,dx'dy' = 1.$$

The model above assumes a continuous distributed population. In this paper, however, we will consider the case in which the population is distributed in separate cells.

We assume that the population is distributed in a grid of cells. The individuals inside each cell are free to move within their cell, but there is no direct contact (contagion) among the individuals of different cells. The infection is transmitted within cells at rate β, and between cells by a vector or vehicle at transmission rate α. Individuals recover with a rate γ and become immune to the disease. We also assume that the dynamics of the disease are on a fast time scale compared to the birth and death rates of the population so that the population can be considered fixed. Then we have the following deterministic version of the model describing this system:

$$\begin{aligned}
\frac{dS_{x,y}}{dt} &= -\left(\beta I_{x,y} + \alpha \sum_{k,m} W(k,m) I_{x+k,y+m}\right) \frac{S_{x,y}}{N_{x,y}} \\
\frac{dI_{x,y}}{dt} &= \left(\beta I_{x,y} + \alpha \sum_{k,m} W(k,m) I_{x+k,y+m}\right) \frac{S_{x,y}}{N_{x,y}} - \gamma I_{x,y} \\
\frac{dR_{x,y}}{dt} &= \gamma I_{x,y},
\end{aligned}$$

where $N_{x,y} = S_{x,y} + I_{x,y} + R_{x,y}$ (the total number of individuals in cell (x, y)), $S_{x,y}$, $I_{x,y}$, and $R_{x,y}$ are the number of susceptible, infectious and recovered individuals, respectively, and W is a nonnegative weighting function satisfying $\sum_{k,m} W(k,m) = 1$.

The above model is quite general for most spatial processes where populatins are confined locally or migration is on a longer time scale than that of the disease. Examples are diseases in breeding farms, where the affected animals are confined but transmission can take place by pests or vehicles such as maintenance tools or feed. This model could also be applied to hospitals, where a disease could be transmitted between wards by staff or visitors.

3. Simulations

The stochastic version of the above model is too complicated to be studied analytically. Computer simulations are an alternative of studying complicated systems such as this. In our model α, β and γ are as above, and

we assume that a cell can only be infected by its four immediate neighbors (nondiagonal), as the next diagram shows:

In the diagram we represent the process inside each cell (x, y) as susceptibles becoming infected, and after a time recovering and then becoming immune to the disease. The dotted lines represent indirect transmission of the disease from the neighboring cells. This particular case is then described by the set of equations

$$\begin{aligned}
\frac{dS_{x,y}}{dt} &= -\left(\beta I_{x,y} + \frac{\alpha}{4}\sum I_{k,m}\right)\frac{S_{x,y}}{N} \\
\frac{dI_{x,y}}{dt} &= \left(\beta I_{x,y} + \frac{\alpha}{4}\sum I_{k,m}\right)\frac{S_{x,y}}{N} - \gamma I_{x,y} \\
\frac{dR_{x,y}}{dt} &= \gamma I_{x,y},
\end{aligned}$$

where the sum is taken over the four immediate neighbors of cell (x, y). Note that here

$$W(k,m) = \begin{cases} \frac{1}{4} & k = \pm 1 \qquad m = 0 \\ \frac{1}{4} & k = 0 \qquad m = \pm 1 \\ 0 & otherwise \end{cases}$$

since we are assuming that all contiguous cells have equal weight with respect to direction in the external transmission of the disease. The grid size was 10×10 on a torus. To simulate the stochastic process, then, we define the following:

Call the rate of infection B. Then

$$B_{x,y} = \left(\beta I_{x,y} + \frac{\alpha}{4}\sum I_{k,m}\right)\frac{S_{x,y}}{N}$$

and call the rate of recovery D. Then $D_{x,y} = \gamma I_{x,y}$. The total event rate is then $\sum B_{x,y} + D_{x,y}$ or equivalently the mean time between events is

$$\tau = \left(\sum_{x,y} B_{x,y} + D_{x,y}\right)^{-1}.$$

The time between events (the inter-event times) can be simulated as an exponential with $S = -\tau ln(U_1)$ where U_1 is a uniform (0,1) random variable.

