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QUASI-STATIONARY DISTRIBUTIONS AND BEHAVIOR OF BIRTH-DEATH MARKOV PROCESS WITH ABSORBING STATES

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ABSTRACT

In this paper the continuous-time Markov process for a closed stochastic SIS epidemic model is modified in such a way that transitions to the absorbing state are substituted by transitions to the initial state. This modified process has a limiting distribution $\underline{\Pi}$ which is used to calculate the number of units of time-disease (UTD's) and the expected incidence. It is also shown how $\underline{\Pi}$ can be used to calculate the exact value of the mean time to extinction. This later is compared against current expressions using the quasi-stationary distribution.An approximation to the expected number of different persons infected and hence to the probability of escaping infection is given.

1. INTRODUCTION

Finite Markov-process with non-absorbing states have a limiting distribution $\underline{\eta}' = \{\eta_1,\eta_2,\eta_3,...\eta_N\}$with a nice interpretation: if the process runs for a long time, the probability that the process will be in state i is η_i. Consequently, η_i can also be interpreted as the total proportion of time the process is in state i. In contrast, finite Markov process with absorbing states have degenerate stationary distributions, that concentrate all the probability in the absorbing states. An important question is then how will the process behave given that it starts at state i_0. The term *behavior* is vague and in the context of the problem it may well be for instance, the collection of visited states indexed by time. In this paper, by behaviour it is understood some measure (absolute or relative) of the amount of time that the process spends in every state before absorption as well as to any quantity derived from that. It will be shown how in the epidemic S-I-S model this information will be used to calculate the expected total incidence before the disease vanishes.

In section 2 the modified stochastic process (MSP) is introduced, and some numerical comparisons are made between the limiting distribution of the MSP with the quasi-stationary distribution (QSD) for specific cases. In section 3 the limiting distribution of the MSP is used to derive the expected time to extinction using Renewal theory. In section 4 the units of time disease, defined in an analog way to man-work hours is introduced, and it is shown how the expected incidence can be calculated from this

value. An approximation to the expected number of different persons infected and hence to the probability of escaping infection is given. In section 5 asymptotic approximations of these results are given for $N \to \infty$.

2. THE MODIFIED MARKOV PROCESS

We have a closed population of size N. Let $p_{i_0,n}(t)$ be the probability that there are n infected individuals at time t given that it started in an arbitrary but fixed state i_0, $n = 0, 1, 2, ..., N$ In order to simplify the notation we write this probability as $p_n(t)$. The Forward Kolmogorv equations can be written as:

$$p'(t) = p(t)A$$

where A is a tridiagonal matrix given by:

$$A = \begin{bmatrix} -r_0 & \lambda_0 & 0 & \cdots & 0 \\ \mu_1 & -r_1 & \lambda_1 & \cdots & 0 \\ 0 & \mu_2 & -r_2 & \cdots & 0 \\ \vdots & \vdots & \vdots & & \vdots \\ 0 & 0 & 0 & \cdots & -r_N \end{bmatrix}$$

where λ_i and μ_i are the birth and death rates in state i, and $r_i = \lambda_i + \mu_i$. Since λ_0=0 the process has the origin as an absorbing state that makes the stationary distribution degenerated with 1 at 0. For the SIS epidemic model $\lambda_i = \lambda i(N-i)/N$, $\mu_i = \mu i$.

Modifying the Markov process in such a way that it allows for a return to the initial state i_0 instead of going to the absorbing state 0 is the same as running the process an infinite number of "cycles", with no delay in state 0. This requires that in matrix A transitions from state 1 to state 0 are replaced by transitions from 1 to i_0. This is refered as the Modified Markov Process (MMP).

The Forward Kolmogorov equations for the MMP are:

$$\begin{aligned} u_1'(t) &= u_2(t)\lambda_2 - u_1(t)r_1 + u_1(t)\lambda_1 I_{[1]} \\ u_2'(t) &= u_1(t)\lambda_1 + u_3(t)\mu_3 - u_2(t)\, r_2 + u_1(t)\lambda_1 I_{[2]} \\ u_3'(t) &= u_2(t)\lambda_2 + u_4(t)\mu_4 - u_3(t)\, r_3 + u_1(t)\lambda_1 I_{[3]} \\ &\vdots \\ u_N'(t) &= u_{N-1}(t)\lambda_{N-1} - u_N(t)\, r_N + u_1(t)\lambda_1 I_{[N]} \end{aligned} \tag{2.2}$$

where $u_n(t)$ is the probability that the process will be in state n at time t, in the MMP, and $I_{[n]} = 1$ the indicator function for the event "initial state is n".

The previous equations can be written in compact form in terms of matrix A as:

$$u'(t) = u(t)\,U$$

were U is identical to the matrix Q except that $D(1)$ is added to the element in row i_0, column 1. The stationary distribution for this MMP exists and is non-degenerated, this is called the Modified Stationary Distribution (MSD) and denoted $\underline{\Pi}'=\{\pi_1,\pi_2,\pi_3,...\pi_N\}$.

Let $\underline{S} = \{S_1, S_2, S_3, ..., S_N\}$ be the vector corresponding to the total amount of time spent in every state before the process goes to absorption. It will be shown how relevant morbidity measures as the expected total number of infection cases before absorption (total incidence) can be drawn from $E\{\underline{S}\}$.

Let r be an arbitrary but fixed state, $r = 1, 2, ...N$. We have:

$$E\{S_r\} = E\left\{k^{-1}\sum_{j=1}^{k} S_{rj}\right\} = \lim_{k\to\infty}\frac{E\left\{\sum_{j=1}^{k} S_{rj}\right\}}{k} \tag{2.1}$$

Note that in the MMP

$$\lim_{k\to\infty}\frac{\sum_{j=1}^{k} S_{rj}}{\sum_{j=1}^{k}\sum_{i=1}^{N} S_{ij}} = \pi_r \tag{2.3}$$

with S_{rj} being the total time spent in state r in j-th cycle, $r = 1, 2, ...N$, $j = 1, 2, ...k$. and π_r the corresponding element from $\underline{\Pi}$. Note the following equality holds:

$$E\{S_{rj}\} = E\{S_r\}$$

that is, the expected total amount of time spent in state r in j-th cycle is equal to that spent in the original process before absorption. Observe that

$$\pi_r = \lim_{k\to\infty} \frac{\sum_{j=1}^{k} S_{rj}}{\sum_{j=1}^{k}\sum_{i=1}^{N} S_{ij}} = \lim_{k\to\infty} \frac{k^{-1}\sum_{j=1}^{k} S_{rj}}{k^{-1}\sum_{j=1}^{k}\sum_{i=1}^{N} S_{ij}}$$

$$= \frac{\lim_{k\to\infty} k^{-1}\sum_{j=1}^{k} S_{rj}}{\lim_{k\to\infty} k^{-1}\sum_{j=1}^{k}\sum_{i=1}^{N} S_{ij}} = \frac{E\{S_r\}}{E\{\sum_{i=1}^{N} S_i\}}$$

Since $E\{\sum_{i=1}^{N} S_i\}$ is the expected time the process will spend in all states in a given cycle, this correspons to the expected time to extinction, T_E , it follows that

$$E\{S_r\} = \pi_r T_E \tag{2.4}$$

It will be shown later (section 3) that $T_E = (\pi_1 \mu_1)^{-1}$, thus we can write

$$E\{S_r\} = \frac{\pi_r}{\pi_1 \mu_1} \tag{2.5}$$

Figs. 1.1 and 1.2 show the comparison between the total amount of time spent in every state, averaging over 5000 cycles and the predicted according to (2.5) for the $S-I-S$ logistic epidemic with $\lambda_i = \lambda\, i\,(N-i)/N$ and $\mu_i = \mu\ i$, with $R_0 = 1.1$ and 1.4, at different initial number of infectives. Simulations were also performed in Matlab. Observe that the total amount of time spent in state 1 is not affected by the initial number of infectives, which is due to the fact that the number of visits to state 1 before absorption is a Geometric random variable with parameter $\theta = \mu_1/(\mu_1 + \lambda_1)$.

Comparison of the MSD with the quasi-stationary distribution

The probability that the process is in state n at time t conditioning in non-extinction is given by:

$$q_n(t) = \frac{p_n(t)}{1 - p_0(t)} \tag{2.6}$$

The limit $t \to \infty$ of the last expression is called the quasi-stationary distribution (QSD). Since $p_0'(t) = \mu_1 p_1(t)$ the system of equations for the QSD can be rewritten as

$$q'(t) = q(t)Q + \mu_1 q_1(t) q(t) \tag{2.7}$$

where Q is equal to matrix A with the first row and first column deleted. The non-linearity of (2.7) makes impossible to find an explicit solution for the QSD for arbitrary N, altough in [3] it is shown how the explicit solution can be found for N=2. It is easy to see that the MSD and the QSD are different since the latter does not deopend of i_0. After computing the MSD and the QSD for several values of N and R_0 we found that they look quite similar when R_0 increases, but the difference is remarkable when $R_0 < 1$. It is interesting to mention that computational difficulties when calculating the QSD led to an approximation which consists in modifying the process by making state 0 a reflecting state, that is, the process goes back to state 1 if there is a death in state 1. The limiting distribution for this process $p^{(0)}$, has been proved [4] to be stochastically smaller than the QSD in the sense that

$$\sum_{i=1}^{N} p_i^{(0)} \geq \sum_{i=1}^{N} q_i$$

Note that if the initial number of infectives is 1, then the MSD and $p^{(0)}$, the approximation to the QSD are the same. Figs 2.1 and 2.2 show the MSD and the QSD for $N = 50$ and $R_0 = 1.2$, 1.4 and 1.7 with different number of initially infected individuals. We can see that when R_0 increases both distributions tends to a normal distribution. This will be used later for asymptotic approximations.

3. EXPECTED TIME TO ABSORPTION.

In this section we showe how Renewal theory can be applied to the MMP to calculate the expected time to absorption. The main result is that the expected time to extinction can be calculated without error once the MSD is known.