The event occurs in a particular cell (i, j) if a second unform random variable (U_2) is

$$\frac{\sum_{x,y}^{i-1,j-1}(B_{x,y}+D_{x,y})}{\sum_{x,y}^{n,n}(B_{x,y}+D_{x,y})} < U_2 \leq \frac{\sum_{x,y}^{i,j}(B_{x,y}+D_{x,y})}{\sum_{x,y}^{n,n}(B_{x,y}+D_{x,y})}.$$

The probability of an infection given that an event has occurred $= B_{i,j}\tau$ and the probability of a recovery given that an event has occurred $= D_{i,j}\tau$. Then to decide if the event is an infection or a recovery we pick a third uniform random variable (U_3) and if

$$0 \leq U_3 < \frac{B_{i,j}}{B_{i,j}+D_{i,j}},$$

then $S_{i,j} \to Si, j-1$, $I_{i,j} \to Ii, j+1$, and $R_{i,j} \to Ri, j$ (an infection occurs) and if

$$\frac{B_{i,j}}{B_{i,j}+D_{i,j}} \leq U_3 \leq 1,$$

then $S_{i,j} \to Si, j$, $I_{i,j} \to Ii, j-1$, and $R_{i,j} \to Ri, j+1$ (a recovery occurs).

We simulated the system with initial conditions $I_{5,5} = I$ and $I_{x,y} = 0$ for all other (x, y), and $R_{x,y} = 0$ for all x and y. Figure 1 represents the results after 100 simulations for several pairs (α, β) with $\gamma = 1$ and $N = 10$. Setting $\gamma = 1$ changes our time units to the mean recovery period. The surfaces represent the average number of survivors (individuals who remained susceptible during the whole development of the epidemic), the average times for the epidemic to finish, the average maximum of infectious individuals at a certain time and the average time when this maximum occurs. The colors represent the variance of the results.

Figure 1 shows the effects that the parameters α and β have on the system. Our choice of parameter values was severely limited by computer time for large values of α and β. In order to better understand the effect of the parameters on the model we established the following relationship. The basic reproduction number for the development of the infection inside an isolated cell is given by $\mathcal{R}_0 = \beta/\gamma$. The spatial aspect of the problem leads to $\mathcal{R}_0' = (\beta + \alpha)/\gamma$.

We define the *spatial infection number* S_0 by

$$S_0 = \frac{\alpha}{\beta},$$

the quotient between the transmission rates inside and outside the cells, which can be interpreted as the ability of the disease to spread throughout the cells. We can then write $\mathcal{R}_0' = (1 + S_0)\,\beta/\gamma = (1 + S_0)\mathcal{R}_0$.

Figures 2, 3, 4 and 5 show the results after 100 simulations with $\gamma = 1$ and $N = 10$, for the values of $\mathcal{R}_0 = 1$, 2, 4 and 8 (since $\gamma = 1$ these correspond to the values of $\beta = 1$, 2, 4 and 8), and the values of $S_0 = 1/100$, $1/200$, $1/400$, $1/800$ and $1/1600$. The points plotted are the values of α that correspond to the values of S_0 mentioned above and the average results after the set of simulations, where the calculations correspond to the same calculations as in Figure 1. The vertical lines represent one standard deviation of the data.

Note that for $\mathcal{R}_0 = 1$ (Figure 2) the average times for the disease to die out are around 1, since we just need to wait for the infected individual to recover. As we increase $\mathcal{R}_0$, we see that an epidemic develops, and that as we increase S_0 the number of survivors (those that never contract the disease) decreases, since the disease attacks more cells. Note that for $\mathcal{R}_0 = 8$ (Figure 5), as we increase the value of S_0, the time for the epidemic to finish decreases, assuming a maximum of around 15 at $S_0 = 1/400$. This means that S_0 also tells us the speed of the development of the epidemic. Note that the epidemic finishes with maximum average time of 15 recovery periods.

Simulations of the stochastic process lead to two interesting conclusions. First, even though the spatial aspect of the infection leads to lower numbers of survivors as the spatial infection number increases (the result one would expect from the deterministic process), the variability of the number of survivors increases even more dramatically. And second, the time for the infection to run its course reaches a maximum of variability at intermediate values of the spatial infection number.