Once the original Markov process is modified in such a way that transitions to state 0 are substituted by transitions to the initial state i_0, then the mean time between

transitions $1 \rightarrow i_0$ in the MSP corresponds to the mean time to absorption in the original process. Let $N_{i,j}(t)$ be the number of transitions form state i to a state j up to time t in an ergodic Markov chain. In [17] it is shown that:

$$\lim_{t\to\infty} t^{-1} E\{N_{i,j}(t)\} \rightarrow \pi_i \, q(i,j)$$

where π_i is the i-th element of $\underline{\Pi}$, and $q(i,j)$ is the transition rate from state i to j. Hence

$$\lim_{t\to\infty} t^{-1} E\{N_{1,i_0}(t)\} \rightarrow \pi_1 \, q(1,i_0)$$

since $q(1,i_0) =$ death rate in state $1 \; = \mu_1$, we have

$$\lim_{t\to\infty} t^{-1} E\{N_{1,i_0}(t)\} \rightarrow \pi_1 \mu_1$$

On the other hand, the Elementary Renewal Theorem states that

$$\lim_{t\to\infty} t^{-1} E\{N_{1,i_0}(t)\} \rightarrow 1/E\{T\}$$

where T is the time between transitions $1 \rightarrow i_0$. It follows that

$$T_E = (\pi_1 \mu_1)^{-1} \tag{3.1}$$

It is interesting to compare (3.1) with two other expressions related for the mean time to extinction

:

$$T_E = (q_1 \mu_1)^{-1} \tag{3.2}$$

and

$$T_E = (p_1^{(0)} \mu_1)^{-1} \tag{3.3}$$

where q_1 is the first element of the quasi-stationary distribution and $p_1^{(0)}$that of the "reflecting state 1 approximation" to the QSD. Expression (3.2) was suggested by [?] and gives the expected time to extinction starting from the quasi-stationary distribution,

whereas (3.3) was suggested in [14] for use if the initial state is 1. No simple expression exists for arbitrary i_0. We can see that if $i_0 = 1$ the (3.1) and (3.3) coincides, since the MMP is the same as the "reflecting state 1 approximation". For a detailed study of the QSD and their approximations see [3].

Numerical evaluation of expressions (3.1) and (3.3) was performed for a population of size $N = 50$ and R_0 values of 0.9, 1.1 and 1.4. The initial number of infectives was 1,2,5 and 10. Simulations were performed with Matlab.

Table 1. Comparison between observed and predicted time to absorption.

R_0									
	0.9			1.1			1.4		
i_0	Obs.(1)	Pred.(2)	Pred.(3)	Obs.	Pred.	Pred.	Obs.	Pred.	Pred.
1	2.183	2.179	2.179	3.520	3.429	3.429	14.285	14.616	14.616
2	3.601	2.179	3.517	5.509	3.429	5.683	25.164	14.616	24.540
5	5.729	2.179	5.845	9.575	3.429	9.649	40.340	14.616	40.373
10	7.691	2.179	7.718	12.727	3.429	12.638	49.014	14.616	49.359

(1) Average mean time to absorption over 5000 cycles.

(2) Predicted time to absorption using (3.3).

(3) Predicted time to absorption using (3.1).

Fig 3 shows the expected time to extinction according to (3.1) and (3.3) as a function of R_0. Note (3.3) is not affected by i_0 and this is indicated by a single dotted line.

Notice that the expected time to extinction starting from the QSD can also be calculated by conditioning in being in state i . Let T_E^* be this expectation, thus:

$$T_E^* = \sum_{i=1}^{N} P(state = i/i > 0)\, E\{T_i\}$$

where $E\{T_i\}$ is the expected time to extinction starting in state i. This can be rewritten in terms of the QSD as:

$$T_E^* = \sum_{i=1}^{N} \frac{q_i}{\pi_i\, \mu_1}$$

comparing this result with (3.2), we get to the interesting relationship between the the QSD and the MSD :

$$\sum_{i=1}^{N} \frac{q_i}{\pi_i} = q_1^{-1}$$

4. TOTAL INCIDENCE IN AN SIS MODEL

We define a unit of time-disease as one sick person during a unit of time. This quantity is very useful because a cost function can be added to every unit, either due to cost of medical treatment and/or to a reduction in the labor force. This will allow us to study a different aspect of the development of the disease under different control strategies.

The total number of units time-disease (UTD) for the duration of the epidemic is:

$$UTD = \sum_{i=1}^{N} i\, S_i$$

where S_i as in (2.1) is the total time there were i infected individuals before the epidemic vanishes. Then, from (2.4)

$$E\{UTD\} = \sum_{i=1}^{N} i\, E\{S_i\} = T_E \sum_{i=1}^{N} i\, \pi_i \qquad (4.1)$$

The previous expression can be used to used to calculate the expected number of cases of infection (total incidence) before the epidemic vanishes. Observe that UTD is a random variable made by the sum of the duration times of a random number of infections W, the total incidence. The duration of every one of these W cases is independent of the others, and thus UTD is a random sum. Therefore

$$E\{UTD\}=E\{W\}E\{X\}$$

where X is the random (exponential) duration of an illness state of an infected individual, with expectation μ^{-1}. It follows that

$$E\{W\}=E\{UTD\}\,\mu \tag{4.2}$$

which corresponds to the total incidence up to absorption time.

Table 2 shows the comparison between the observed (averaged over 5000 cycles) and the expected total incidence W for a population of size $N = 50$ for $R_0 = 0.9$, 1.1 and 1.4, and initial number of infectives 1,2,5 and 10.

Table 2. Comparison between observed and predicted expected value of the Total Incidence (W).

	R_0					
	0.9		1.1		1.4	
i_0	Observed[1]	Predicted[2]	Observed	Predicted	Observed	Predicted
1	5.53	5.53	15.14	14.70	153.56	158.25
2	11.23	10.67	26.53	27.41	279.81	272.87
5	23.68	25.90	55.93	56.91	469.73	469.39
10	41.29	41.89	89.76	88.87	590.92	596.38

(1) Average over 5000 cycles of the observed number of infections before absorption.

(2) Expected value calculated according to (11).

we leave further analytisis of the results for next section

5. ASYMPTOTIC APPROXIMATIONS

In this section we deal with the most common case in which N is big and $R_0 > 1$. In this case the mean time to extinction T_E is not relevant by itself, since very likely it would be beyond the mean duration of life of individuals, but it is neccesary to calculate the UTD in (4.1) . Although a normal distribution can be used to approximate the MSD, it is natural to expect a poor fit in the tails of the distribution. Nasell [3] provided a good account of approximations for both the QSD in general and for q_1 in particular. He proved that the asymptotically the QSD follows a normal distribution with mean and variance $N(R_0 - 1)/R_0$ and N/R_0 respectivelly. He also proved that for $R_0 > 1$ and $N \to \infty$ then the expected time to extinction from state j is approximately equal to

$$\frac{1}{\mu_1 q_1}(1 - R_0^{-j}) \tag{5.1}$$

with

$$q_1 \sim \sqrt{N}\,\frac{(R_0 - 1)^2}{R_0}\varphi(\beta_1)$$

where, for $R_0 > 1$

$$\beta_1 = \sqrt{2N\left(Ln(R_0) - \frac{R_0 - 1}{R_0}\right)}$$

and $\varphi(.)$ is the standard normal density function. Combining these results with (4.1) we get an asymptotic approximation for $E\{UTD\}$ if the process starts in state j:

$$E\{UTD\} \approx \frac{N(R_0 - 1)}{\mu_1 q_1 R_0}(1 - R_0^{-j}) \tag{5.2}$$

Fig. 5.1 shows the numerical results of compartison of expressions (4.1) and (5.2), for different R_0values with $N = 100$, for an initial number of infective individuals of 1,2,5 and 10. In this graph the ratio of both expressions is plotted against R_0. We can see that the approximation (5.2) is accurate.

We now explore how $E\{UTD\}$ is affected by a reduction in the mean time of the duration of the infectious state of infected individuals. Let $UTD(N, R_0, j)$ be the total number of units of time disease for an epidemic that starts with j infected, with N and R_0 fixed.If the expected value of the mean duration of the infectious period is reduced from μ^{-1} to $\alpha\,\mu^{-1}$ with $0 < \alpha < 1$, then R_0 is reduced to $\alpha\,R_0$and the relative reduction accomplished is:

$$\frac{E\{UTD(N, \alpha R_0, j\}}{E\{UTD(N, R_0, j)\}} \tag{5.3}$$

Fig. (5.2) shows the value of this ratio as a function of α and R_0, wheras (5.3) shows the ratio as a function of α and N. When N and R_0 increases the influence of j, the initial state is negliigible.

References

[1] Darroch and Seneta (1967) On quasi-stationary distributions in absorbing continuous-time finite markov chains. *J. Appl. Prob.* **4**, 192-196.

[2] Nasell, I. (1991) On the Quasi-Stationary Distribution of the Ross Malaria Model. *Math. Biosc.* **107** 187-207

[3] Nasell , I. (1993) The quasi-stationary distribution of the closed endemic S-I-S model. Preprint

[4] Cavender (1978) Quasi-Stationary Distributionss for birth and death processes. *Adv. Appl.Probab.* **10**, 570-586.

[5] Kryscio, R.J. and Lefevre,C. (1989) On the extinction of the S-I-S stochastic logistic epidemic. *J. Appl. Prob.* **27**, 685-694.

[6] Cox, D.R. (1962) Renewal Theory. Wiley, New York

[7] Karlin,S. and Taylor, H.M. (1975) A First Course in Stochastic Processs. Acadenmic Press. New York.

[8] Resnick, S. (1992). Adventures in Stochastic Processes. Birkhäuser, Boston.

[13] Bailey, N.T. J.(1964) The Elements of stochastic Processes with Applications to the natural Sciences.

[14] Nisbet, R.M. and Gurney, W.S.C. (1982). Modelling Fluctuating Populations. Wiley, Chichester.

[15] Casella, G. and Berger, R.L. (1990). Statistical Inference. Duxbury Press, California.

[16] Renshaw , E. (1991). Modelling Biological Populations in Space and Time. Cambridge University Press.