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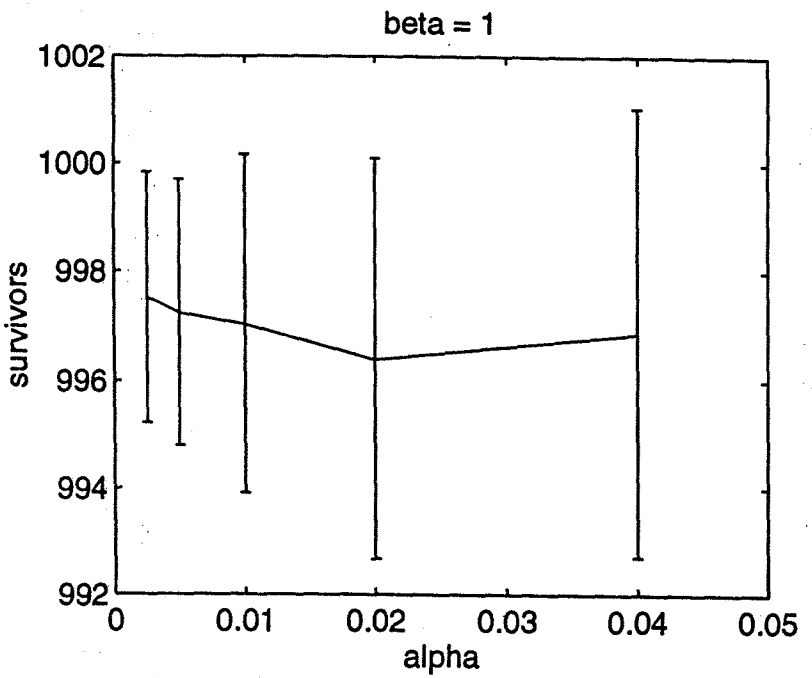
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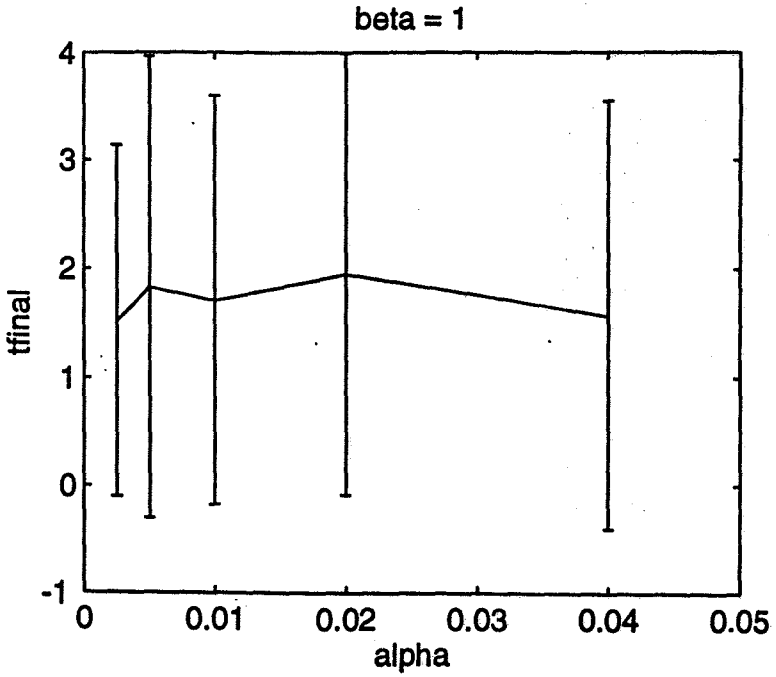
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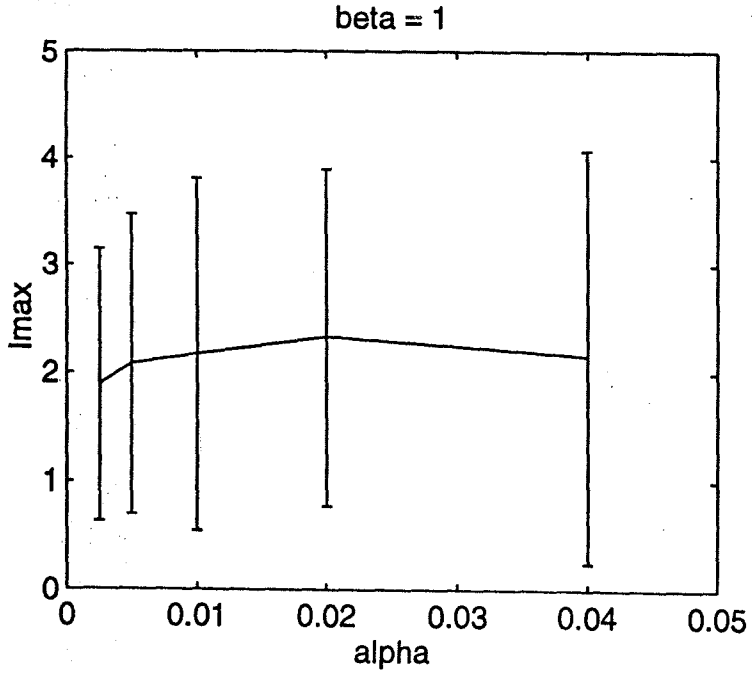