[17] Albert, A. (1962) Estimating the infinitesimaql generator of a Continuous time, finite state Markov Process. *Ann. Math. Stat.* 33, 727-753

Fig. 1.1 Comparison between averaged (dotted line) and expected total time. Numbers next to lines indicate the initial states

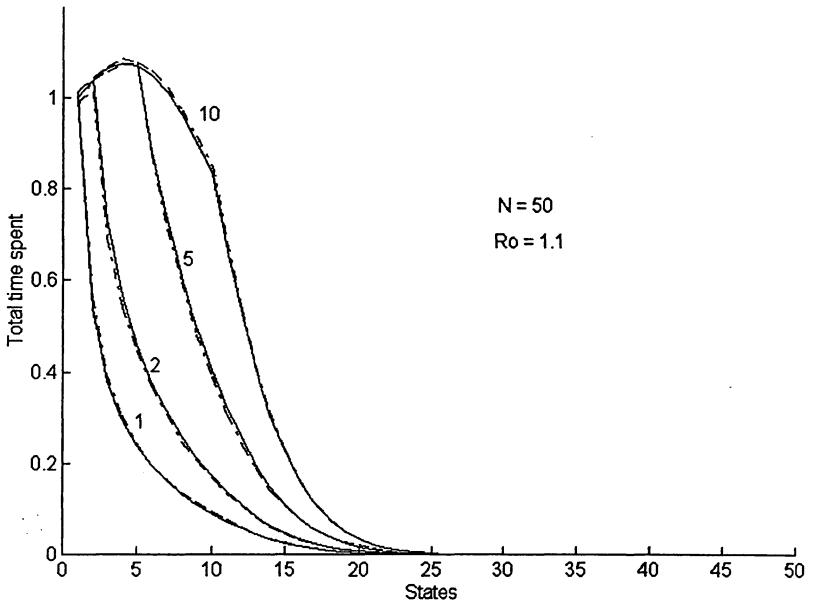


Fig. 1.2 Comparison between averaged (dotted line) and expected total time. Numbers next to lines indicate the initial states