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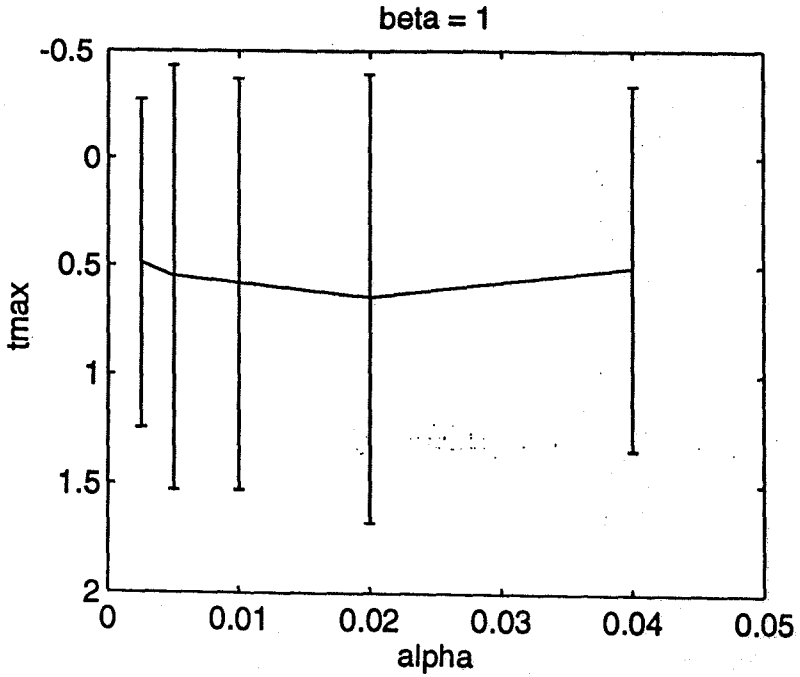
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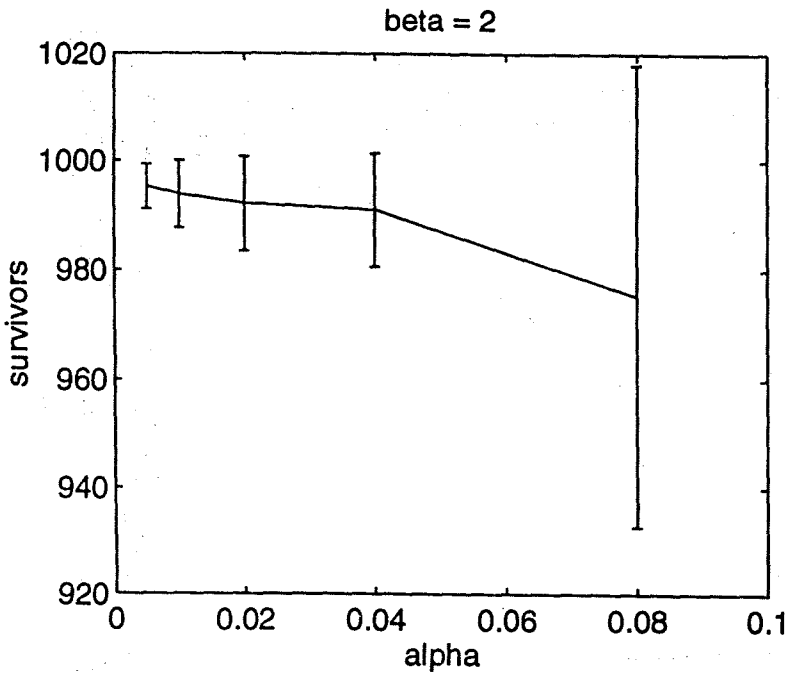
Figure 2.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