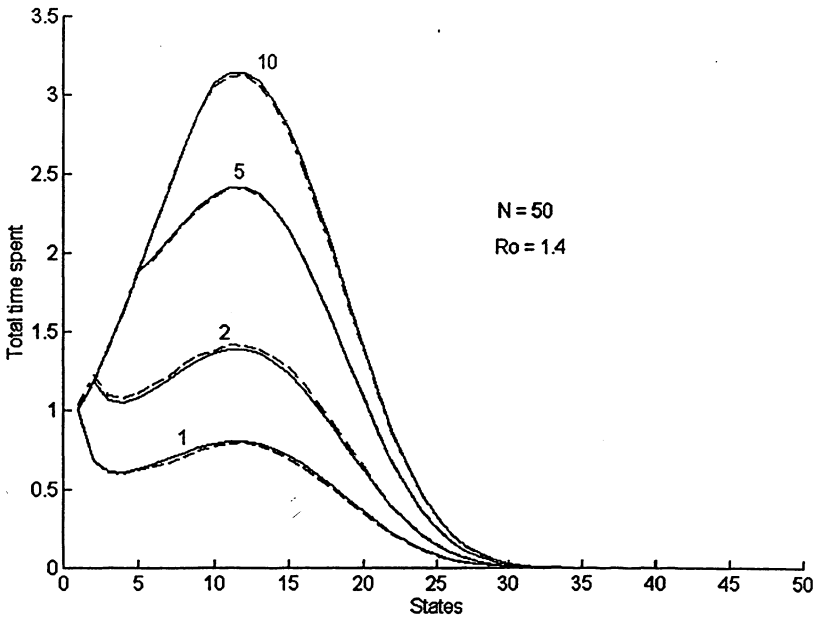


Fig. 2.1

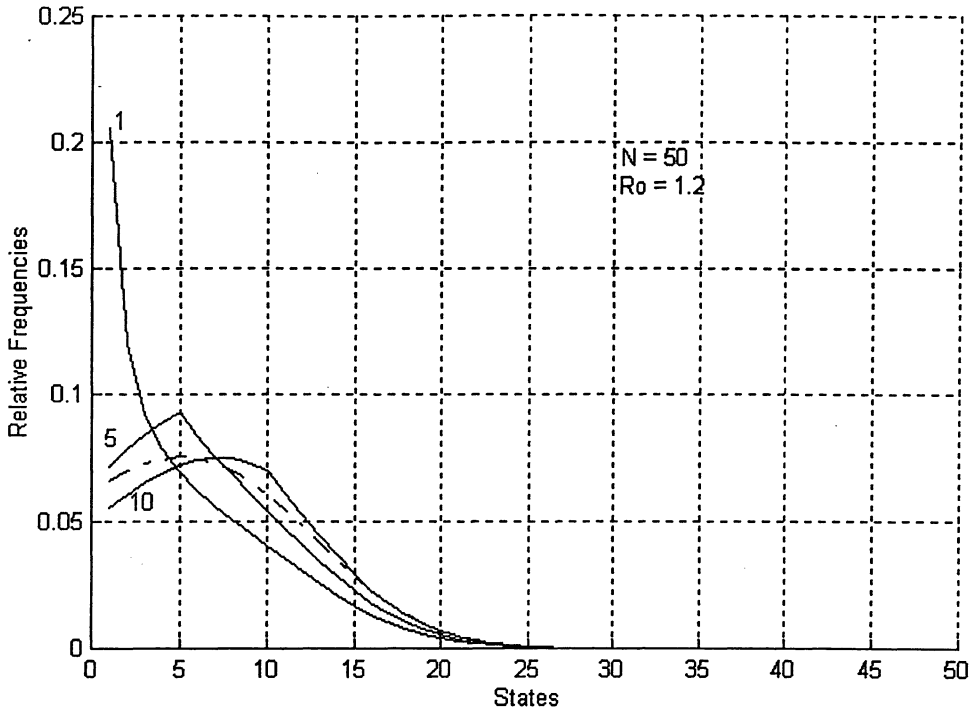
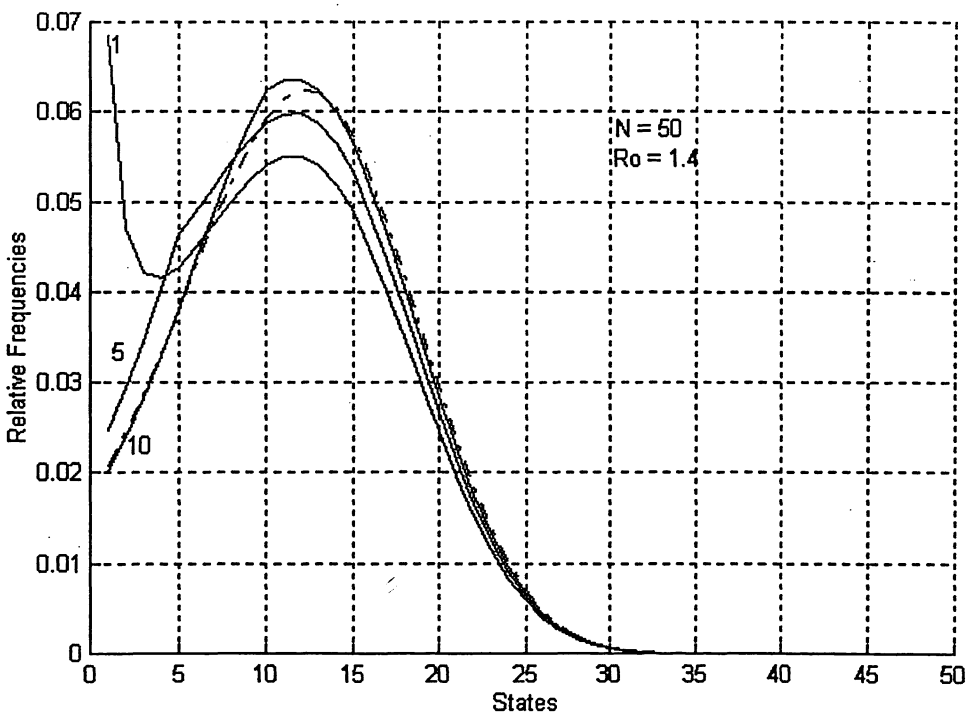

0.25
0.2
0.15
0.1
0.05
0
Relative Frequencies
1
5
10
N = 50
Ro = 1.2
0
5
10
15
20
25
30
35
40
45
50
States

Fig. 2.2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0.02
0.01
0
Relative Frequencies
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Ro = 1.4
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5
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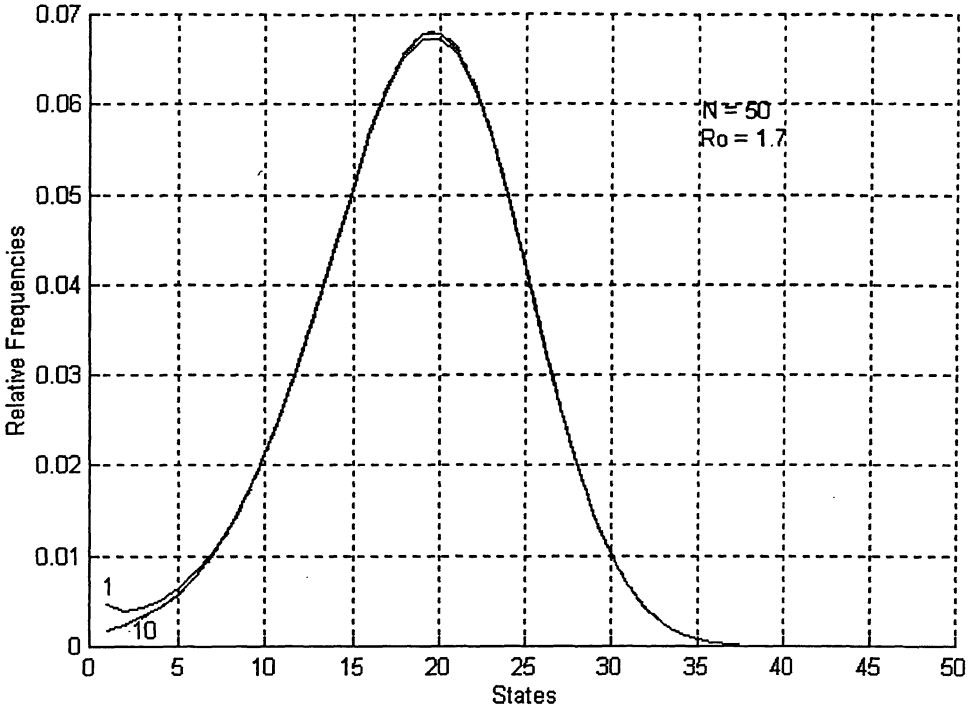
15
20
25
30
35
40
45
50
States

Fig 2.3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0.05
0.04
0.03
0.02
0.01
0
Relative Frequencies
N = 50
Ro = 1.7
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10
0
5
10
15
20
25
30
35
40
45
50
States

Fig. 3 Expected time to extinction as a function of R_0

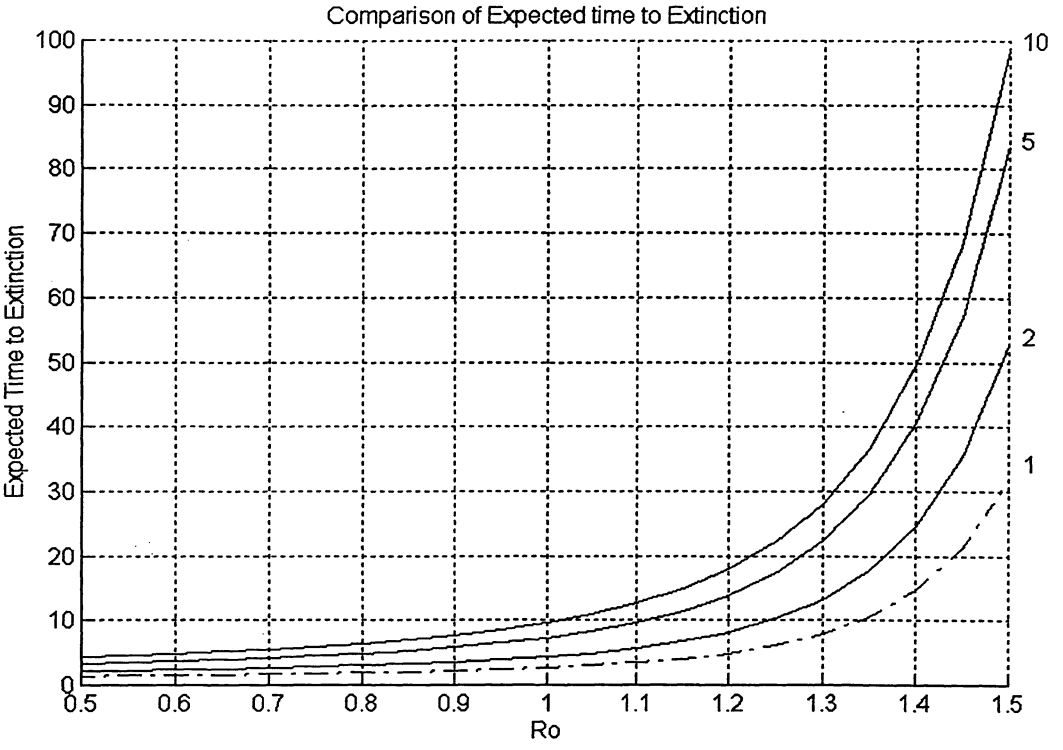
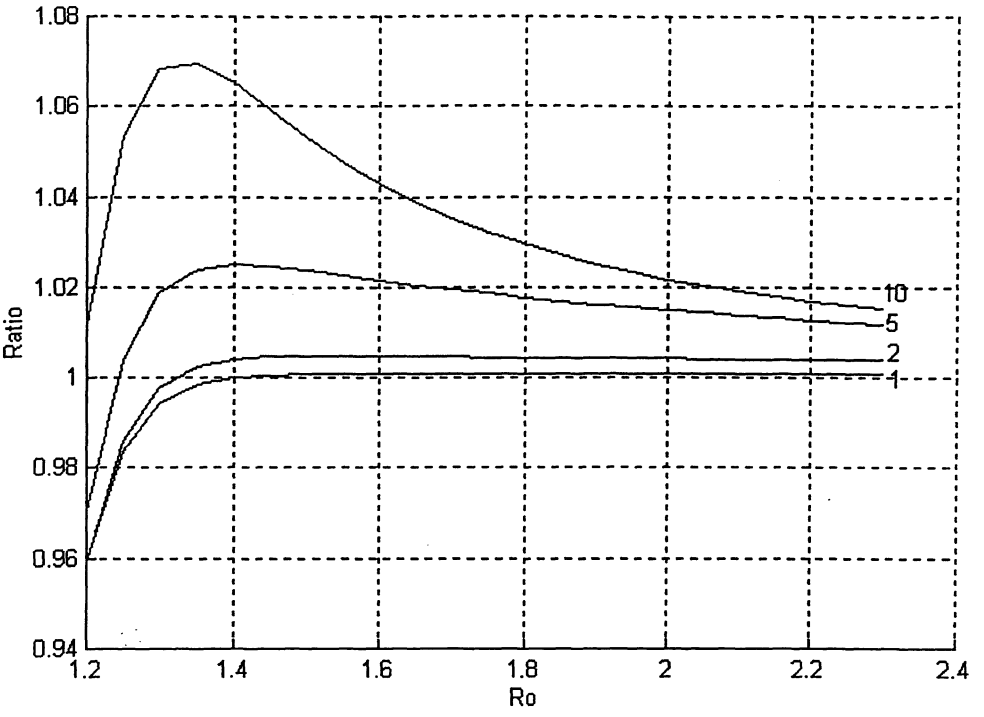