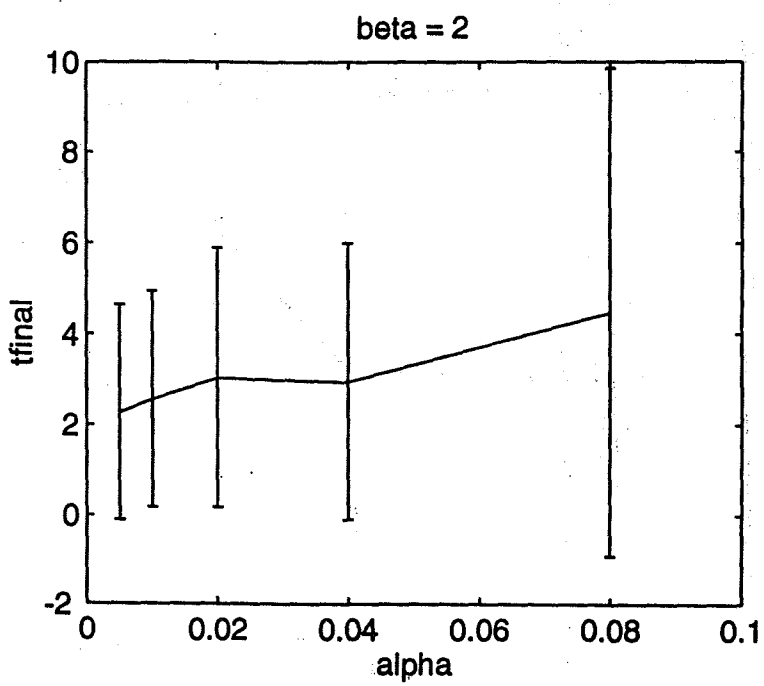
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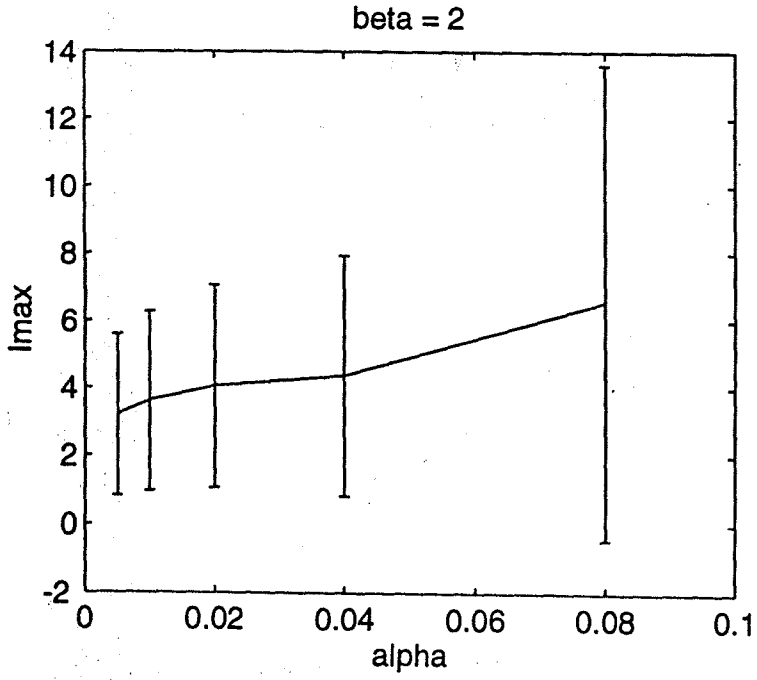
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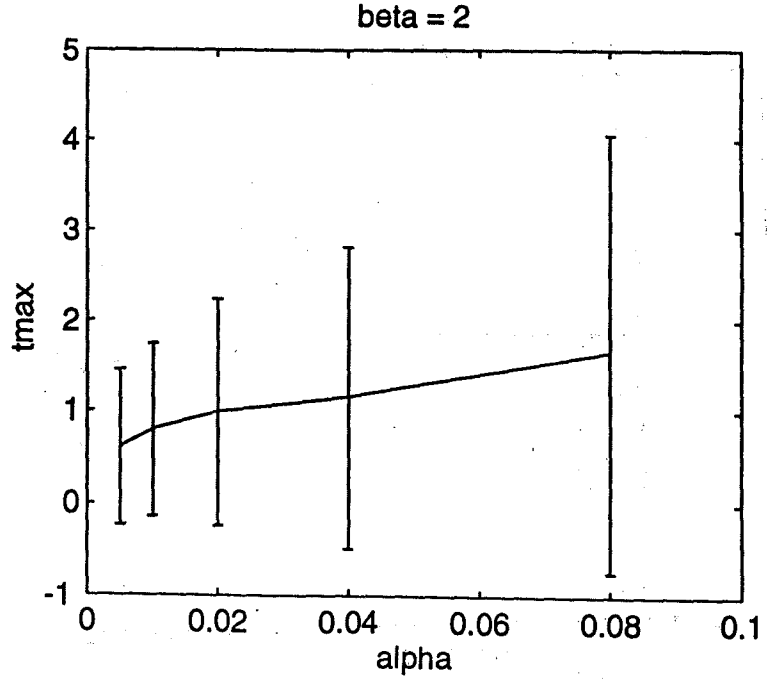
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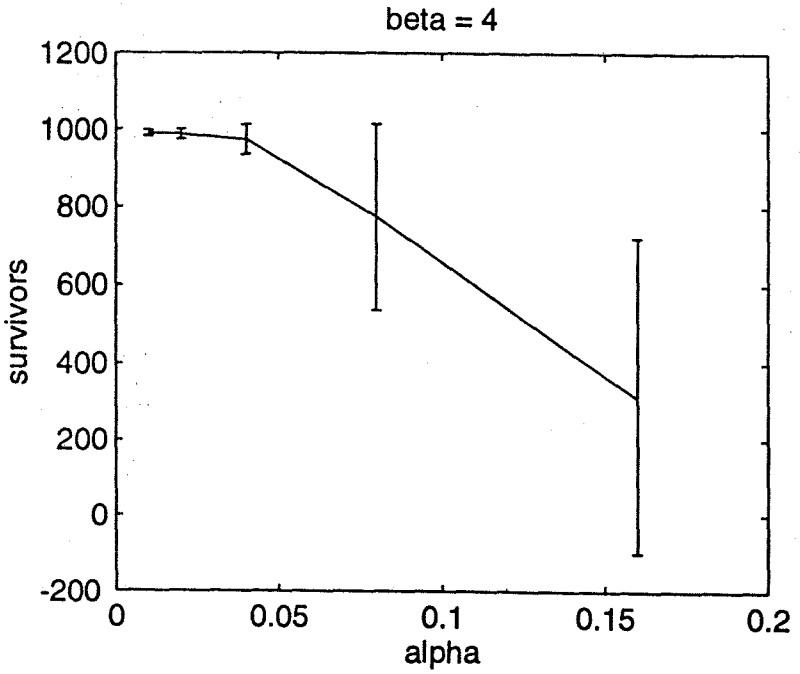
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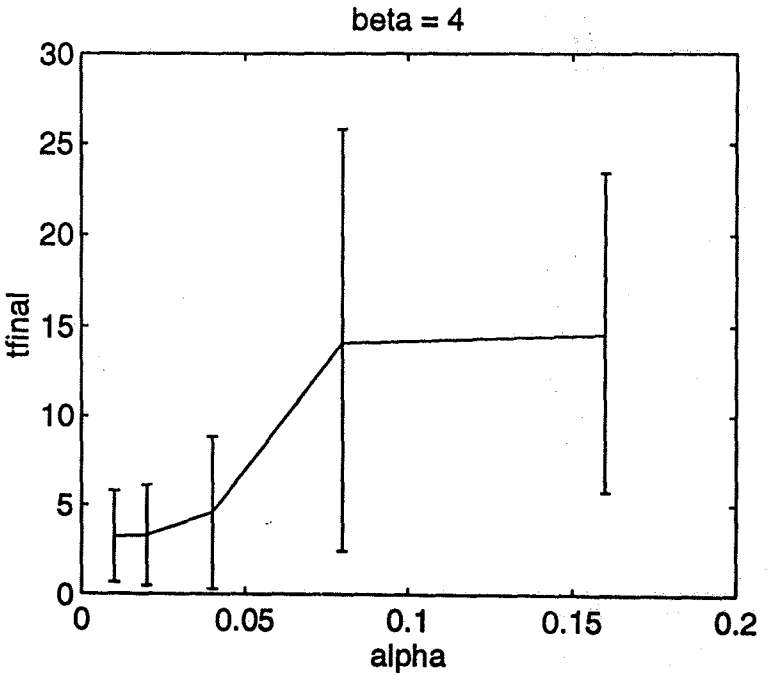
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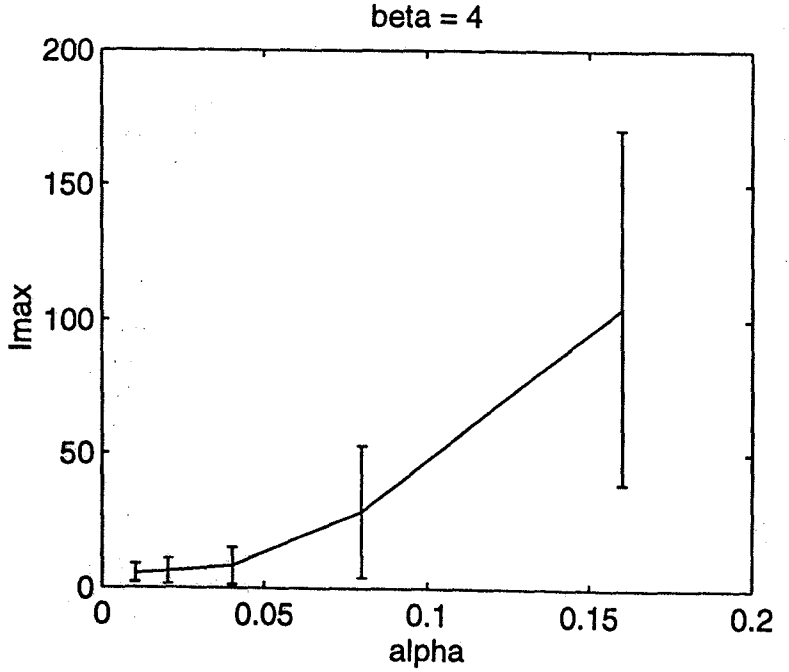