Fig. 5.1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1.06
1.04
1.02
1
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0.96
0.94
Ratio
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1.4
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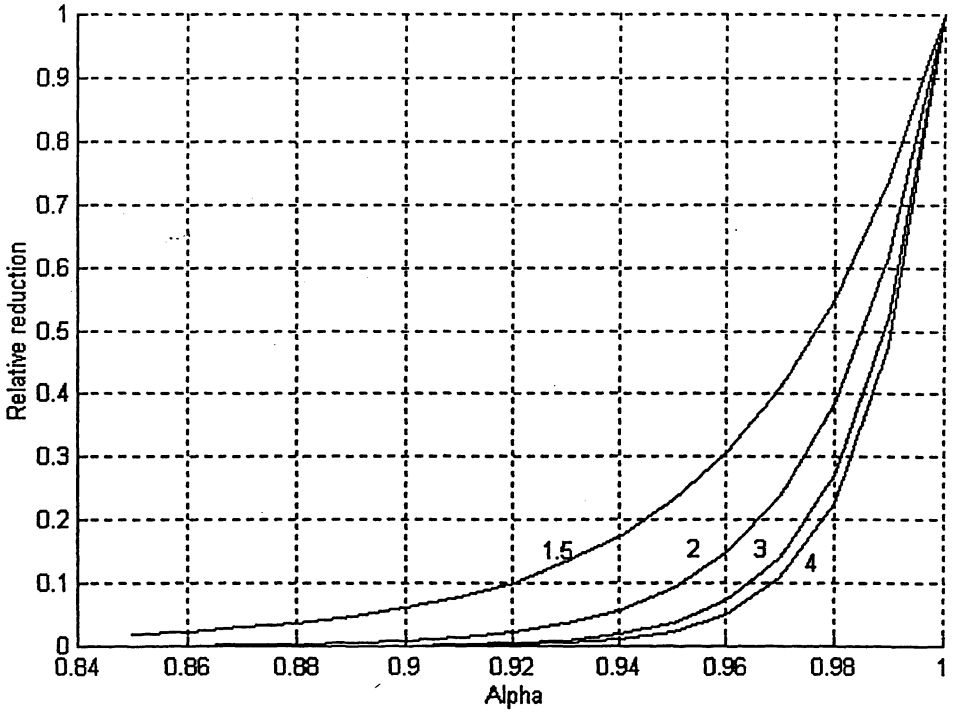
2
2.2
2.4
Ro
10
5
2
1

Fig 5.2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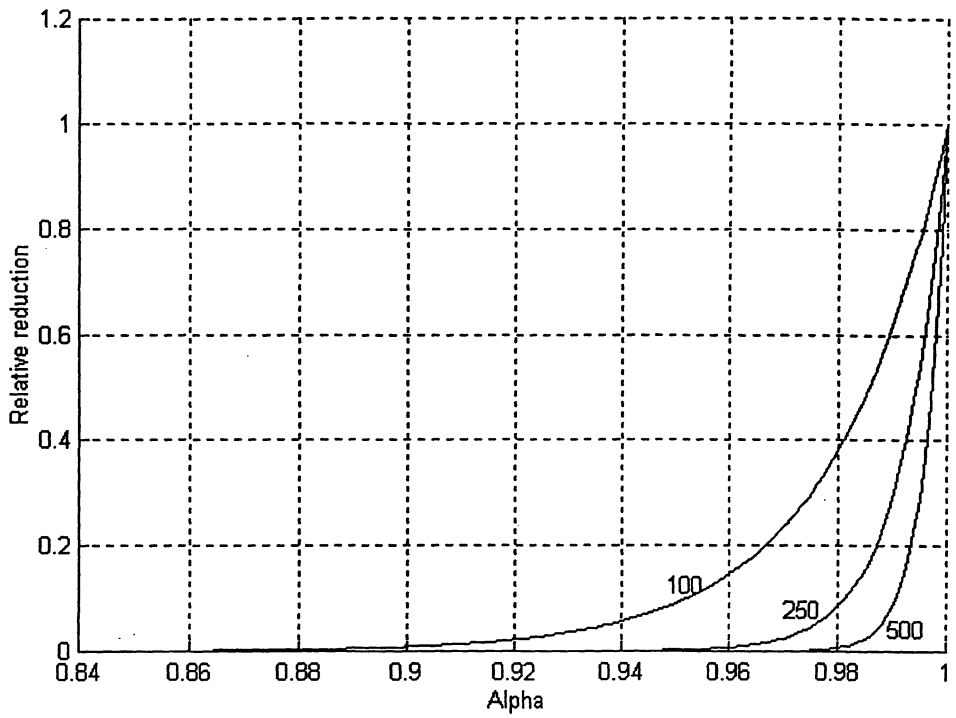
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
Relative reduction
0.84
0.86
0.88
0.9
0.92
0.94
0.96
0.98
1
Alpha
1.5
2
3
4

Fig. 5.3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1
0.8
0.6
0.4
0.2
0
Relative reduction
0.84
0.86
0.88
0.9
0.92
0.94
0.96
0.98
1
Alpha
100
250
500