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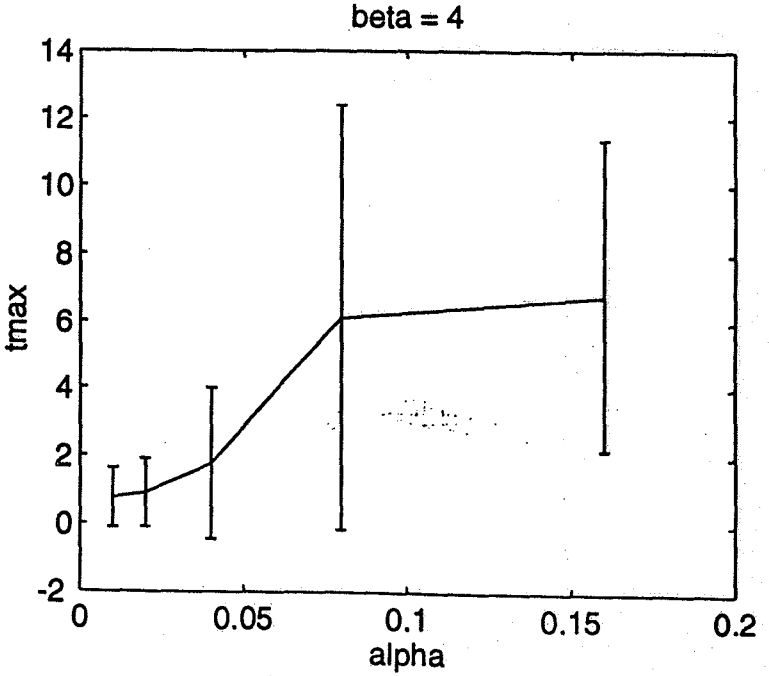
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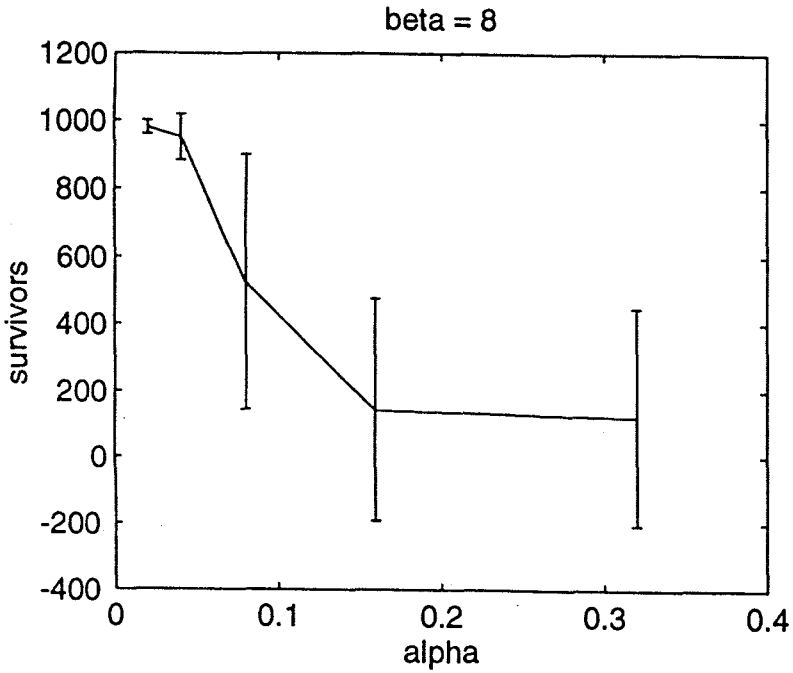
Figure 4.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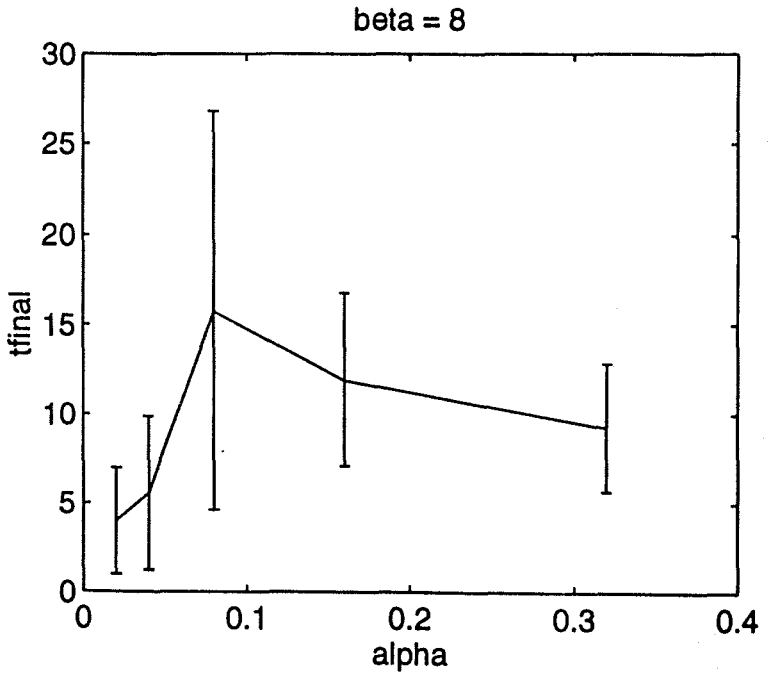
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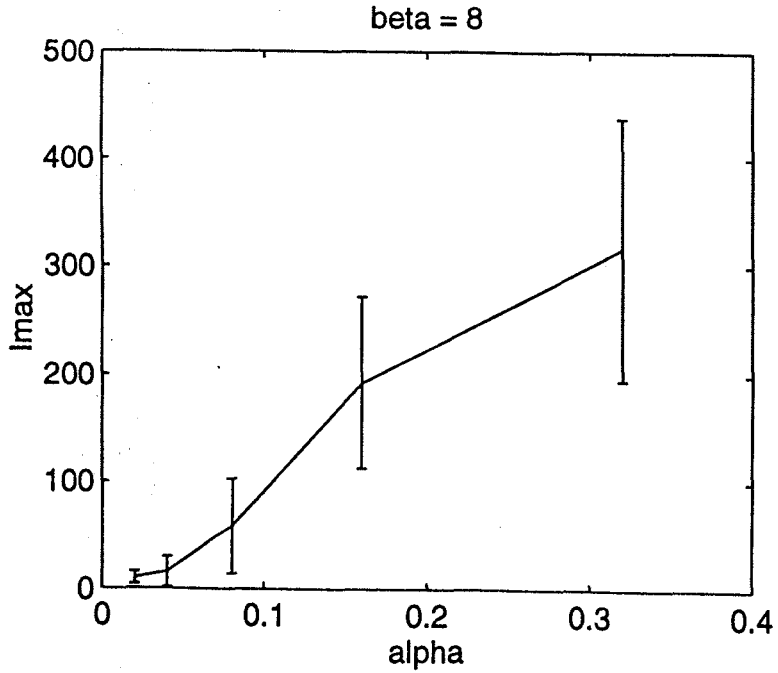
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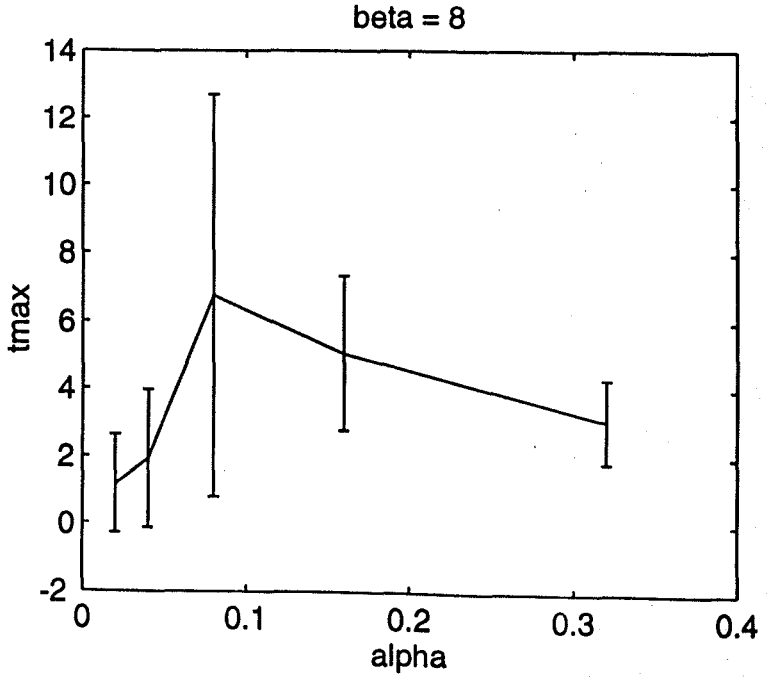
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Figure 5.